

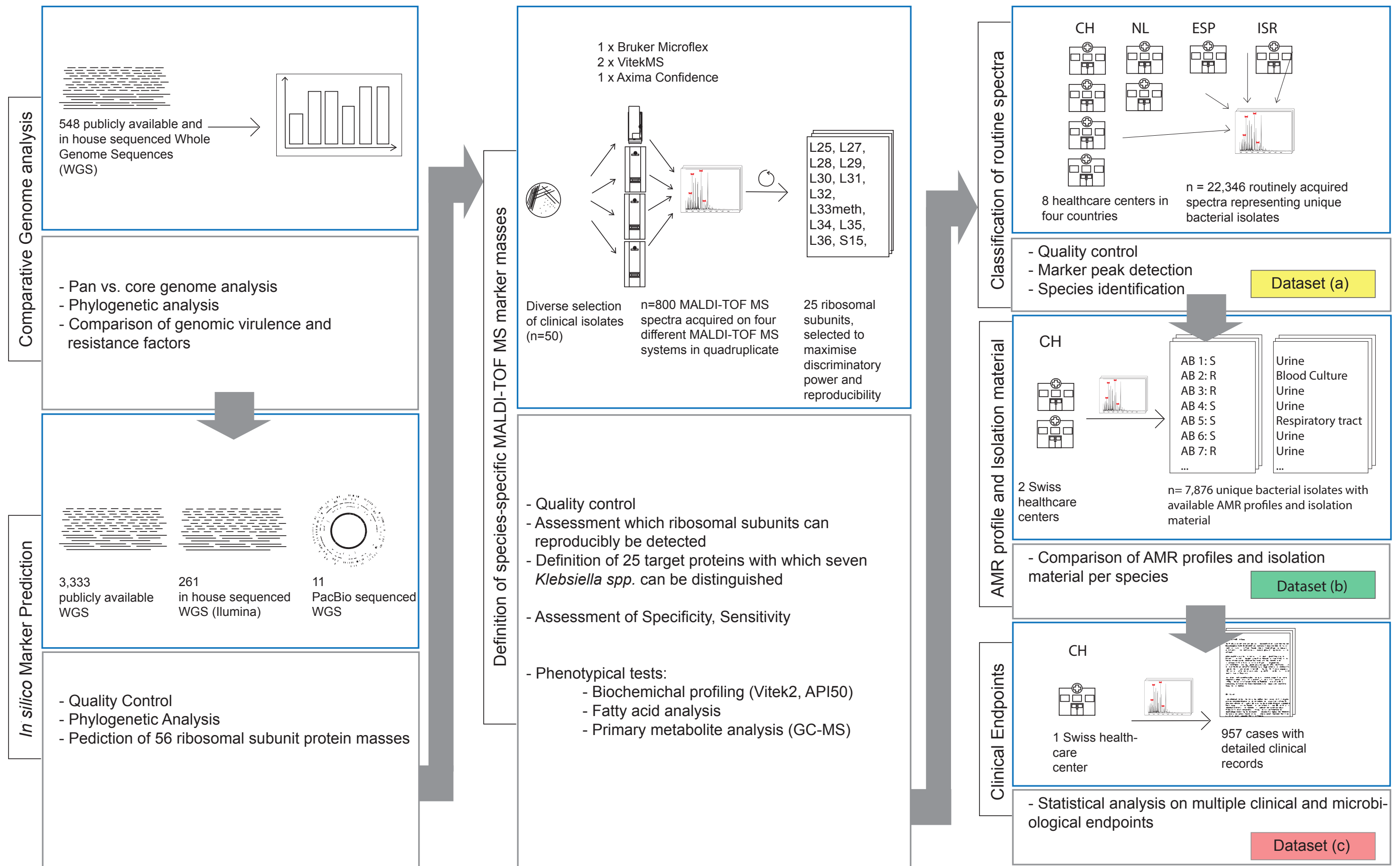


Figure S1: Workflow of the Project. Blue framed boxes indicate the data analysed whereas the grey framed boxes indicate which analysis and measurements have been done. The yellow, green and red boxes depict the datasets used in the statistical analysis comparing the occurrence of *Klebsiella spp.* as well as multiple microbiological and clinical endpoints.

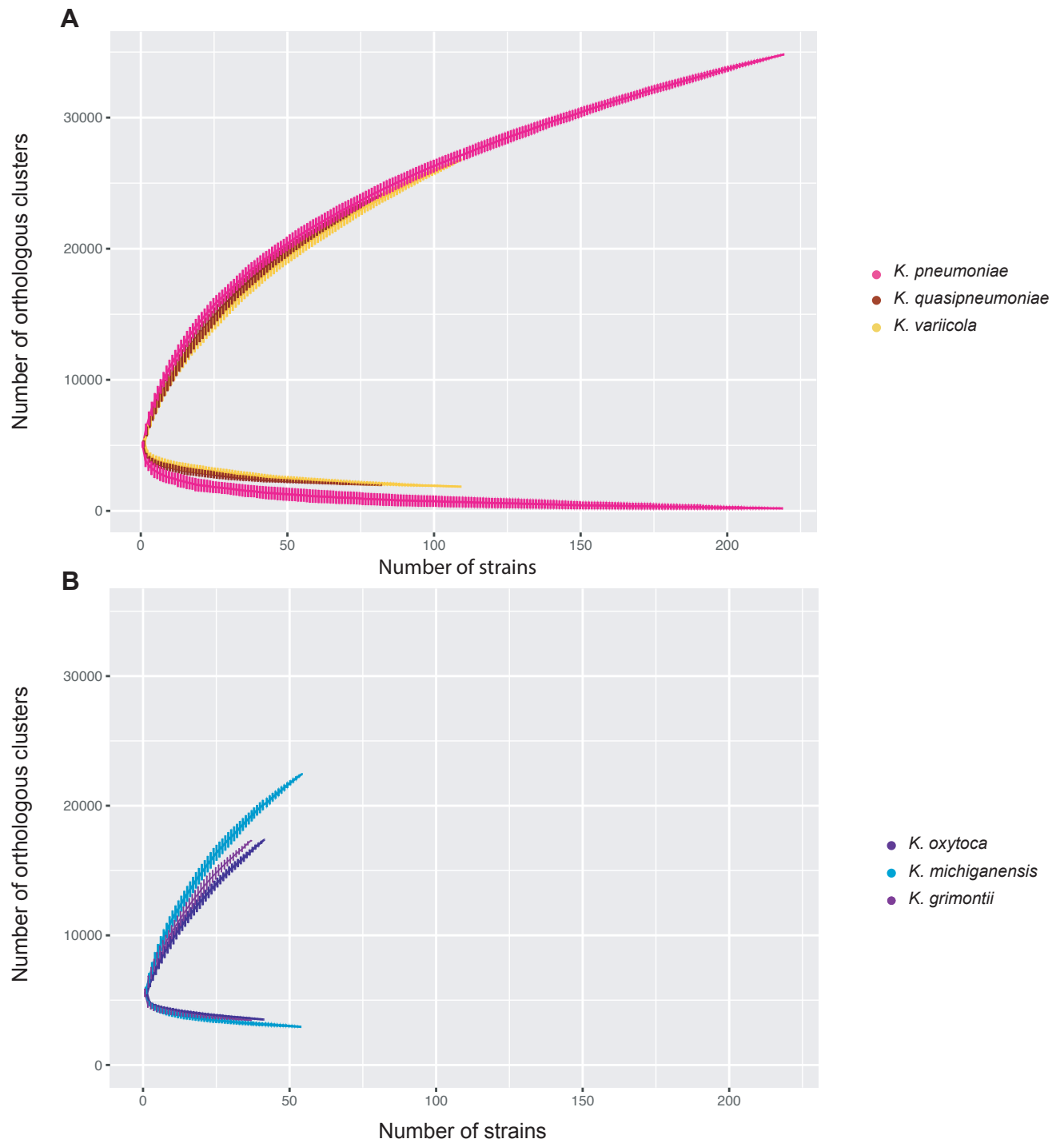


Figure S2: Gene accumulation curves for species of the *K. pneumoniae* group (A) and the *K. oxytoca* group (B)

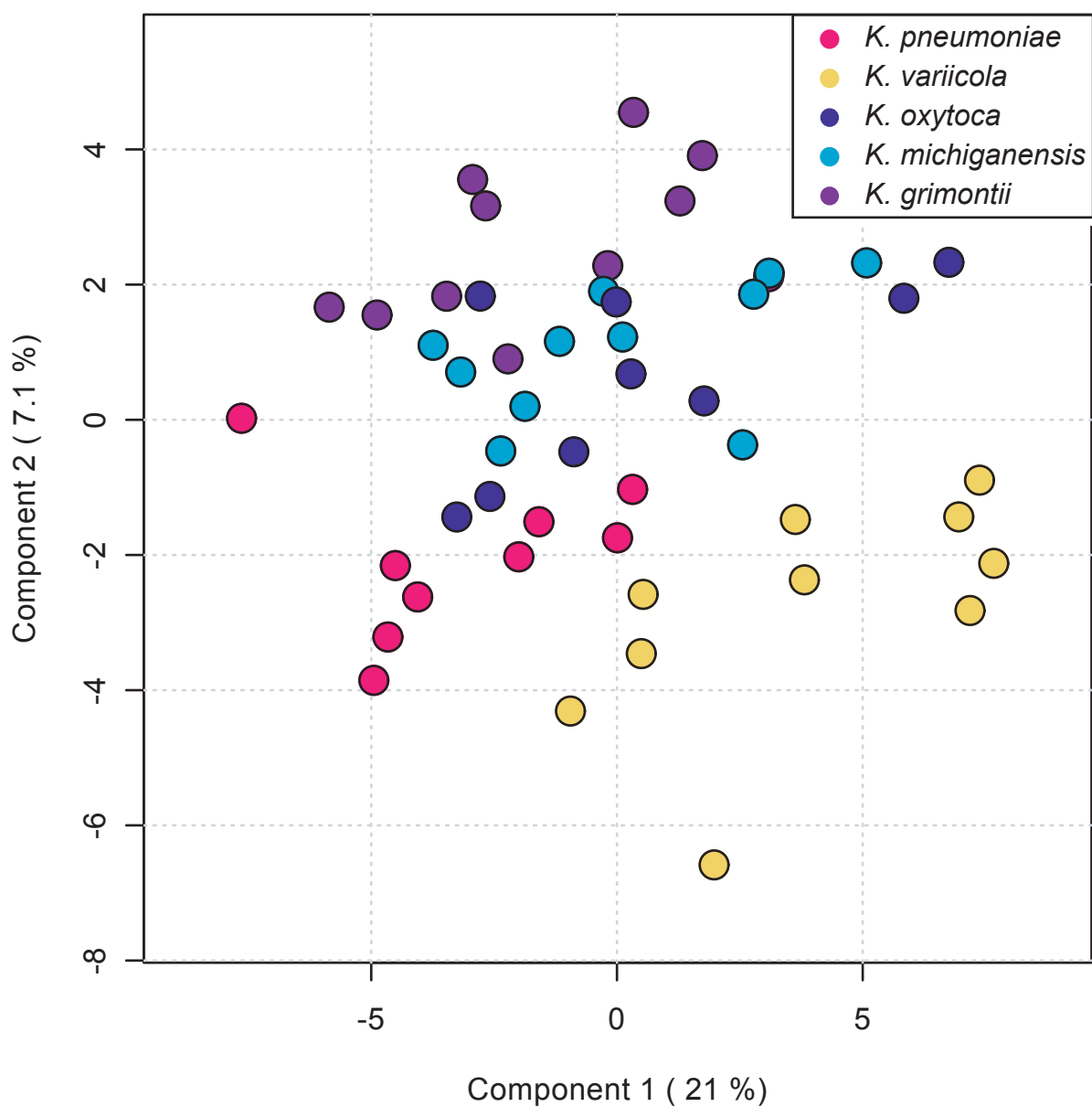


Figure S4: Partial least squares discriminant analysis (PLS-DA) score plot containing primary metabolites measured of five *Klebsiella* spp (n=50). The primary metabolite profile does not allow clustering of the strains according to their species identity.

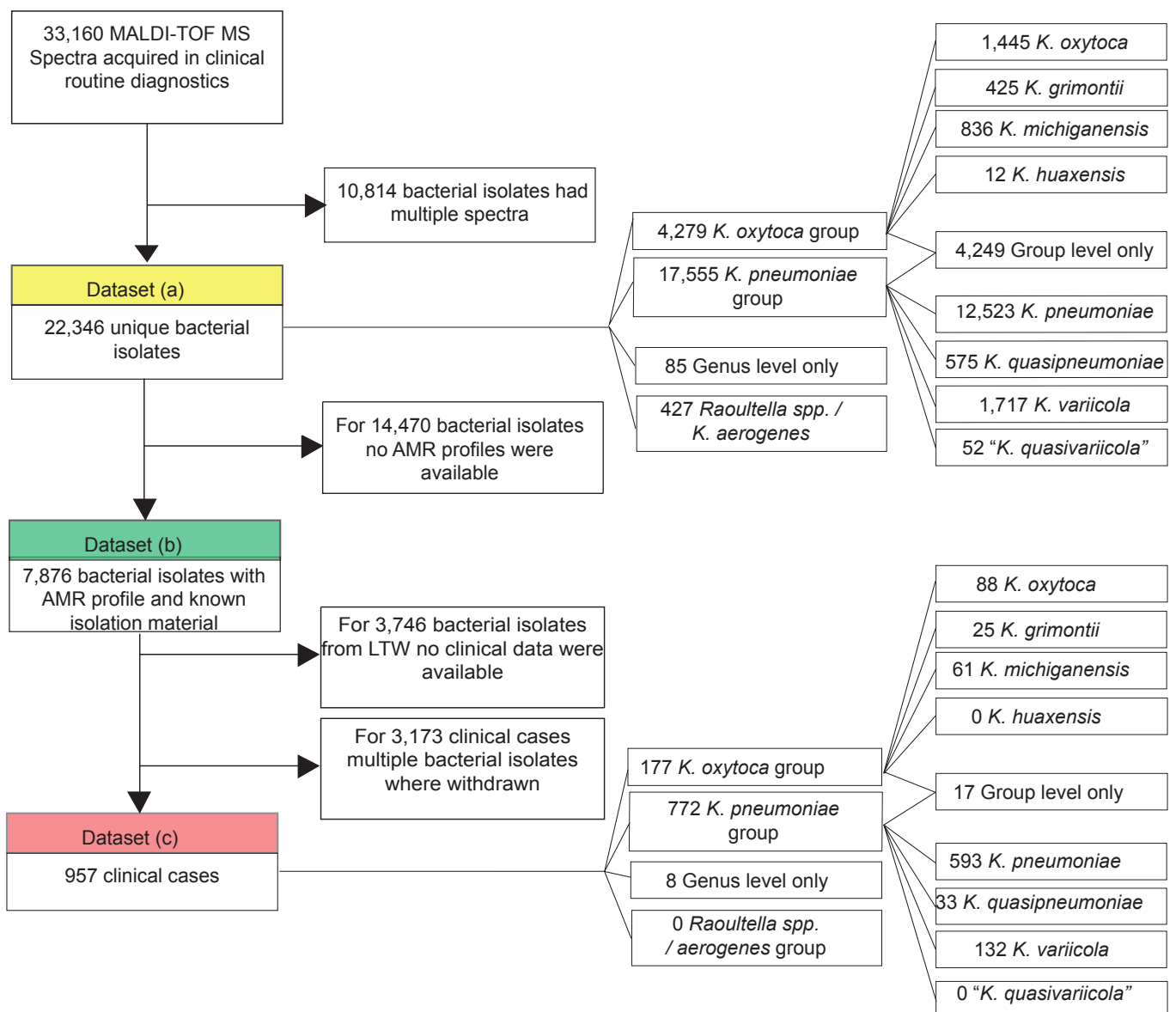


Figure S5: Species identity of datasets (a), (b) and (c) included in the statistical analysis. These three datasets were analysed with the objectives: (i) to investigate the relative distribution of *Klebsiella* spp. (and species groups) identified in samples from patients presenting with infection, with regard to center, country, sample material, and resistance to antibiotics; and (ii) to examine the link between clinical outcome of the patients and the *Klebsiella* spp. causing the infection and relevant patient characteristics.