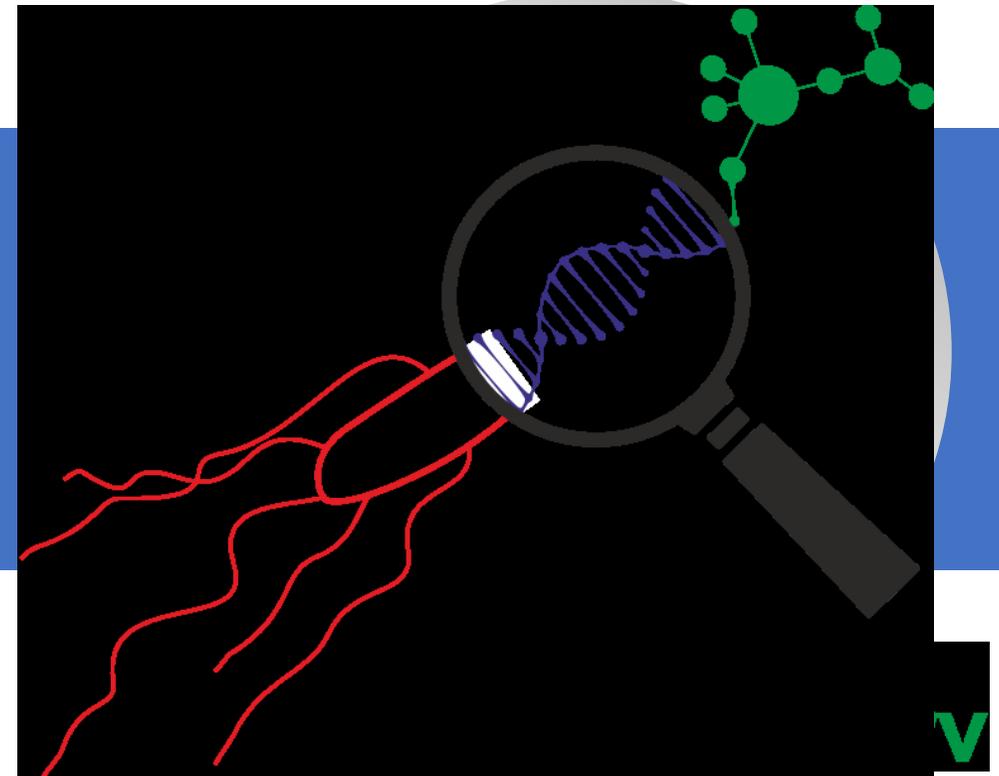


# GenoSalmSurv screencasts



# GenoSalmSurv screencasts

das Projekt

die Pipelines

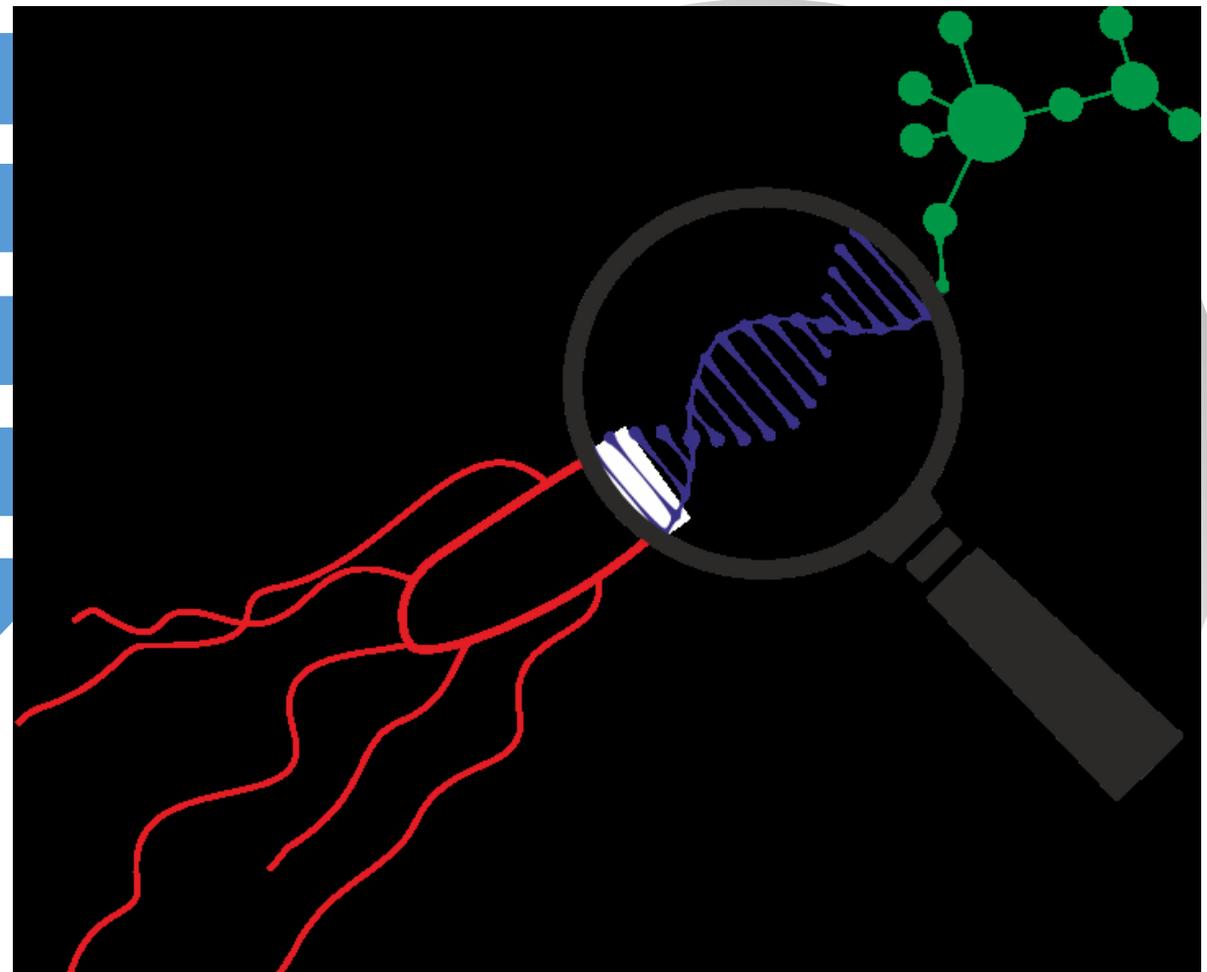
AQUAMIS und die QC Entscheidung

das allele calling: chewieSnake

Metachewiereport + Interpretation 5

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### Salmonella Derby Ausbruch - Hintergrundinformationen

- November 2013 – Januar 2014
- Berlin und Brandenburg
- 145 Fälle; vor allem ältere Menschen in Krankenhäusern und Pflegeheimen
- Quelle: rohe Teewurst

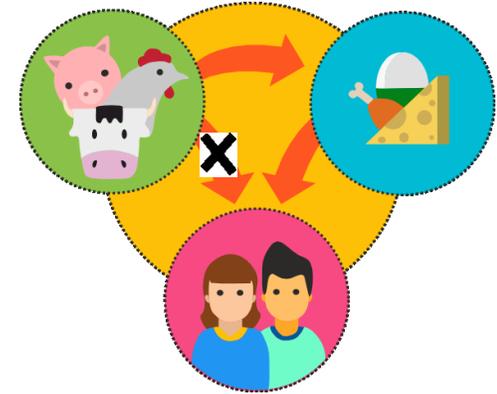
Evaluation of WGS based approaches for investigating a food-borne outbreak caused by *Salmonella enterica* serovar Derby in Germany

Sandra Simon <sup>a,\*</sup>, Eva Trost <sup>a</sup>, Jennifer Bender <sup>b</sup>, Stephan Fuchs <sup>b</sup>, Burkhard Malorny <sup>c</sup>, Wolfgang Rabsch <sup>a</sup>, Rita Prager <sup>a</sup>, Erhard Tietze <sup>a</sup>, Antje Flieger <sup>a</sup>

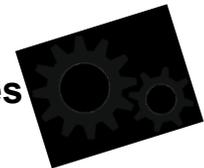
<sup>a</sup> Robert Koch Institute, National Reference Centre for Salmonella and Other Bacterial Enteric Pathogens and Unit of Enteropathogenic Bacteria and Legionella, Wernigerode, Germany

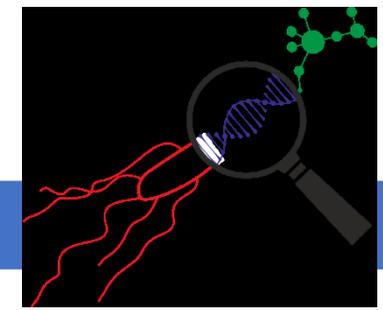
<sup>b</sup> Robert Koch Institute, Unit of Nosocomial Pathogens and Antibiotic Resistances, Wernigerode, Germany

<sup>c</sup> Federal Institute for Risk Assessment, Max-Dohrn-Str. 8-10, 10589 Berlin, Germany

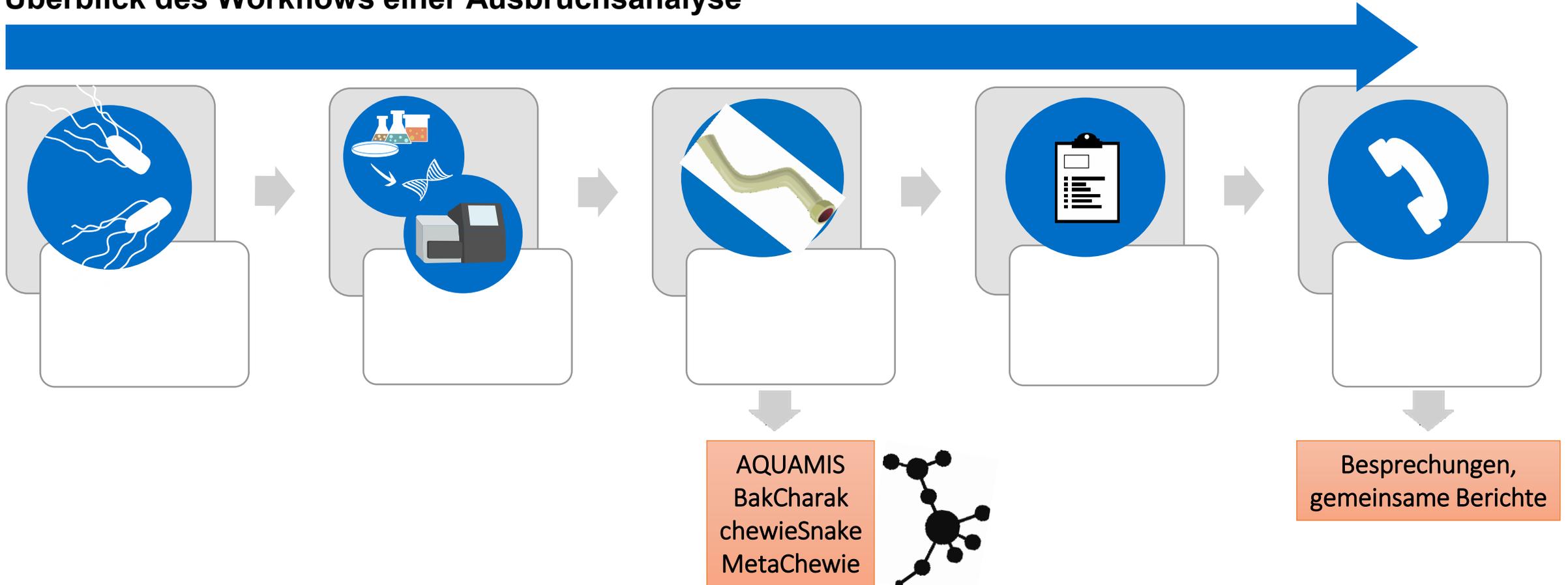


- Retrospektive WGS Analysen (SNP und cgMLST): Simon et al. 2017, Food Microbiology
- Datensatz n=55
  - bestätigte Ausbruchsstämme (n=26)
  - Stämme mit unsicherer Korrelation zum Ausbruch (n=7)
  - Kontroll-Set (n=22)
- Analyse mittels GenoSalmSurv Pipelines





### Überblick des Workflows einer Ausbruchsanalyse



### AQUAMIS: Assembly

AQUAMIS report ist in Produktion

Short summary report

#### Assembly report for run results

[Overview](#)
[Short summary table](#)
[Detailed assembly table](#)
[Detailed trimming table](#)
[Kraken2 results](#)
[Plots per run](#)
[Plots per sample](#)
[Program versions/ log](#)
[Help](#)

Show  entries

sample name	species	total length	# contigs >1000 bp	Q30 base fraction	coverage depth	fraction majority species	single-copy orthologs	duplicated orthologs
<input type="text" value="All"/>								
21-0247762-001-01	Salmonella enterica	4728813	37	0.90	78.3	1.00	0.99	0.00
21-0252809-001-01	Salmonella enterica	9501539	102	0.90	44.4	0.51	0.14	0.80
21-0272167-001-01	Salmonella enterica	4868637	44	0.90	72.6	0.98	0.99	0.00
21-0281461-001-01	Salmonella enterica	4814437	43	0.90	96.0	1.00	0.99	0.00
21-0295546-001-01	Salmonella enterica	4942762	53	0.91	96.6	1.00	0.99	0.00
21-0299976-001-01	Salmonella enterica	4776687	25	0.89	62.6	1.00	0.99	0.00
21-0299978-001-01	Salmonella enterica	4796020	38	0.89	76.5	1.00	0.99	0.00

### AQUAMIS: Assembly

AQUAMIS report ist in Produktion   
kraken

#### Assembly report for run results

Overview Short summary table Detailed assembly table Detailed trimming table **Kraken2 results** Plots per run Plots per sample Program versions/ log Help

Three most abundant species according to read-based taxonomic classification with kraken2 and abundance estimation with braken based on the kraken2 minikraken database.

Copy Print Download Column visibility Show **10** entries

Sample	hit1_name	hit1_abundance	hit2_name	hit2_abundance	hit3_name	hit3_abundance
All	All	All	All	All	All	All
21-0247762-001-01	Salmonella enterica	0.99882	Escherichia coli	0.00051	Klebsiella pneumoniae	0.00009
21-0252809-001-01	Salmonella enterica	0.51043	Citrobacter amalonaticus	0.19509	Citrobacter sp. 86	0.0722
21-0272167-001-01	Salmonella enterica	0.98135	Escherichia coli	0.0178	Salmonella phage 118970_sal3	0.00011
21-0281461-001-01	Salmonella enterica	0.99866	Escherichia coli	0.00077	Klebsiella pneumoniae	0.00008
21-0295546-001-01	Salmonella enterica	0.99781	Escherichia coli	0.00137	Klebsiella pneumoniae	0.0001
21-0299976-001-01	Salmonella enterica	0.99789	Escherichia coli	0.00137	Klebsiella pneumoniae	0.00011
21-0299978-001-01	Salmonella enterica	0.99813	Escherichia coli	0.00109	Klebsiella pneumoniae	0.00011

### BakCharak: Typisierung

[Summary table](#)
[Overview of resistance genes](#)
[Overview of plasmidfinder marker genes](#)
[Overview of virulence genes](#)
[List of resistance genes](#)
[List of plasmid markers](#)
[List of virulence genes](#)
[Extra reports for species Salmonella](#)
[Data files](#)
[Database info](#)

The database table is searchable and sortable.

Show  entries

Sample	Details	MLST_ST	MLST_Formula_short	mash_serovar	serovar	serovar_cgmlst	count_resgenes	resgenes
<input type="text" value="04-05621"/>	<input type="text" value="Details"/>	<input type="text" value="39"/>	<input type="text" value="All"/>					
04-05621	<a href="#">Details</a>	39	19;20;3;20;5;2;22	Derby	Derby	Derby	1	446864678 WP_000941934NA1 NG_054942 1 1 fosA7 fosA7_fam thiol_transferase fosfomycin_resistance_glutathione_transferase_FosA7
07-01167	<a href="#">Details</a>	71	39;35;8;36;29;9;36	Derby	Derby	Derby	6	446602081 WP_000679427NA1 NG_048042 1 1 qacEdelta1 qacE_gen efflux quaternary_ammonium_compound_efflux_SMR_transporter_QacI_resistant_dihydrofolate_reductase_DfrA10;447180584 WP_001257840.1 NG_051907 1 1 tet(G) tet(G) efflux tetracycline_efflux_MFS_transporter_la_family_aminoglycoside_nucleotidyltransferase_AadA2;487652940 WP_001747811.1 NG_047861 1 1 floR floR efflux chloramphenicol/florfenicol blaPSE hydrolase PSE_family_carbenicillin-hydrolyzing_class_A_beta-lactamase_CARB-2
07-02601	<a href="#">Details</a>	774	224;20;3;20;5;2;22	Derby	Derby	Derby	4	1391852856 WP_109545041NA1 NG_056002 1 1 aph(3'')-Ib aph(3'')-Ib phosphotransferase aminoglycoside_O-phosphotransferase_APH(3'')-Ib phosphotransferase aminoglycoside_O-phosphotransferase_APH(6)-Ic;446864678 WP_000941934.1 NG_054942 1 1 fosA7 fosA7_fam thiol_transferase fosfomycin_resistance_glutathione_transferase_FosA7;545_resistant_class_A_broad-spectrum_beta-lactamase_TEM-40
07-04162	<a href="#">Details</a>	-	19;20;3;20;20;5;22;22	Derby	Derby	Derby	1	446864678 WP_000941934NA1 NG_054942 1 1 fosA7 fosA7_fam thiol_transferase fosfomycin_resistance_glutathione_transferase_FosA7

Typisierung gibt einen ersten Hinweis auf Zusammengehörigkeit der Isolate

alleles which have exact matches (100% DNA identity)  
with previously identified alleles

### ChewieSnake: cgMLST

inferred new alleles using Prodigal CDS predictions

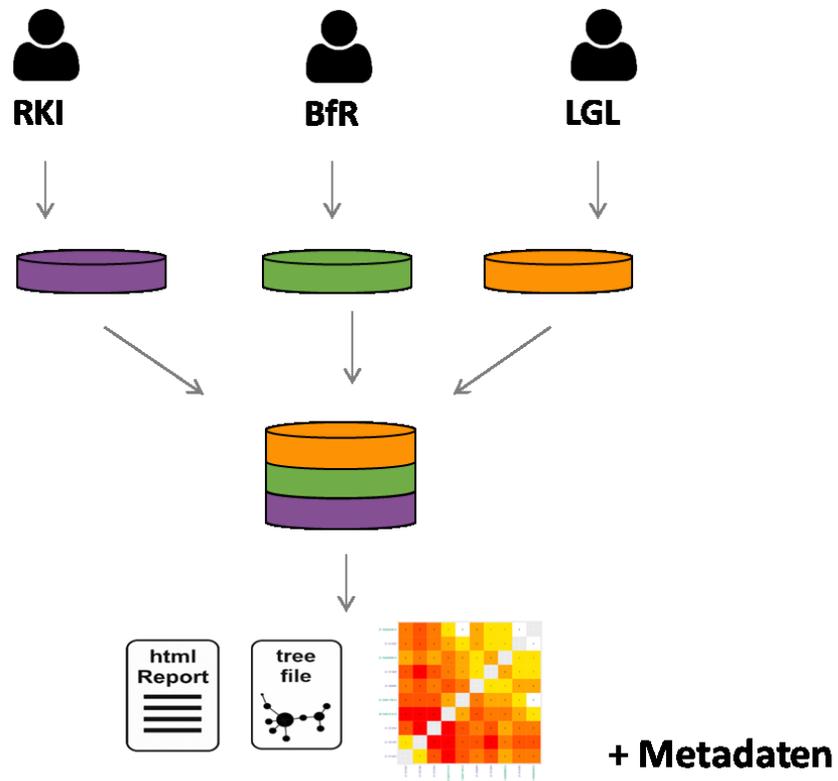
loci not found

Overview | **Allele statistics** | Allele distance table | Allele distance matrix | Clustering | Minimum spanning tree | Links to files | Config and parameters | Help

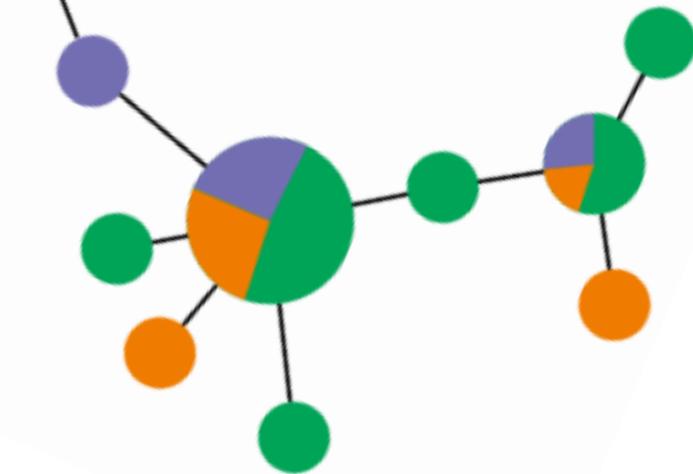
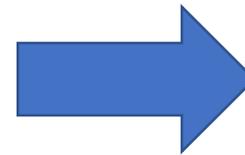
Copy | Print | Download | Column visibility | Show 10 entries

Sample	Fraction of loci found	Fraction of missing loci	EXC	INF	LNF	PLOT	NIPH	ALM	ASM
All	All	All	All	All	All	All	All	All	All
07-04162	0.94	0.06	2832	0	46	0	109	9	4
14-00751	0.98	0.02	2930	0	53	0	7	7	3
12-01254	0.98	0.02	2926	0	46	1	15	9	3
14-00117	0.98	0.02	2927	0	46	0	15	9	3

### Datenzusammenführung und MetaChewie

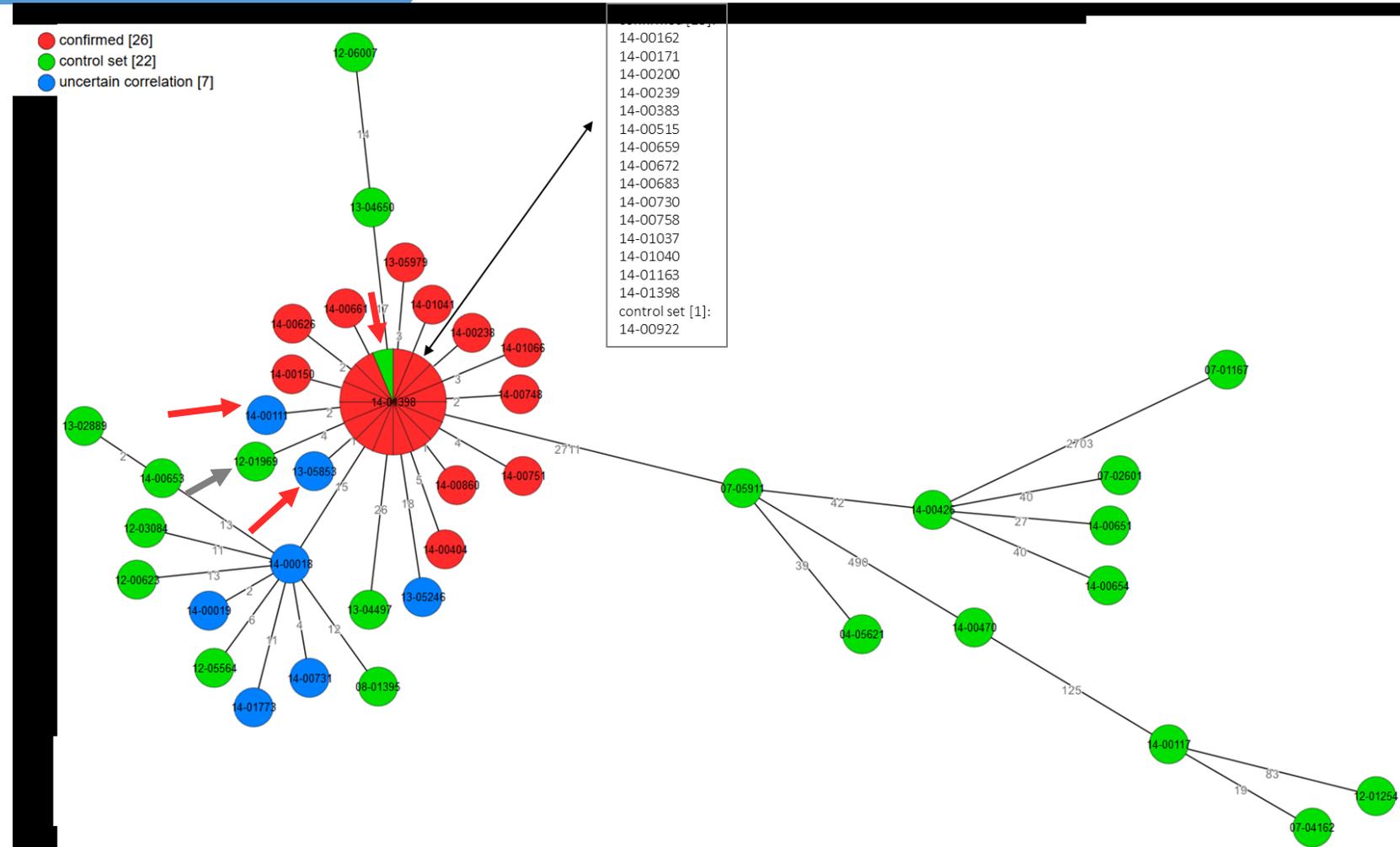


### Minimum Spanning Tree (MST)



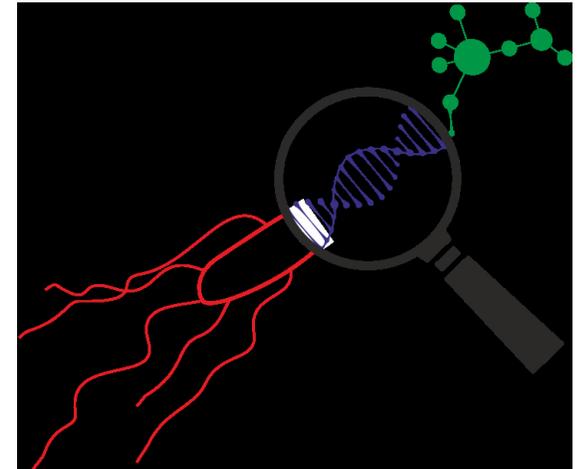
### Clusteranalyse

- bestätigte Ausbruchsstämme (rot, n=26)
  - ✓ clustern zusammen
  - ✓ max. 5 AD
- Stämme mit unsicherer Korrelation zum Ausbruch (blau, n=7)
  - ✓ 2 Stämme gehören zum Ausbruch
  - ✓ max. 2 AD
- Kontroll-Set (grün, n=22)
  - ❖ 2 Kontrollen clustern zu Ausbruchsstämmen
  - ❖ max. 4 AD



### Fazit der Clusteranalyse

- Bundesländerübergreifende Ausbrüche werden erkannt
- Ausbruchsaufklärung mittels Clusteranalyse:
  - ✓ Bestätigung der Ausbruchszugehörigkeit (epidemiologischer Link)
  - ✓ Abklärung der Ausbruchszugehörigkeit (fehlender epidemiologischer Link)
  - ❖ überraschende Ergebnisse (control set)
- Sinnvolle Interpretation nur möglich in Kombination mit Metadaten!



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das allele calling: chewieSnake

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