Supplemental Table 1. Average log decay for H1N1pdm09 or Spn in droplets						
		$Log_{10}$ Decay H1N1pdm09 ± SEM		$Log_{10}$ Decay $Spn \pm SEM$		
ASL Donor	HBE Donor Condition	H1N1pdm09	H1N1pdm09/Spn	Spn	H1N1pdm09/Spn	
0223	COPD	$2.333 \pm 0.068*$	$1.667 \pm 0.068*$	3.187 ± 0.067*	$2.565 \pm 0.002*$	
0259	COPD	$1.083\pm0.136$	$1.125\pm0.118$	$3.071 \pm 0.101*$	$2.577 \pm 0.033*$	
0284	IPF	$0.958 \pm 0.180$	$1.292\pm0.180$	$4.950 \pm 0.415 *$	$2.848 \pm 0.148*$	
0305	COPD	$1.00\pm0.118$	$0.708 \pm 0.272$	$4.237\pm0.333$	$3.256\pm0$	

An asterisk indicates the p-value was less than 0.05 when comparing droplets of individual microbes to droplets with both microbes using a Welch's unpaired t-tests.

## 208 Supplemental Materials and Methods

## 209 Virus and Bacteria

- A/California/07/2009 (H1N1pdm09) was grown in minimum essential media in Madin-Darby
- 211 Canine Kidney (MDCK) cells at 37°C for 48 hours and collected by centrifuging supernatant to
- remove cell debris. Quantification of virus was performed using the 50% tissue culture infectious
- dose assay (TCID<sub>50</sub>) of 10-fold serial dilution on MDKC cells in 96-well plates and subsequent
- assessment for cytopathic effects 4 days after plating.
- *S. pneumoniae* D39 (Spn) was grown in Columbia broth at 37°C. Quantification of bacterial
- burden was performed by plating 10-fold serial dilutions on blood agar plates and counting
- colony-forming units after incubation at 37°C overnight.
- 218 Animals
- 219 Experiments involving ferrets were performed at the University of Pittsburgh under BSL2 safety

conditions (IACUC protocol 19075697). Four to six-month male ferrets were confirmed to be

seronegative for influenza infection prior to purchase. Animals were intranasally infected with

- $10^{6}$  TCID<sub>50</sub> of H1N1pdm09 in 500 µL total volume and  $10^{7}$  CFU of Spn in 500 µL. Ferrets were
- sedated using isoflurane prior to nasal wash collection, performed by collecting the flow-through
- of PBS passed through the nostrils.

225 Air Sampling

226 Infectious virus and bacteria were collected using the Liquid Spot Sampler (Aerosol Devices Inc,

227 Series 110), which uses condensation to collect aerosols into a collection vial. Air was collected

from infected animals in a 7 liter chamber connected to the Spot sampler via anti-static tubing for

15 minutes each day at a rate of 1.4L/minute (Supplemental Figure 1). Sampling was performed on days 3, 4, and 5 post-H1N1pdm09 infection (days 1, 2, and 3 post-Spn infection) and prior to nasal wash collection. Condensed aerosols were collected in 700µL 0.5% BSA in PBS. Samples were immediately plated to quantify expelled bacteria and the remaining sample was used for virus titration as described above.

Aerosol sampling of H1N1pdm09/Spn-infected ferrets was performed using cyclone-based air

samplers (BC251 developed by NIOSH) on days 3, 4, and 5 post-H1N1pdm09 infection to

collect microbial genomic material. Samplers, calibrated to collect 3.5L of air per minute, were

237 placed downwind of infected animals in cages with directional airflow and were run for 1 hour.

Samplers fractionated aerosols into three sizes: aerosols  $>4\mu$ m,  $1-4\mu$ m, and  $<1\mu$ m diameter.

After aerosol collection, samplers were washed with isopropanol and allowed to air-dry to avoidcontamination.

241 RNA was isolated using 500µL MagMAX Lysis/Binding Solution Concentrate in each collection

tube with thorough vortexing. QIAamp viral RNA mini kit was used to isolate DNA and RNA

243 from lysis solution. Viral and bacterial genome copies were quantified using RT-qPCR with

244 primers against influenza M gene (Forward 5'-AGATGAGTCTTCTAACCGAGGTCG-3';

245 Reverse 5'-GCAAAGACACTTTCCAGTCTCTG-3'; Probe 5'-

246 [FAM]TCAGGCCCCCTCAAAGCCGA[3BHQ1] -3') or S. pneumoniae lytA gene (Forward 5'-

247 ACGCAATCTAGCAGATGAAGCA-3'; Reverse 5'-TCGTGCGTTTTAATTCCAGCT-3';

248 Probe 5'-[HEX]GCCGAAAACGCTTGATACAGGGAG[BHQ1]-3'). In vitro transcribed RNA

249 was used to make a standard curve for influenza virus, and *S. pneumoniae* genomic DNA was

serially diluted to generate a standard curve for Spn. Limits of detection were determined by a Ct

251 = 40 or a positive day 0 sample.

## 252 Stability Experiments

253	Inside a biosafety cabinet, a saturated salt solution of K <sub>2</sub> CO <sub>3</sub> was used to condition a glass
254	chamber to 43% relative humidity, and a HOBO UX-100-011 logger was used to record
255	temperature and humidity conditions during each ASL replicate (Figure 2E). Experimental
256	solutions were generated using 10 <sup>7.15</sup> CFU/mL Spn, 10 <sup>7.15</sup> TCID <sub>50</sub> /mL H1N1pdm09, and a 1:5
257	dilution in PBS of airway surface liquid collected from human bronchial epithelial cells. Ten 1
258	$\mu L$ droplets were incubated on polystyrene tissue culture plates in the conditioned chamber for
259	two hours. Controls were 10 $\mu$ L samples of each microbial solution in closed tubes that were
260	incubated for 2 hours at ambient temperature during the chamber experiments. $Log_{10}$ decay was
261	calculated as previously described and represents the loss in virus or bacterial infectivity (21).
262	Log <sub>10</sub> decay was determined for each droplet replicate by subtracting the titer of the droplets
263	from the average of the controls for the corresponding ASL. Experiments were performed using
264	technical triplicates for droplets and technical duplicates for controls.
265	Human lung tissue collected using an approved protocol was used to differentiate human
266	bronchial epithelial cells as previously described (22). Airway surface liquid was collected by
267	washing differentiated cells with 150 $\mu$ L PBS and collecting the wash (3). All HBE donors were
268	diagnosed with chronic obstructive pulmonary disease (COPD), except for HBE 0284, which
269	came from a patient diagnosed with idiopathic pulmonary fibrosis.

## 270 Data Availability

The data that supports the findings shown here will be made openly available in FigShare at
DOI: 10.6084/m9.figshare.22129055 upon publication. Some of the stability experiments were
previously made available on BioRxiv at https://doi.org/10.1101/2020.11.10.376442

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