to identify the sources of infection, and the virus evolution as well as host/virus interaction. In our study, using 454/Illumina sequencing, we have obtained large amount of whole genome sequences. We designed a preliminary bioinformatics analysis pipeline to classify these NGS reads. First we mapped our nucleotide reads to GenBank reference sequences using BLAST, and classified them by their taxonomic family, such as host, virus and unclassified. Then, for a specific type of virus (e.g. influenza virus, MERS coronavirus), we conducted de novo and reference based assembly of the reads to obtain the full genome sequences for further phylogenetic study. In the future, through advanced bioinformatics tools, we hope to get more detailed information from our large amount of NGS sequences of field/clinical samples, experimental data, especially in the following areas: (i) finding novel pathogens in unclassified sequences; (ii) virus/virus interactions; (iii) pathogen/host interaction.

**S25** Phylogenetic analysis of the nucleocapsid and RNA-dependent RNA polymerase fragments of the first imported case of middle east respiratory syndrome coronavirus (MERS-CoV) infection in the Philippines

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We report the first laboratory-confirmed case of Middle East Respiratory Syndrome Coronavirus (MERS-CoV) infection from Saudi Arabia, February 2015.

**S26** Transmission patterns and evolution of RSV in a community outbreak identified by genomic analysis

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Detailed information on the source, spread and evolution of respiratory syncytial virus (RSV) during seasonal community outbreaks remains sparse. Molecular analyses of attachment (G) gene sequences from hospitalised cases suggest that multiple genotypes and variants co-circulate during epidemics and that RSV persistence over successive seasons is characterized by replacement and multiple new introductions of variants. No studies have defined the patterns of introduction, spread and evolution of RSV at the local community and household level. We present a whole genome sequence analysis of 131 RSV group A viruses collected during six-month household-based RSV infection surveillance in Coastal Kenya, 2010 within an area of 12 km². RSV infections were identified by regularly screening of all household members twice weekly. Phylogenetic analysis revealed that the RSV A viruses in 9 households were closely related to genotype GA2 and fell within a single branch on the global phylogeny. Genomic analysis allowed the detection of household-specific variation in seven households. For comparison, using only G gene analysis, household-specific variation was found only in 1 of the 9 households. Nucleotide changes were observed intra-host (viruses identified from same individual in follow-up sampling) and inter-host (viruses identified from different household members) and these coupled with sampling dates enabled partial reconstruction of the within household transmission chains. The genomic evolutionary rate for the household dataset was estimated as 2.307 × 10⁻³ (95% highest posterior density: 0.93513–4.1636 × 10⁻³) substitutions/site/year. We conclude that (i) at the household level, most RSV infections arise from the introduction of a single virus variant followed by accumulation of household specific variants and (ii) analysis of complete virus genomes is crucial to better understand viral transmission in the community. A key question arising is whether prevention of RSV introduction or spread within the household by vaccinating key household members in these functions would lead to a reduced onward community wide transmission.

**S27** Using whole genome sequence data and minority variant profiles to elucidate transmission patterns during RSV household outbreaks

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Reconstructing transmission chains for outbreaks is important in understanding how viruses spread. Furthermore, defining the main underlying determinants of transmission chains is important for developing effective interventions. Whole