Table S1 Primers and Probes for IAV, IBV, NoV GI and NoV GII detection via RT-dPCR

Primer/probe target	Description	Sequence (5'–3')
Influenza A	InfA For1	CAA GAC CAA TCY TGT CAC CTC TGA C
	InfA For2	CAA GAC CAA TYC TGT CAC CTY TGA C
	InfA Rev1	GCA TTY TGG ACA AAV CGT CTA CG
	InfA Rev2	GCA TTT TGG ATA AAG CGT CTA CG
	InfA Probe	FAM/TGC AGT CCT CGC TCA CTG GGC ACG/BHQ-1
Influenza B	InfB For	TCC TCA AYT CAC TCT TCG AGC G
	InfB Rev	CGG TGC TCT TGA CCA AAT TGG
	InfB Probe	HEX/CCA ATT CGA GCA GCT GAA ACT GCG GTG/BHQ-1
Norovirus GI	LZIF	GGA GAT CGC RAT CTC CTG CCC GA
	LZIR-A	CTC YGG TAC CAG CTG GCC
	LZIR-B	CCT CYG GHA CCA GCT GAC C
	LZIP	HEX/CGT CCT TAG ACG CCA TCA TCA TTT AC/BHQ-1
Norovirus GII	LZIIF-A	GTG GGA TGG ACT TTT ACG TGC CAA G
	LZIIF-B	GGT GGM ATG GAT TTT TAC GTG CCC AG
	LZIIR	CGT CAY TCG ACG CCA TCT TCA TTC AC
	LZIIP	FAM/AGC CAG ATT GCG ATC GCC/BHQ-1

Table S2 Linearised DNA positive-control sequences after in vitro amplification

| NoV GI	5'_GGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGAAAGGCAATTGGGTACCGAGCTCGCGGCCGCAAGCGGACA**GGAGATCGCAATCTCCTGCCCGA***ATTCGTAAATGATGATGGCGTCTAAGGACGCCCCAACATCCCCTGATGGCGCCAGTGGCGCC**GGCCAGCTGGTACCGGAGGC**TAATAACCTGCTTTTGCTCGCTTGGATCCGAATTCAAAGGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTG_3'
NoV GII	5'_GGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGAAAGGCAATTGGGTACCGAGCTCGCGGCCGCAAGCAGAAG***GTGGGATGGACTTTTACGTGCCAAG*GCAGGAACCCATGTTCAGGTGGATGAGGTTTTCTGACTTGAGCACGTGGGAGGGCGATCGCAATCTGGCTCCCAATTTT*GTGAATGAAGATGGCGTCGAATGAGC***CGCTCACCTGCTTTTGCTCGCTTGGATCCGAATTCAAAGGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTG_3'
IAV	5'_GGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGAAAGGCAATTGGGTACCGAGCTCGCGGCCGCAAGCAAAGA***CAAGACCAATCCTGTCACCTCTGAC*TAAGGGGATTTTAGGGTTTGTGTTCACGCTCACCGTGCCCAGTGAGCGAGGACTGCAG*CGTAGACGCTTTGTCCAAAATGC*CCTAAACCTGCTTTTGCTCGCTTGGATCCGAATTCAAAGGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTG_3'
IBV	5'_GGAGCAGACAAGCCCGTCAGGGCGCGTCAGCGGGTGTTGGCGGGTGTCGGGGCTGGCTTAACTATGCGGCATCAGAGCAGATTGTACTGAGAGAAAGGCAATTGGGTACCGAGCTCGCGGCCGCAAGCTCGGA***TCCTCAATTCACTCTTCGAGCG*TCTTAATGAAGGACATTCAAAGCCAATTCGAGCAGCTGAAACTGCGGTGGGAGTCTTATC*CCAATTTGGTCAAGAGCACCG*ACTATACCTGCTTTTGCTCGCTTGGATCCGAATTCAAAGGTGAAATTGTTATCCGCTCACAATTCCACACAACATACGAGCCGGAAGCATAAAGTGTAAAGCCTG_3'
Pex-plasmid-residue, overhang, *selective primer-region,* **target-sequence with probe-region**	
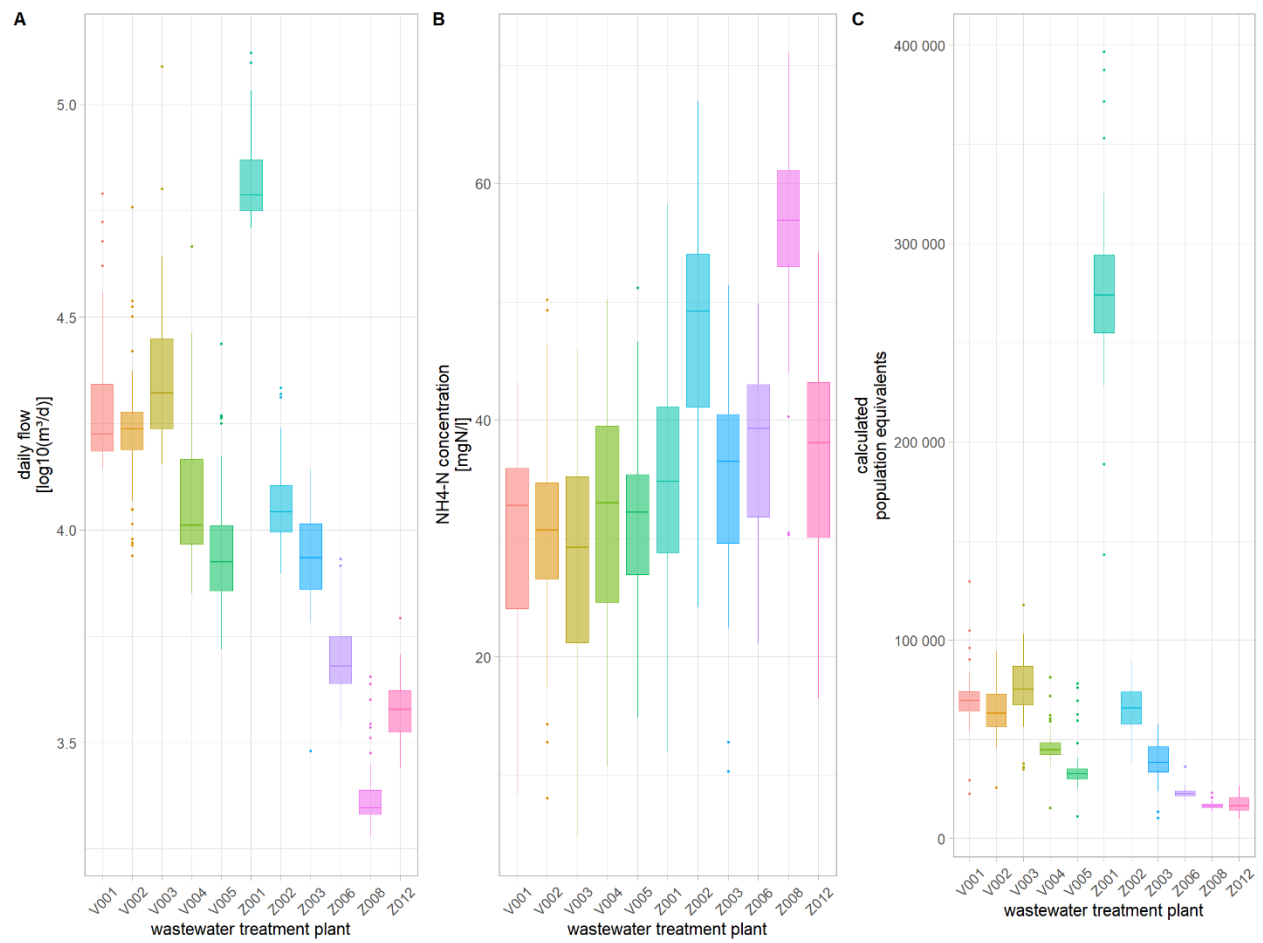
Figure A1 Flow rate, NH₄-N concentration and calculated population size according to NH₄-N normalization.
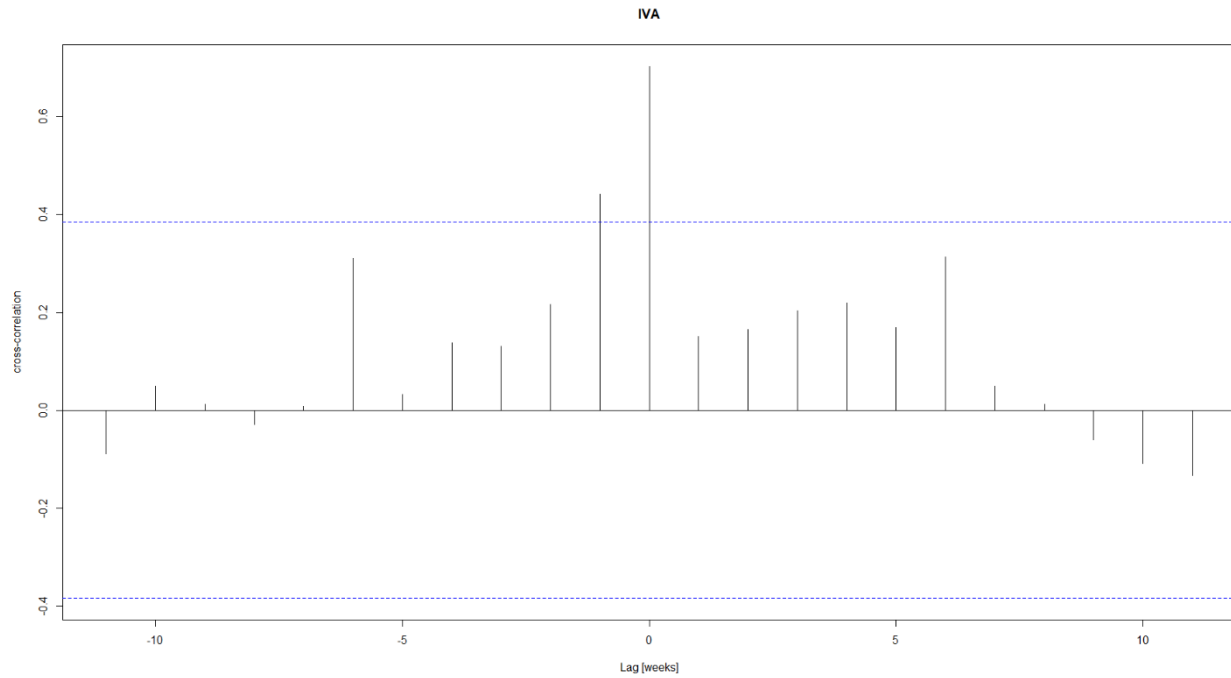
Figure A2 Cross correlation analysis for IVA and inpatients infected with influenza virus
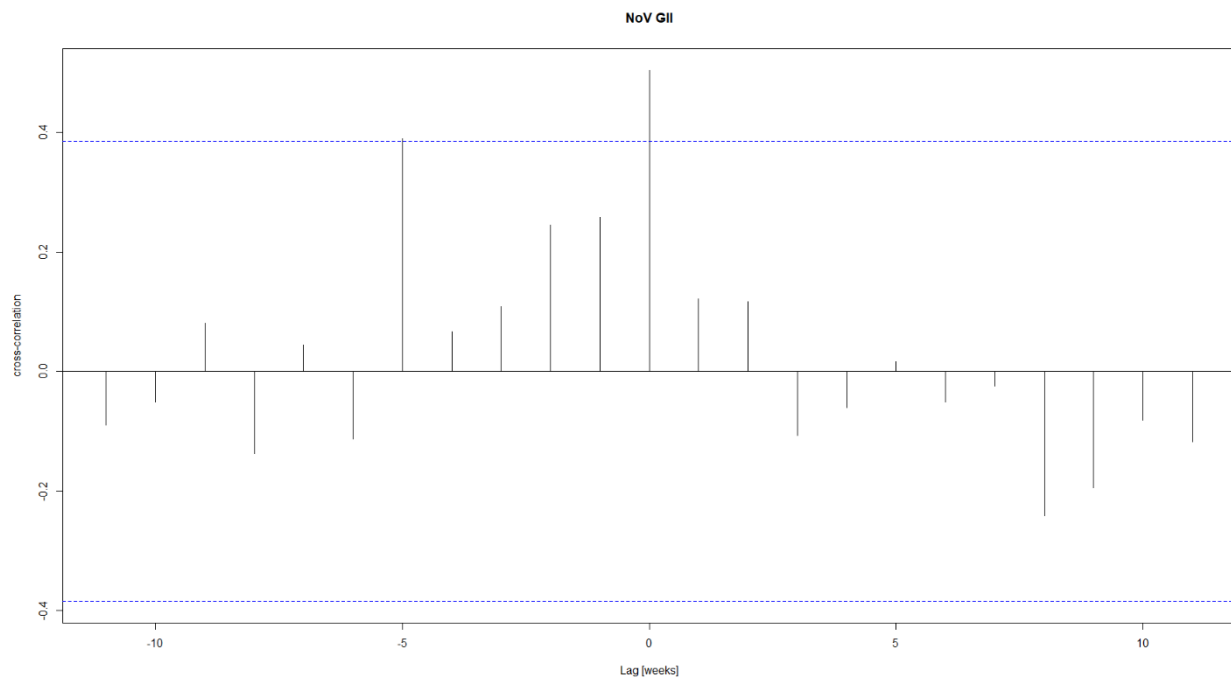

Figure A3 Cross correlation analysis for NoV GII and inpatients infected with NoVs.