

PlasmidID:

a mapping based tool for plasmid identification, annotation, typing and visualization.

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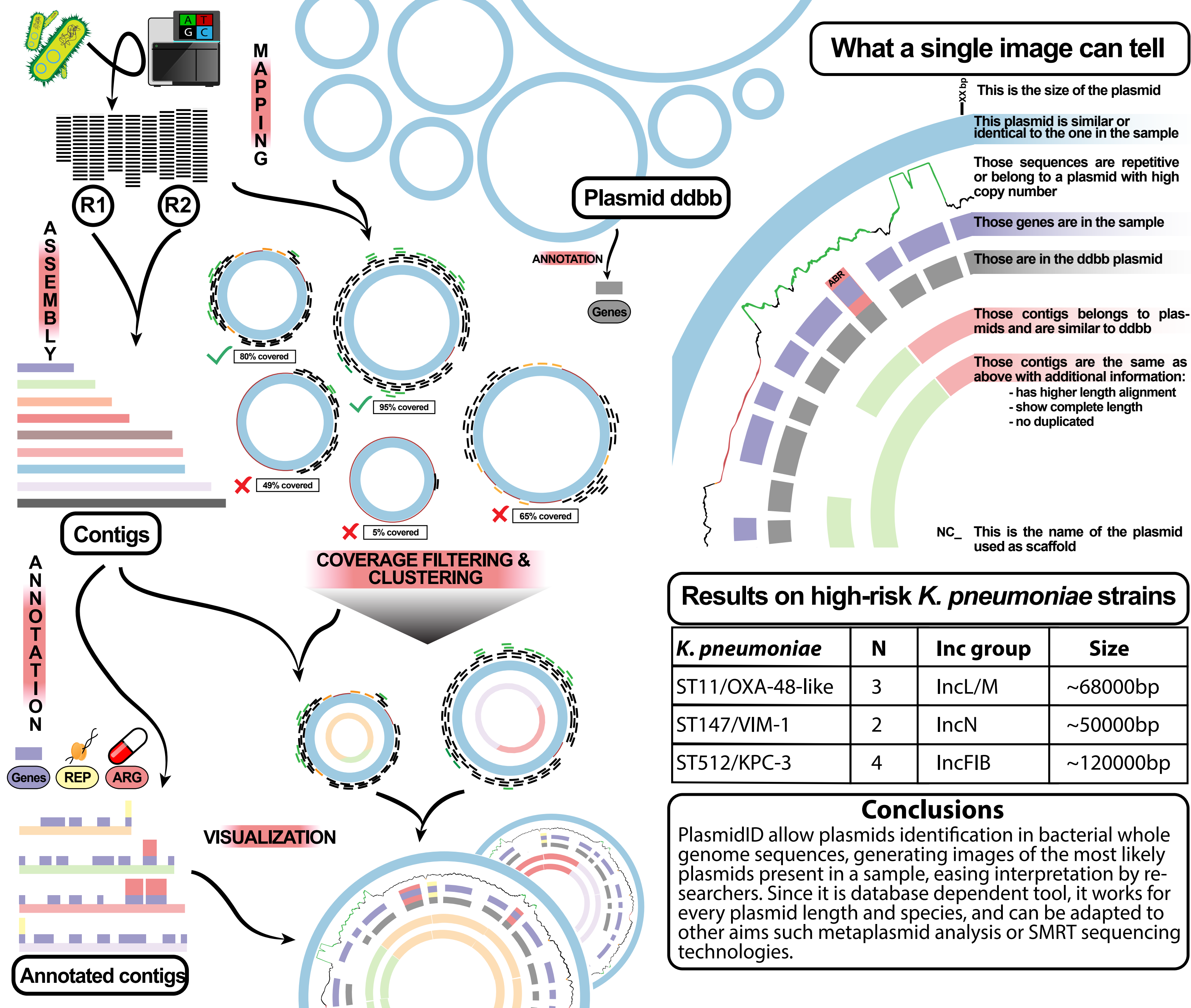
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Background

- Plasmids are key elements in ARG and virulence factors horizontal transfer
- Modular nature hinder recovery from WGS data
- Local alignment & *de novo* assembly are limited strategies

Results

PlasmidID is a new method that maps Illumina reads over plasmid database sequences. The most covered sequences are clustered by identity to avoid redundancy and the longest are used as scaffold for plasmid reconstruction. Reads are assembled and annotated. All information generated from mapping, assembly, annotation and local alignment analyses is gathered and accurately represented in a circular image which allow user to determine plasmidic composition in any bacterial sample.



Results on high-risk *K. pneumoniae* strains

<i>K. pneumoniae</i>	N	Inc group	Size
ST11/OXA-48-like	3	IncL/M	~68000bp
ST147/VIM-1	2	IncN	~50000bp
ST512/KPC-3	4	IncFIB	~120000bp

Conclusions

PlasmidID allow plasmids identification in bacterial whole genome sequences, generating images of the most likely plasmids present in a sample, easing interpretation by researchers. Since it is database dependent tool, it works for every plasmid length and species, and can be adapted to other aims such metaplasmid analysis or SMRT sequencing technologies.