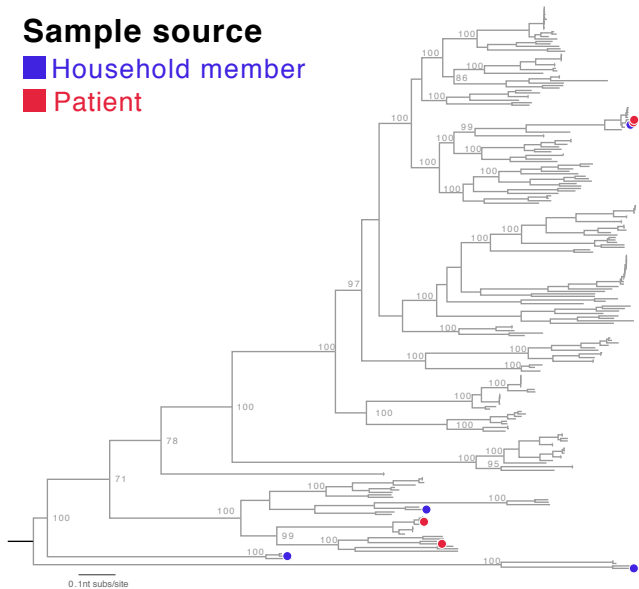


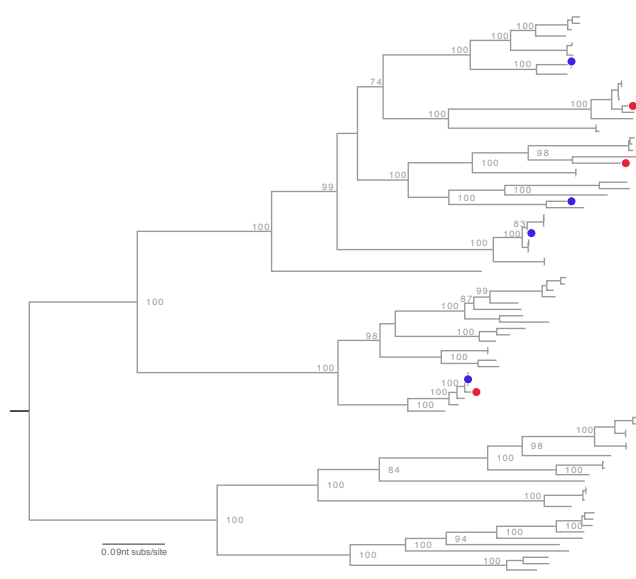
Supplementary Figure S2

Sample source

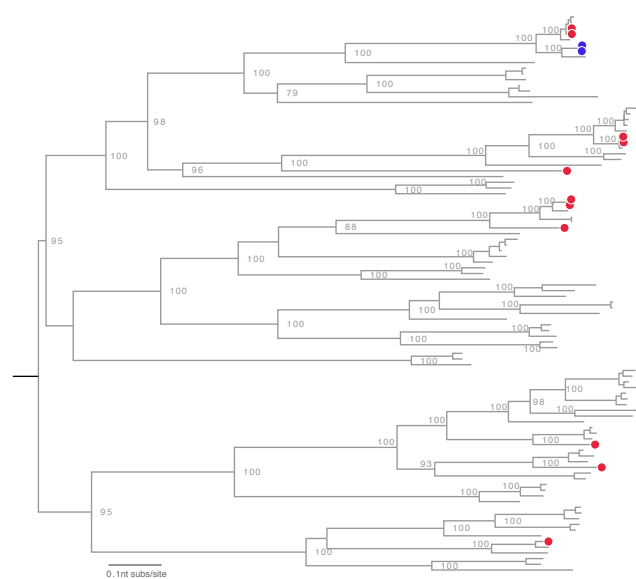
- Household member
- Patient



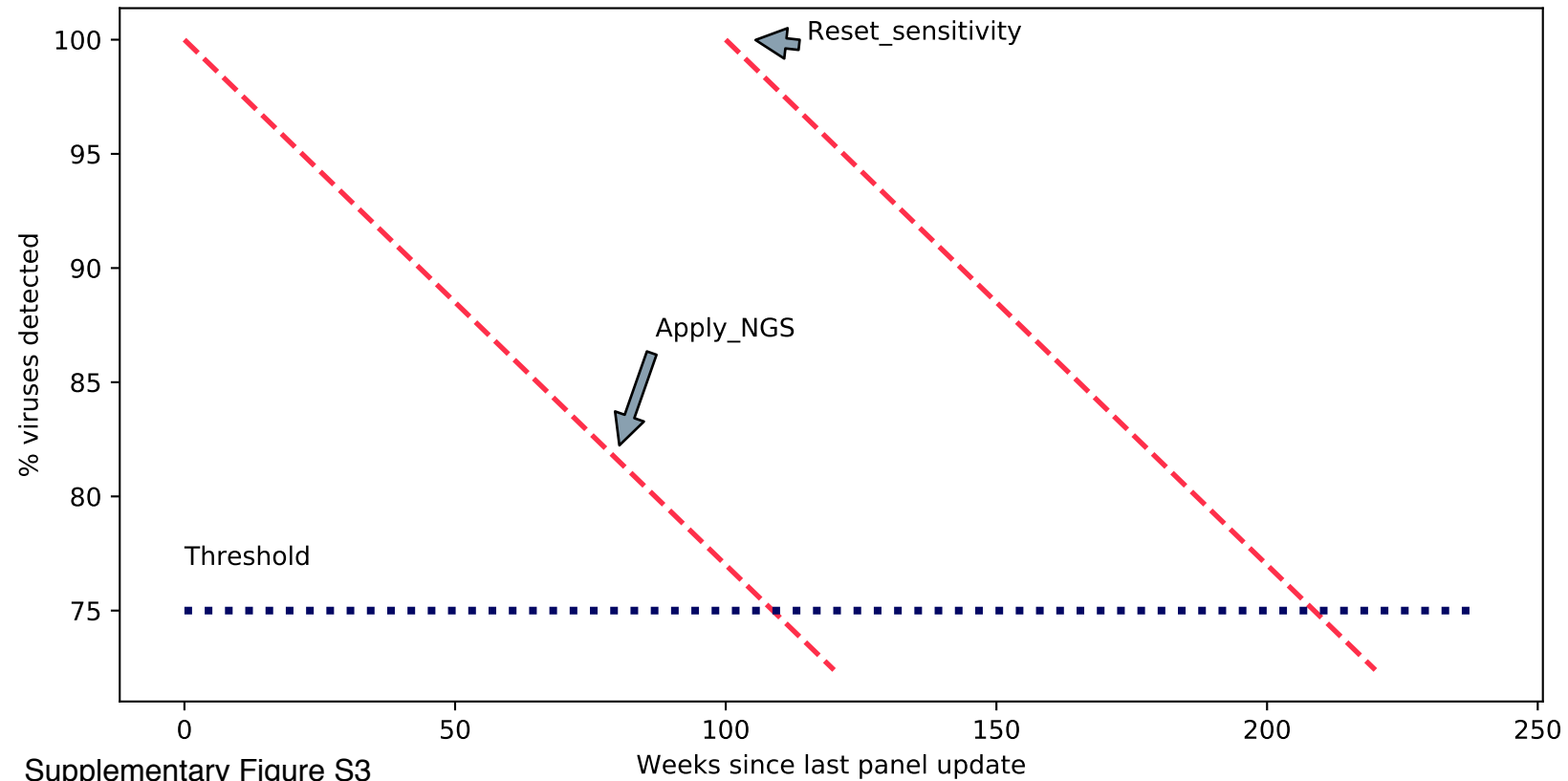
A - ML tree HRV-A



B - ML tree HRV-B



C - ML tree HRV-C



Supplementary Figure S3

Supplementary Table 1. List of diagnostic primers and probes used in the local respiratory viruses screening assays.

Target #	Organism	Target	Sequence (5' to 3')	5' Modification	3' Modification	Reference
1	Influenza A	Matrix	F, AAGACAAGACCAATYCTGTCCACCTCT R, TCTACGYTGACAGTCCYCGCT P, TYACGCTCACCGTCCAGTG	- - FAM	- - BHQ1	(1) Gunson et al, 2010
2	Influenza B	NS	F, ATGATCTTACAGTGGAGGATGAAGAA R, CGAATTGGCTTGRATGTCCTT P, ATGGCCATCGGATCCTCAAYCACTCT	- - CY5	- - BHQ2	(2) Gunson et al, 2011
3	Influenza C	Matrix	F, GGCAAGCGACATGCTGAAYA R, TCCAGCTGCYTTCAATTGCTTT P, CTCTTCTTCTGATTTTTTCAAA	- - VIC	- - MGBNFQ	(2) Gunson et al, 2011
4	HMPV A	Fusion	F, GCGYAGCTTCAGTCAATTCAA R, TCCAGCATTGTCTGAAAATTGC P, CAACATTAGAAAACCTTCT	- - VIC	- - MGBNFQ	(2) Gunson et al, 2011
5	HMPV B	Fusion	F, GCGYAGCTTCAGTCAATTCAA R, GTTATCCCTGCATTGTCTGAAAAT P, CGCACAACTTAGGAATCTTCT	- - VIC	- - MGBNFQ	(2) Gunson et al, 2011
6	PIV-1	HN	F, GTGATTTAAACCCGTAATTTCTCA R, CCTTGTCTGCAGCTATTACAGA P, ACCTATGACATCAACGAC	- - FAM	- - MGBNFQ	(2) Gunson et al, 2011
7	PIV-2	HN	F, ATGAAAACCTTACCTAAGTGATGGA R, CCTCCYGGTATRGACGACTGAAC P, TCAATCGCAAAAGC	- - VIC	- - MGBNFQ	(2) Gunson et al, 2011
8	PIV-3	HN	F, CCAGGGATATAYTAYAAAGGCAAAA R, CCGGRCACCCAGTTGTG P, TGGRTTCAAGACCTCCATAYCCGAGAAA	- - FAM	- - BHQ1	(2) Gunson et al, 2011
9	PIV-4	Fusion	F, CAGAYAACATCAATCGCCTTACAAA R, TGTACTATGACTGCCCAAAA P, CCMATCACAAAGCTCAGAAATYCAAAAGTCGT	- - CY5	- - BHQ2	(2) Gunson et al, 2011
10	HCoV 229E	Nucleocapsid	F, CAGTCAAATGGGCTGATGCA R, AAAGGGCTATAAAGAGAATAAAGGTATTCT P, CCCTGACGACCAGTTGTGGTTCA	- - FAM	- - BHQ1	(2) Gunson et al, 2011
11	HCoV OC43	Nucleocapsid	F, CGATGAGGCTATCCGACTAGGT R, CCTTCTGAGCCTTCAATATAGTAACC P, TCCGCTGGCAGGTAATCCCT	- - CY5	- - BHQ3	(2) Gunson et al, 2011
12	HCoV NL63	1a gene	F, ACGTACTTCTATTATGAAGCATGATTTAA R, AGCAGATCTAATGTTACTTAAAACTACG P, ATTGCCAAGGCTCTAAACGTACAGGTGT	- - VIC	- - TAMRA	(2) Gunson et al, 2011
13	RSV A	NP	F, AGATCAACTTCTGTATCCAGCAA R, TTCTGCACATCATAATTAGGAG P, CACCATCCAACGGAGCAGGAGAT	- - FAM	- - BHQ1	(2) Gunson et al, 2011
14	RSV B	NP	F, GCATCATTGCTGCTTAATCAATT R, GGTGTACTCTRACTCTCCATTATG P, TCAAGTGTGCTYTAGGYAATGCAGC	- - VIC	- - TAMRA	(3) Kamau et al, 2017
15	HRV	5'UTR	F, TGGACAGGGTGTGAAGAGC R, CAAAGTAGTCCGTCCTCCATCC P, TCCTCGGCCCTGAATG	- - VIC	- - TAMRA	(2) Gunson et al, 2011
16	Adv	Matrix	F, GCCACGGTGGGGTTCTAAACT R, GCCCCAGTGGTCTTACATGCATC P, TGCACCAGACCCGGGCTCAGTACTCCGA	- - CY5	- - BHQ2	(2) Gunson et al, 2011
17	<i>M. pneumoniae</i>	Cytoadhesin P1 gene	F, AAGCAGGAGTGACGGAAACAC R, CACCACATCATTCCCGTATT P, CTCACCAACAACCTCGGCCTA	- - CY5	- - BHQ2	(2) Gunson et al, 2011

Abbreviations

FAM=6-carboxyfluorescein;BHQ= black hole quencher; NS=nonstructural; HN=hemagglutinin; NP=nucleoprotein; UTR=untranslated region; PIV=parainfluenza virus; HCoV=human coronavirus; RSV=respiratory syncytial virus; Adv=Adenovirus; HMPV=human metapneumovirus;

References

(1) Gunson R, Maclean A, Davies E, Bennett S, Miller R, Carman WF. Development of a multiplex real-time RT-PCR that allows universal detection of influenza A viruses and simultaneous typing of influenza A/H1N1/2009 virus. *J Virol Methods*. 2010 Feb;163(2):258-61. doi: 10.1016/j.jviromet.2009.10.006. Epub 2009 Oct 23. PubMed PMID: 19854220.

(2) Gunson RN, Carman WF. During the summer 2009 outbreak of "swine flu" in Scotland what respiratory pathogens were diagnosed as H1N1/2009? *BMC Infect Dis*. 2011 Jul 13;11:192. doi: 10.1186/1471-2334-11-192. PubMed PMID: 21752259; PubMed Central PMCID: PMC3146830.

(3) Kamau E, Agoti CN, Lewa CS, Oketch J, Owor BE, Otieno GP, Bett A, Cane PA, Nokes DJ. Recent sequence variation in probe binding site affected detection of respiratory syncytial virus group B by real-time RT-PCR. *J Clin Virol*. 2017 Mar;88:21-25. doi: 10.1016/j.jcv.2016.12.011. Epub 2017 Jan 5. PubMed PMID: 28107671; PubMed Central PMCID: PMC5331890.

Supplementary Table 2. List of all viral sequences identified with corresponding GenBank accession number and crude read depth coverage.

Sample ID	Virus	Virus Abbreviation	Genome crude coverage*	Genome length	GenBank accession number
20692_1	Rhinovirus_A	HRV-A	3.441	6,822nt	MK989733
20692_1	RSVB	RSVB	253.603	15,287nt	MK989761
20692_3	Parvovirus_B19	B19	10.102	5,593nt	MK989716
20692_6	Rhinovirus_C	HRV-C	240.805	7,113nt	MK989748
20692_7	RVi_KEN_2B	RVi	13.758	9,770nt	MK989764
20692_18	Rhinovirus_C	HRV-C	586.337	7,121nt	MK989749
20692_20	RSVB	RSVB	20.176	15,262nt	MK989762
20692_25	Enterovirus_D68	EV-D68	105.957	7,261nt	MK989723
20692_31	Rhinovirus_C	HRV-C	8.626	6,651nt	MK989750
20692_33	Rhinovirus_B	HRV-B	9.832	7,059nt	MK989741
20692_39	Rhinovirus_C	HRV-C	11.381	7,107nt	MK989751
20692_42	HMPV	HMPV	19.71	13,234nt	MK989730
20692_43	Enterovirus_D68	EV-D68	24.48	7,251nt	MK989724
20692_44	Rhinovirus_A	HRV-A	53.015	7,166nt	MK989734
20692_48	Rhinovirus_B	HRV-B	21.809	6,879nt	MK989742
20692_51	Rhinovirus_C	HRV-C	5.99	7,021nt	MK989760
20692_52	Rhinovirus_A	HRV-A	28.979	7,118nt	MK989735
20692_52	Enterovirus_D68	EV-D68	9.101	7,328nt	MK989725
20692_55	Poliovirus	Polio	20.16	7,397nt	MK989713
20692_57	Rhinovirus_A	HRV-A	147.094	7,051nt	MK989736
20692_62	RSVB	RSVB	29.037	15,367nt	MK989763
20692_64	Bocavirus	HBoV	100.277	5,533nt	MK989727
20692_64	Rhinovirus_B	HRV-B	4.871	7,204nt	MK989743
20692_81	Rhinovirus_C	HRV-C	9.21	6,919nt	MK989752
20692_83	Rhinovirus_C_contig1	HRV-C	314.609	7,103nt	MK989753
20692_83	Rhinovirus_C_contig2	HRV-C	33.611	4,195nt	MK989754
20692_88	Coxsackievirus_A16	CV-A16	214.343	7,411nt	MK989714
20692_88	Enterovirus_D68	EV-D68	35.684	7,288nt	MK989726
20692_90	Rhinovirus_C	HRV-C	79.665	7,086nt	MK989755
20692_92	RVi_KEN_2B	RVi	5.678	9,588nt	MK989765
20692_93	Rhinovirus_C	HRV-C	151.153	7,151nt	MK989756
20692_95	Rhinovirus_C	HRV-C	14.438	7,103nt	MK989757
20693_1	Rhinovirus_A	HRV-A	5.934	7,087nt	MK989737
20693_9	Coxsackievirus_A24	CV-A24	6.018	7,326nt	MK989717
20693_11	Bocavirus	HBoV	11.358	5,497nt	MK989728
20693_14	HMPV	HMPV	7.99	13,303nt	MK989731
20693_16	Rhinovirus_A	HRV-A	42.407	6,866nt	MK989738
20693_21	Rhinovirus_B	HRV-B	3.24	6927nt	MK989744
20693_45	Rhinovirus_A	HRV-A	10.051	7,059nt	MK989739
20693_49	Coxsackievirus_A24	CV-A24	36.418	7,389nt	MK989718
20693_57	Rhinovirus_B	HRV-B	4.526	7,068nt	MK989745
20693_58	Rhinovirus_A	HRV-A	164.936	7,043nt	MK989740
20693_59	Rhinovirus_B	HRV-B	216.215	7,249nt	MK989746
20693_61	HMPV	HMPV	13.172	13,329nt	MK989732
20693_66	Coxsackievirus_A24	CV-A24	12.071	7,422nt	MK989719
20693_67	Coxsackievirus_A24	CV-A24	14.581	7,396nt	MK989720
20693_68	Human_parainfluenza_1	HPIV-1	232.83	15,560nt	MK989715
20693_74	Bocavirus	HBoV	9.595	5,512nt	MK989729
20693_82	Rhinovirus_B	HRV-B	13.571	7,186nt	MK989747
20693_83	Rhinovirus_C	HRV-C	143.663	7,135nt	MK989758
20693_84	Coxsackievirus_A24	CV-A24	32.712	7,477nt	MK989721
20693_86	Rhinovirus_C	HRV-C	4.371	6965nt	MK989759
20693_94	Coxsackievirus_A24	CV-A24	31.566	7,307nt	MK989722

*Depth of sequence coverage was calculated as number of reads mapping with Bowtie2 [28] with "--very-sensitive-local" mapping | to detect possible cross-talk sequences.

28. Langmead, B. & Salzberg, S. L. Fast gapped-read alignment with Bowtie2. *Nat. Methods* 9, 357–359 (2012).