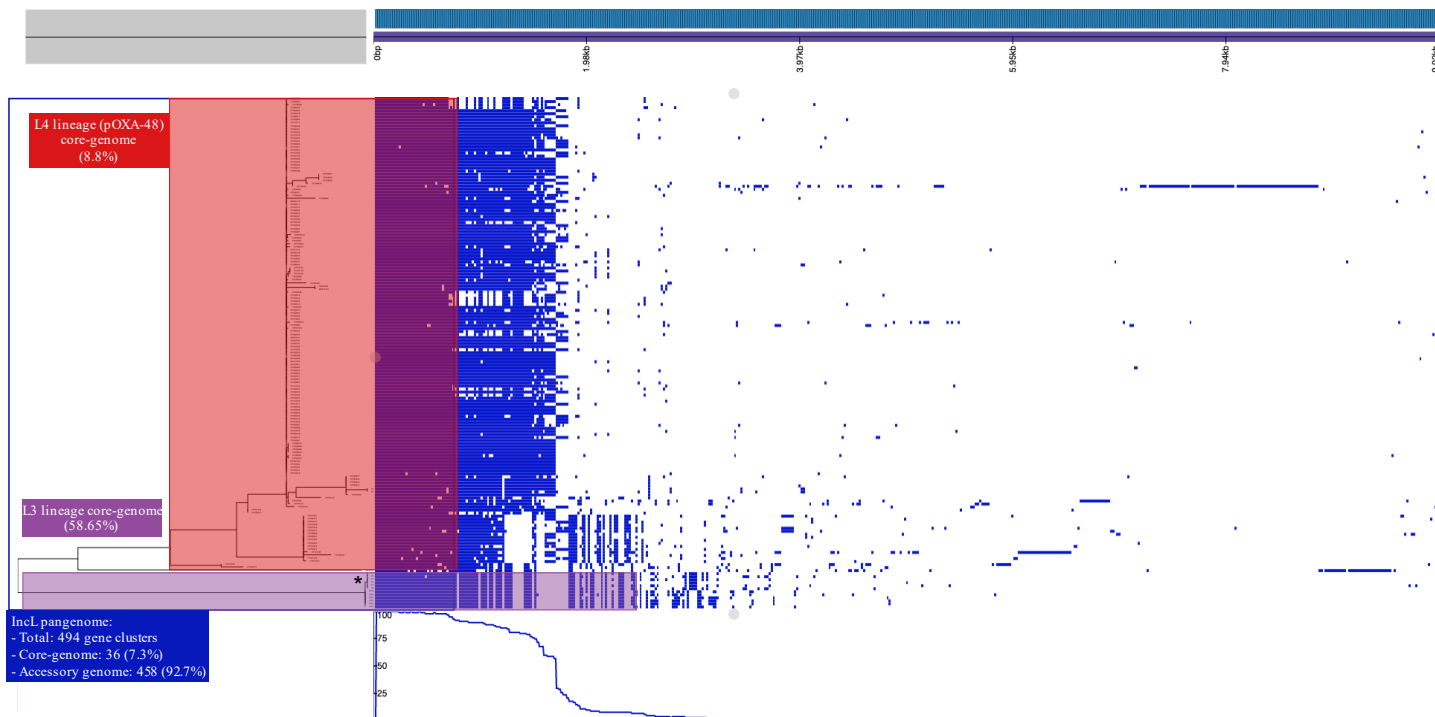


Supplementary Figure 2. SNP-trees of genes considered molecular markers for phylogenetic classification of IncL plasmids (scale bars: substitutions per site). Specific IncL types are indicated by colored shades (center legend) and pRMTE4 plasmids are pointed out by '*'. Substitution rate scale is shown in the bottom-left of each figure panel. A: *repA* SNP-tree. B: *excA* SNP-tree. C: *traX* SNP-tree. D: *traY* SNP-tree.



Supplementary Figure 3. Pan-genome visualization of all IncL type plasmids. Phylogenetic tree was constructed based on SNPs from non-recombinogenic core-genes present in at least 95% of 169 IncL plasmids included in the collection. The graph shows the presence (dark blue) and absence (white) in each plasmid of all gene clusters encompassed in the pan-genome. Total IncL core-genome and pOXA-48 cluster and L3 lineage core-genomes are highlighted by different colored frames, indicating in each case the % of gene clusters belonging to core-genome with respect to the total gene clusters for each IncL plasmid type. pRMTE4 plasmid cluster is pointed out by ‘*’.



Supplementary Figure 4. Resistance gene content of all IncL type plasmids. Phylogenetic tree was constructed based on SNPs from non-recombinogenic core-genes present in at least 95% of 169 IncL plasmids included in the collection. Specific IncL types are indicated by colored shades (top-left legend) and pRMTE4 plasmid cluster is pointed out by ‘*’. The graph shows the presence and absence in each plasmid of all antimicrobial resistance genes identified in the IncL plasmid collection. Key resistance genes for pOXA-48 and pRMTE4 plasmids are emphasized by colored frames.