

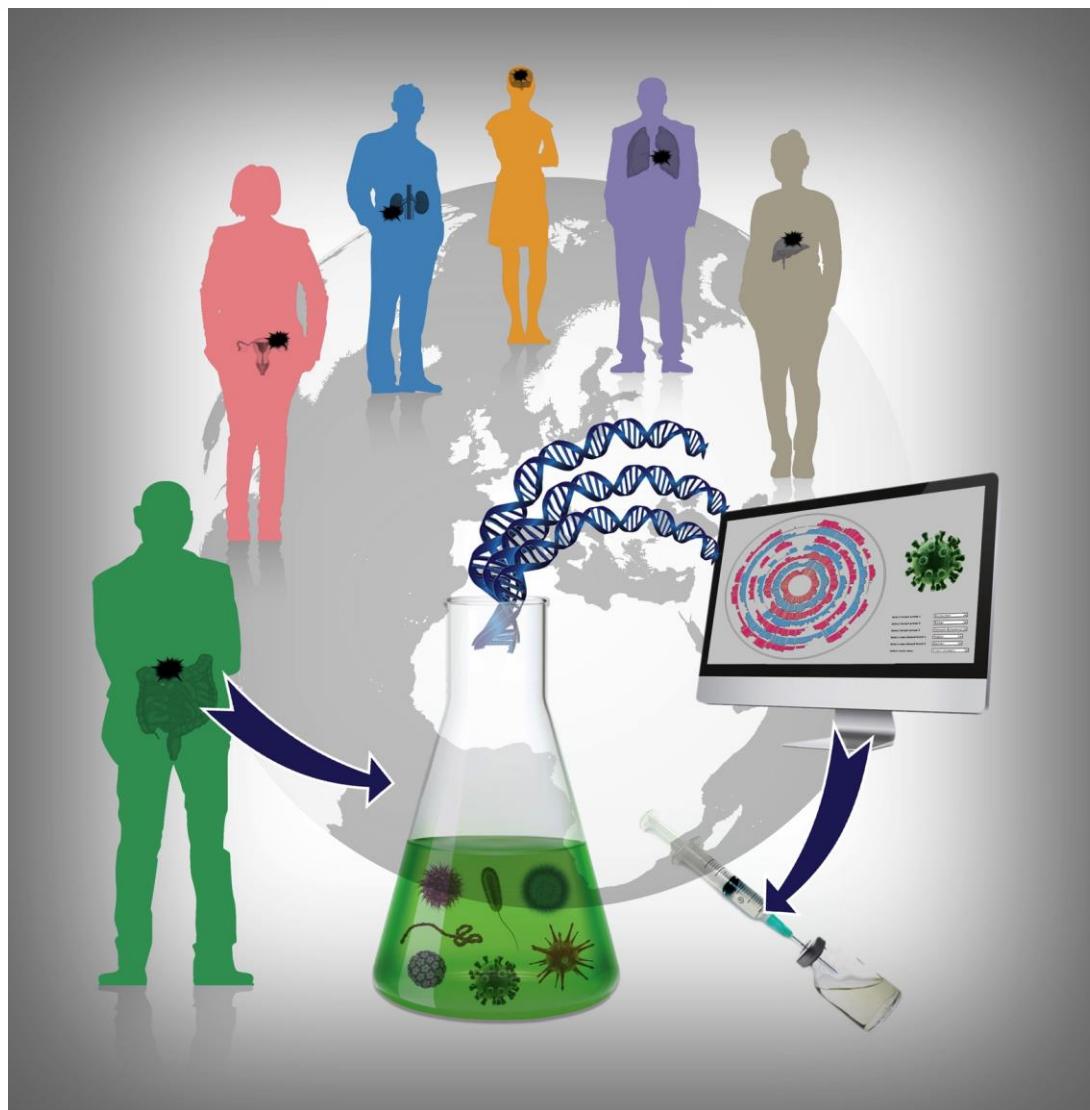


Extensive viral nucleic acid contamination in clinical samples

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Viruses

Need host cell to multiply

Infect animals, plants, algae, fungi, protozoa and bacteria

Host specific

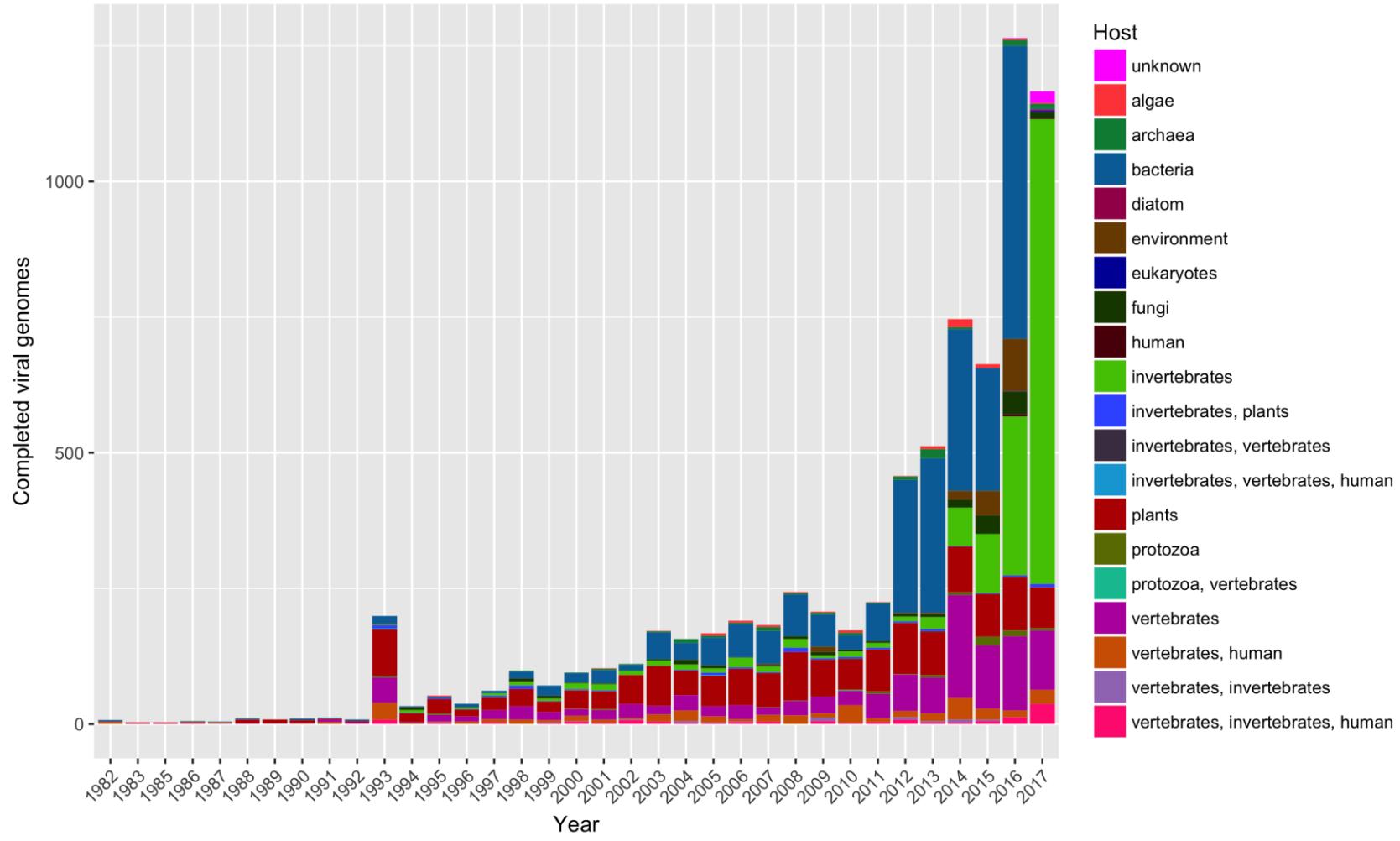


Cause disease/cancer

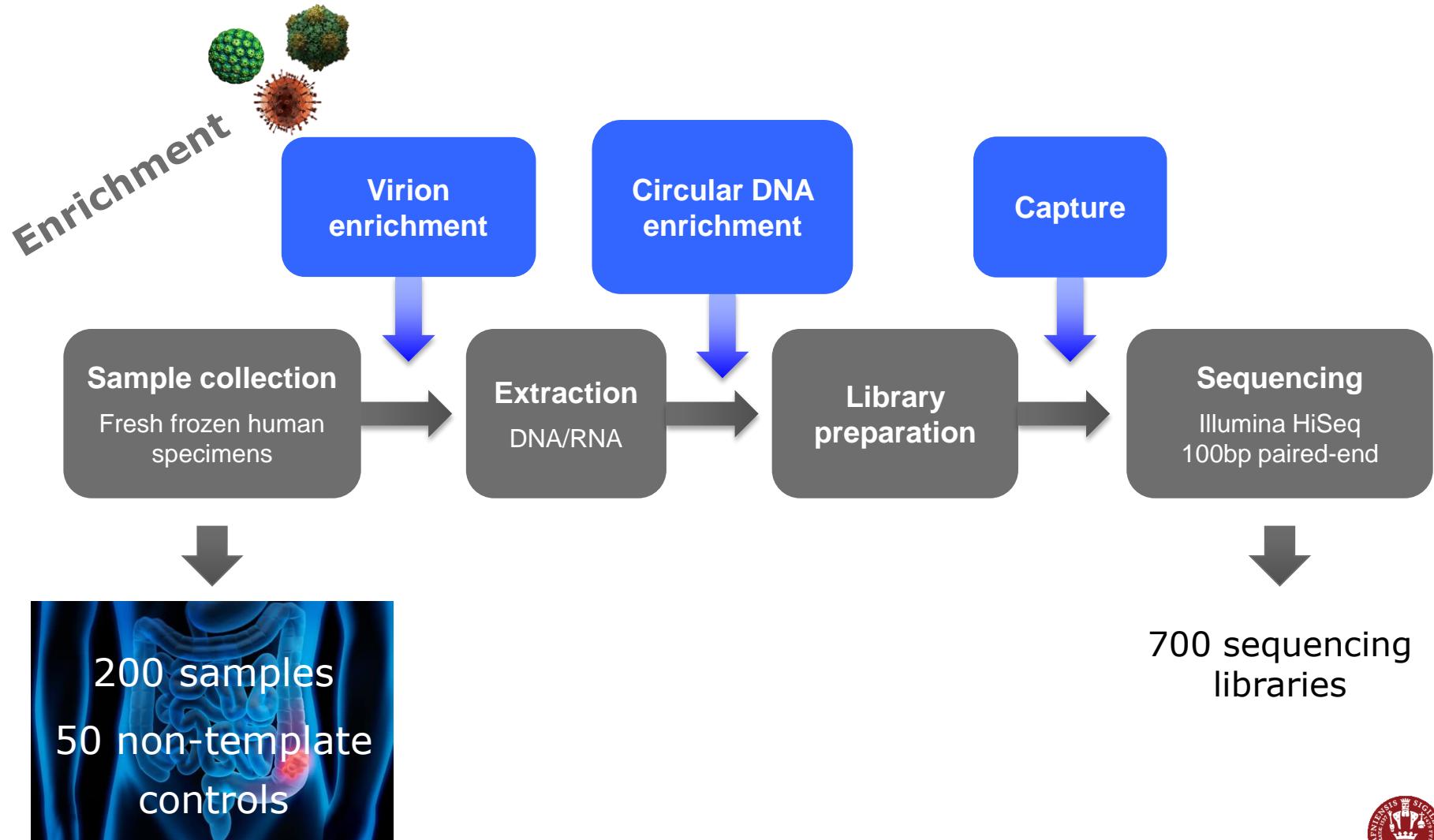


Genetically identifying viruses

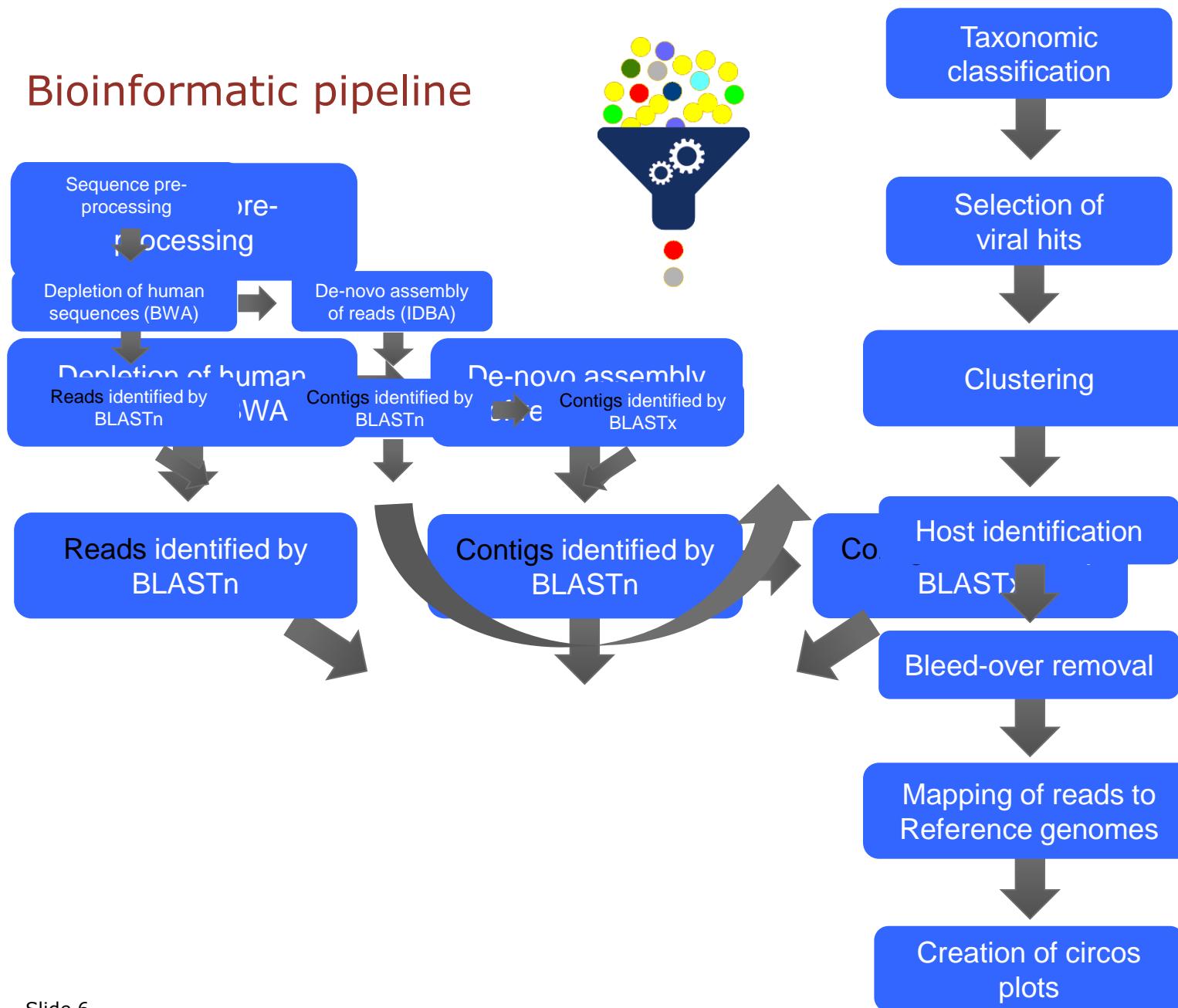
Large part unidentified



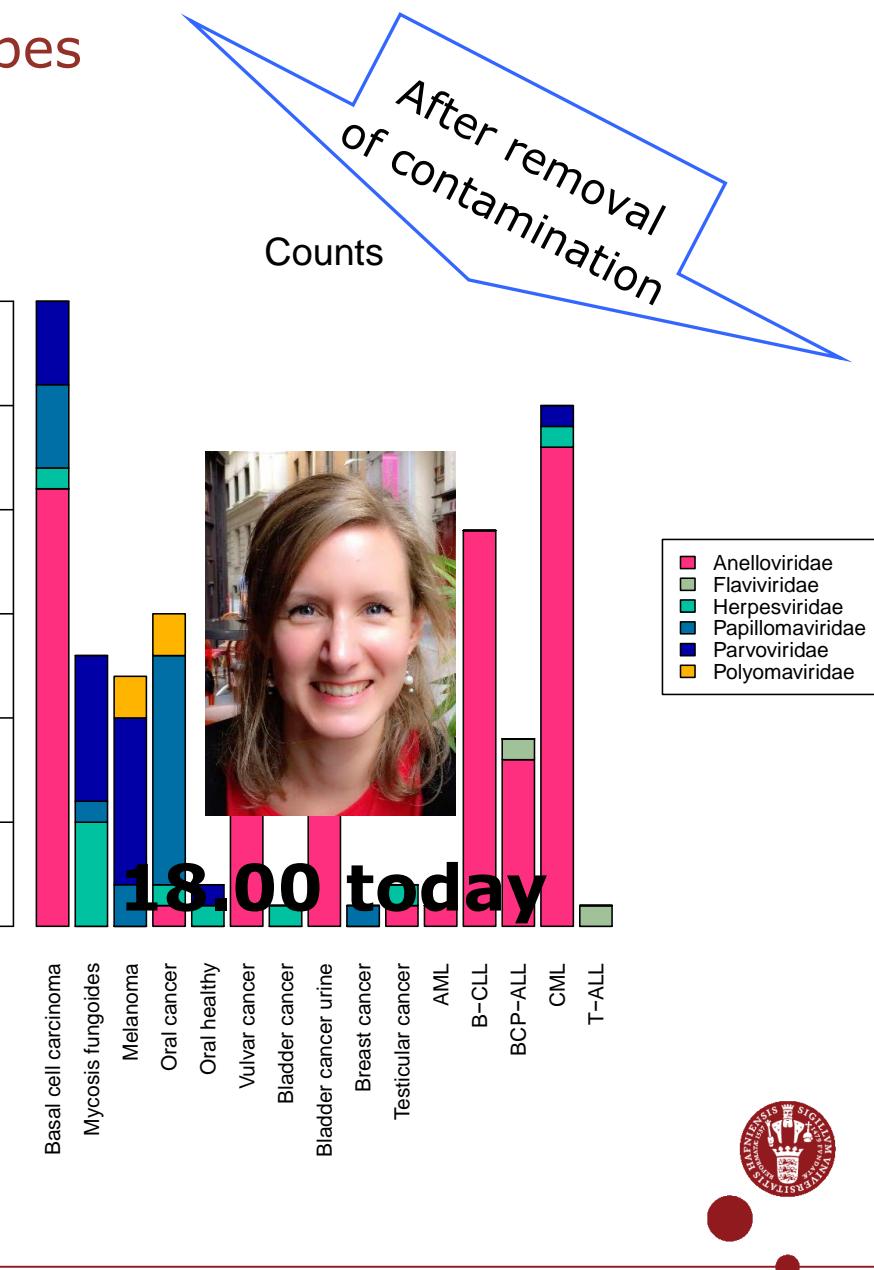
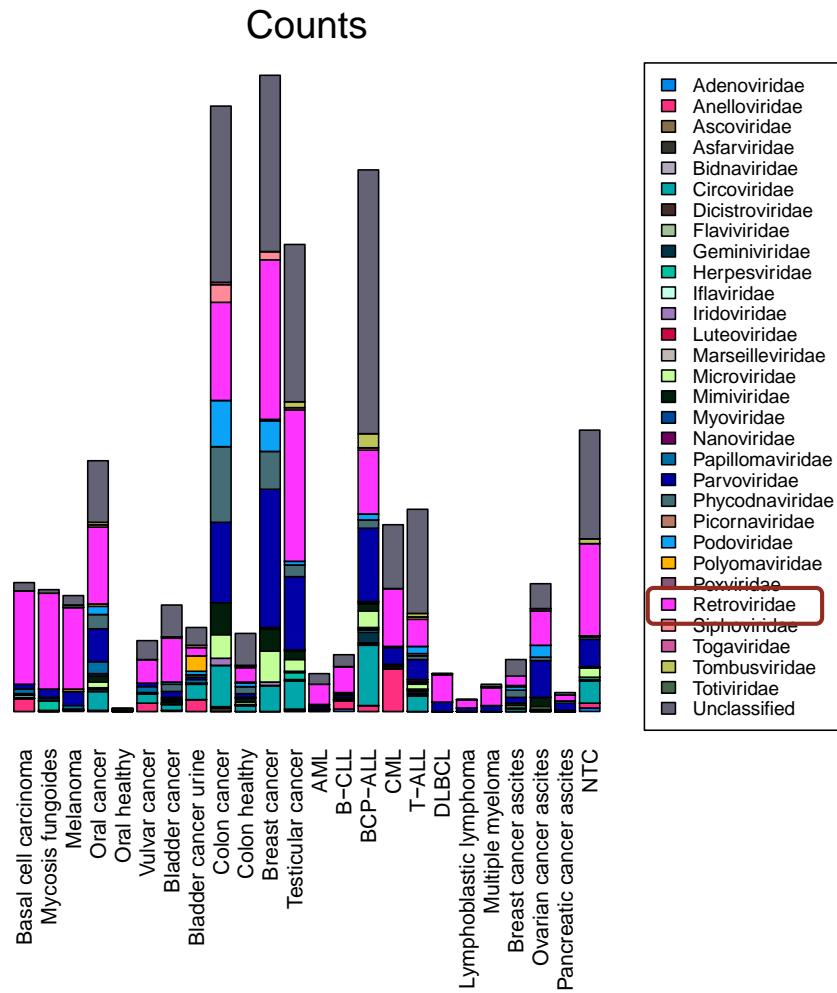
Sample preparation



Bioinformatic pipeline



Viruses detected for cancer types

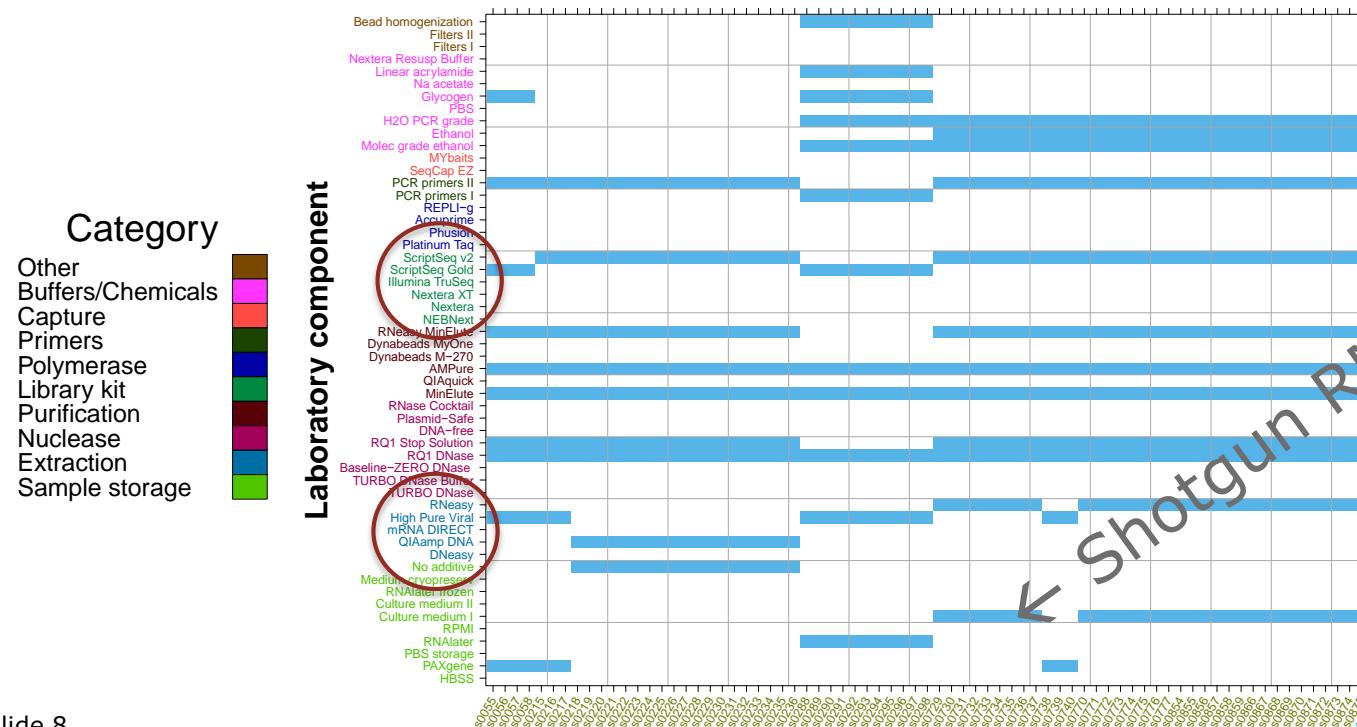


Linking viruses to their source

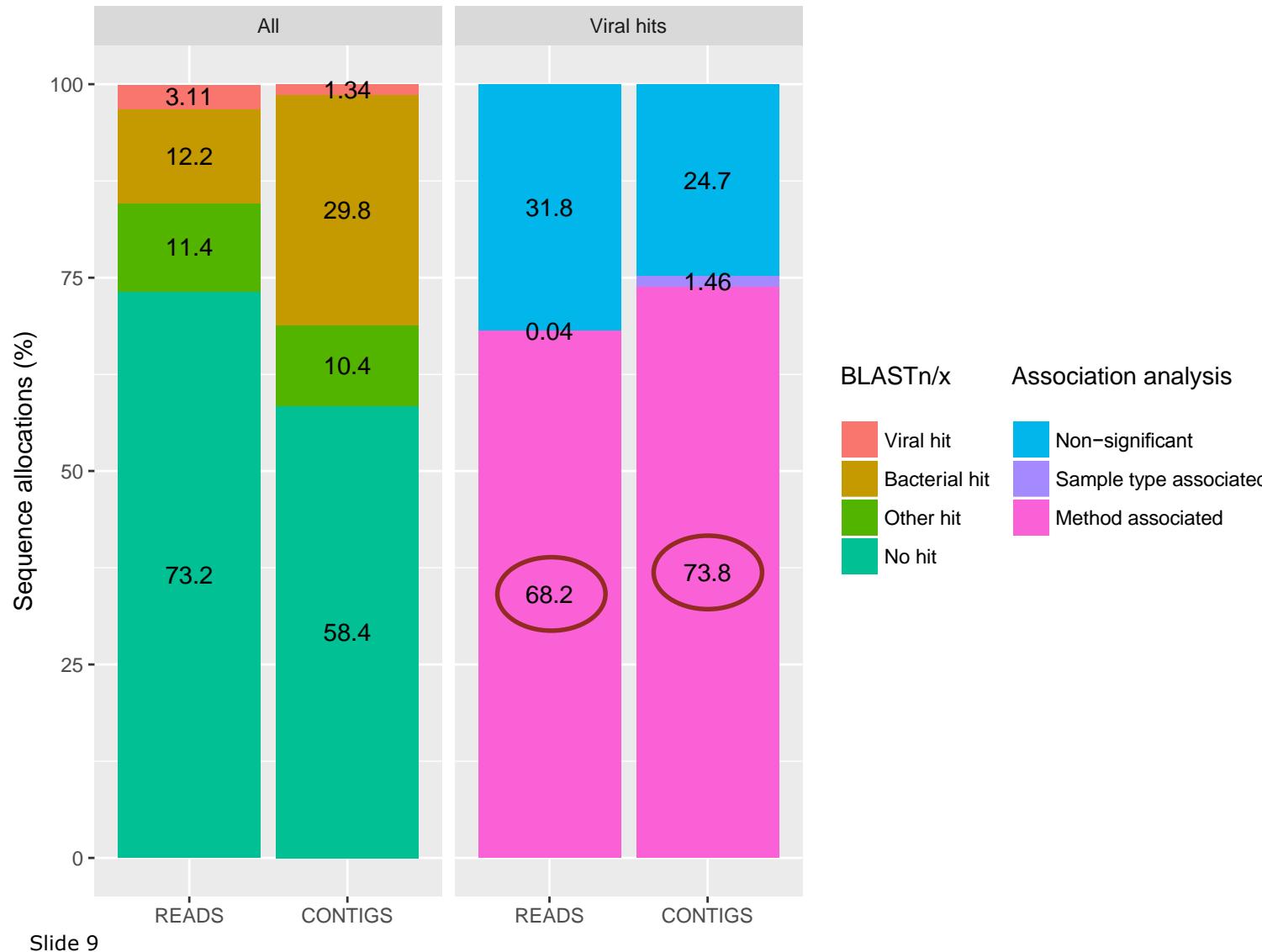
Viral strains identified: 1728 from reads
1252 from contigs

54 laboratory components, 33 tissue types

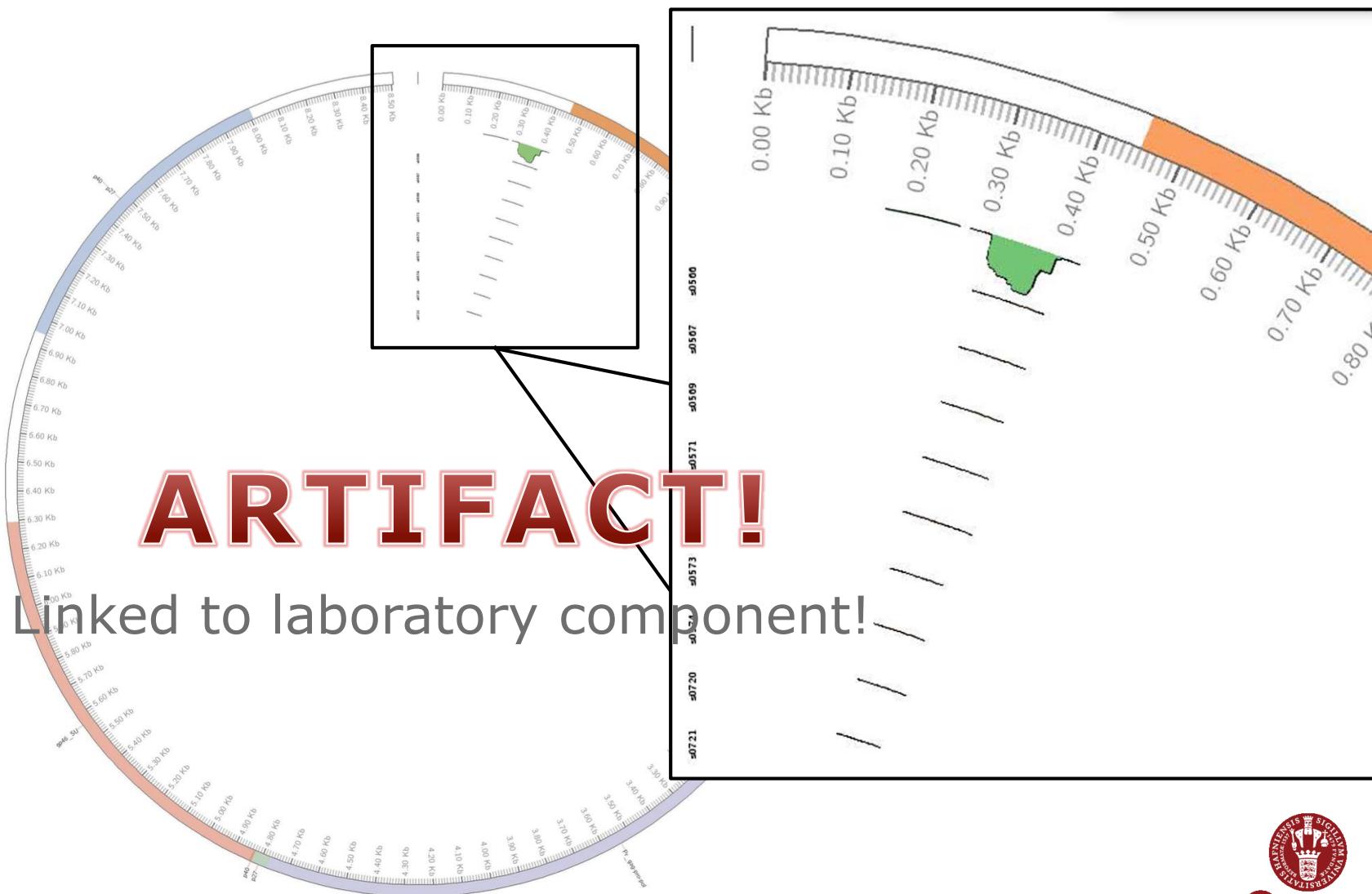
Fisher's exact test – correction multiple comparisons



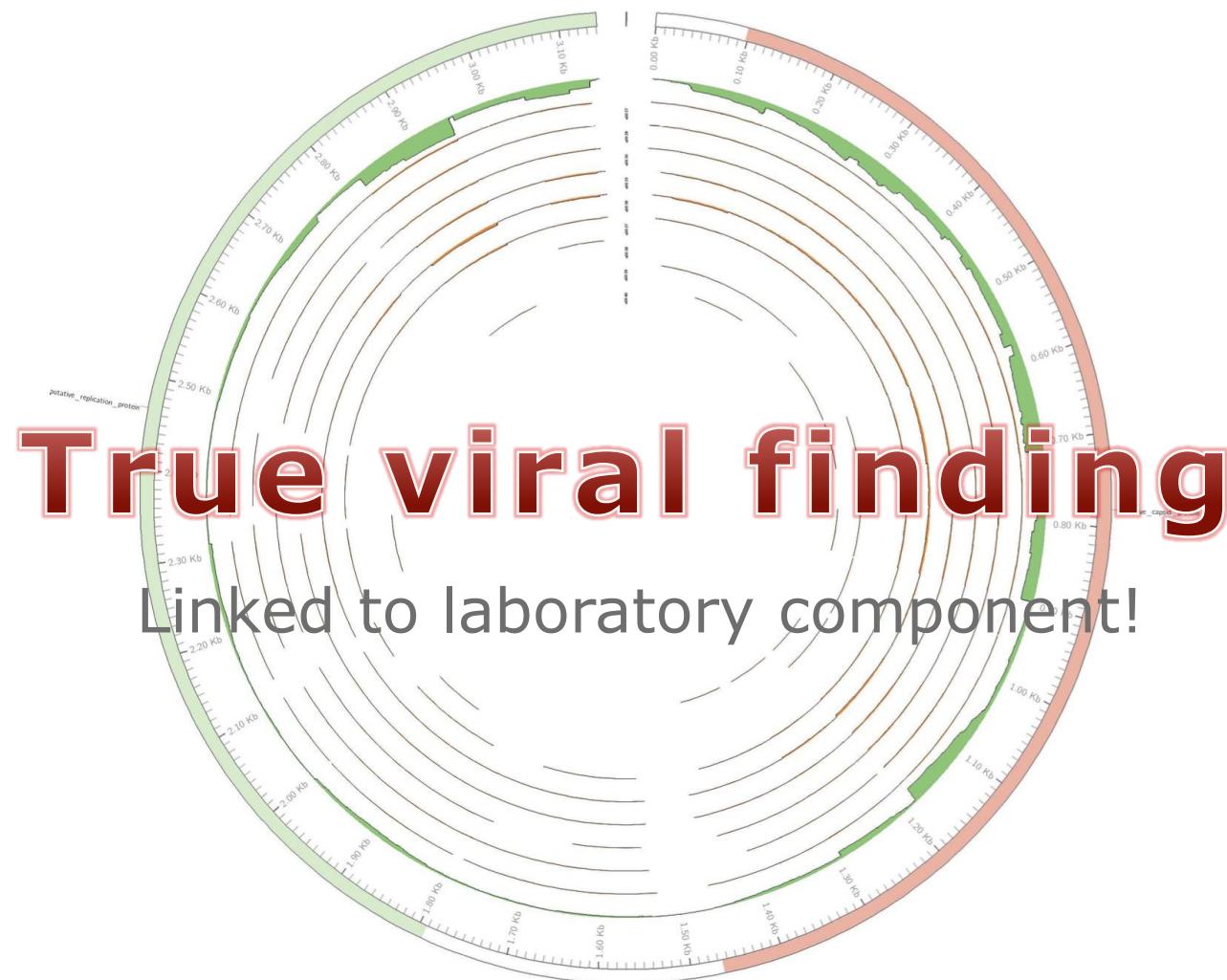
Viral contamination percentage



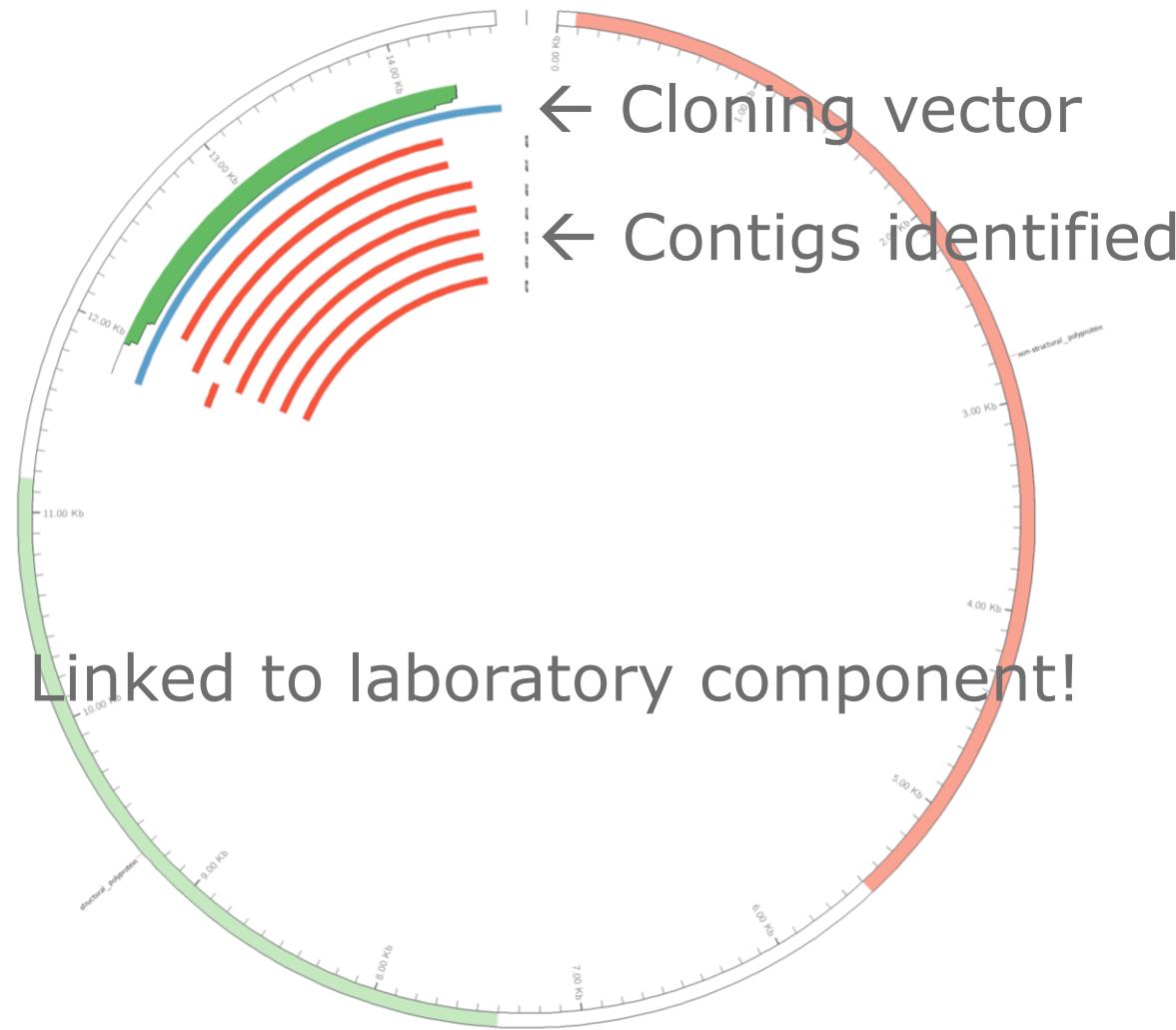
Human T-cell lymphotropic virus



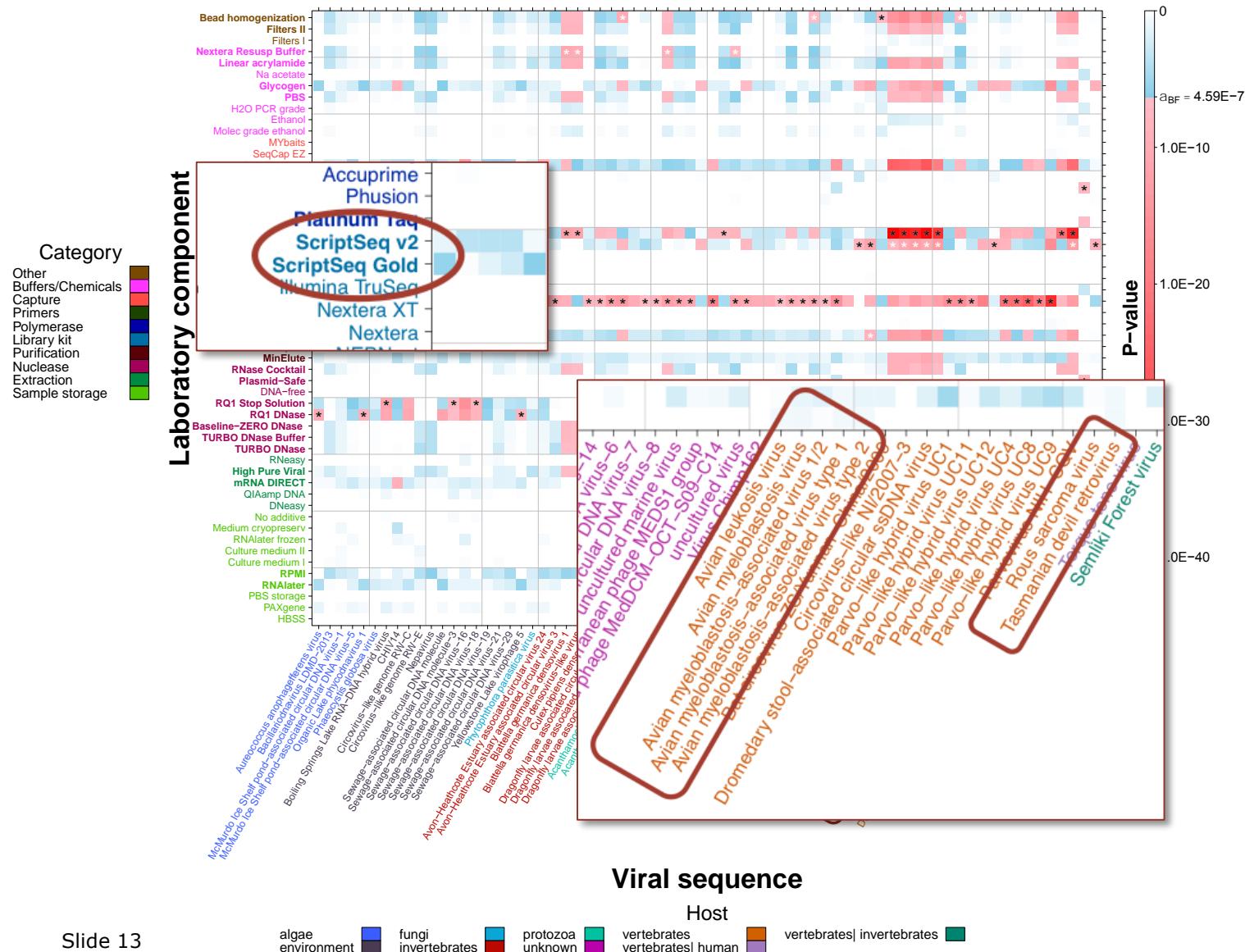
Chimeric virus 14



Semliki Forest virus

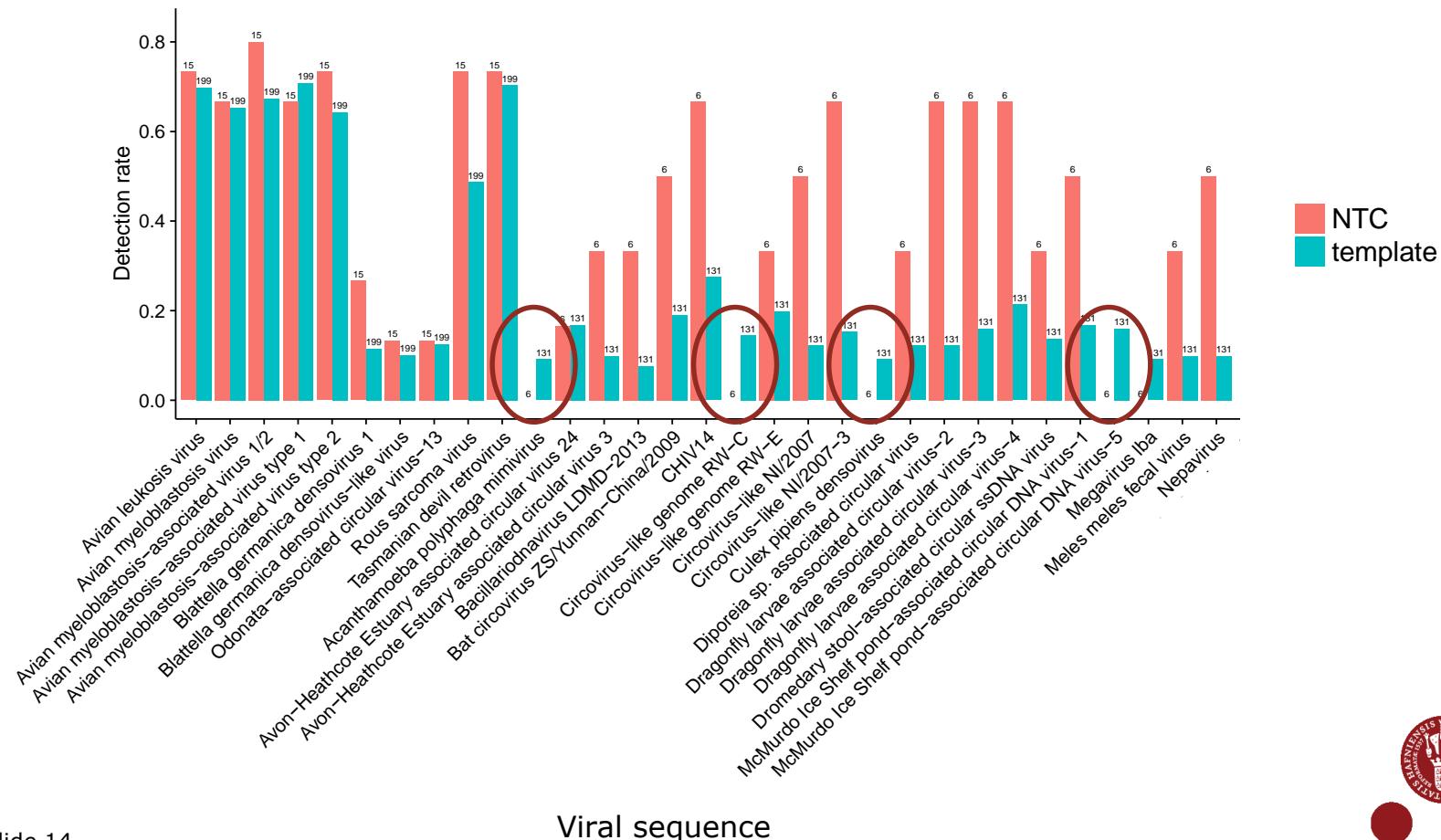


Contaminating viral sequences



Stochastic appearance

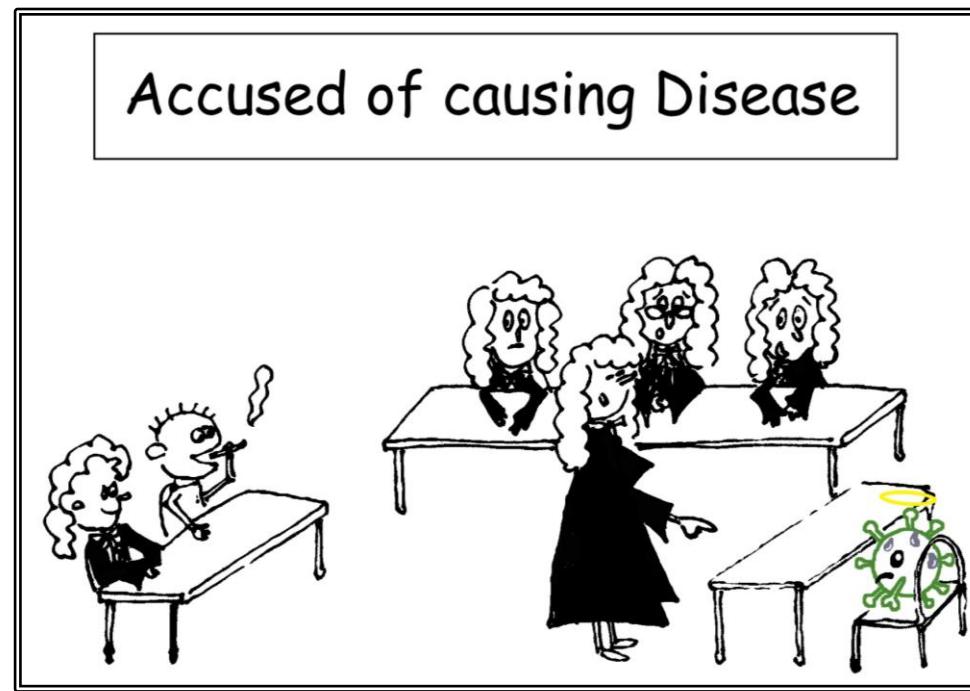
NTC to identify contamination



Conclusions

Contaminating viral sequences from laboratory components is extensive

Viral contamination can be sporadic and not always detected in non-template controls



THANK YOU!

Anders Hansen

Sarah Mollerup

Rós Kjartansdóttir

Thomas Arn Hansen

Tobias Mourier

Helena Fridholm

Lars Nielsen

Txema Gonzalez-Izarzugaza

Jens Friis-Nielsen

Alex Romero Herrera



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