**Thesis Chapters C Goh**

1. Introduction
   1. Sepsis heterogeneity
   2. Omics-based approaches and the importance of the pathogen
   3. New opportunities in clinical microbiology
   4. Challenges in diagnostic metagenomics
   5. Aims and objectives
2. Materials and methods
   1. The GAinS cohort
   2. STOP-HCV and cardiac cohorts
   3. Library preparation optimisation
   4. Probe-based enrichment
   5. Metagenomic analysis
   6. Digital droplet PCR
   7. ELISAs
   8. Transcriptomics data processing
3. Metagenomic sequencing applied to sepsis
   1. Introduction
   2. Results: library preparation optimisation
   3. Results: probe-based enrichment (viral multiplex reference)
   4. Results: data processing and diagnostic models
   5. Discussion
   6. Conclusions
4. Improved classification of microbiological aetiology in sepsis
   1. Introduction
   2. Results: clinical microbiology
   3. Results: metagenomics
   4. Results: recovery of whole genomes
   5. Results: digital droplet PCR
   6. Results: EBV antibody ELISAs
   7. Discussion
   8. Conclusions
5. Integration of metagenomics with the host response
   1. Introduction
   2. Results: evidence for immunosuppression
   3. Results: transcriptomic signatures of different pathogens
   4. Results: genomics (genotyping, HLA, eQTL)
   5. Results: proteomics
   6. Discussion
   7. Conclusions
6. General Discussion