**Supplementary table 1.** The distribution of genotyped picornaviruses.

| Species | Total number of distinct types (number of specimens positive for type) | Number of classical types (number of specimens) | Number of uncharacterised types (number of specimens) |
|---|---|---|---|
| **RV-A** | 31 (142) | A1 (3), A13 (1), A18 (1), A19 (2), A21 (2), A24 (12), A28 (1), A34 (6), A38 (1), A39 (8), A40 (3), A46 (1), A47 (1), A49 (7), A51 (1), A57 (4), A58 (15), A61 (1), A63 (1), A65 (2), A66 (8), A75 (3), A78 (14), A85 (3), A88 (5), A89 (1), A94 (1), A101 (22) | NAT089 (3), LZY25 (1), A71_p1047_sR141_2008 (8) |
| **RV-B** | 5 (11) | B4 (3), B6 (1), B17 (2), B27 (4), B70 (1) | |
| **RV-C** | 30 (113) | C2 (13), C3 (2), C5 (16), C6 (3), C10 (2), C12 (2), C15 (9), C16 (1), C17 (3), C18 (3), C19 (1), C20 (1), C22 (1), C25 (4), C26 (1), C28 (8), C35 (1), C36 (7), C37 (2), C38 (3), C39 (5), C40 (1), C41 (1), C43 (8), C45 (1), C49 (4), C51 (2), C53 (3), Cpat19 (4) | W4 (1) |
| **Untypeable** | (19) | | |
| **EV A-D** | 4 (12) | CV-A2 (2), E-9 (4), EV-D68 (5), PV-1 (1) | |

CV-Coxsackievirus; E-echovirus (EV-B); PV-poliovirus (EV-C) thought to be from inactivated whole-virus OPV vaccine in use at that time thus finding considered incidental and without clinical significance; Underlined types are considered "minor group" RVs using the receptor-based terminology.

**Supplementary table 2.** Correlation matrix for number of positive virus detections per week. The Spearman correlation coefficient 'Rho' is followed by the p-value under the hypothesis that Rho=0. N = 51 weeks.

| | RV | ADV | HMPV | EV | IFAV | HCoV-OC43 | RSV | HCoV-NL63 | PIV | HCoV-HKU1 |
|---|---|---|---|---|---|---|---|---|---|---|
| **RV** | 1 | 0·20, p=0.15 | 0·31, p=0·03 | 0·25, p=0.08 | -0·38, p=0·006 | -0·08, p=0·58 | 0·49, p=0·0003 | 0·13, p=0·36 | 0·04, p=0·75 | -0·11, p=0·46 |
| **ADV** | | 1 | 0·44, p=0·001 | 0·20, p=0·16 | 0·27, p=0·05 | 0·25, p=0·07 | 0·10, p=0·48 | 0·10, p=0·49 | 0·28, p=0·04 | -0·09, p=0·51 |
| **HMPV** | | | 1 | 0·13, p=0·36 | 0·31, p=0·03 | 0·50, p=0·0002 | 0·04, p=0·76 | 0·31, p=0·03 | 0·27, p=0·05 | 0·02, p=0·91 |
| **EV** | | | | 1 | -0·24, p=0·09 | -0·18, p=0·19 | 0·37, p=0·007 | -0·13, p=0·38 | -0·02, p=0·91 | 0·12, p=0·40 |
| **IFAV** | | | | | 1 | 0·63, p<0·0001 | -0·28, p=0·04 | 0·04, p=0·78 | 0·27, p=0·06 | -0·14, p=0·34 |
| **HCoV-OC43** | | | | | | 1 | -0·24, p=0·08 | 0·32, p=0·02 | 0·17, p=0·22 | -0·11, p=0·45 |
| **RSV** | | | | | | | 1 | 0·04, p=0·80 | -0·24, p=0·08 | -0·02, p=0·87 |
| **HCoV-NL63** | | | | | | | | 1 | -0·01, p=0·93 | -0·07, p=0·61 |
| **PIV** | | | | | | | | | 1 | -0·08, p=0·57 |

**Supplementary table 3.** Regression models examining factors that modify the probability of a positive RV test depending on the season, sex, and presence of other viruses.
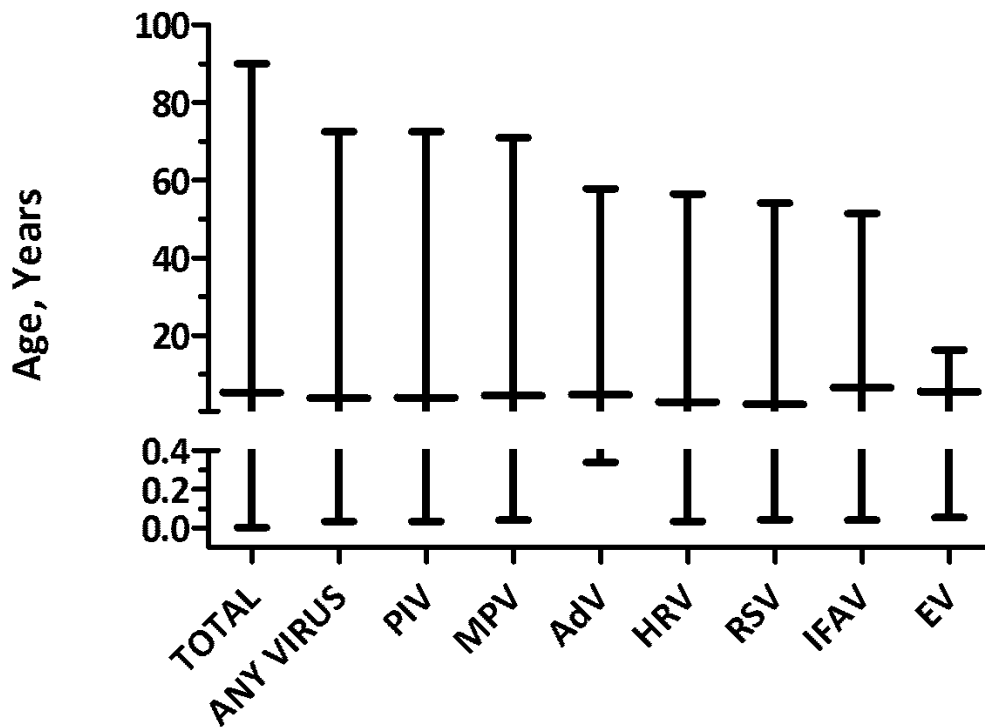
| Outcome variable (HRV positive) | Explanatory variables entered[a] | p-value | Odds ratio for likelihood of RV[b] |
|---|---|---|---|
| **RV** | IFAV | 0·007 | **0·14**, 0·03-0·59 |
| | Sex | 0·16 | |
| | | | |
| | *Season* | 0·001 | |
| | Autumn | <0·0001 | **2·0**, 1·3-3·03 |
| | Spring | 0·005 | **2·72**, 1·80-4·11 |
| | summer | 0·11 | **2·07**, 1·24-3·44 |
| | age group | | |
| **RV** | EV | 0·97 | |
| | Sex | 0·17 | |
| | | | |
| | *Season* | <0·0001 | |
| | Autumn | <0·0001 | **2·51**, 1·67-3·77 |
| | Spring | 0·0002 | **3·33**, 2·22-5·00 |
| | Summer | 0·09 | **2·60**, 1·57-4·23 |
| | Age group | | |
| **RV** | HCoV-OC43 | 0·0542 | |
| | Sex | 0·19 | |
| | | | |
| | *Season* | <0·0001 | |
| | Autumn | <0·0001 | **2·5**, 1·68-3·76 |
| | Spring | 0·0002 | **3·33**, 2·22-5·00 |
| | Summer | 0·08 | **2·60**, 1·57-4·23 |
| | Age group | | |
| **RV** | RSV | 0·052[1] | |
| | Sex | 0·15 | |
| | | | |
| | *Season* | <0·0001 | |
| | Autumn | <0·0001 | **2·51**, 1·67-3·76 |
| | Spring | 0·0002 | **3·33**, 2·22-5·00 |
| | Summer | 0·052 | **2·60**, 1·57-4·23 |
| | Age group | | |

[a]Adjusted for season (winter is the reference category); Significant associations are shown in bold. These are 'nearly significant' at the p-0.05 level.
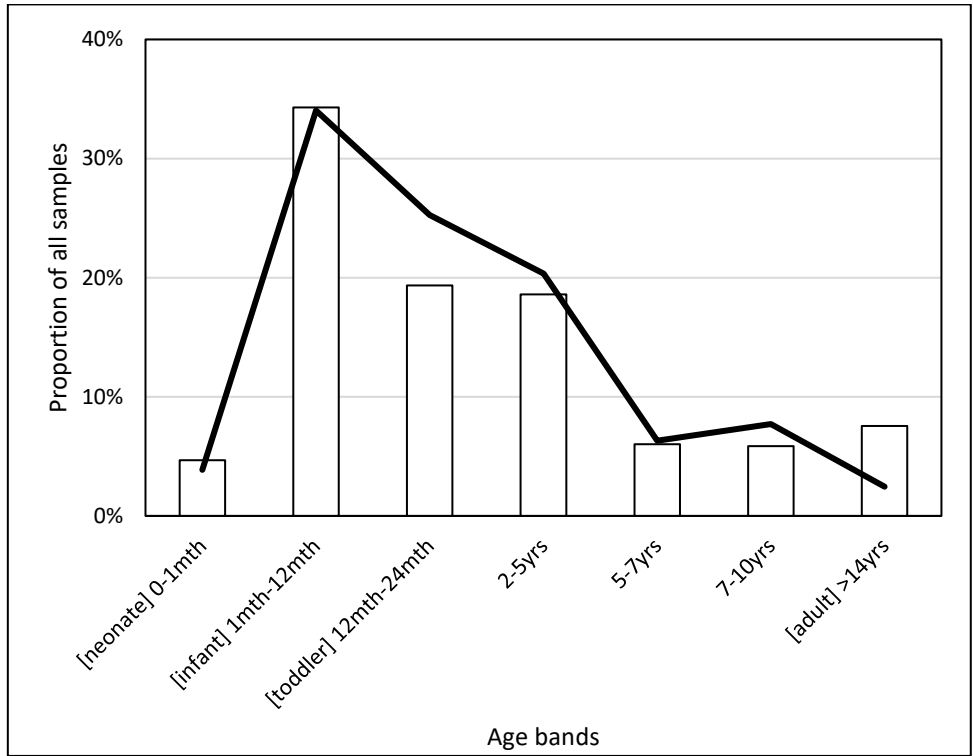
**Supplementary table 4.** Measures of association between virus pairs where co-detections occurred as determined by 2 x 2 contingency tables with Fisher's exact test.

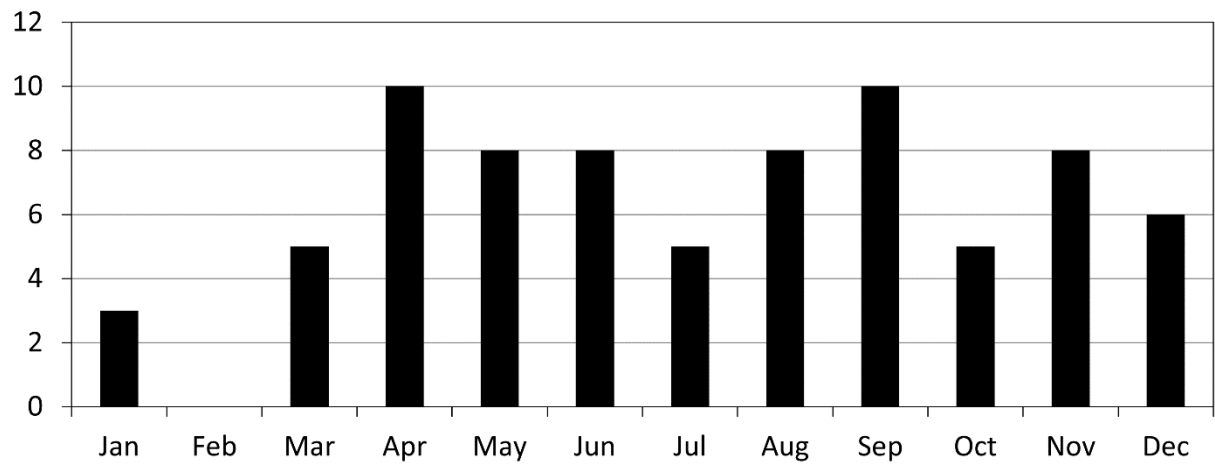| | RV | AdV | HMPV | EV | IFAV | HCoV-OC43 | RSV | HCoV-NL63 | PIV | HCoV-HKU1 |
|---|---|---|---|---|---|---|---|---|---|---|
| **Total Detections** | 285 | 37 | 85 | 12 | 73 | 26 | 101 | 4 | 66 | 5 |
| **Single Detections** | 225 | 25 | 53 | 11 | 66 | 20 | 83 | 4 | 48 | 3 |
| **Co-detections** | 60 | 12 | 32 | 1 | 7 | 6 | 19 | 0 | 18 | 2 |
| **RV** | | 5, 0·2; 0·48 (0·2-1·2) | 21, 1·0; 1·0 (0·6-1·7) | 0, 0·08; 0·12 (0·01-2·1) | 2, **<0·0001;** 0·08 (0·02-0·3) | 2, 0·06; 0·26 (0·06-1·1) | 17, 0·07; 0·60 (0·4-1·0) | 0, 0·58; 0·34 (0·02-6·4) | 16, 1·0; 1·0 (0·6-1·8) | 2, 0·6; 2·10 (0·35-12·64) |
| **AdV** | | | 4, 0·34; 1·57 (0·5-4·5) | 1, 0·32; 2·86 (0·4-22·8) | 0, 0·16; 0·19 (0·01-3·2) | 2, 0·19; 2·67 (0·6-11·7) | 0, 0·07; 0·13 (0·01-2·2) | 0, 1·0; 3·38 (0·2-63·9) | 1, 0·72; 0·46 (0·06-3·4) | 0, 1·0; 2·76 (0·15-50·88) |
| **HMPV** | | | | 0, 1·0; 0·50, (0·03-8·5) | 5, 1·0; 0·93 (0·4-2·4) | 1, 1·0; 0·50 (0·07-3·8) | 2, **0·03**; 0·24 (0·06-0·9) | 0, 1·0; 1·42 (0·07-26·3) | 3, 0·62; 0·59 (0·2-11·3) | 0, 1·0; 1·16 (0·06-21·17) |
| **EV** | | | | | 0, 1·0; 0·60 (0·03-10·2) | 0, 1·0; 1·73 (0·1-29·9) | 0, 0·61; 0·42 (0·02-7·1) | 0, 1·0; 10·36 (0·5-202·8) | 0, 1·0; 0·66 (0·04-11·3) | 0, 1·0; 8·45 (0·44-161·55) |
| **IFAV** | | | | | | 1, 1·0; 0·60 (0·08-4·5) | 0, **0·002**; 0·07 (0·004-1·1) | 0, 1·0; 1·67 (0·09-31·3) | 0, **0·03;** 0·11 (0·0006-1·7) | 0, 1·0; 1·36 (0·07-24·92) |
| **HCoV-OC43** | | | | | | | 0, 0·16; 0·19 (0·01-3·2) | 0, 1·0; 4·83 (0·3-91·9) | 0, 0·39; 0·31 (0·02-5·1) | 1, 0·1; 11·49 (1·24-106·67) |
| **RSV** | | | | | | | | 0, 1·0; 1·16 (0·06-21·8) | 0, **0·005;** 0·07 (0·005-1·2) | 0, 1·0; 0·95 (0·05-17·36) |
| **HCoV-NL63** | | | | | | | | | 0, 1·0; 1·86 (0·1 -34·9) | 0, 1·0; 23·65 (1·13-495·04) |
| **PIV** | | | | | | | | | | 0, 1·0; 1·52 (0·08-27·75) |

The total detections of each virus are divided into whether they occurred by themselves (single detections) or concurrently with one or more other viruses (co-detections; ≥ 2 detections in one sample). The first row in each cell of the table gives the number of co-detections, followed by the probability of association by chance (p-values; bold indicates $p < 0.05$ ). The second row gives the odds ratio for occurrence of co-detection of the virus in the column heading given the presence of the virus in the row heading. Where there are no co-detections the odds ratio is estimated using a correction of 0.5 in every cell of those tables that contain a zero.

**Supplementary figure 1**. The median age range of people positive for different endemic human respiratory viruses. Total-all samples providers including virus positive and negative cases of ARI; Any-samples positive for any virus; PIV-parainfluenza virus; MPV-metapneumovirus; AdV-adenovirus; RV-rhinovirus; RSV-respiratory syncytial virus; IFAV-influenza A virus; EV- a member of an enterovirus species

**Supplementary figure 2.** The proportion of samples (bars) and rhinovirus detection (line) by age band.

**Supplementary figure 3.** Total viral co-detections by month.