

Global antigenic cartography – publication, ongoing cross H1 and H3 antigenic characterisation

OFFLU SIV Group technical meeting, 19-20 March 2014 University of Minnesota, Minneapolis, USA

WHO Collaborating Center for Modeling, Evolution, and Control of Emerging Infectious Diseases and Centre for Pathogen Evolution, Department of Zoology, University of Cambridge

Questions

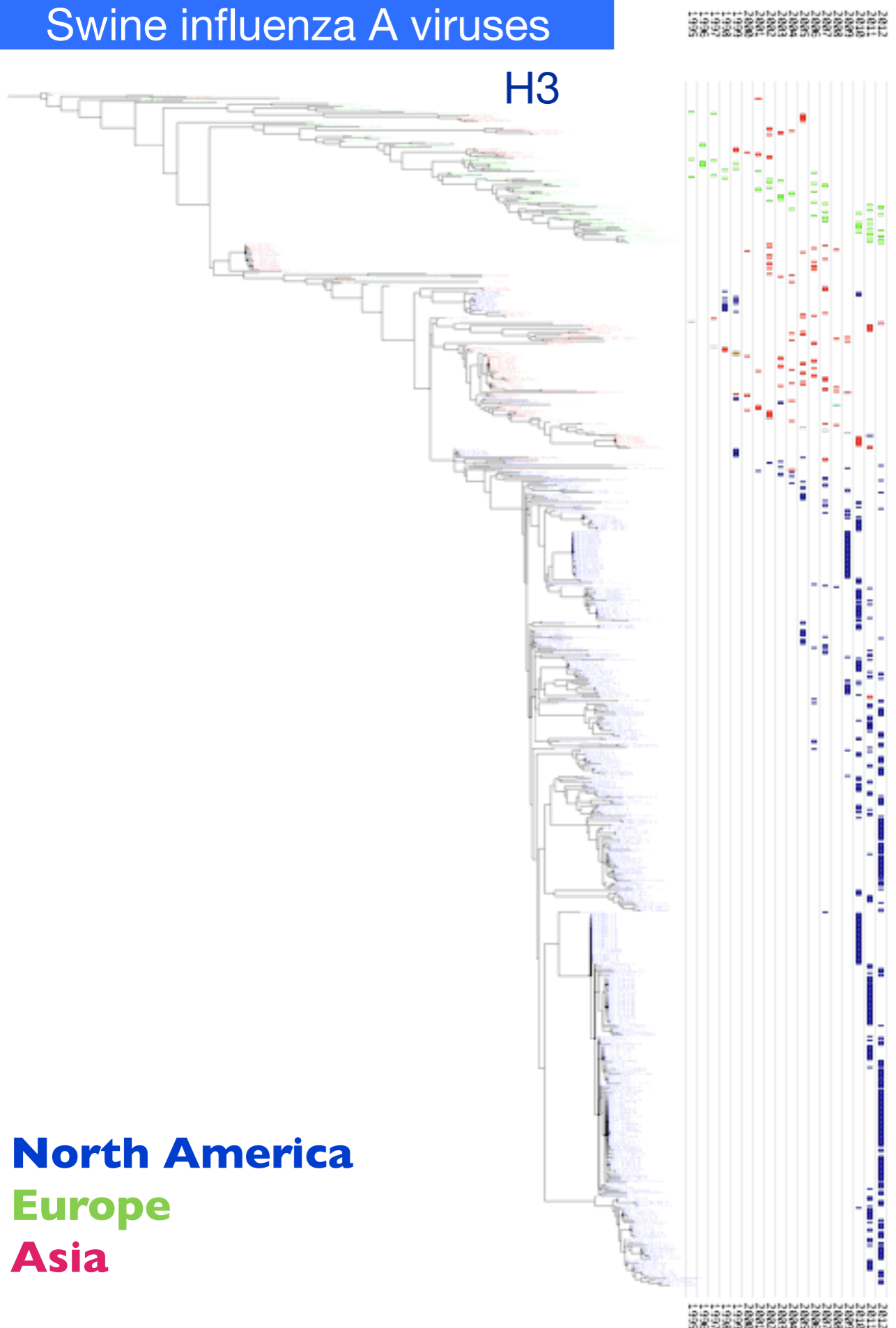
- What are the antigenic relationships among swine influenza H1 and H3 viruses that have circulated in the global pig population and how have they evolved?
- What is the standing antigenic diversity today?
- Geographic distribution and relative antigenic differences among regions?
- Where are viruses circulating in pigs positioned antigenically relative to current and previously circulating human H1 and H3's?

Dataset

- HI assay data, turkey RBC's, swine and ferret sera
- cross-validation experiments to check that swine sera = ferret sera defined antigenic distances for both H1 and H3
- global swine flu data merging achieved by NADC swine serum panel sharing among partners
- Antigenic data: U.S, Canada, EU (numerous countries), Hong Kong (slaughterhouse sampling), Vietnam, Japan + human data
- Genetic data: add Thailand, Australia, Argentina, plus Genbank, plus representative human strains

Swine influenza A viruses

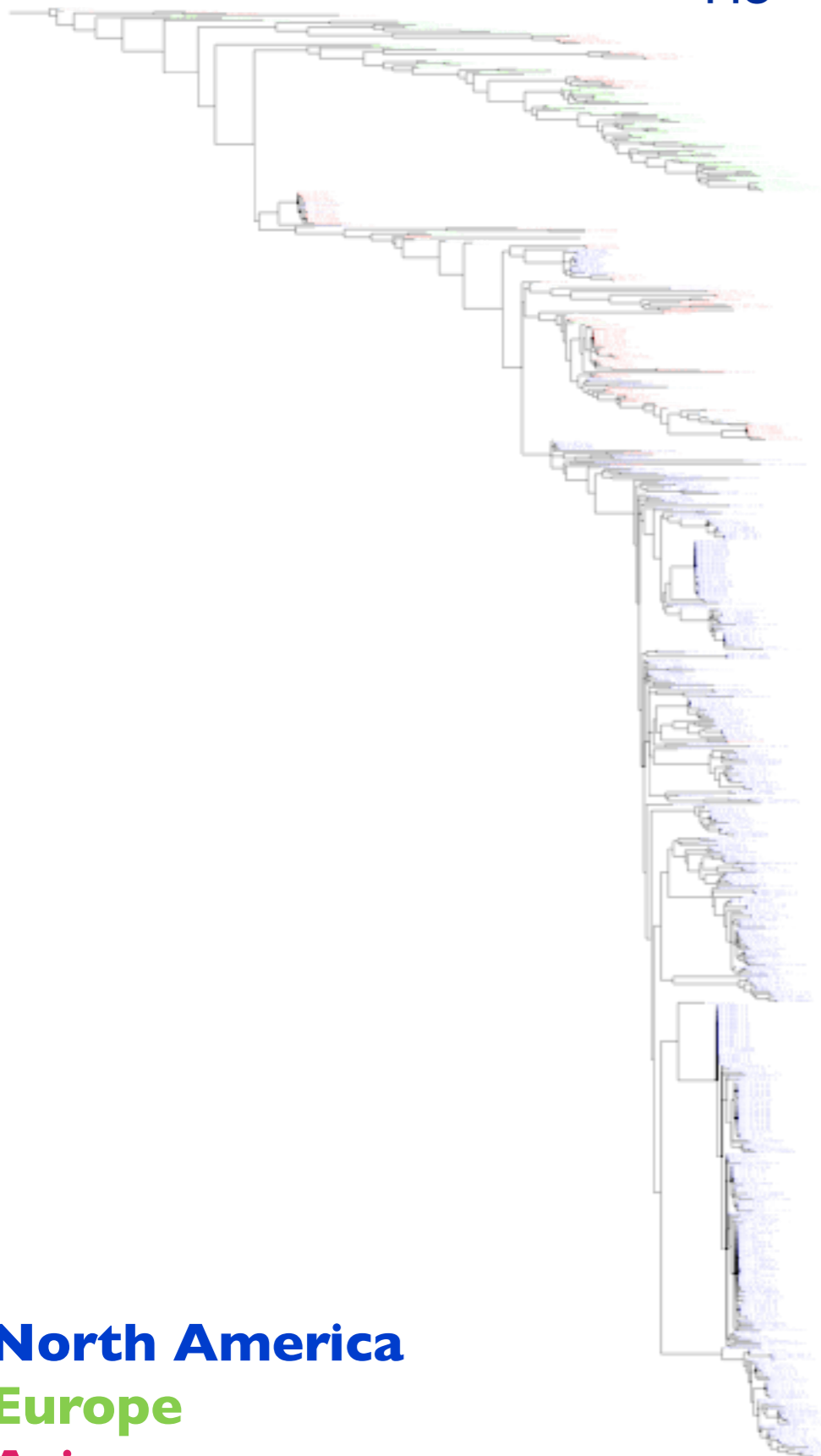
H3



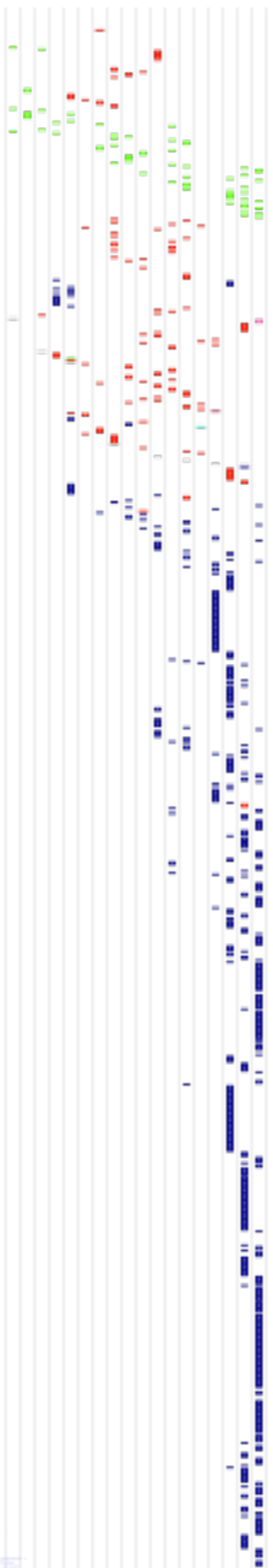
North America
Europe
Asia

Swine influenza A viruses

H3

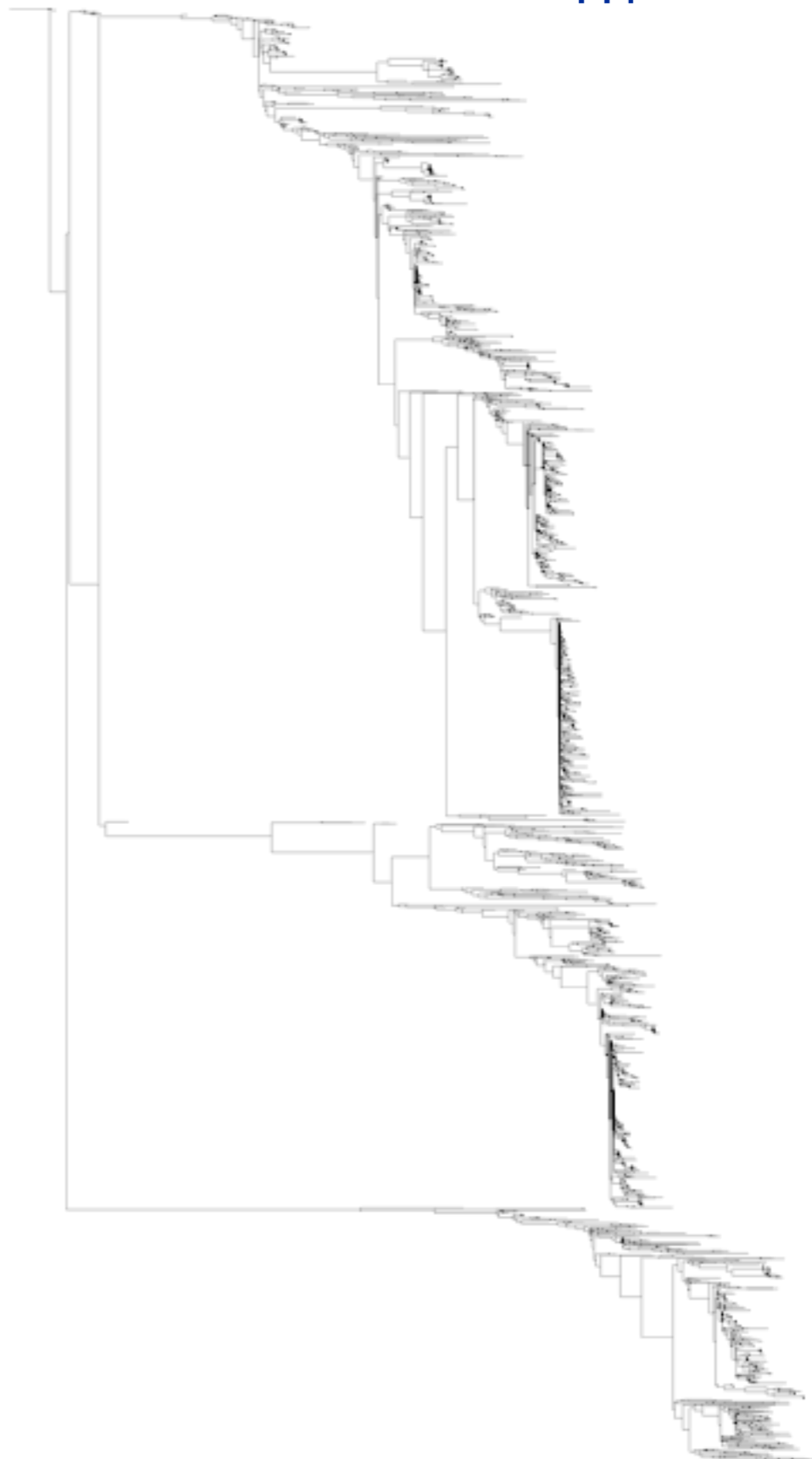


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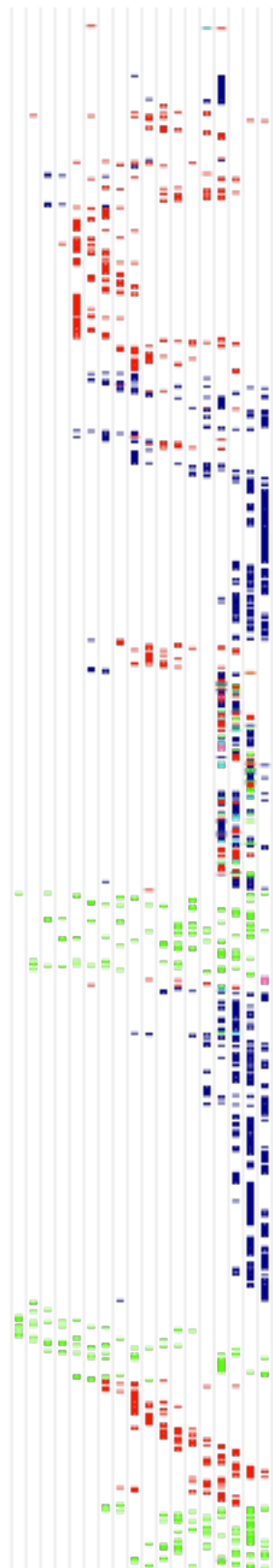


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H1



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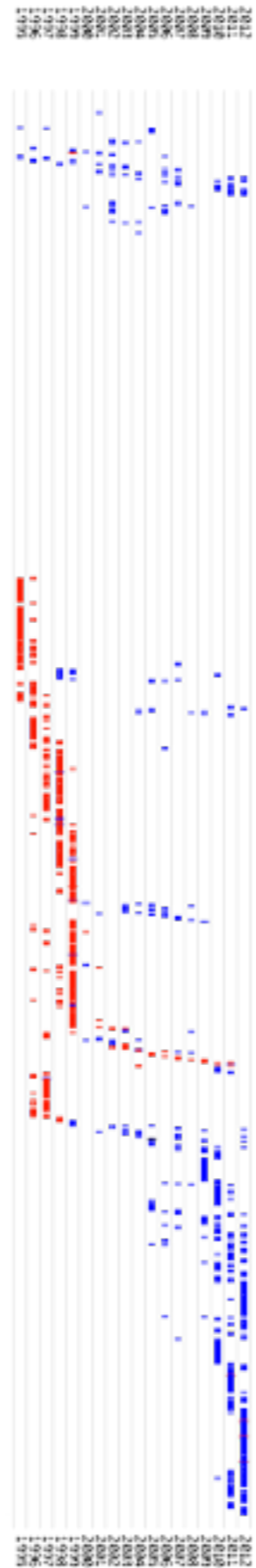
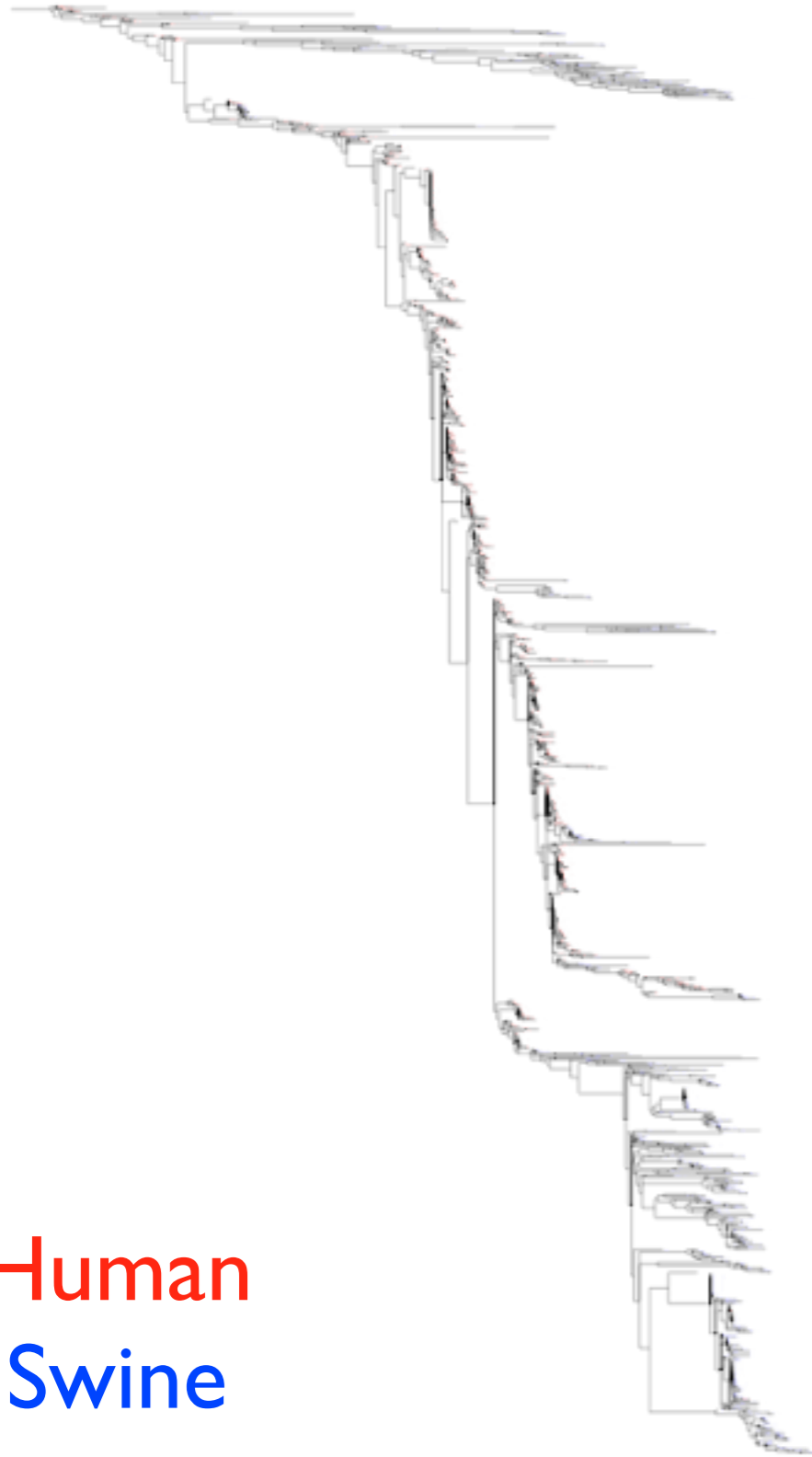


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Human and swine influenza A viruses

H3

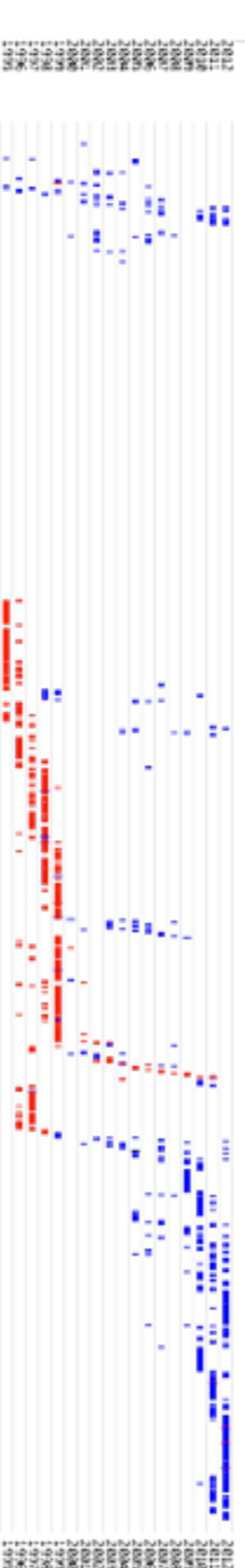


Human
Swine

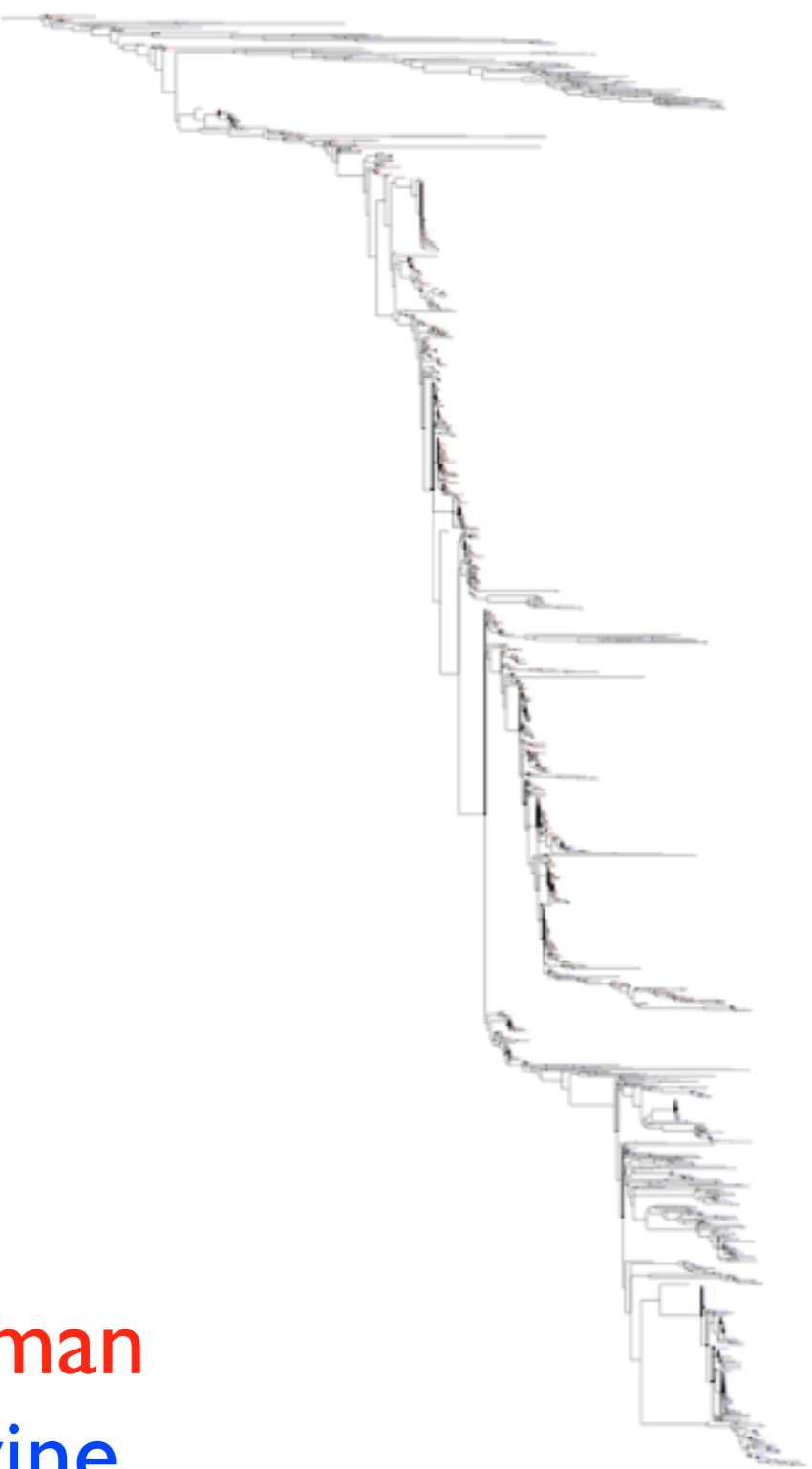
Human and swine influenza A viruses



H1



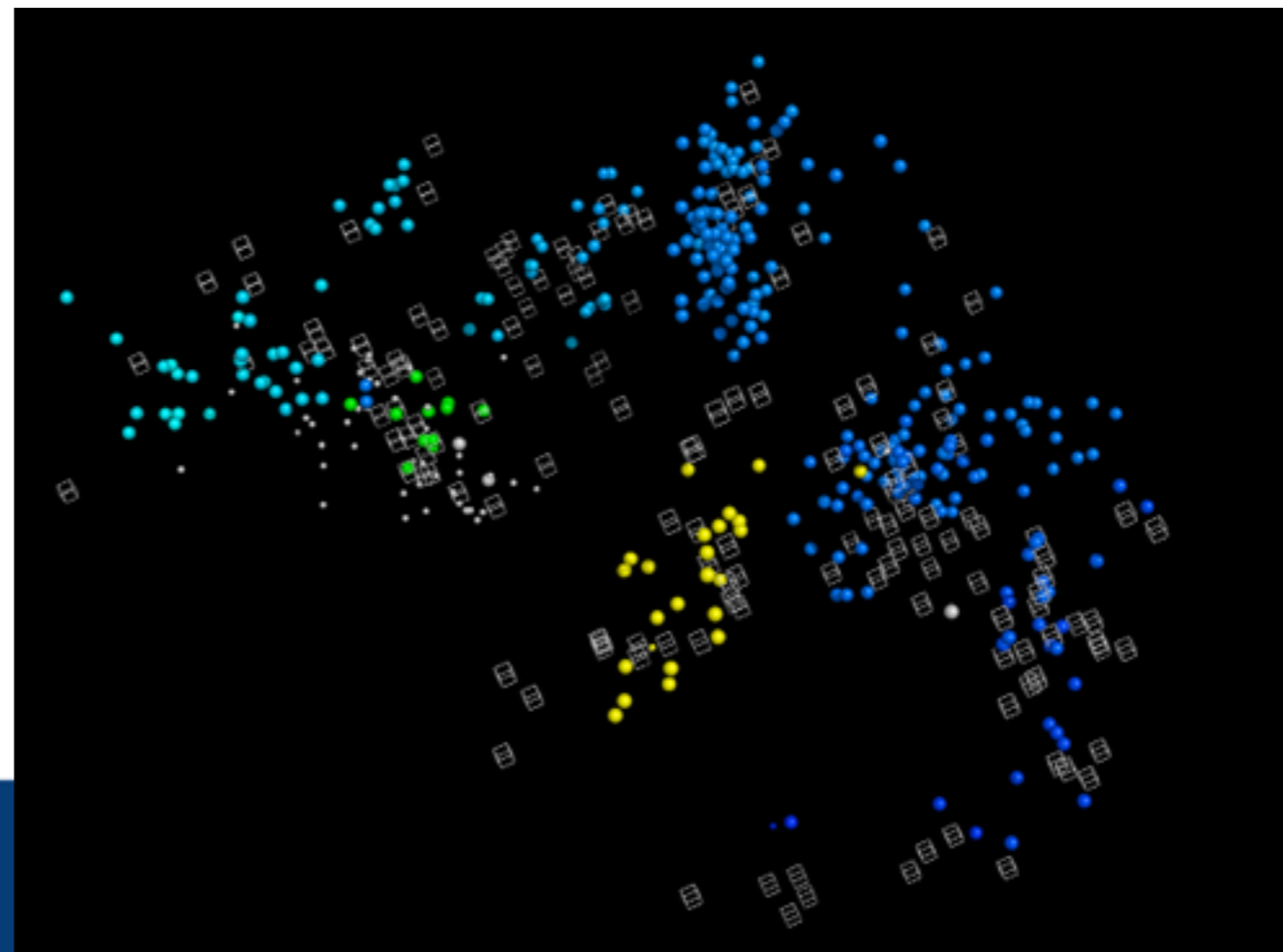
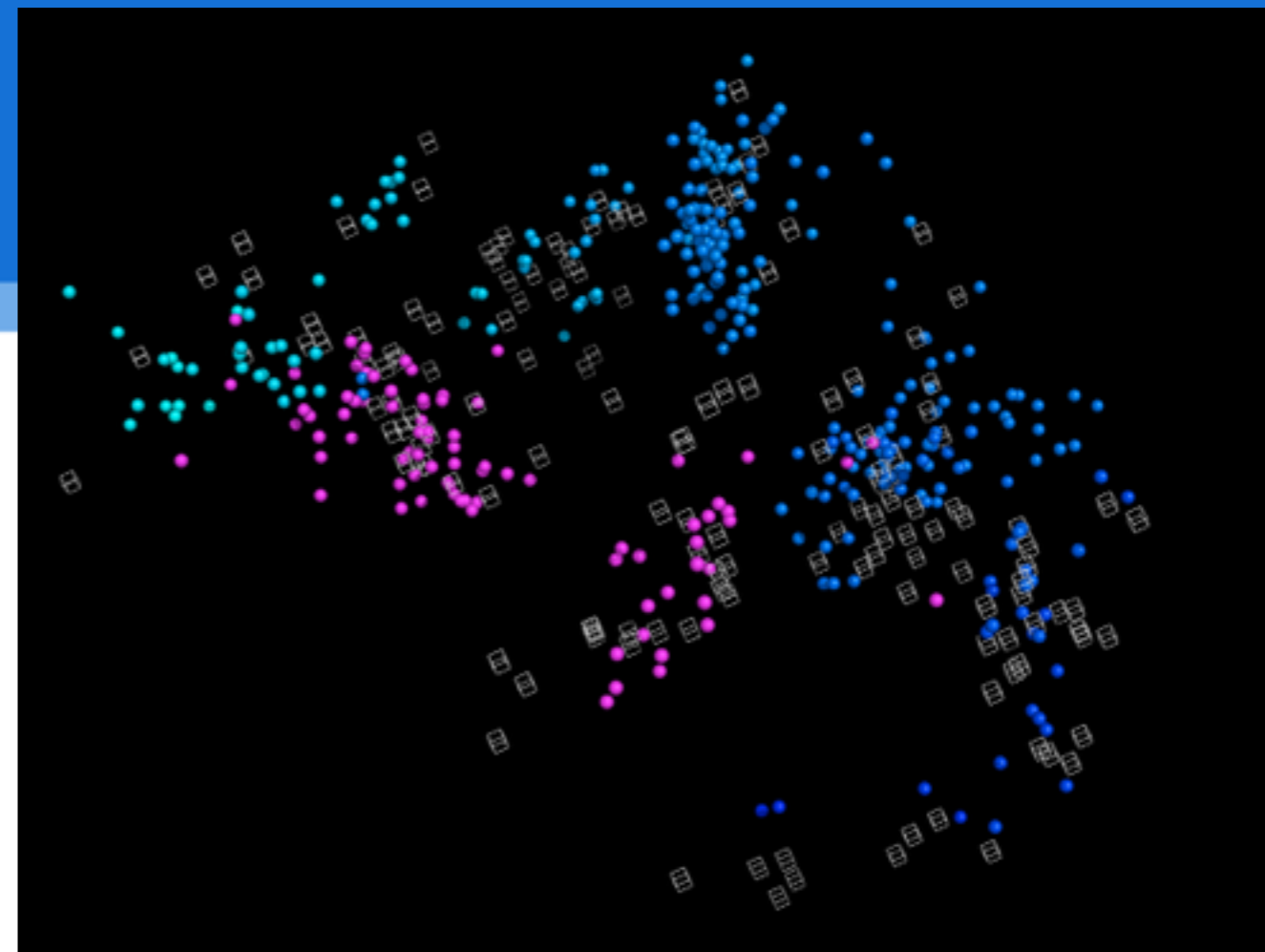
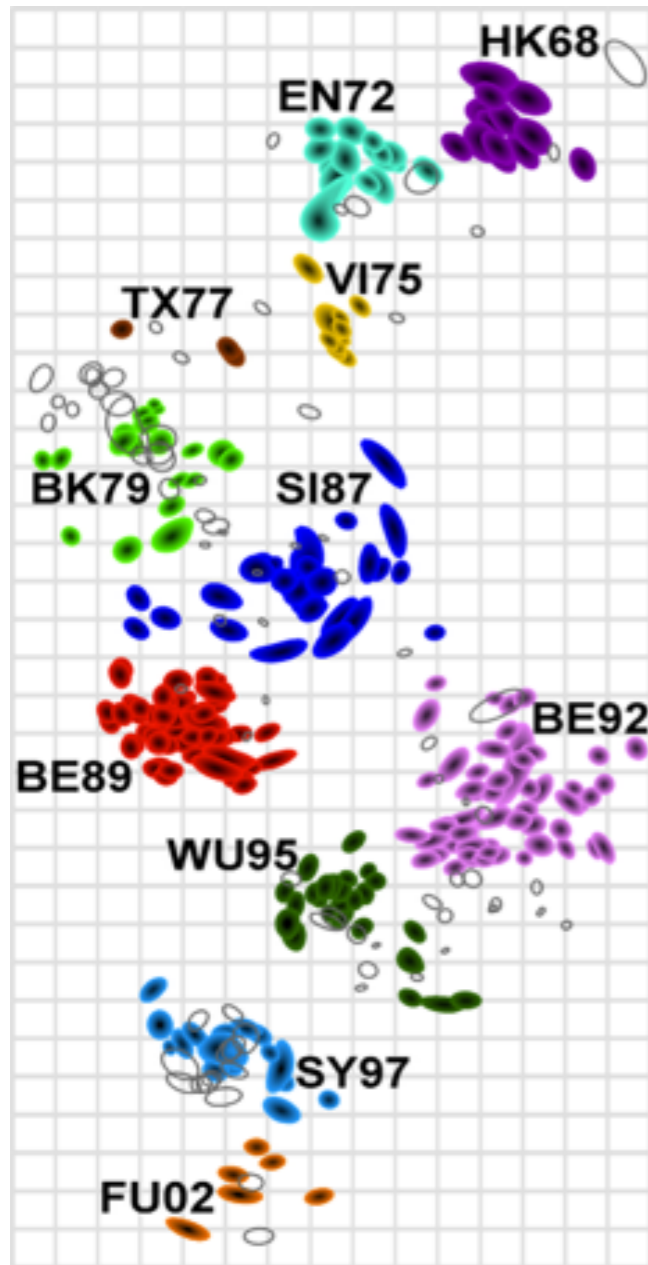
H3



Human
Swine

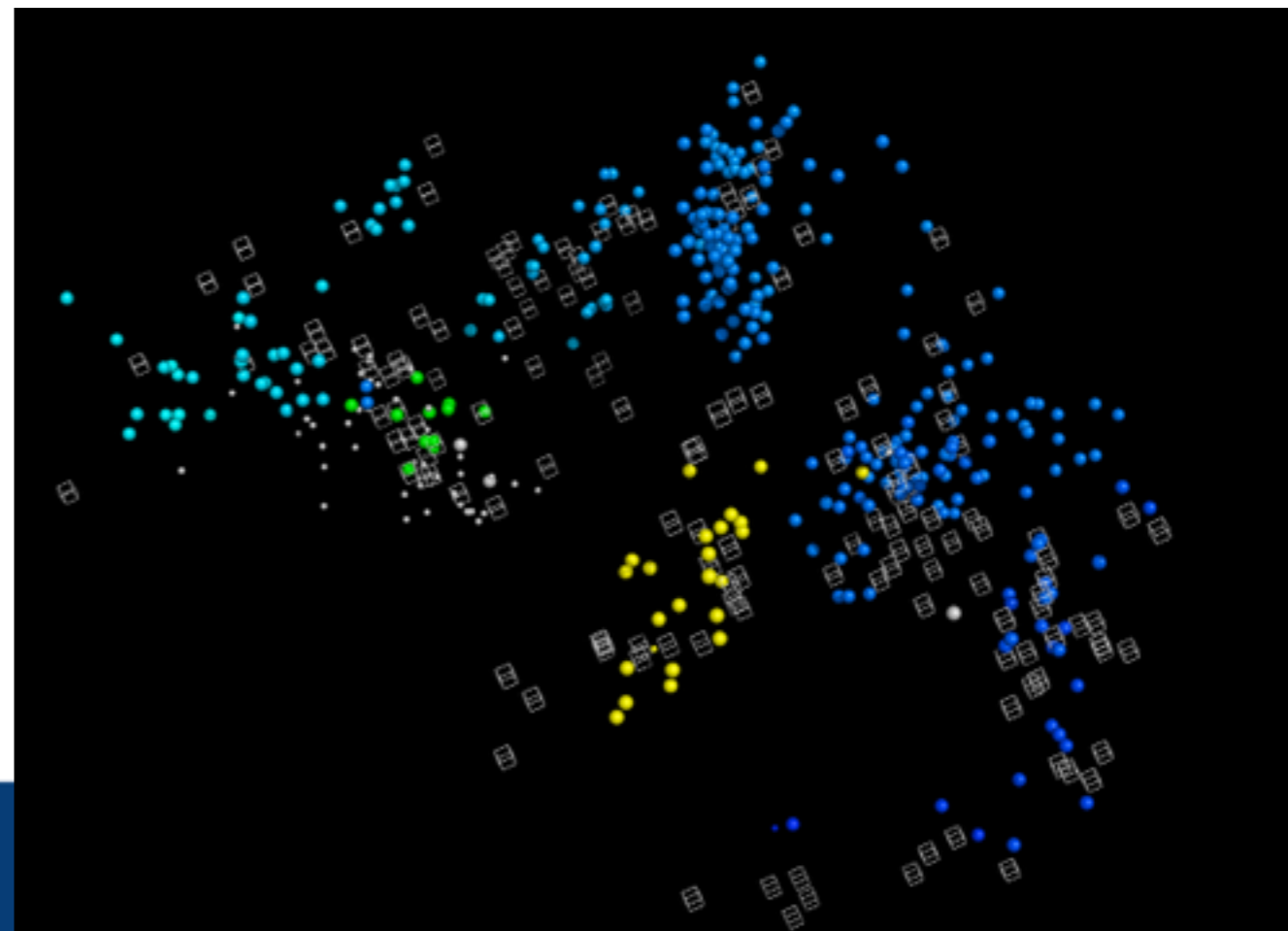
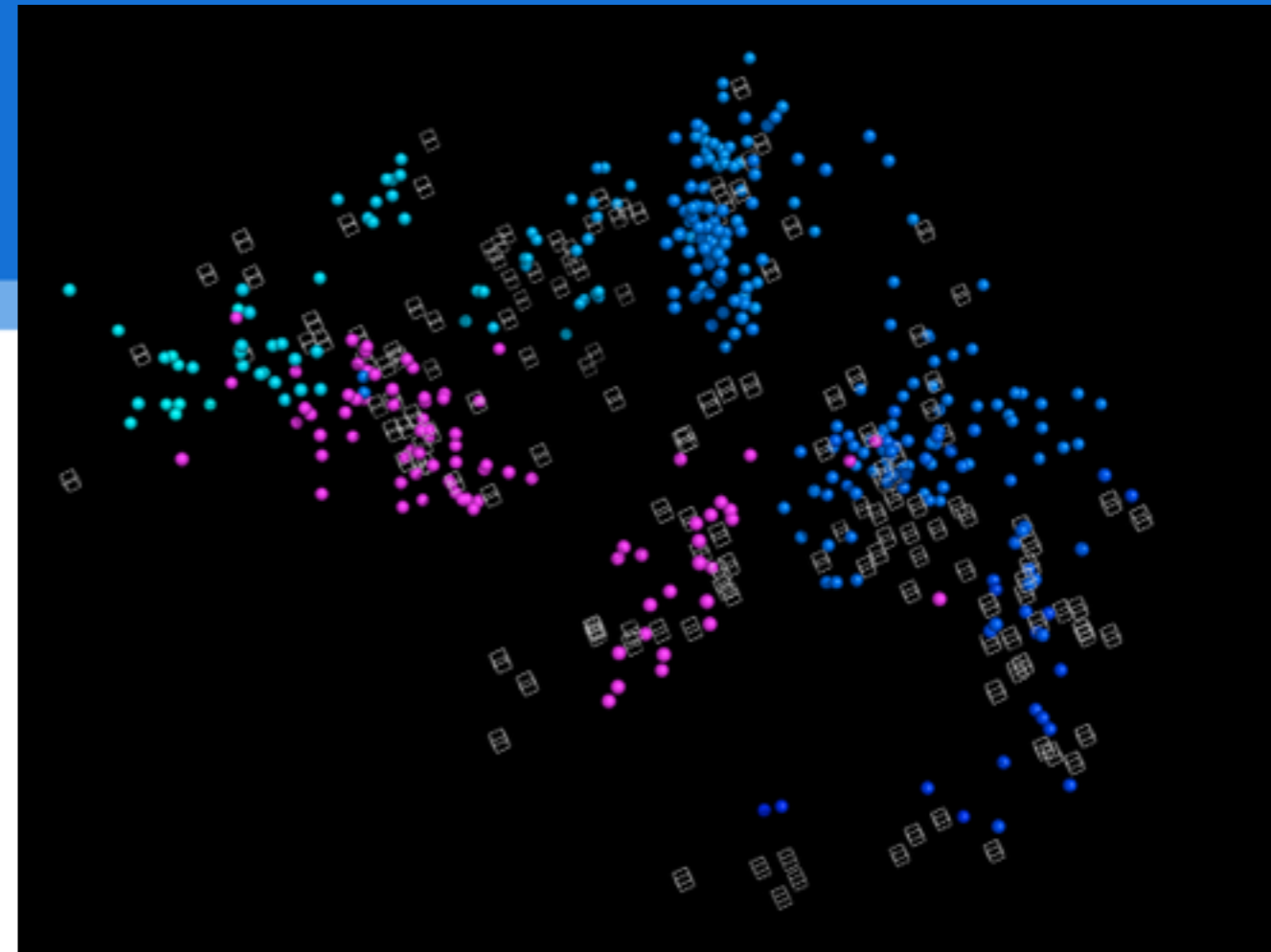
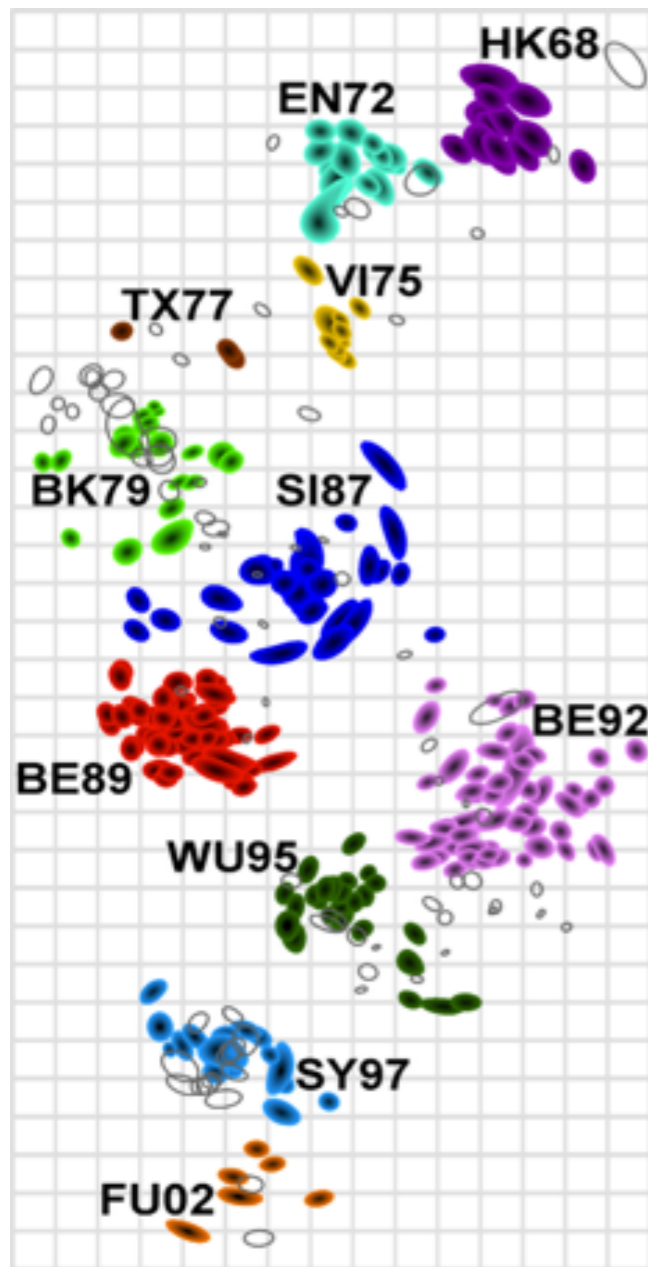
Antigenic characterisation

Methods, dimensions, scale



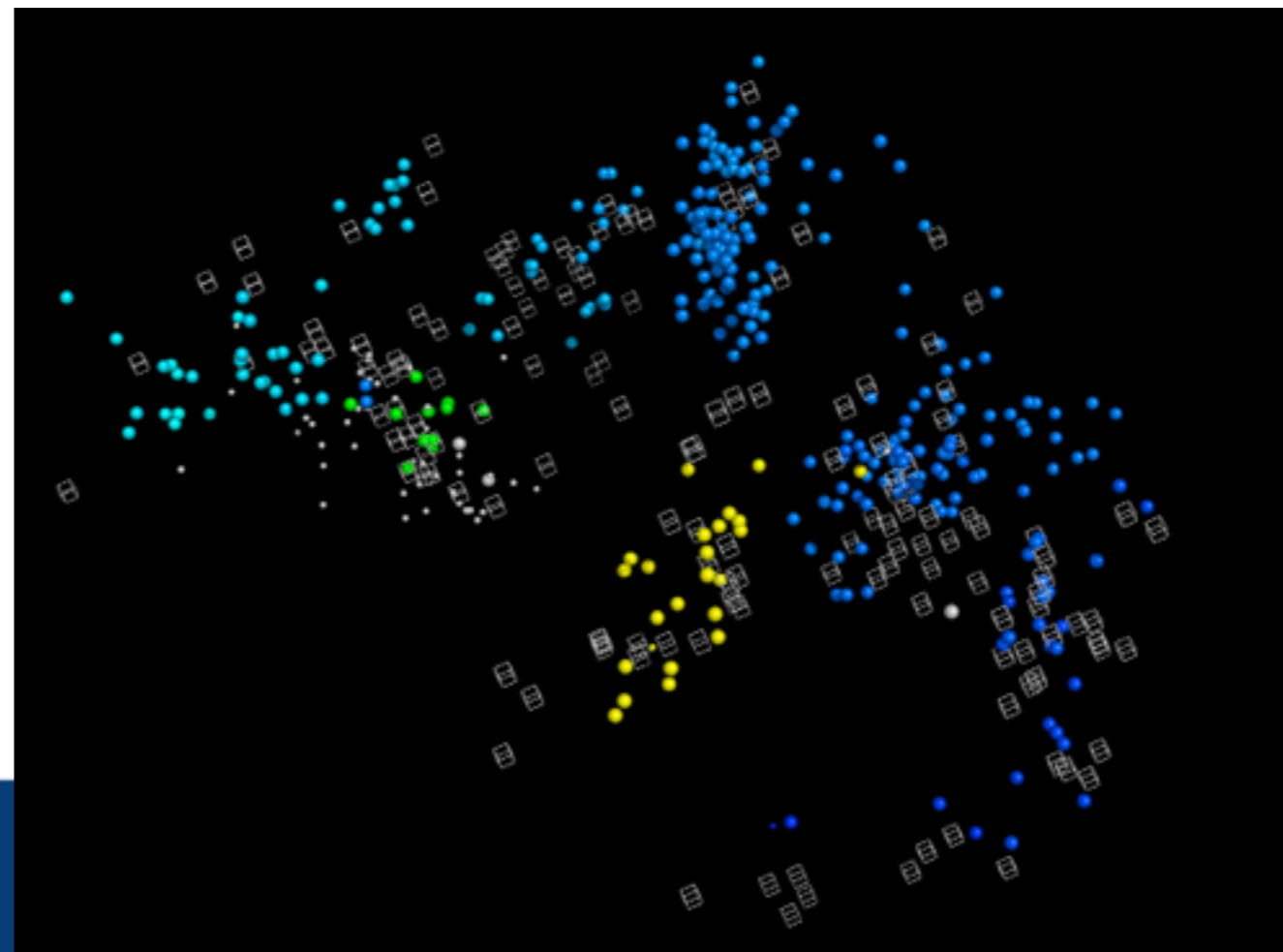
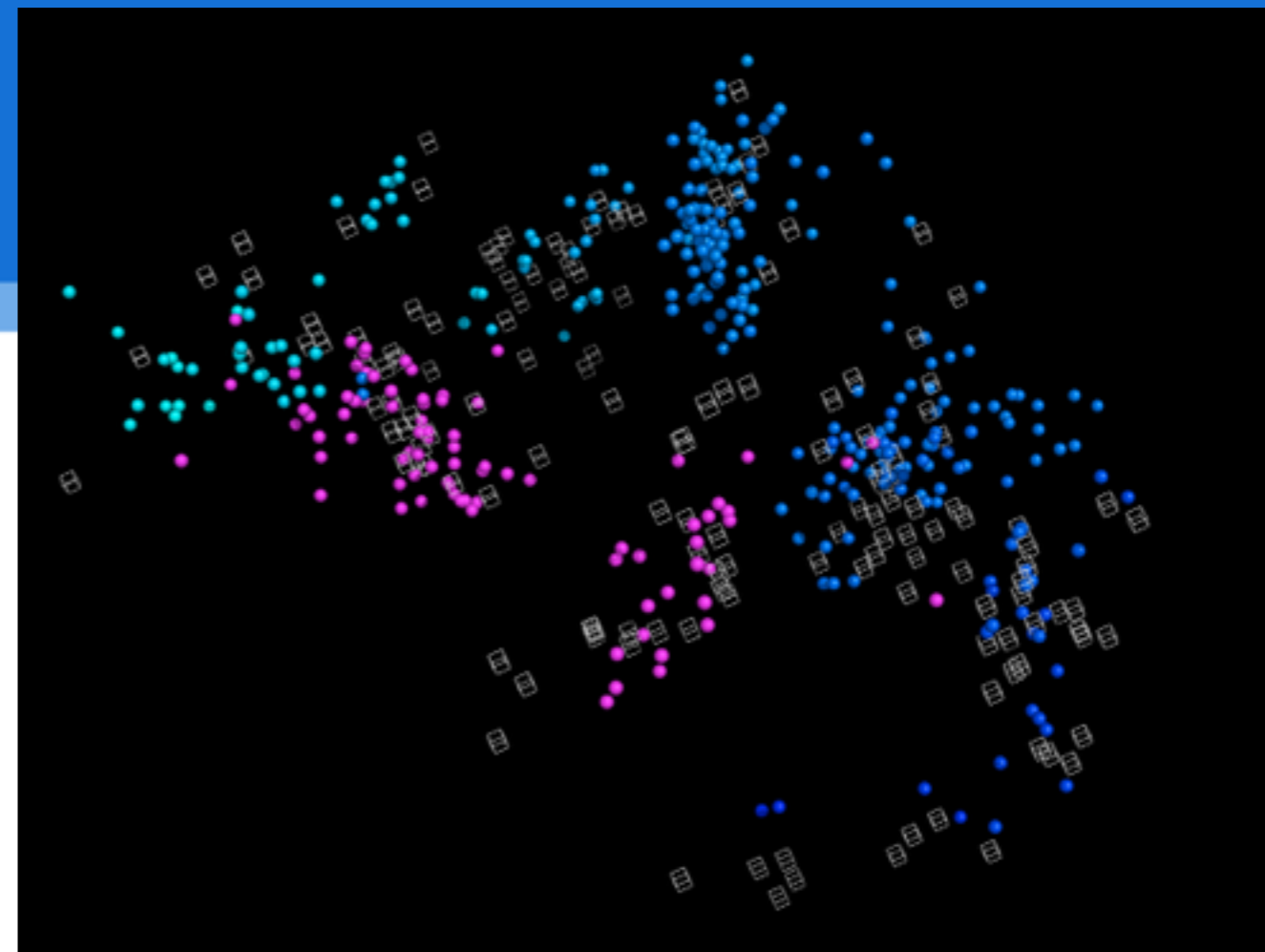
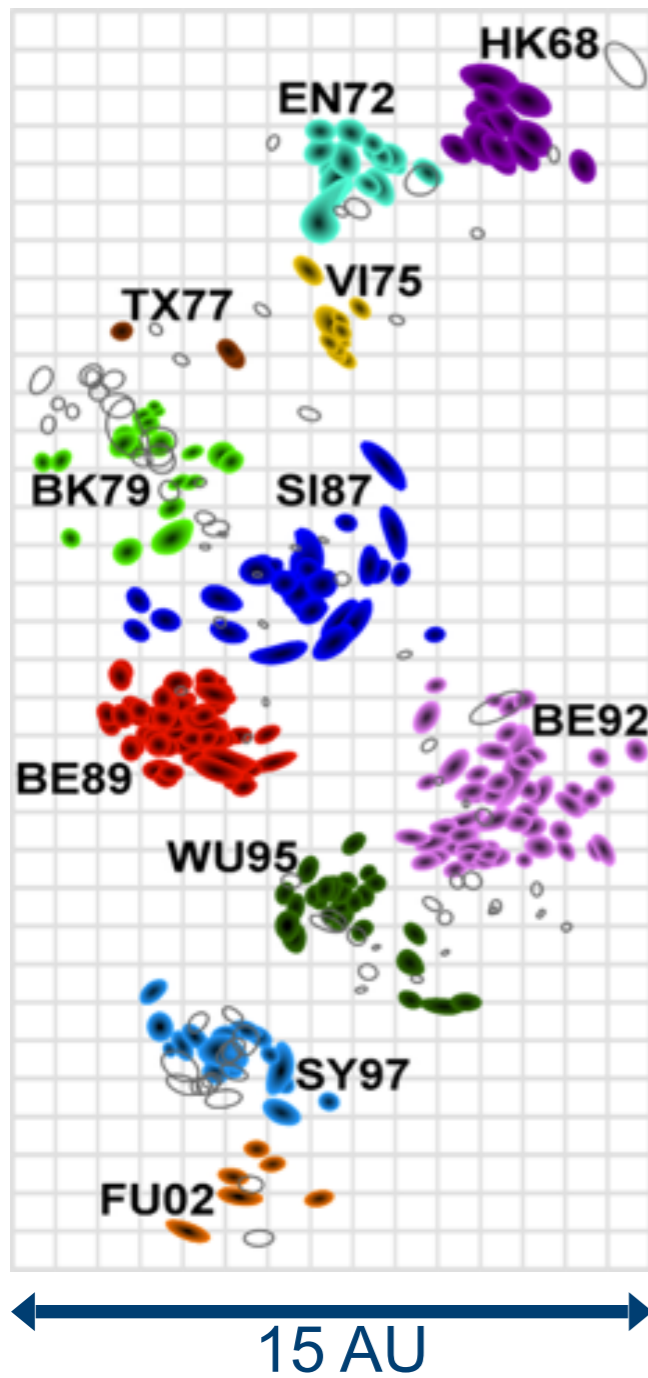
Antigenic characterisation

Methods, dimensions, scale



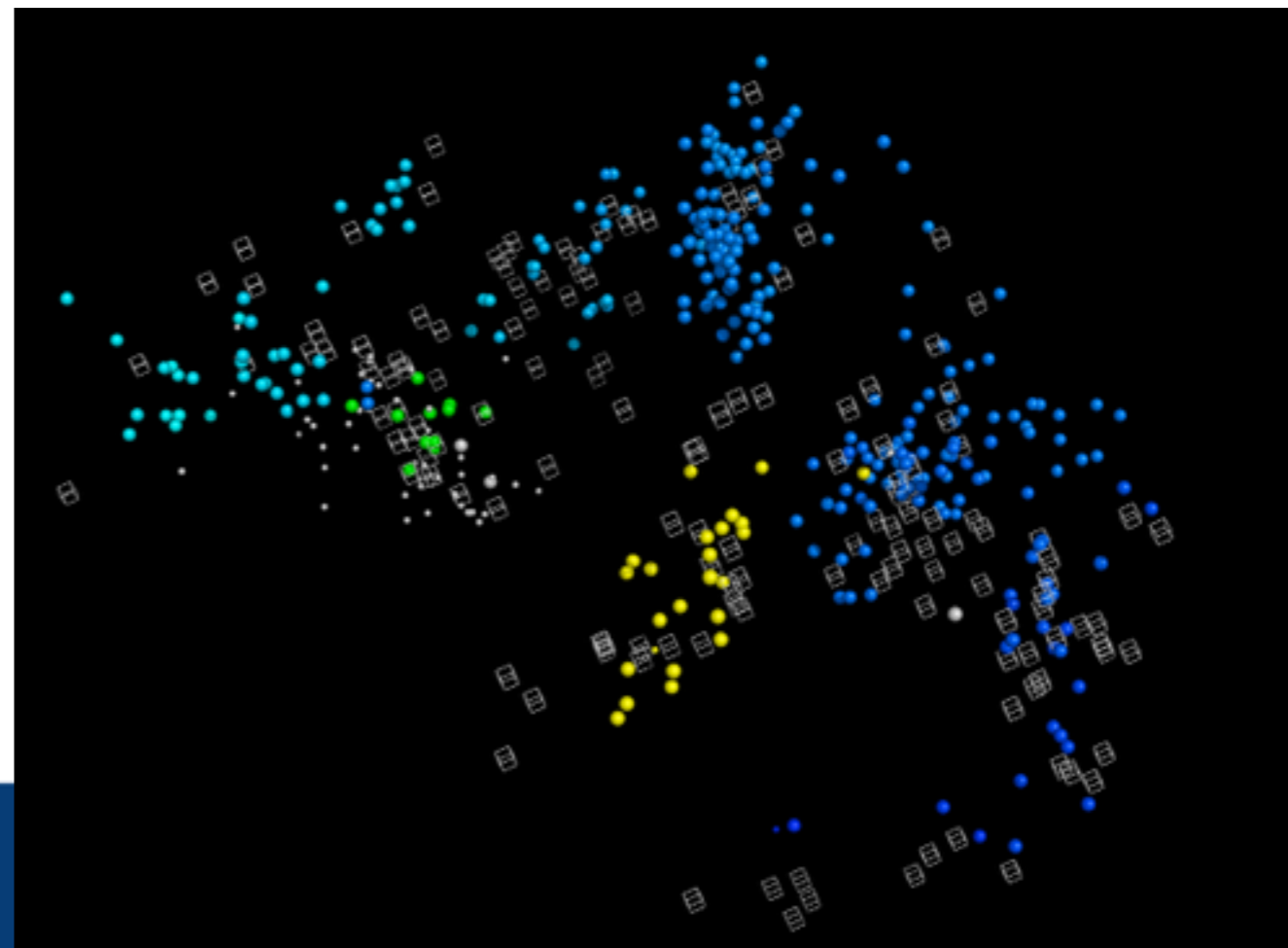
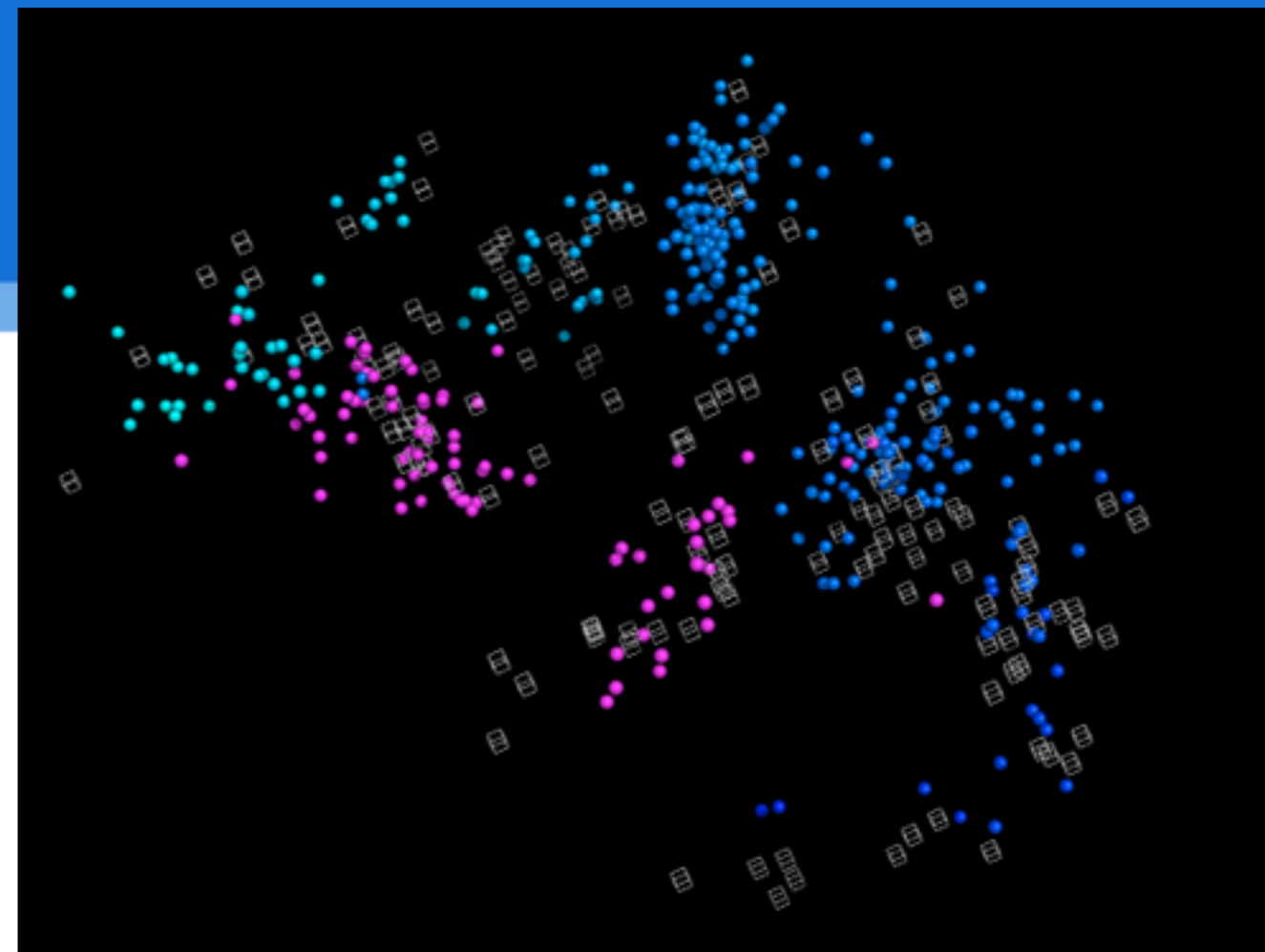
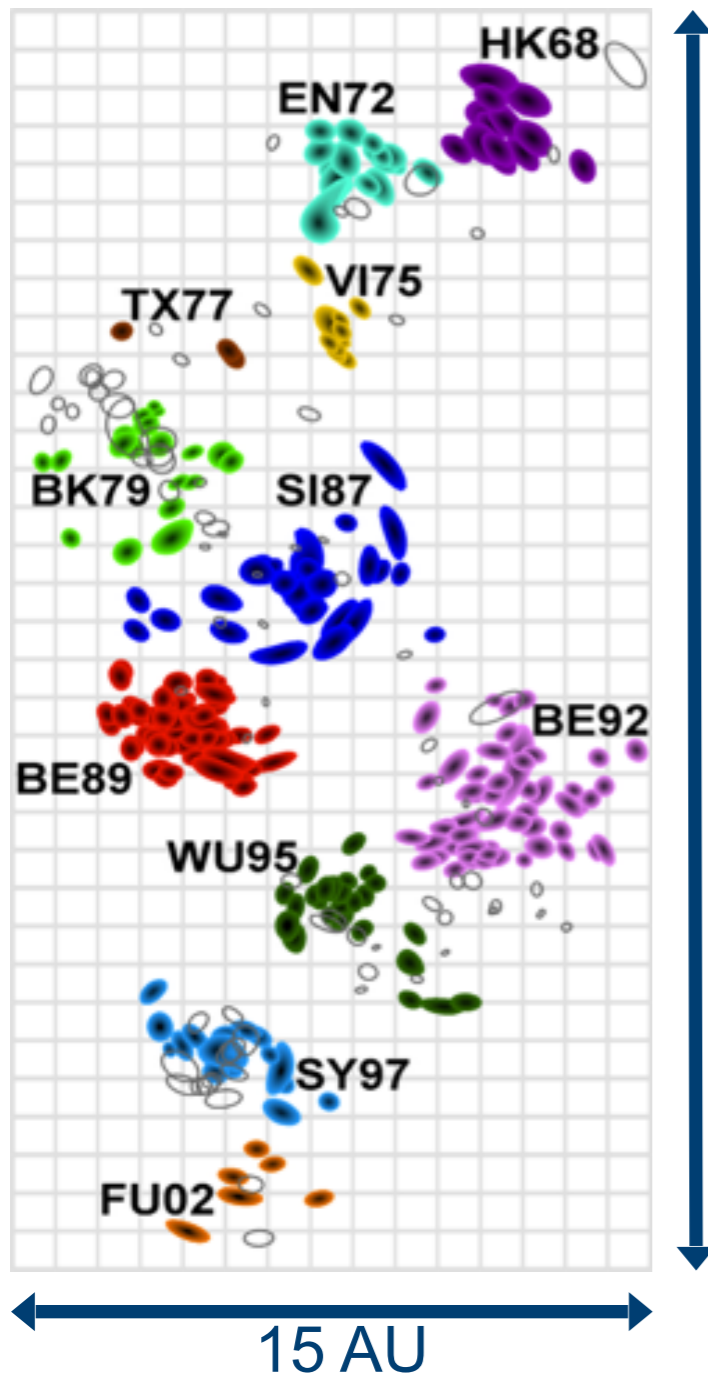
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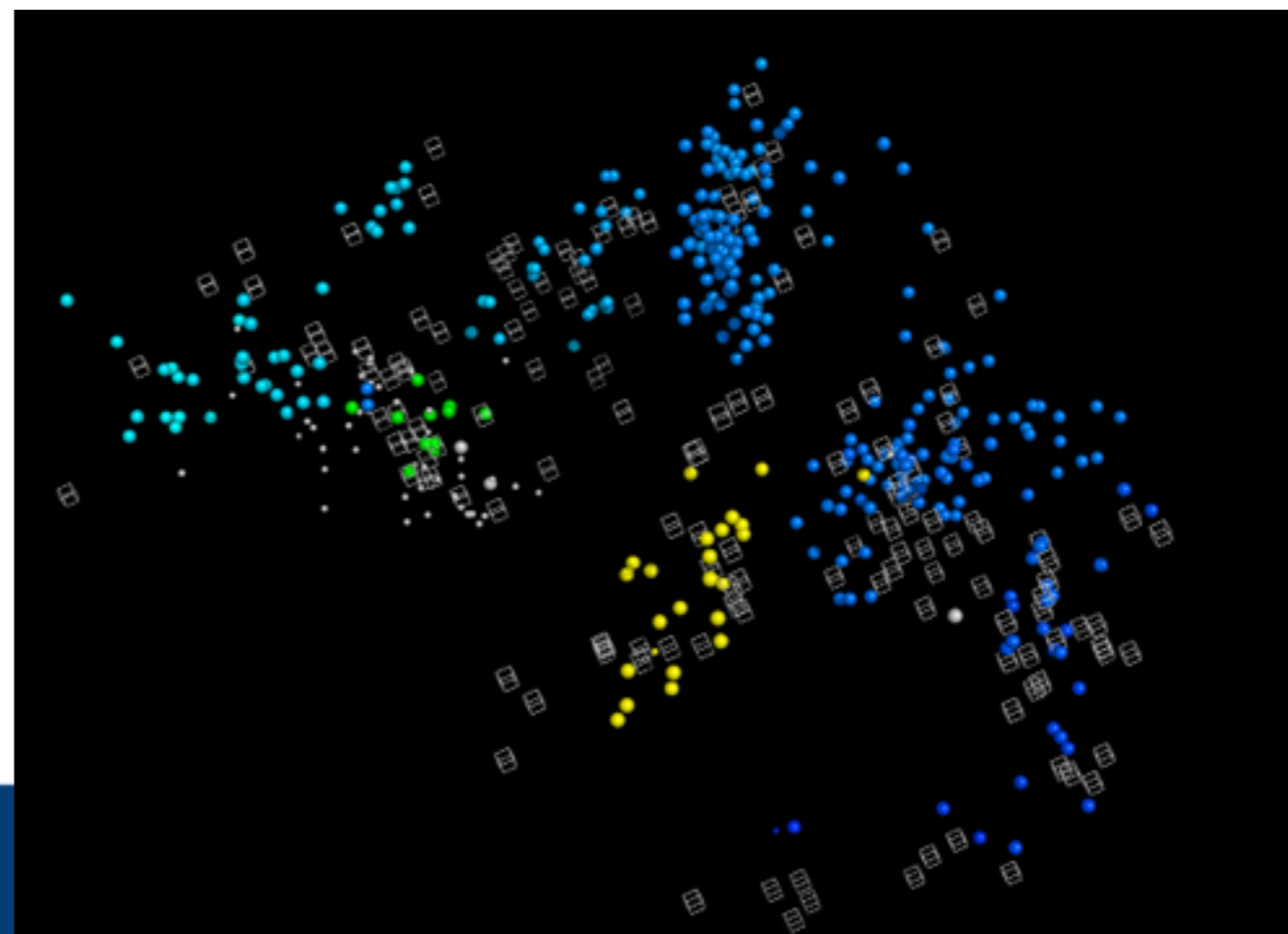
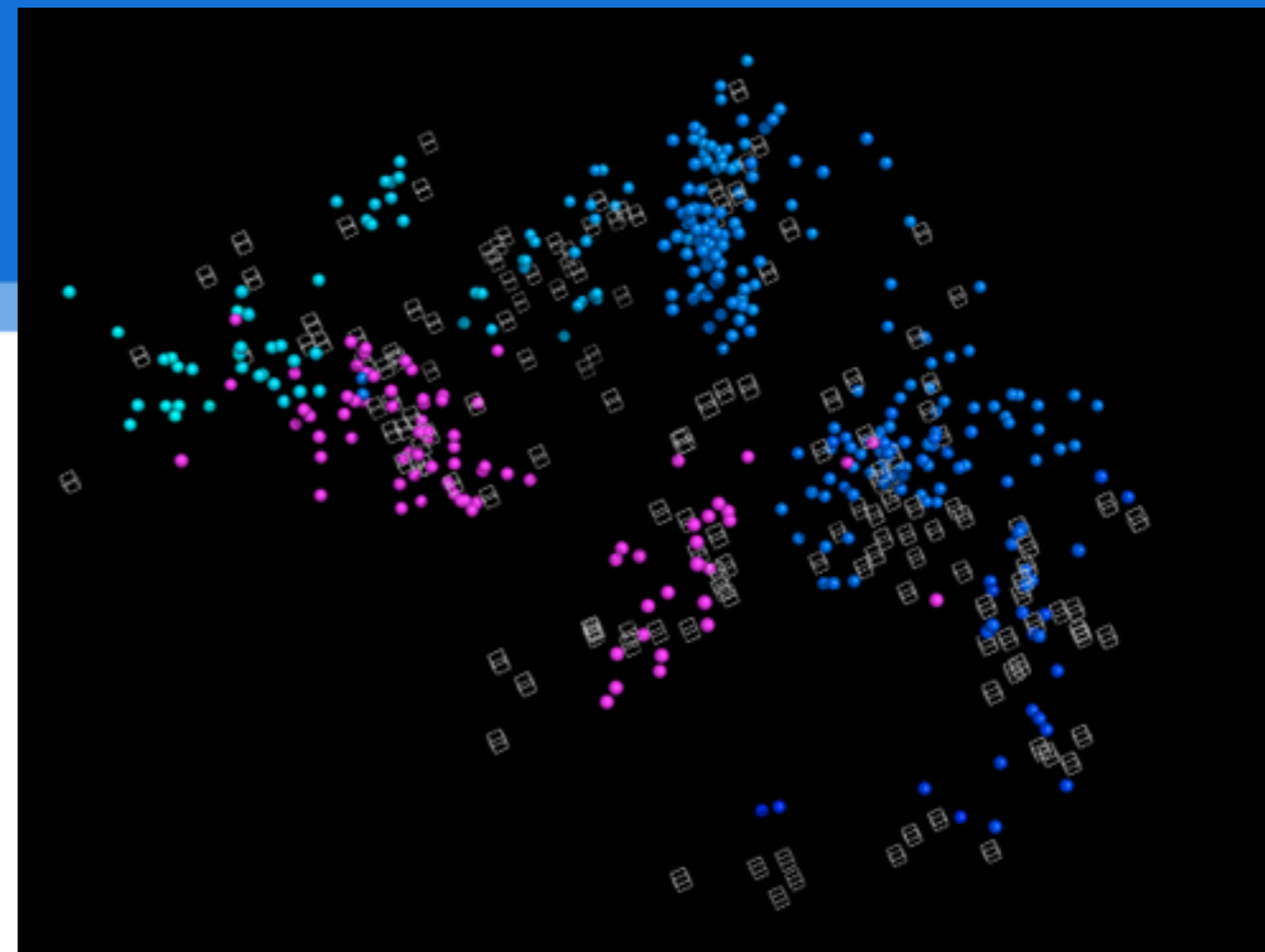
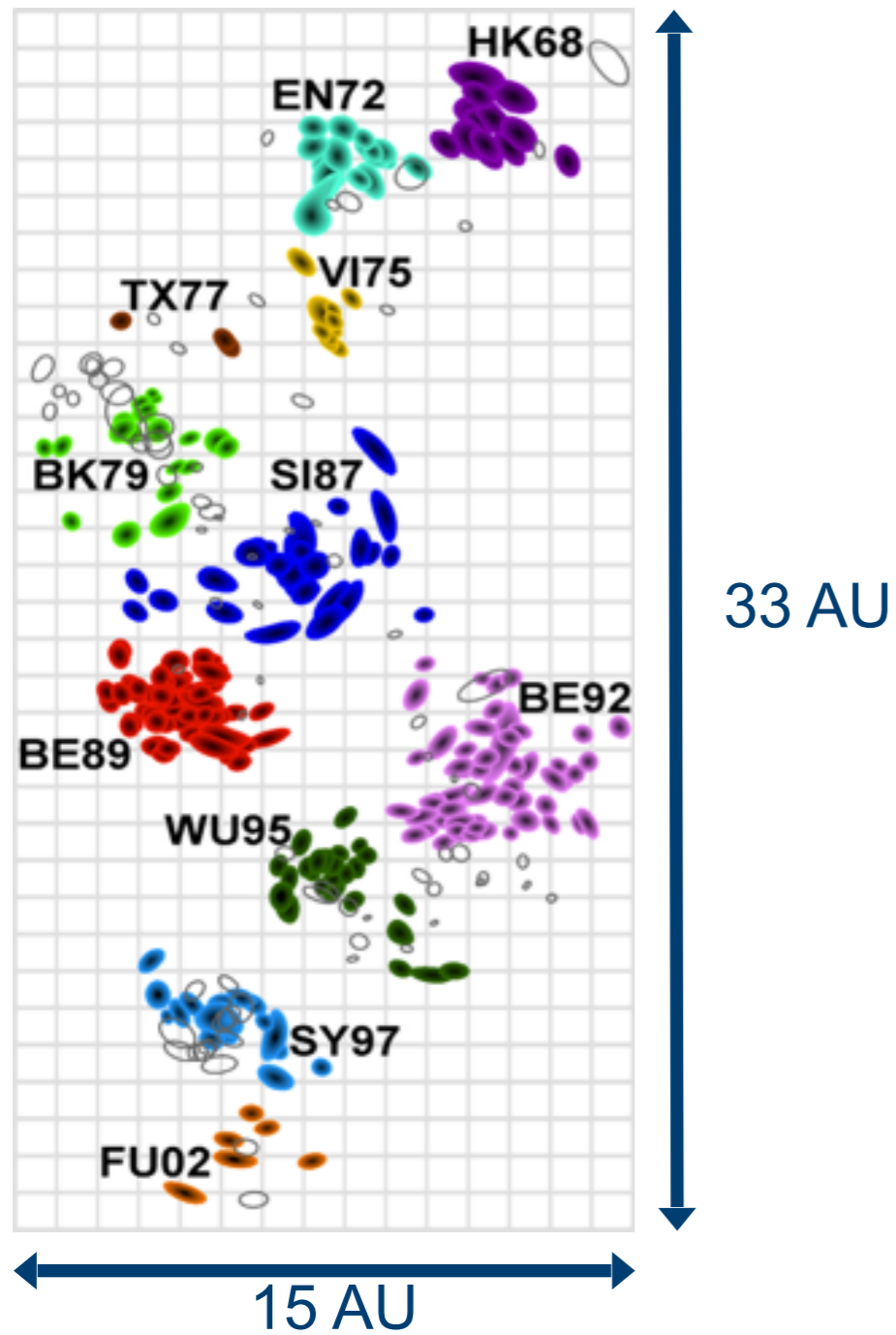
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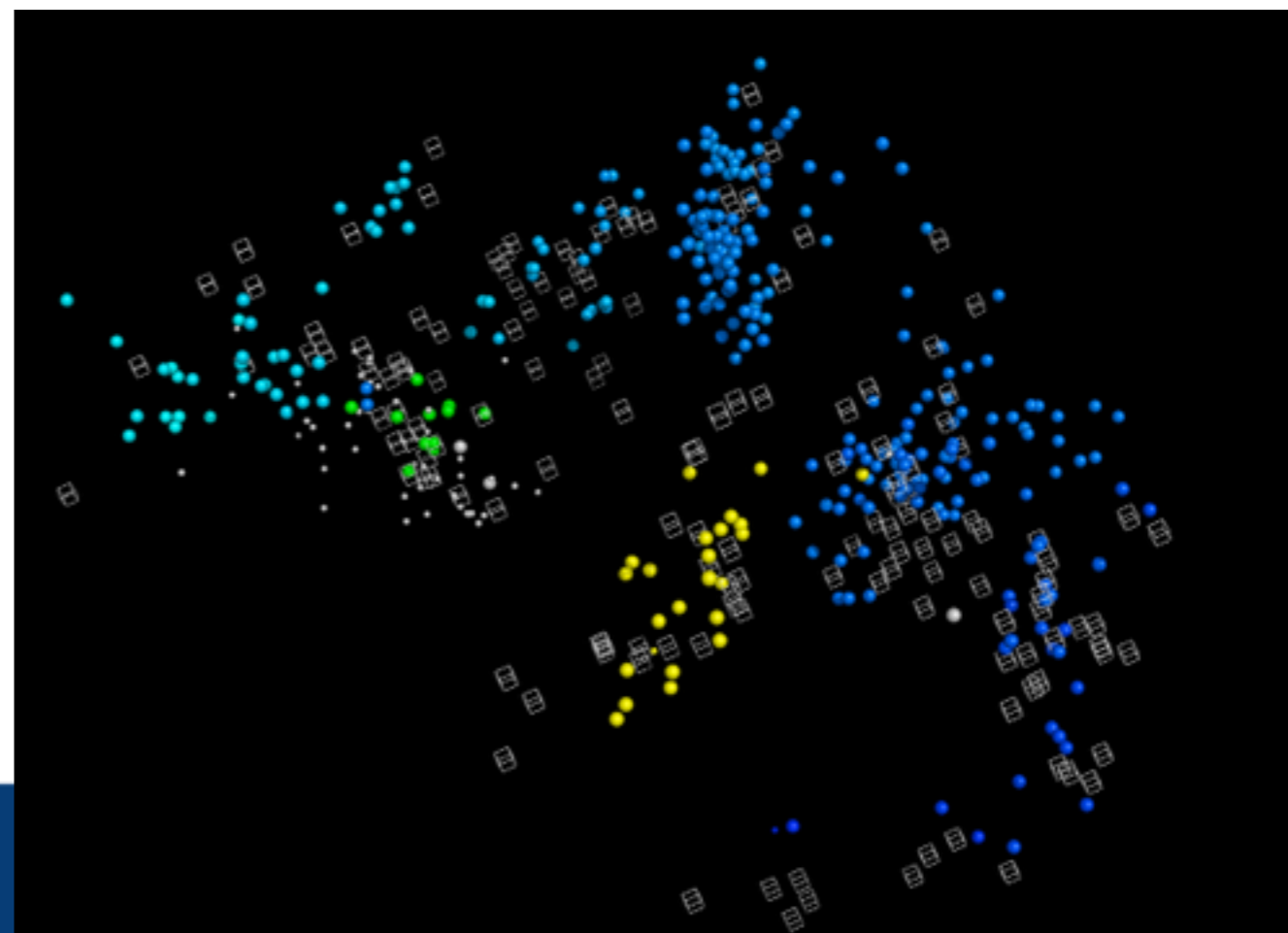
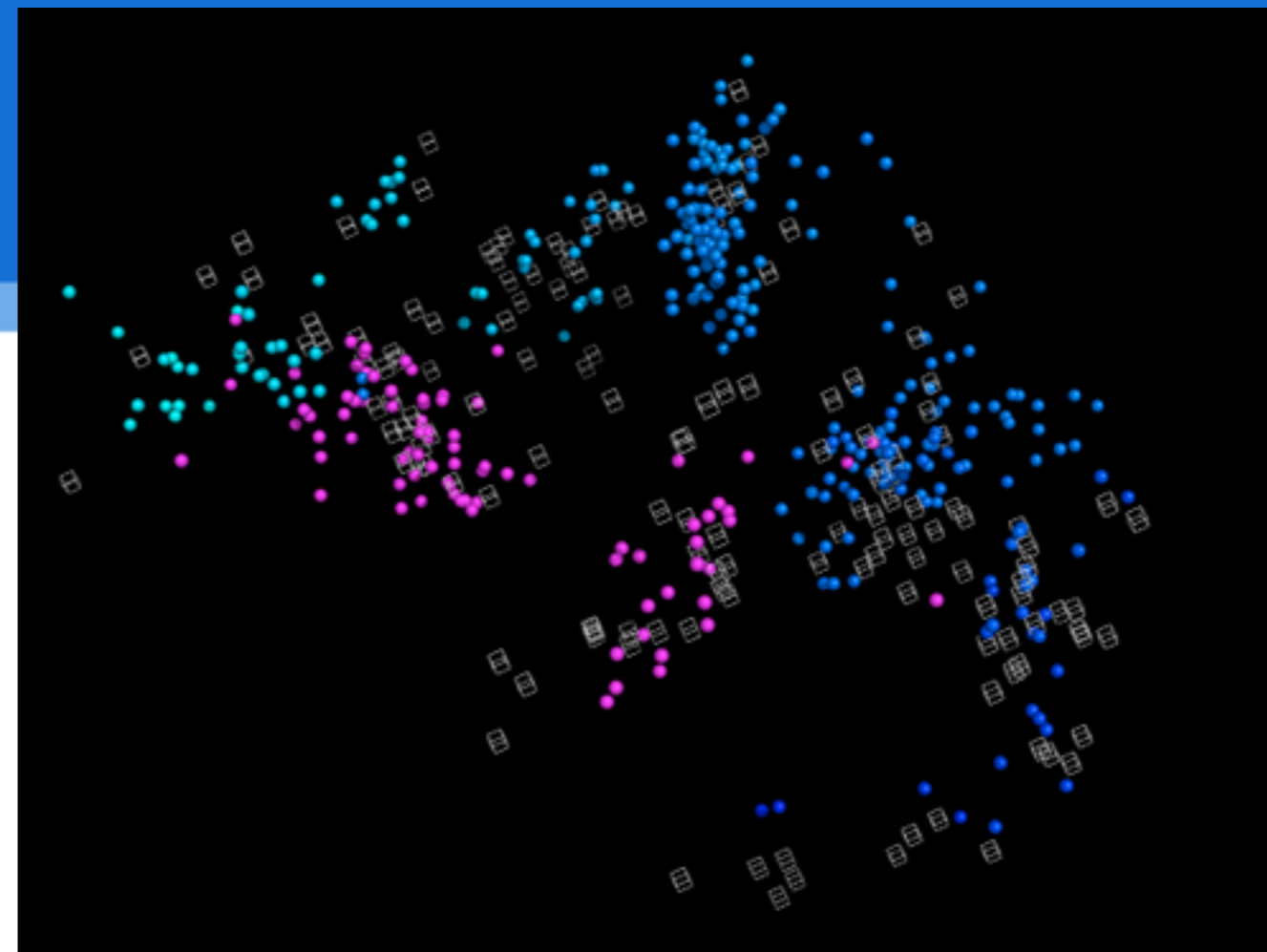
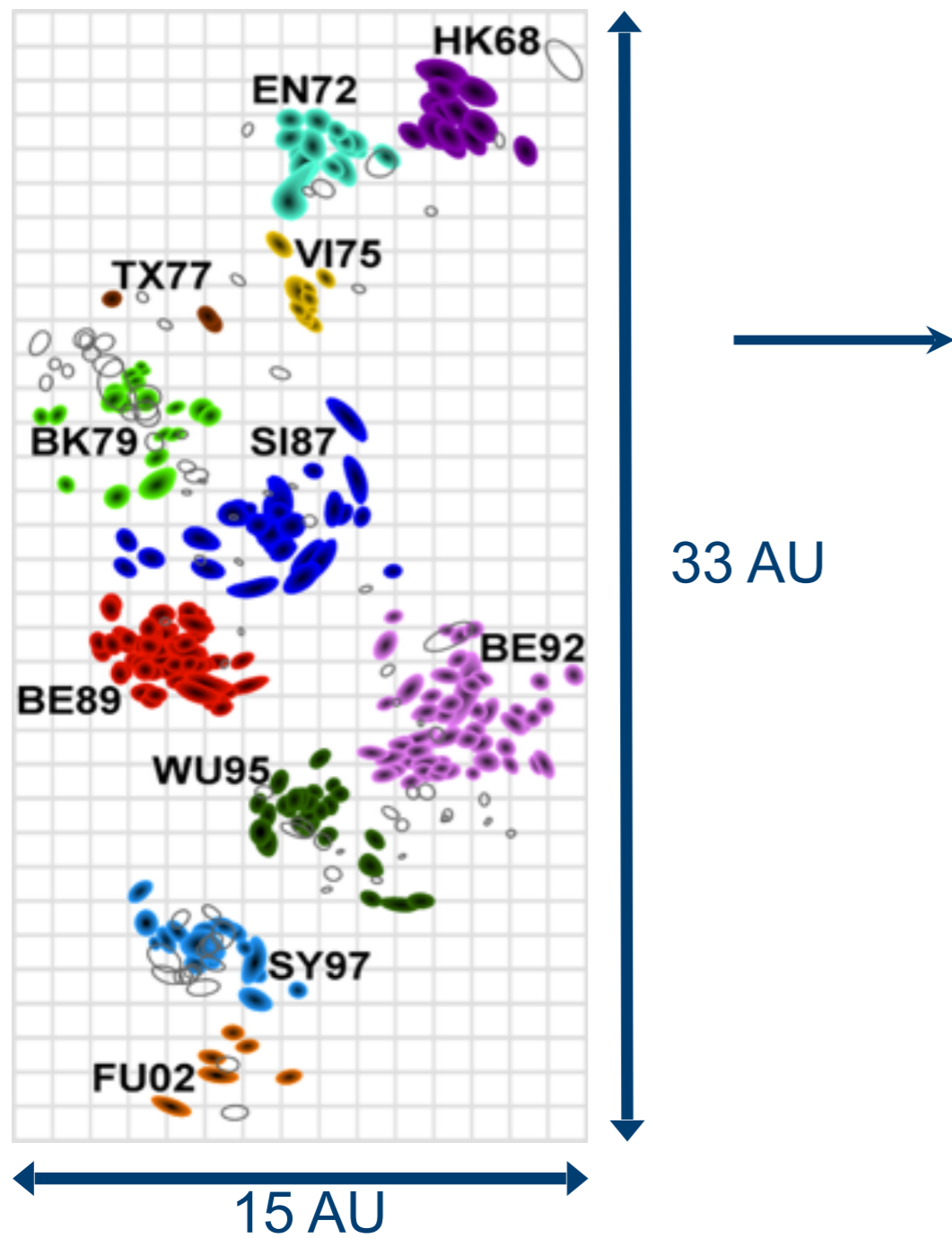
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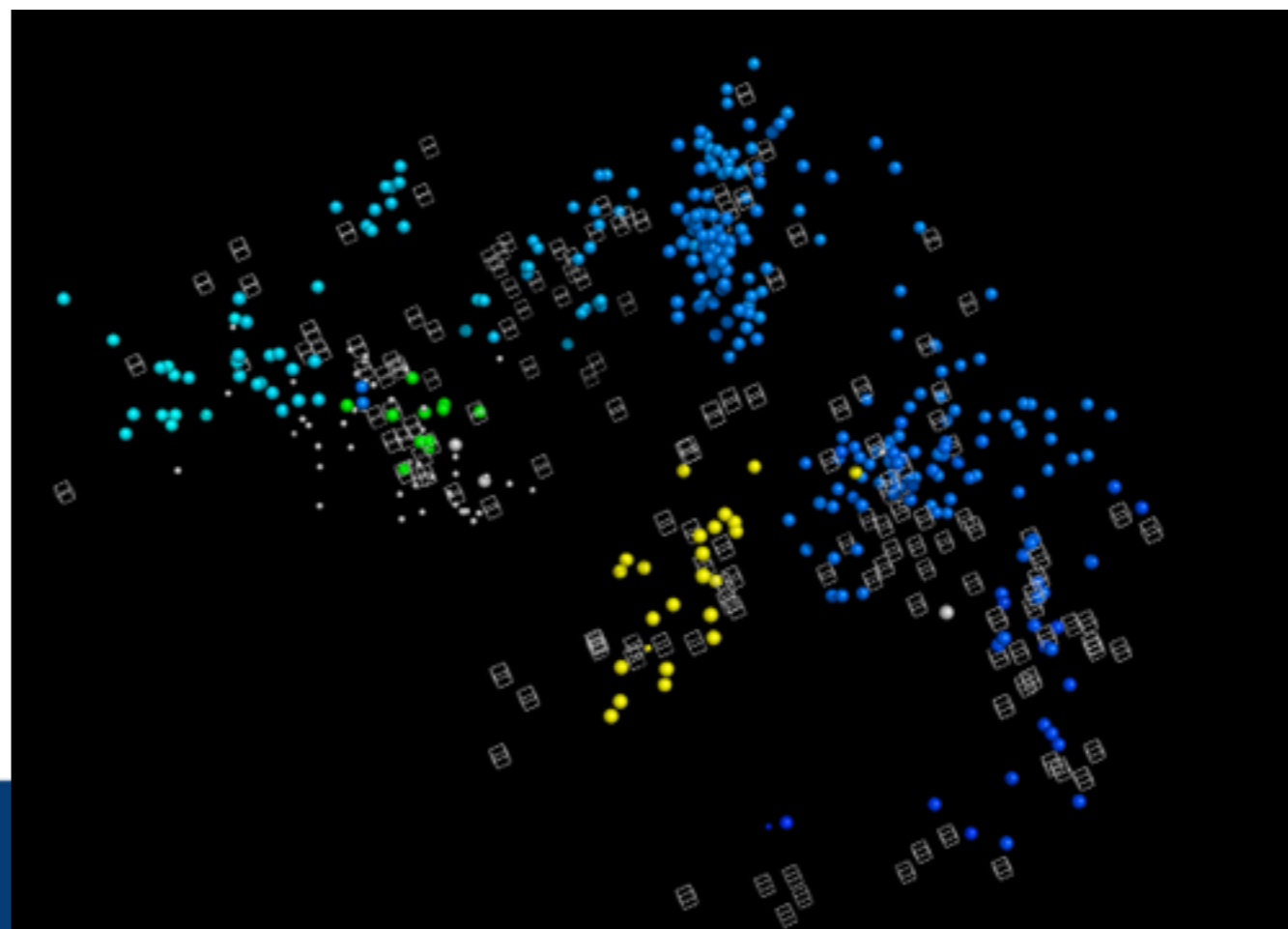
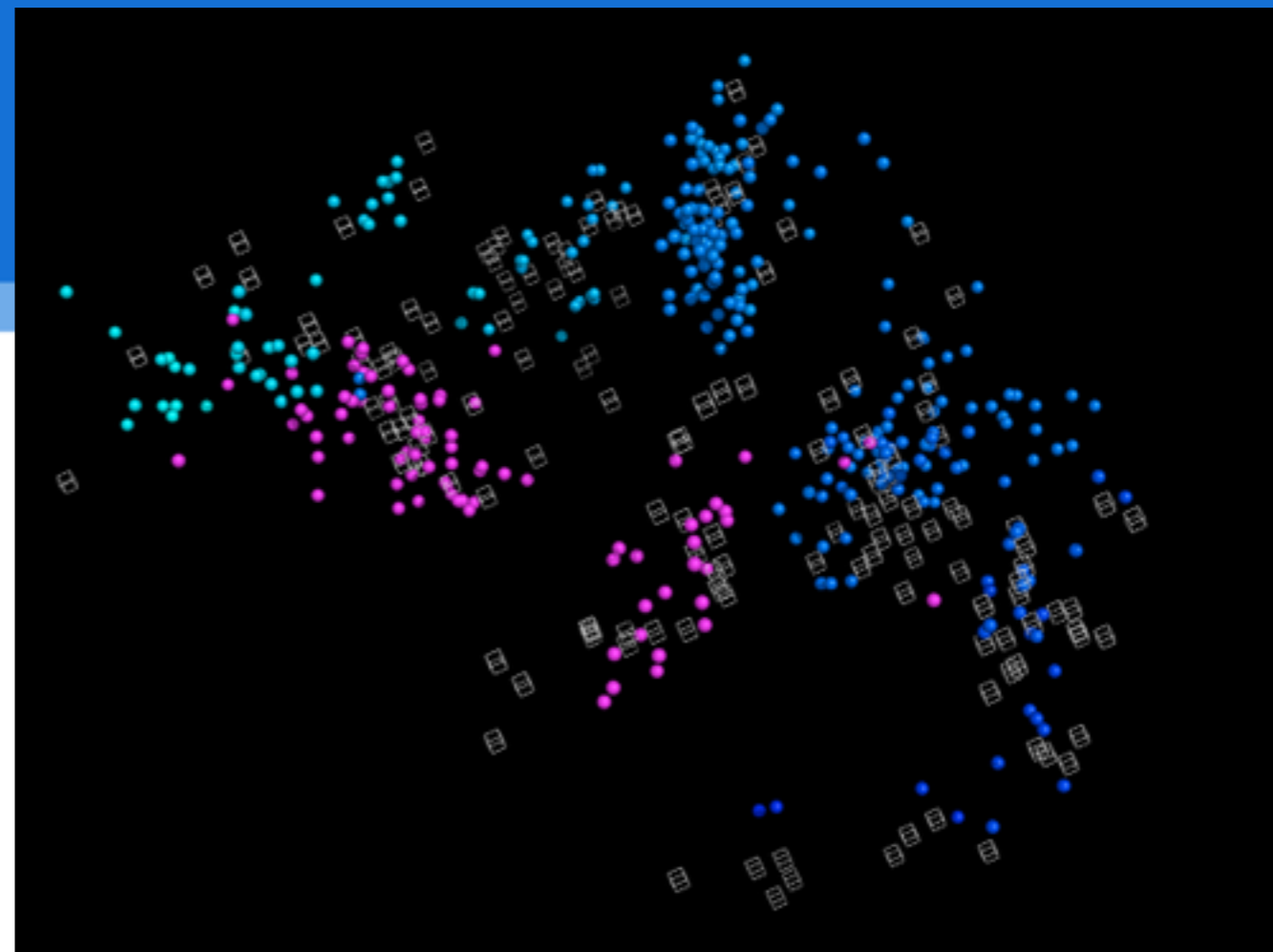
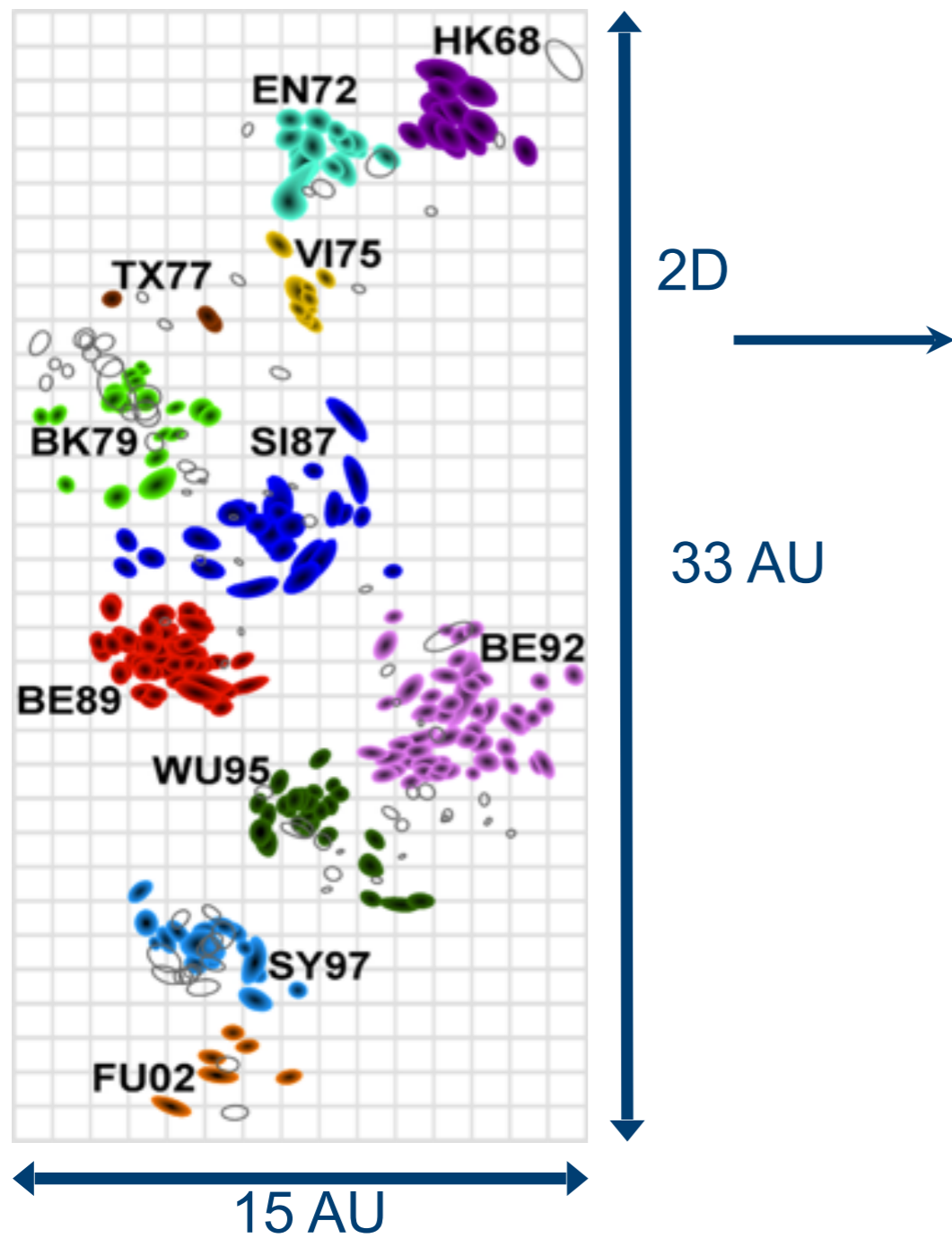
Antigenic characterisation

Methods, dimensions, scale



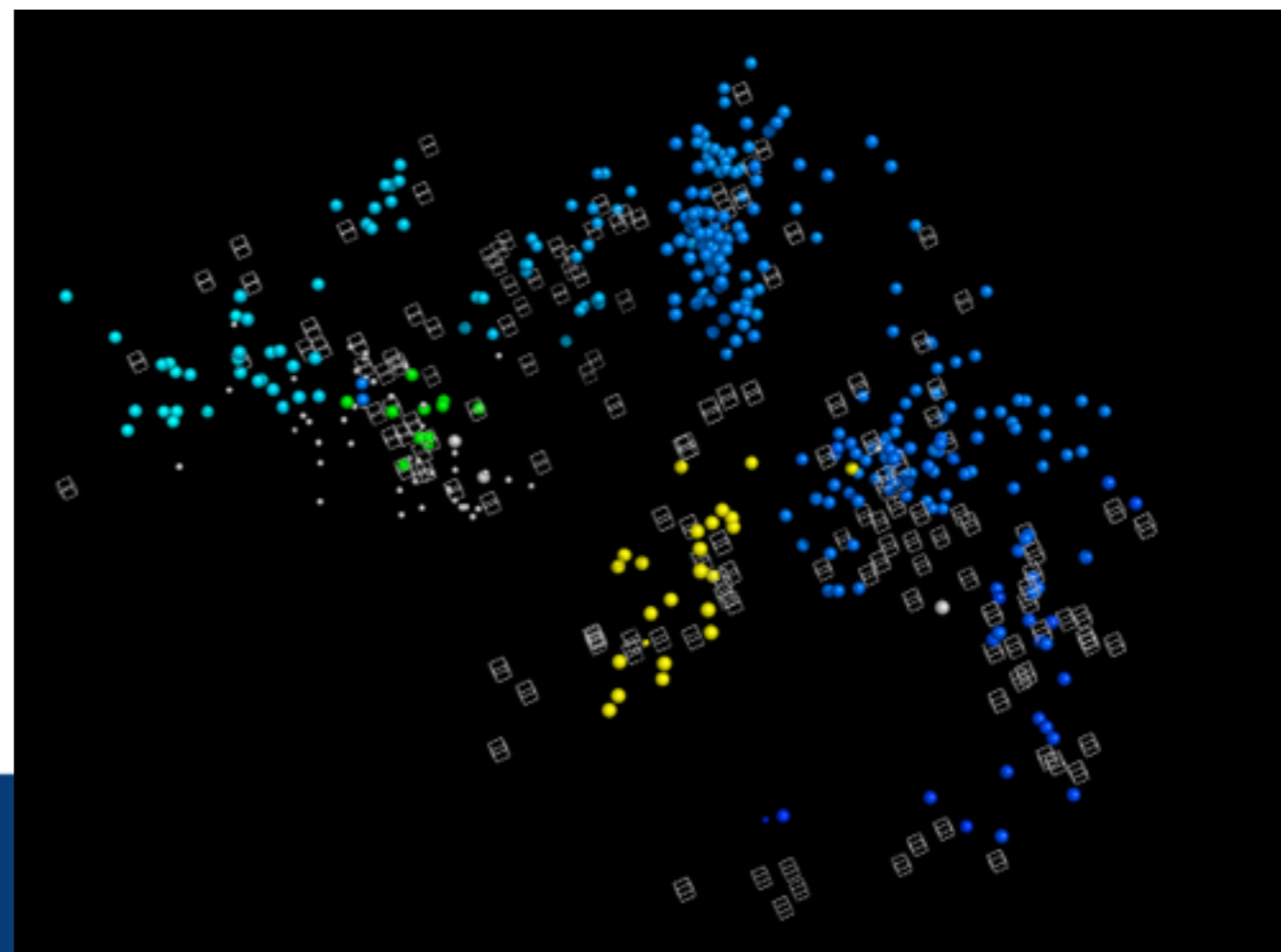
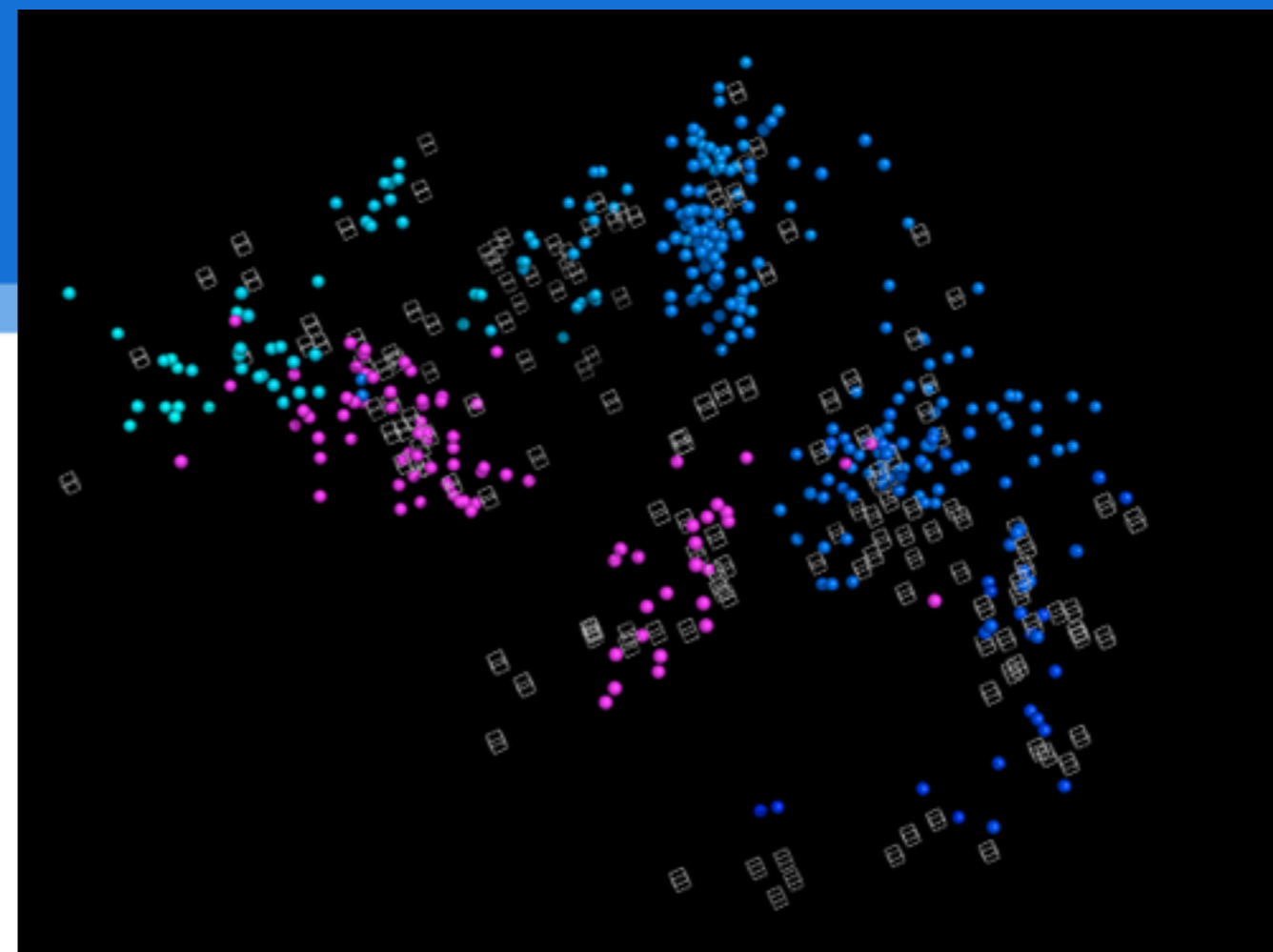
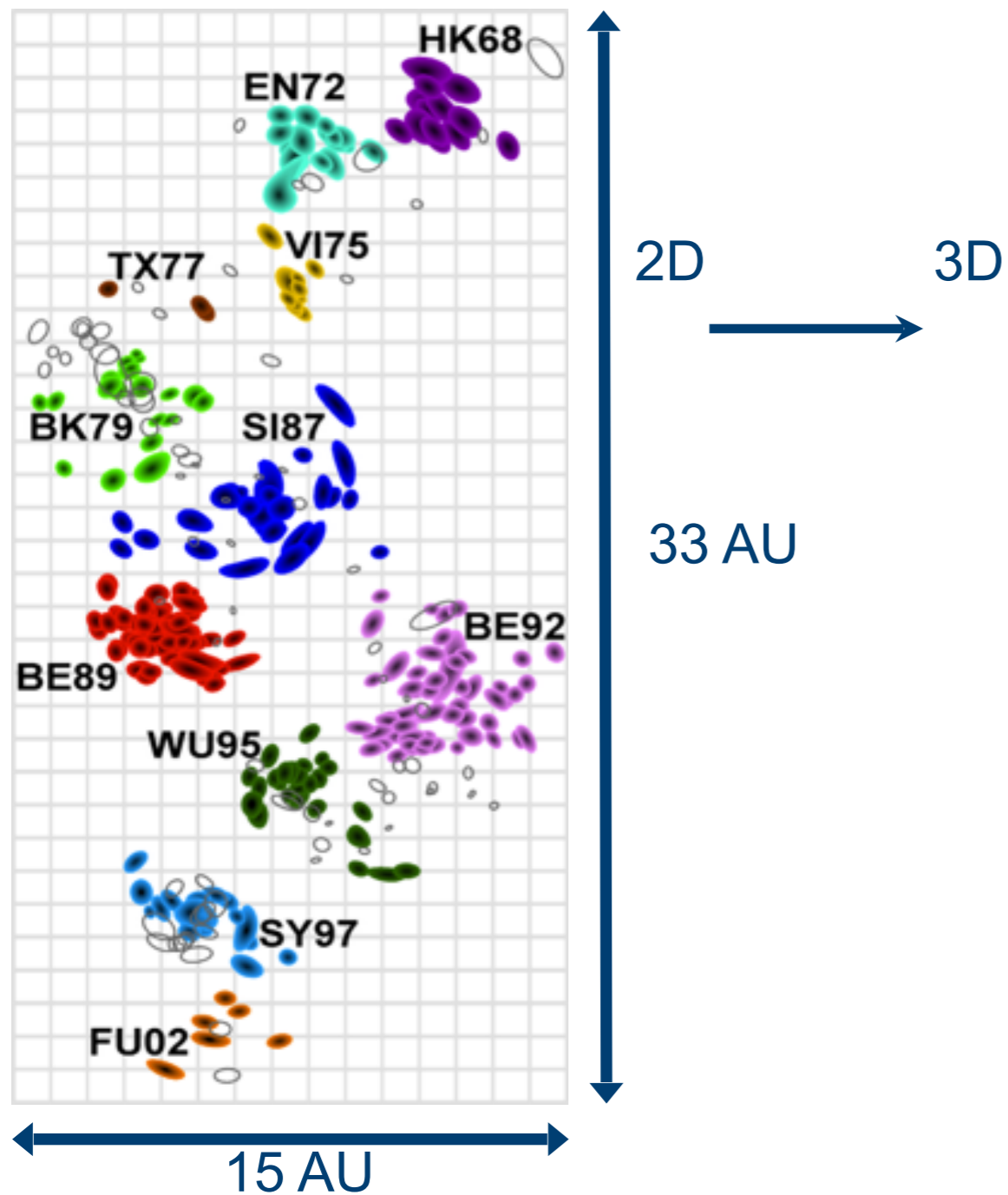
Antigenic characterisation

Methods, dimensions, scale

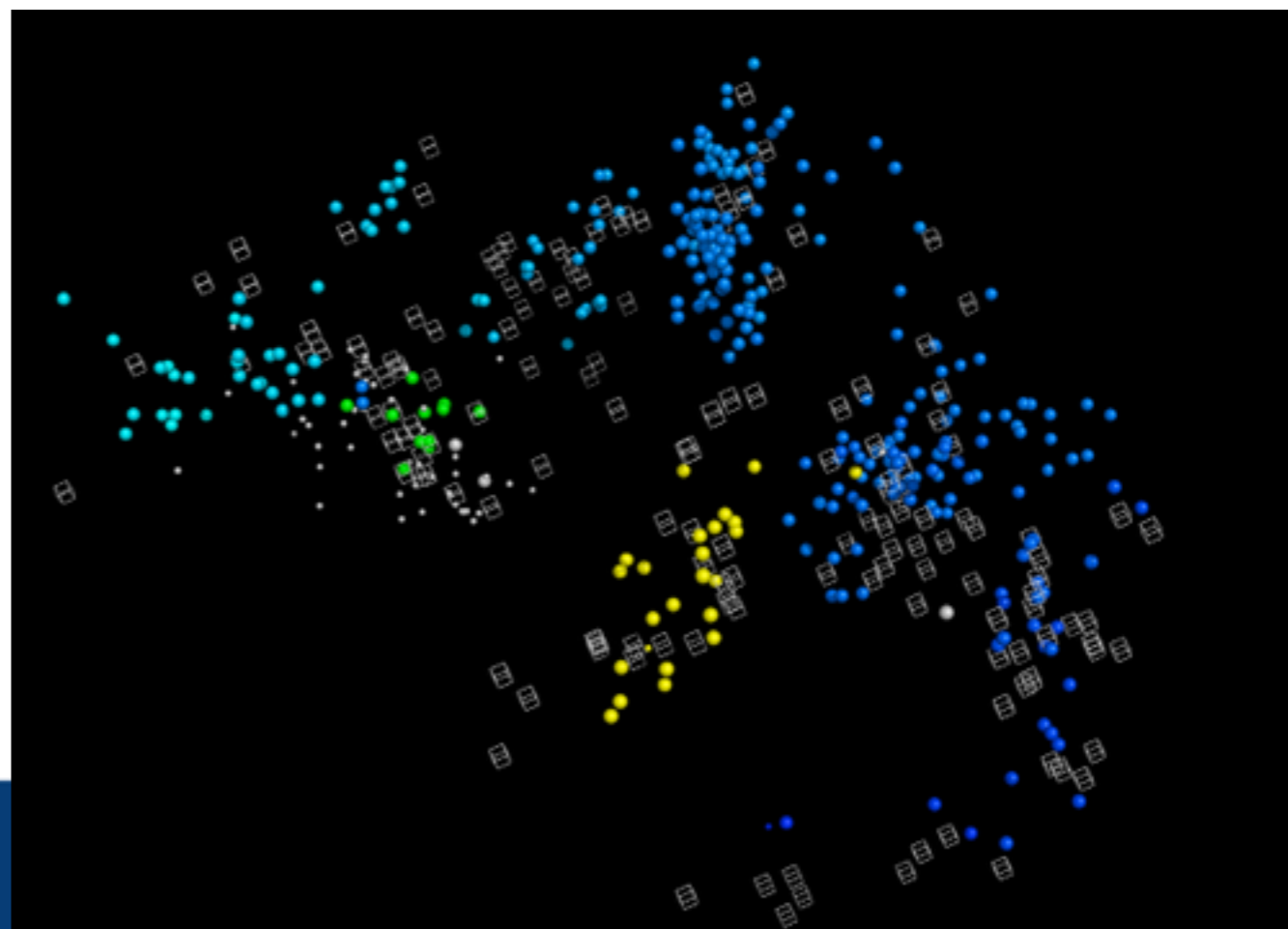
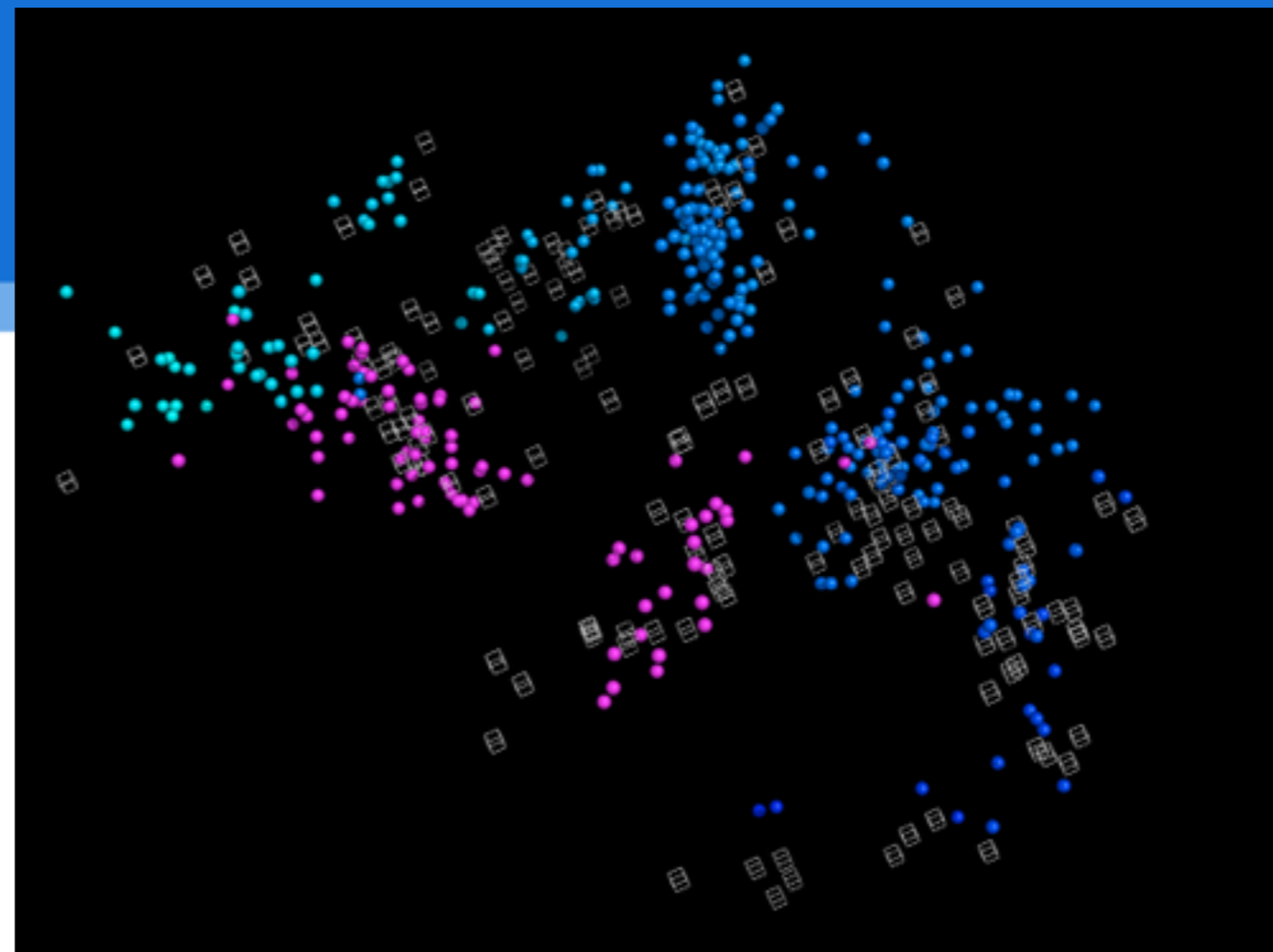
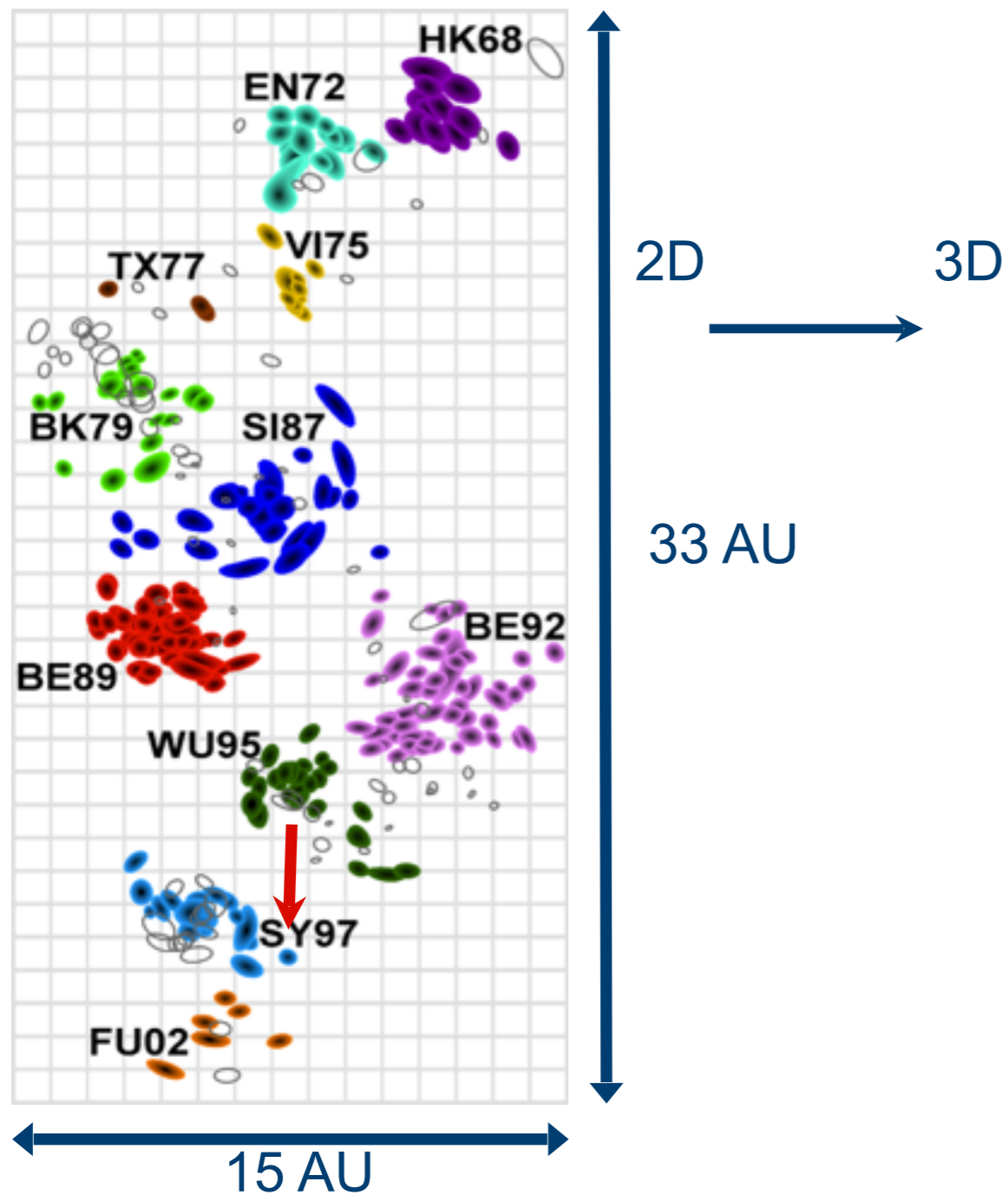


Antigenic characterisation

Methods, dimensions, scale

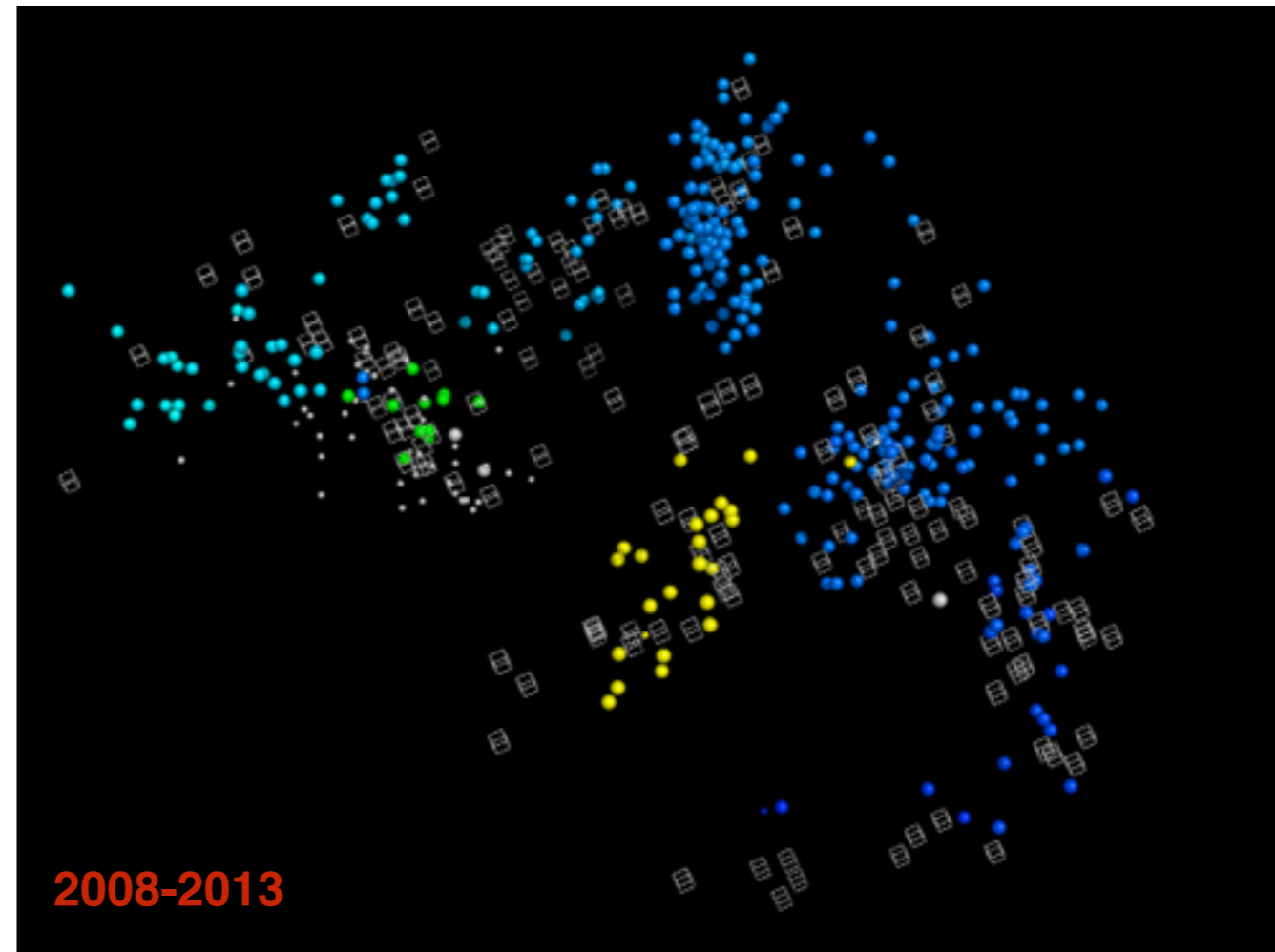
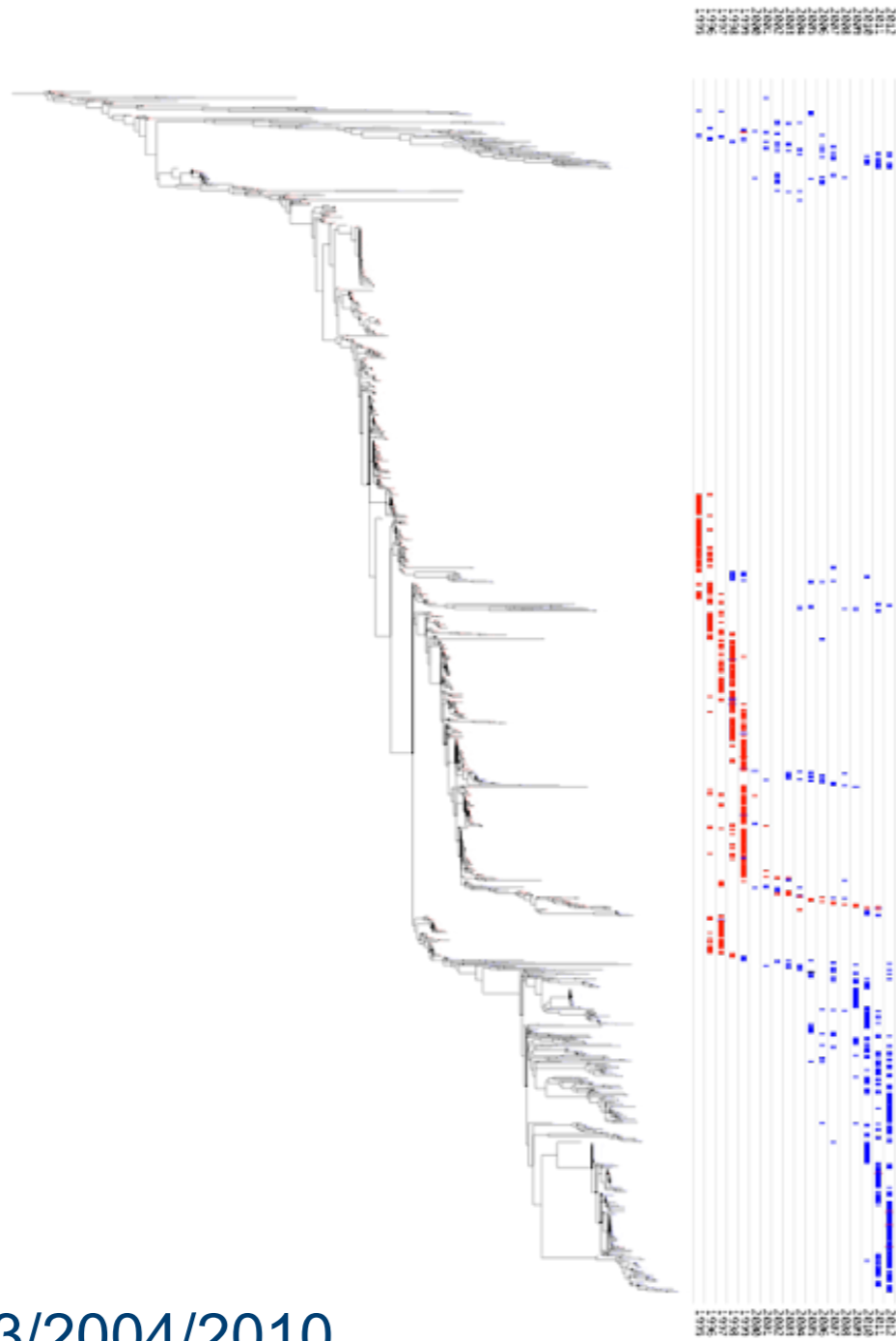


Antigenic characterisation Methods, dimensions, scale



Human and swine influenza A viruses: H3

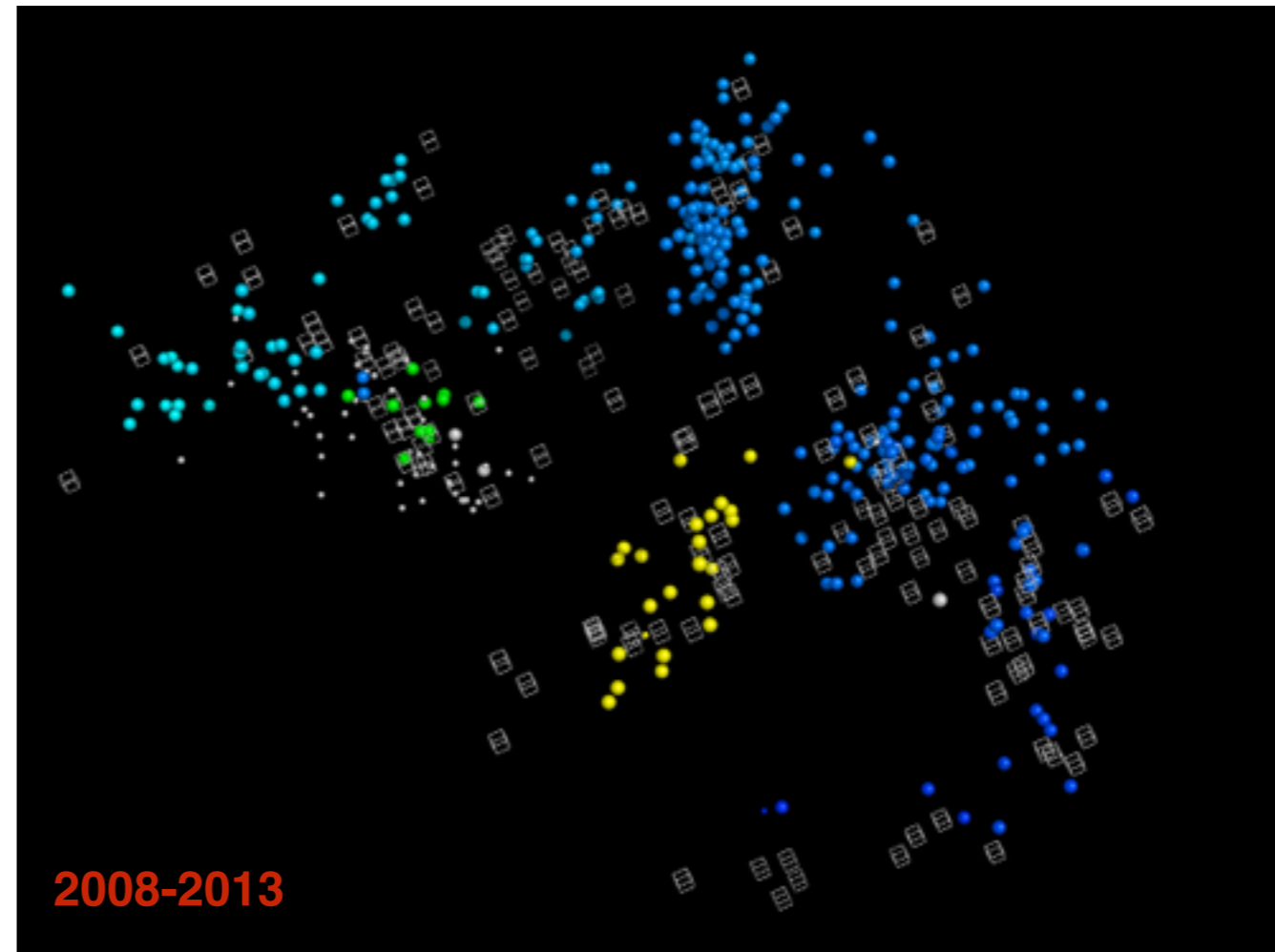
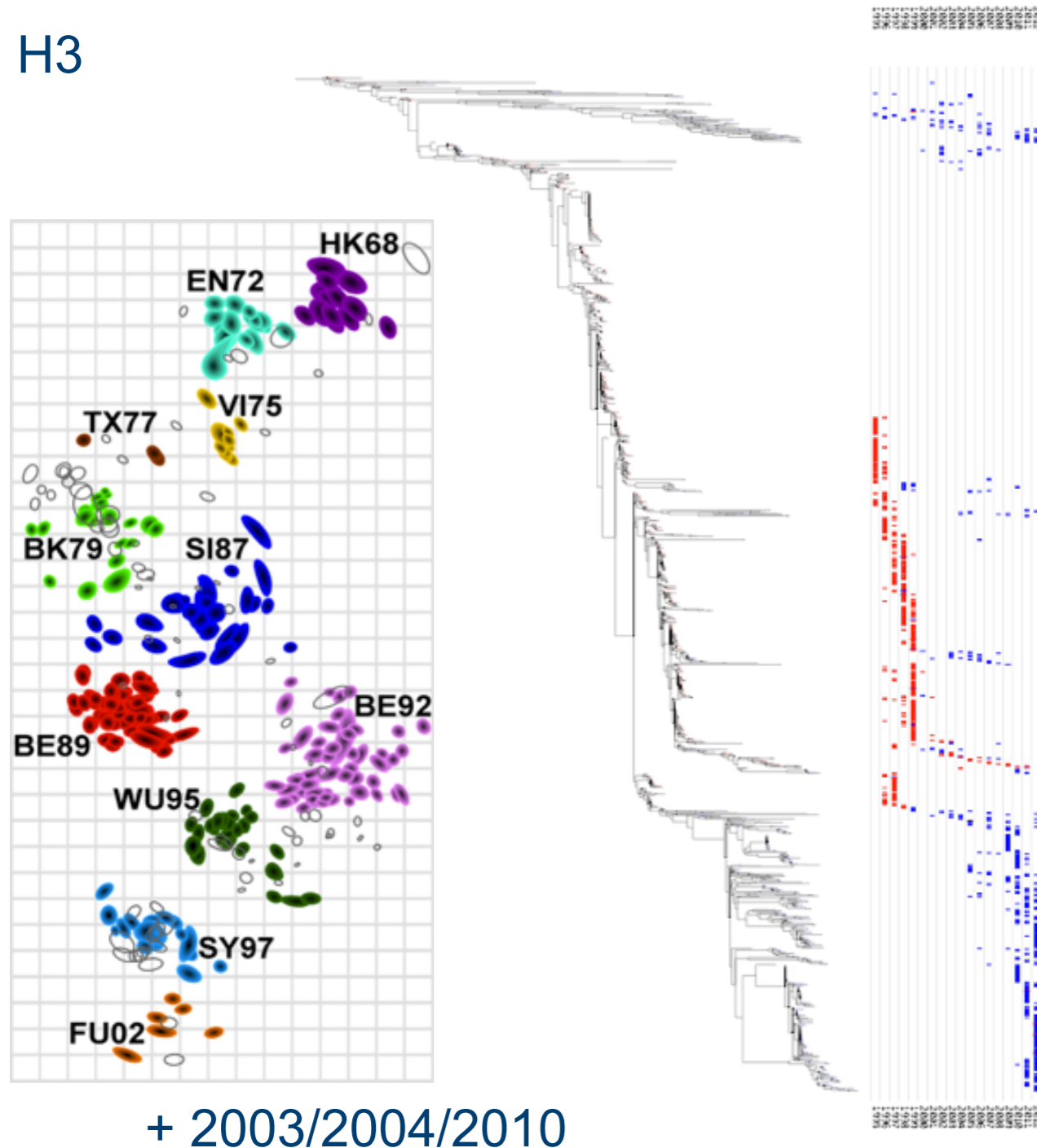
H3



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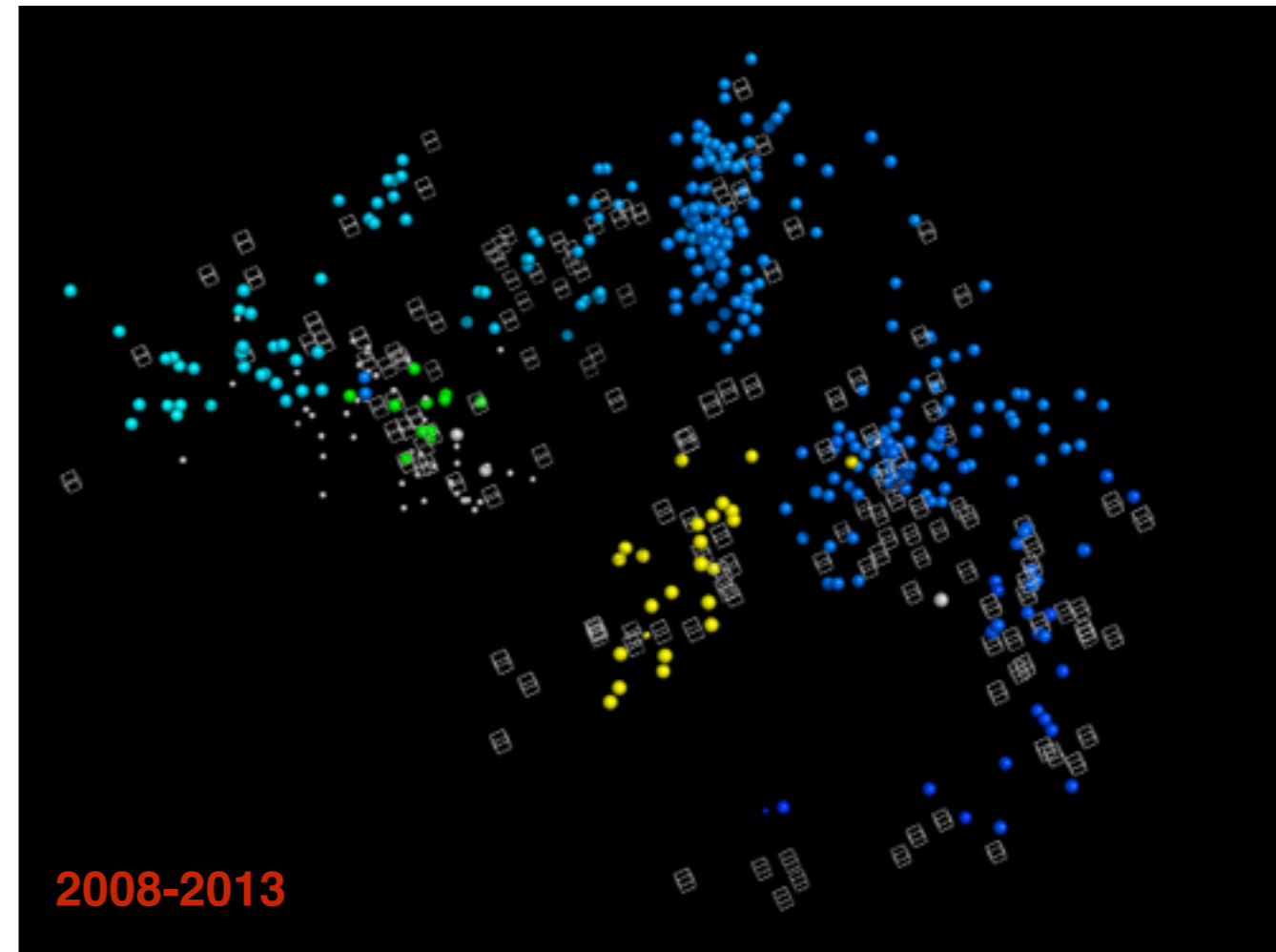
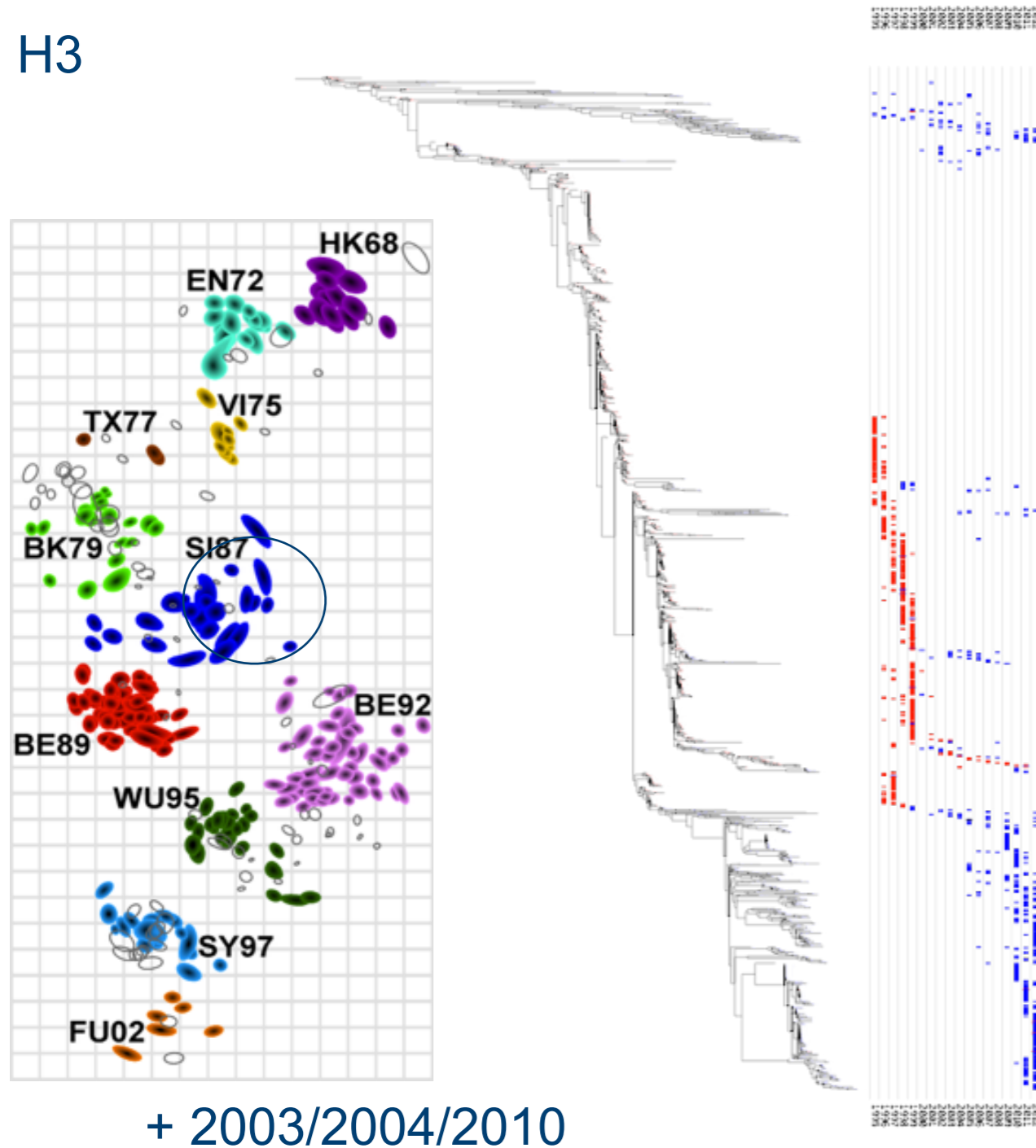
Human and swine influenza A viruses: H3

H3



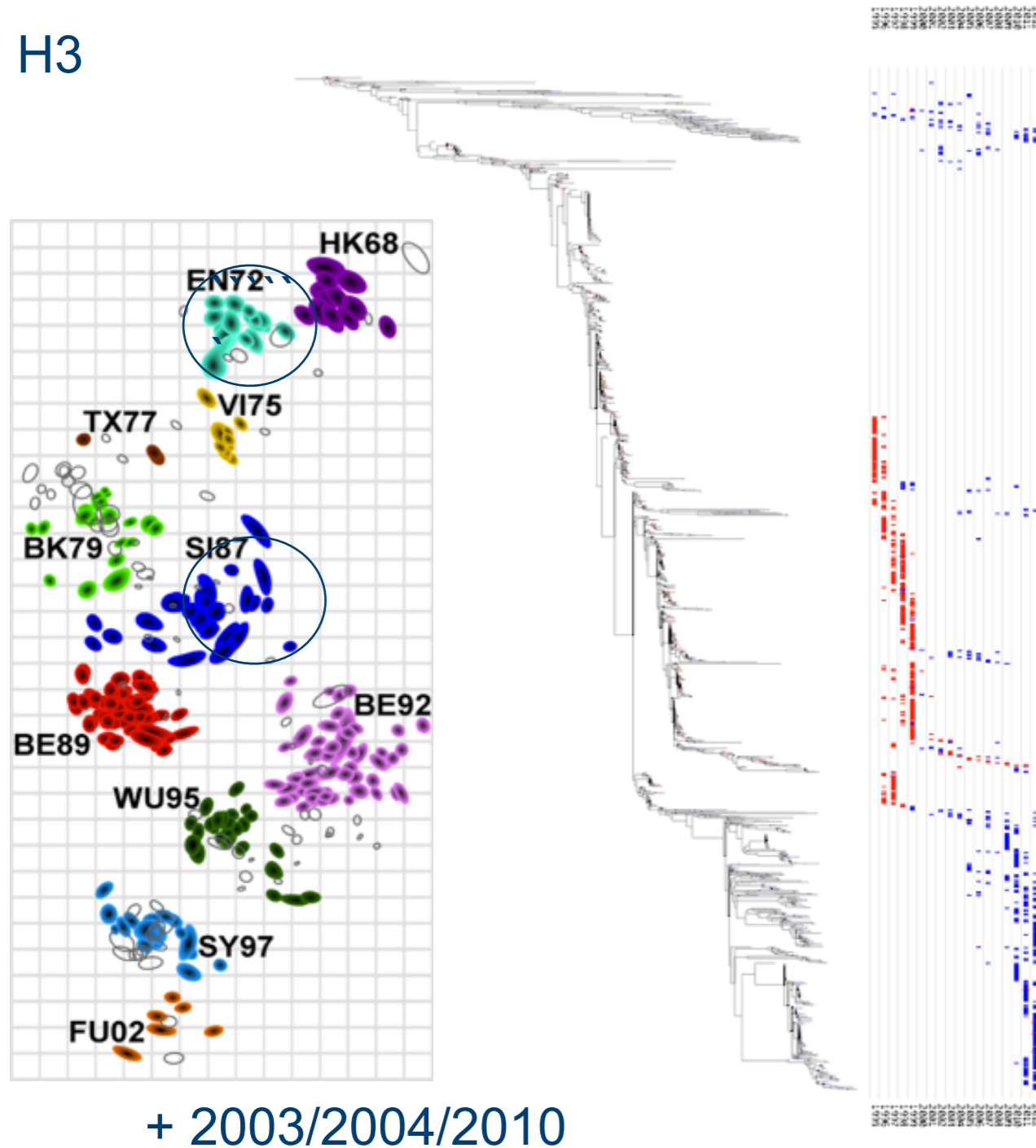
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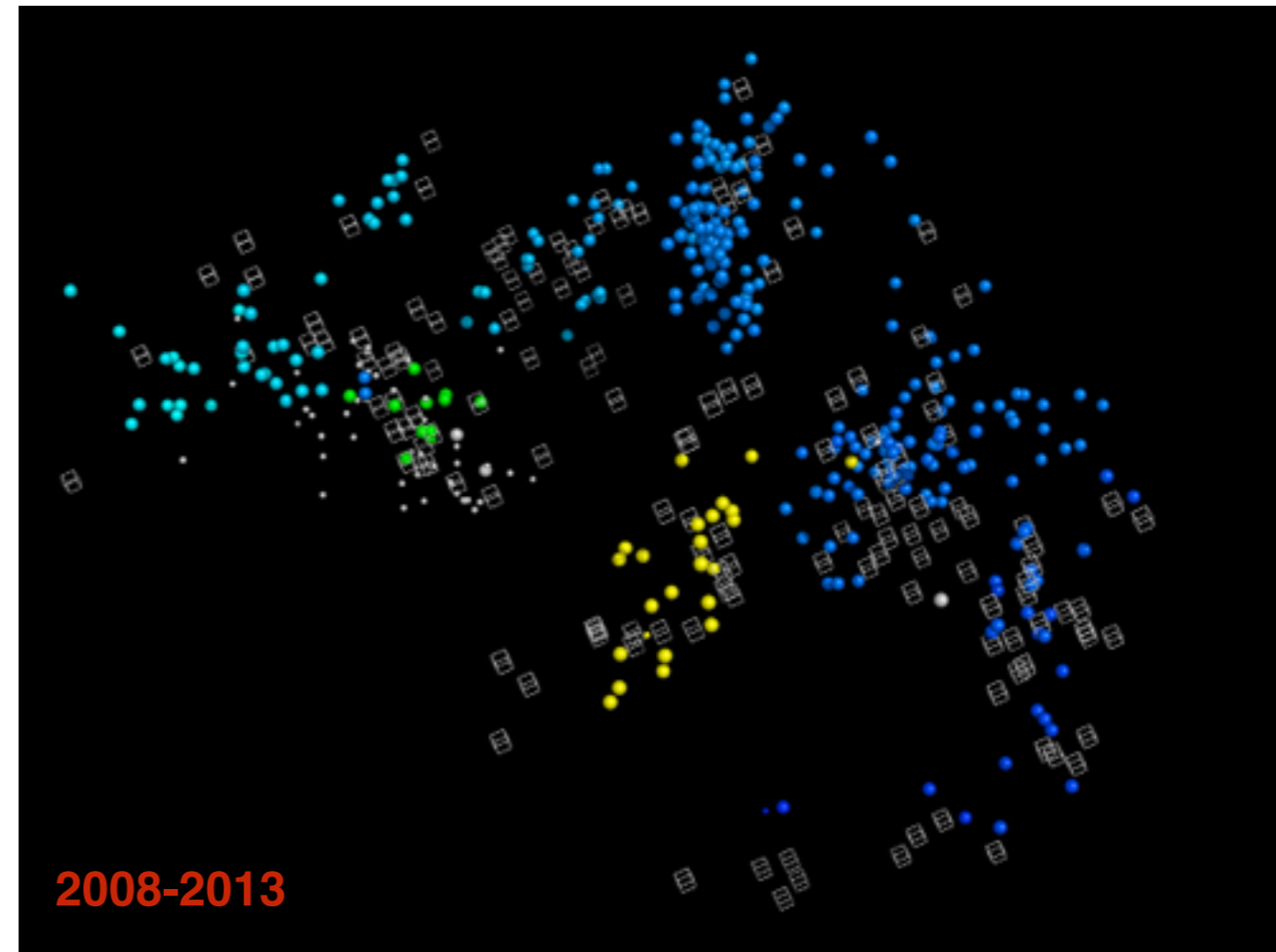


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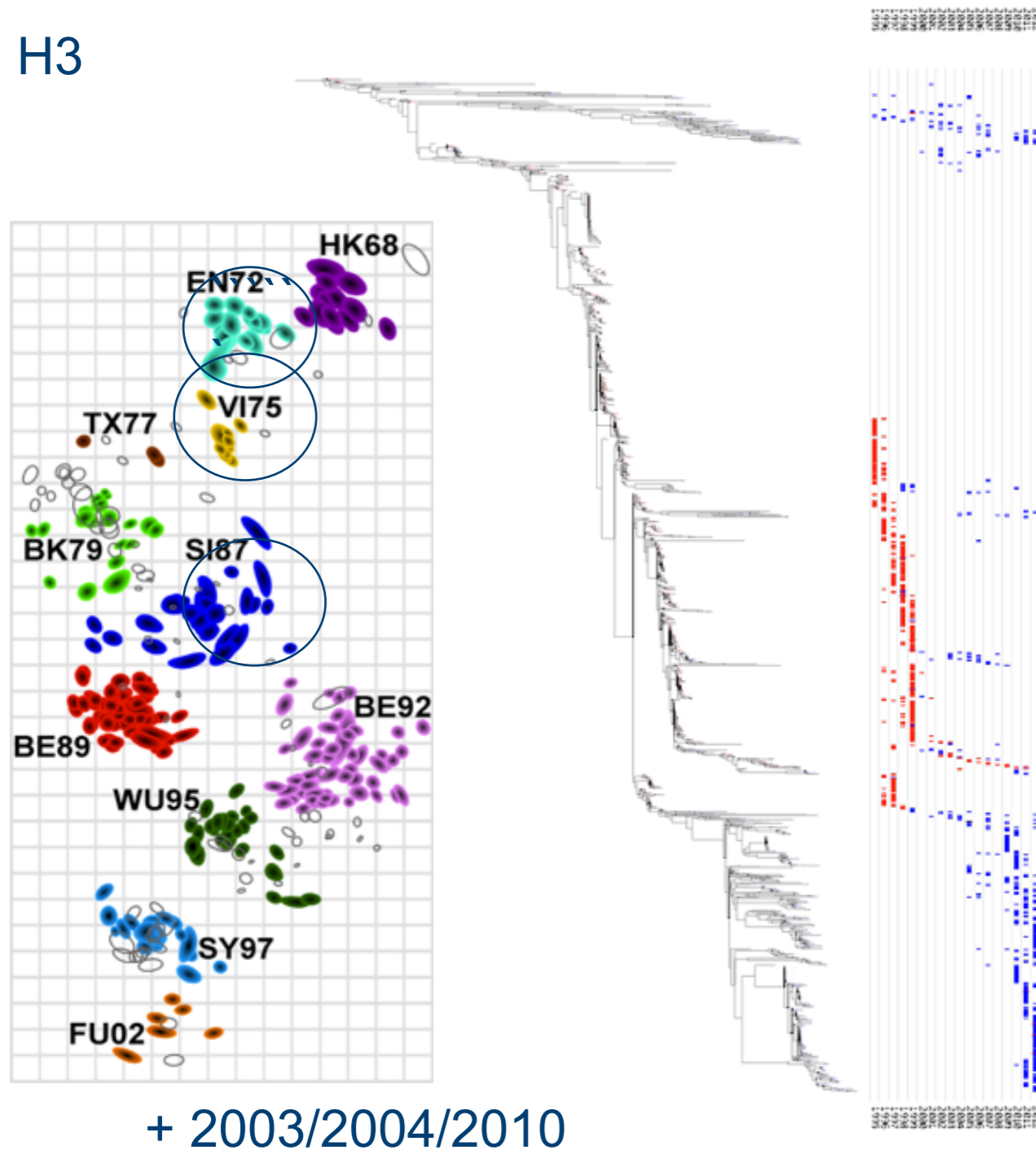


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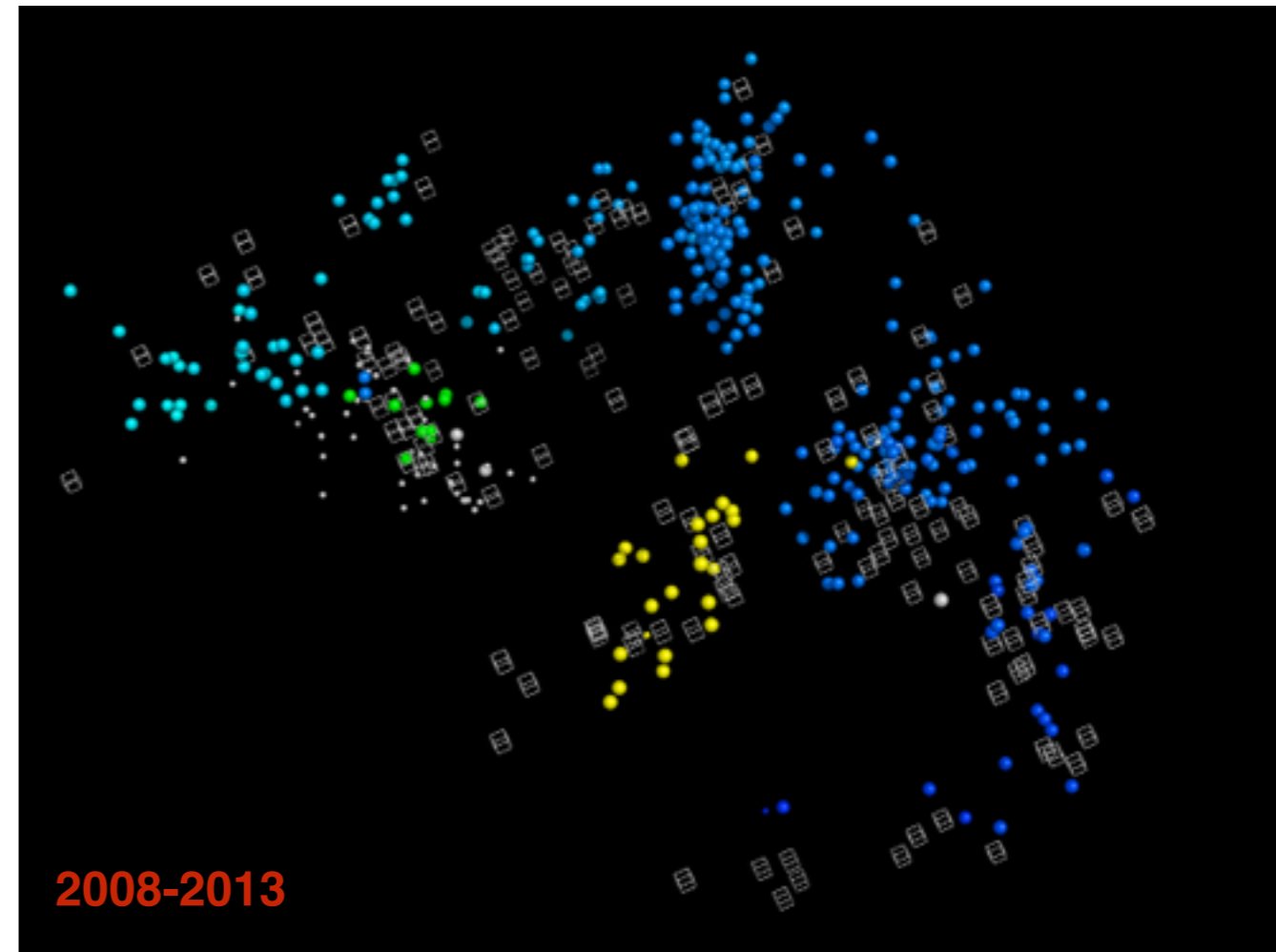


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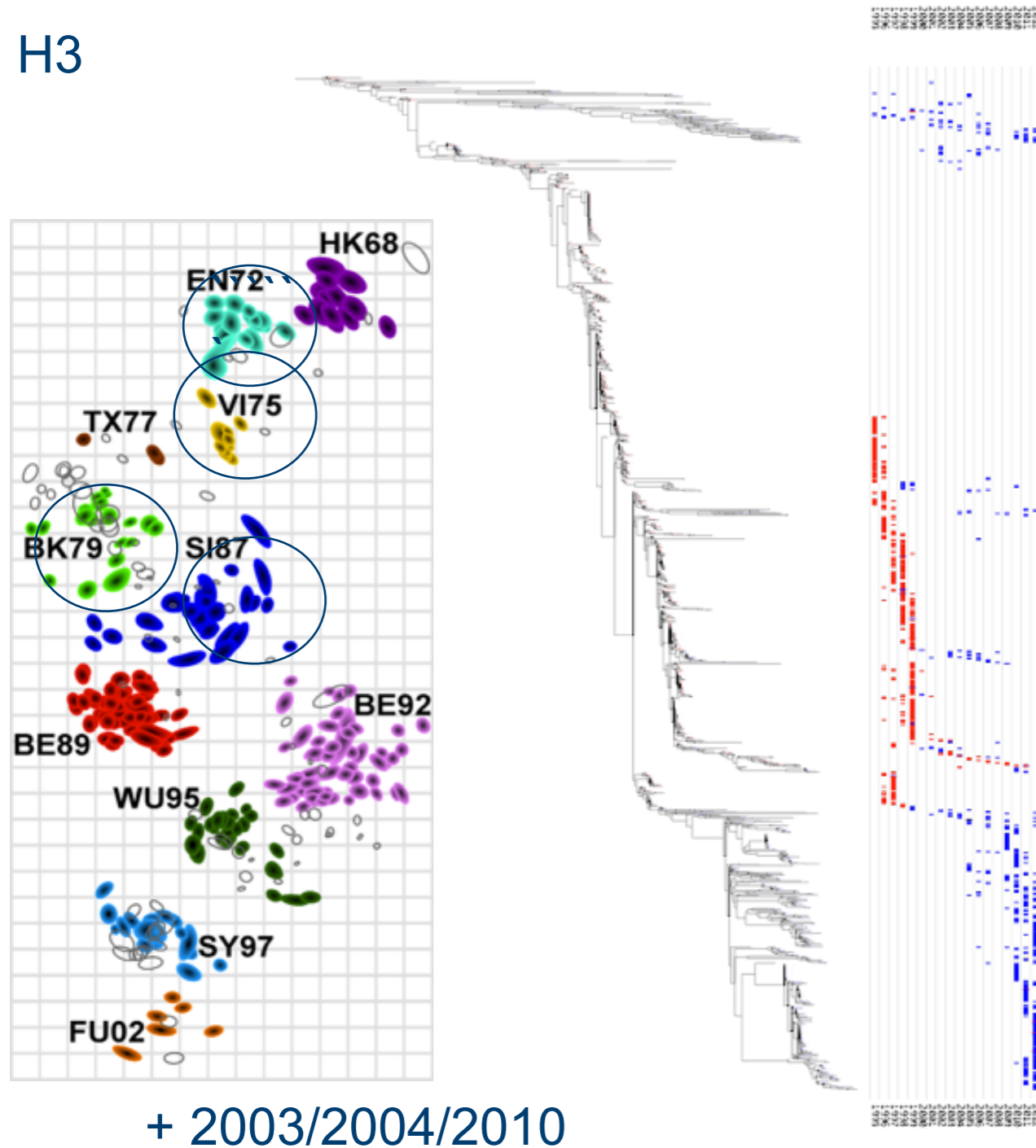


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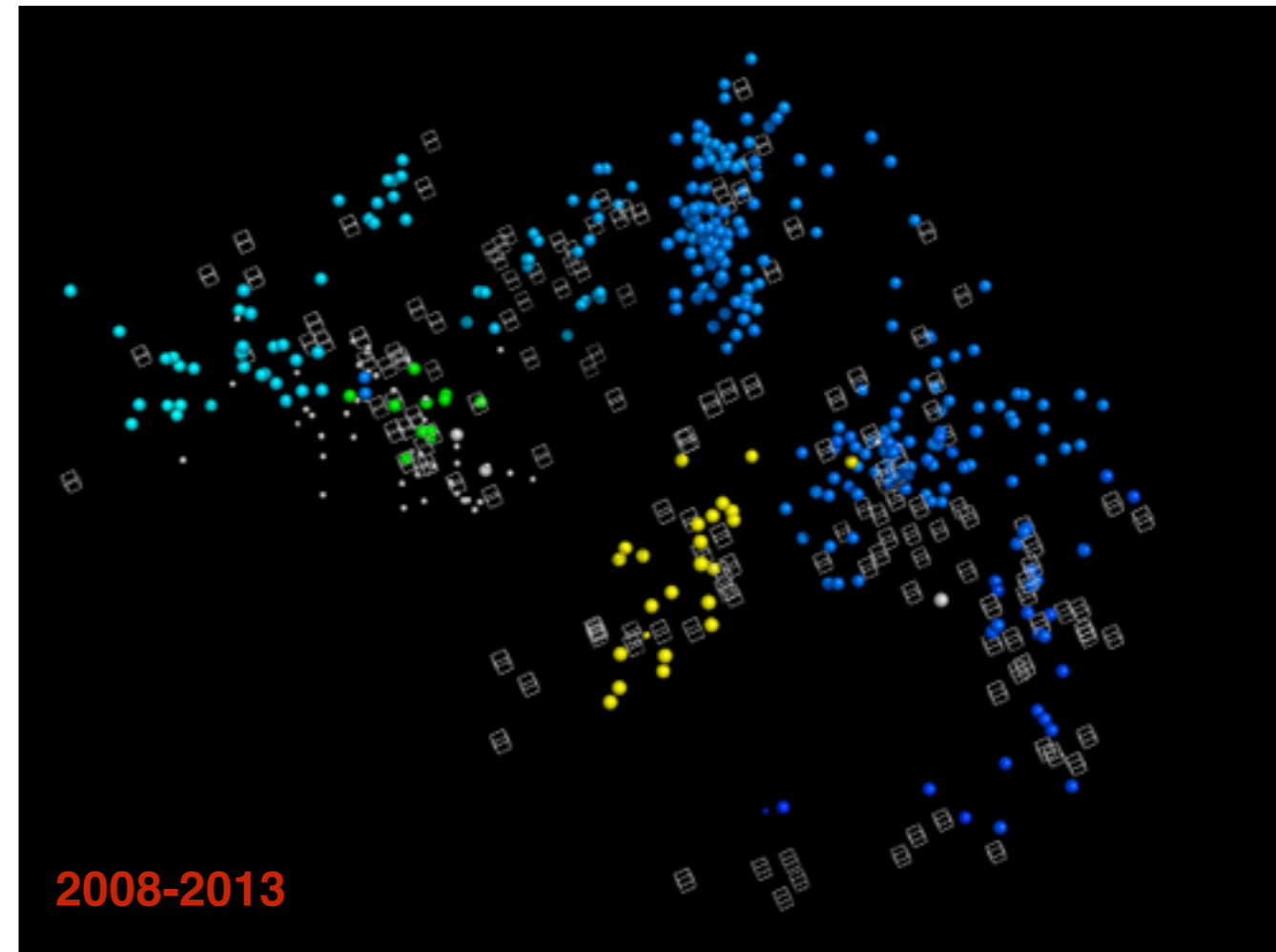


Human and swine influenza A viruses: H3

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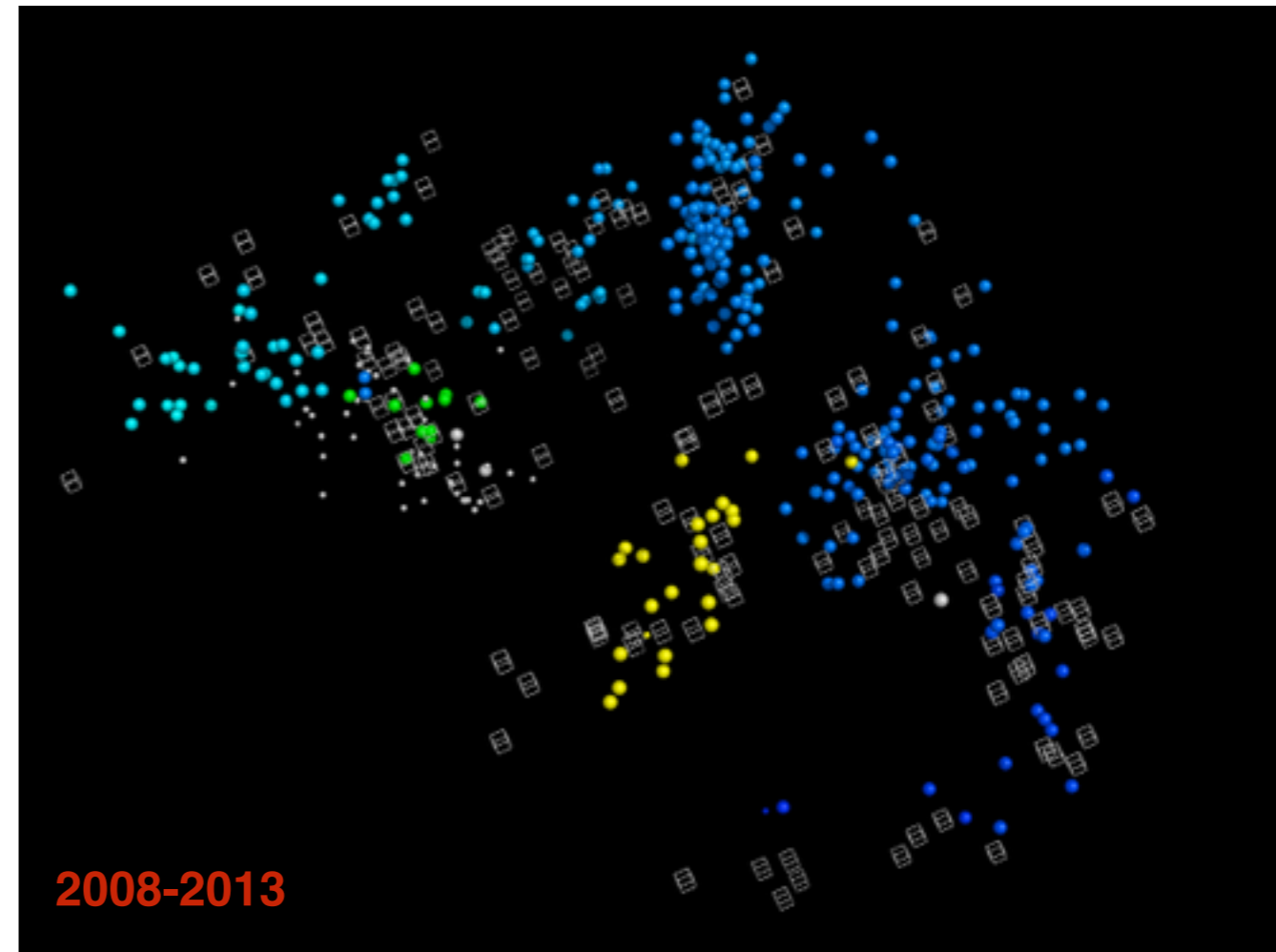
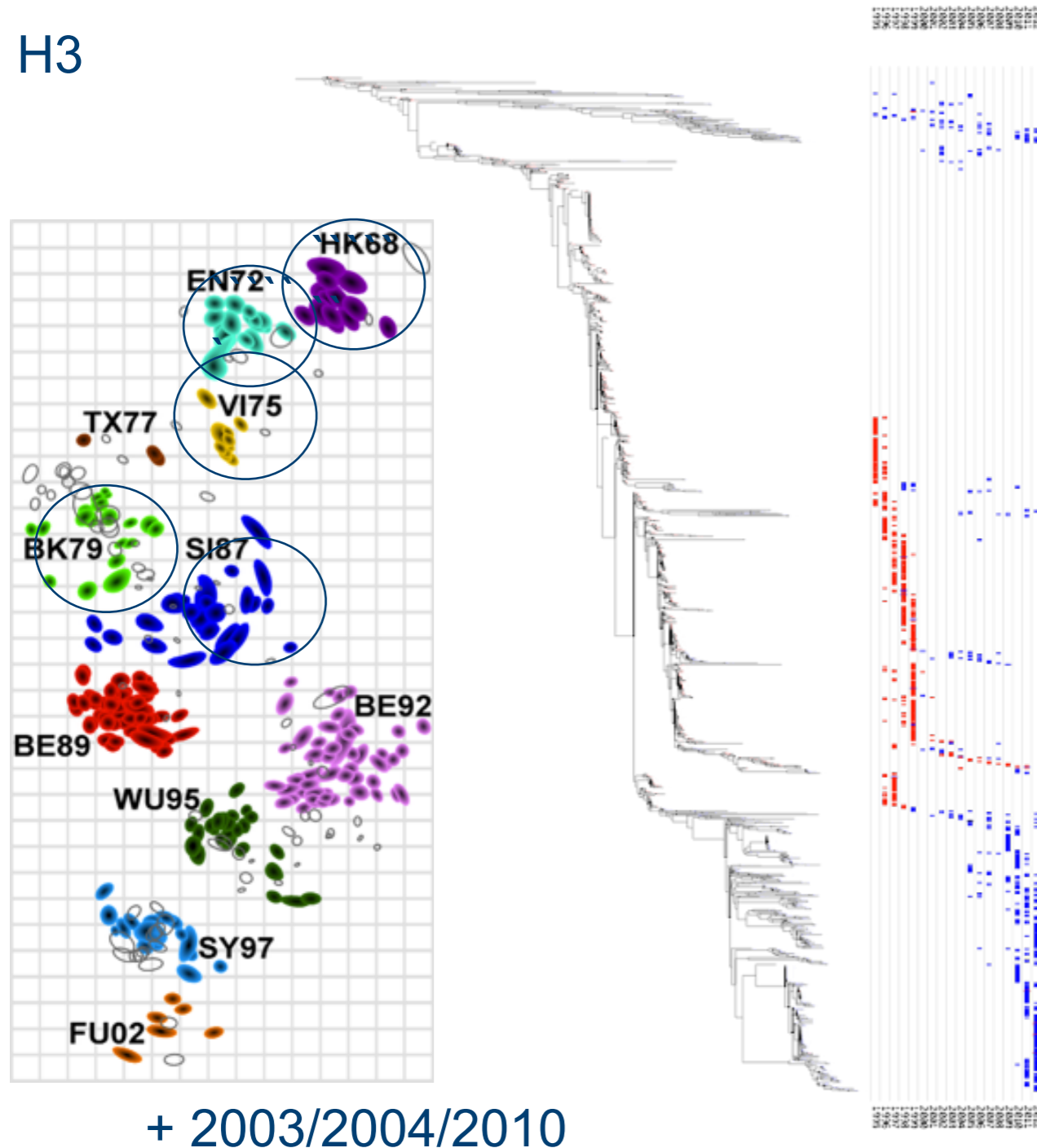
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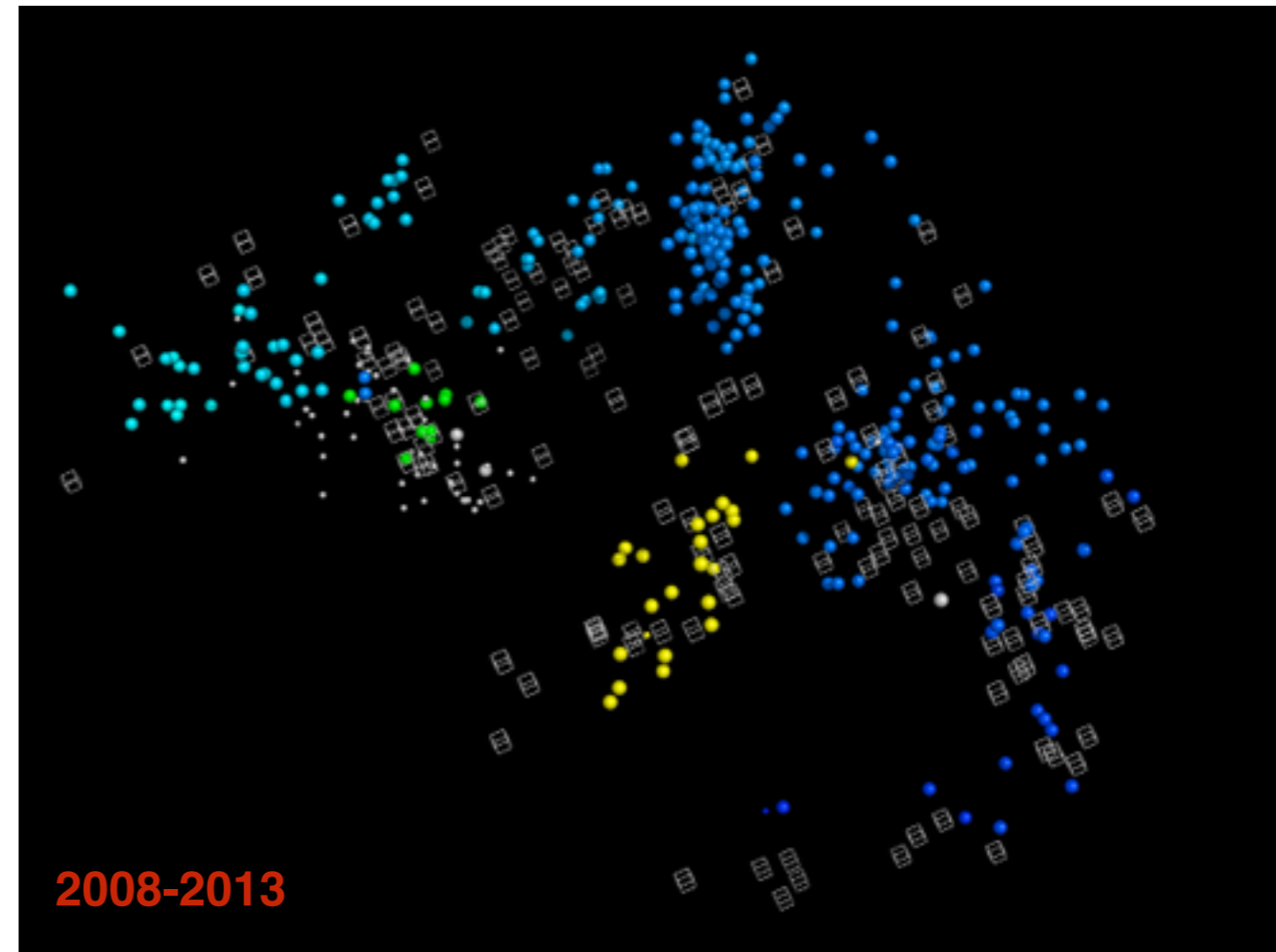
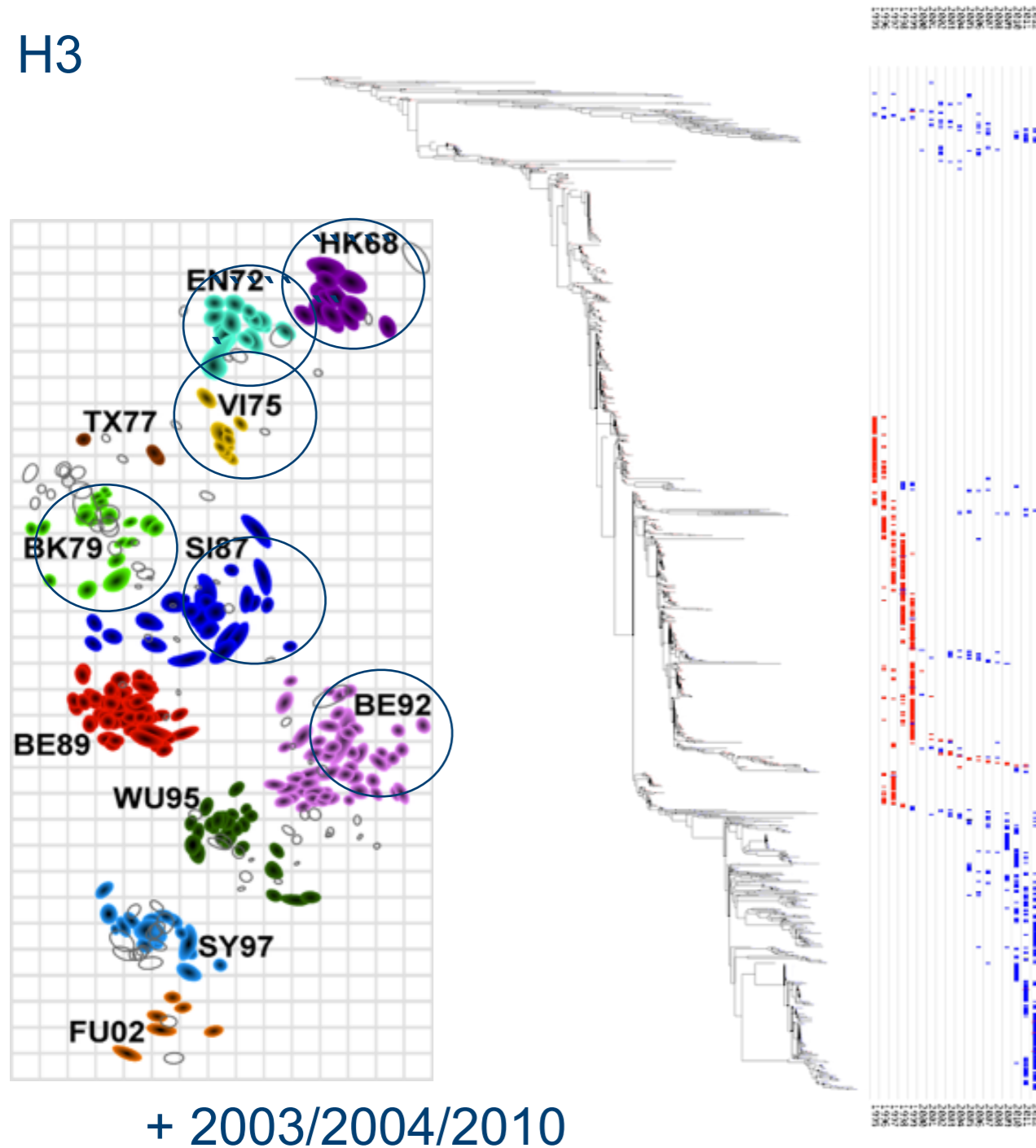
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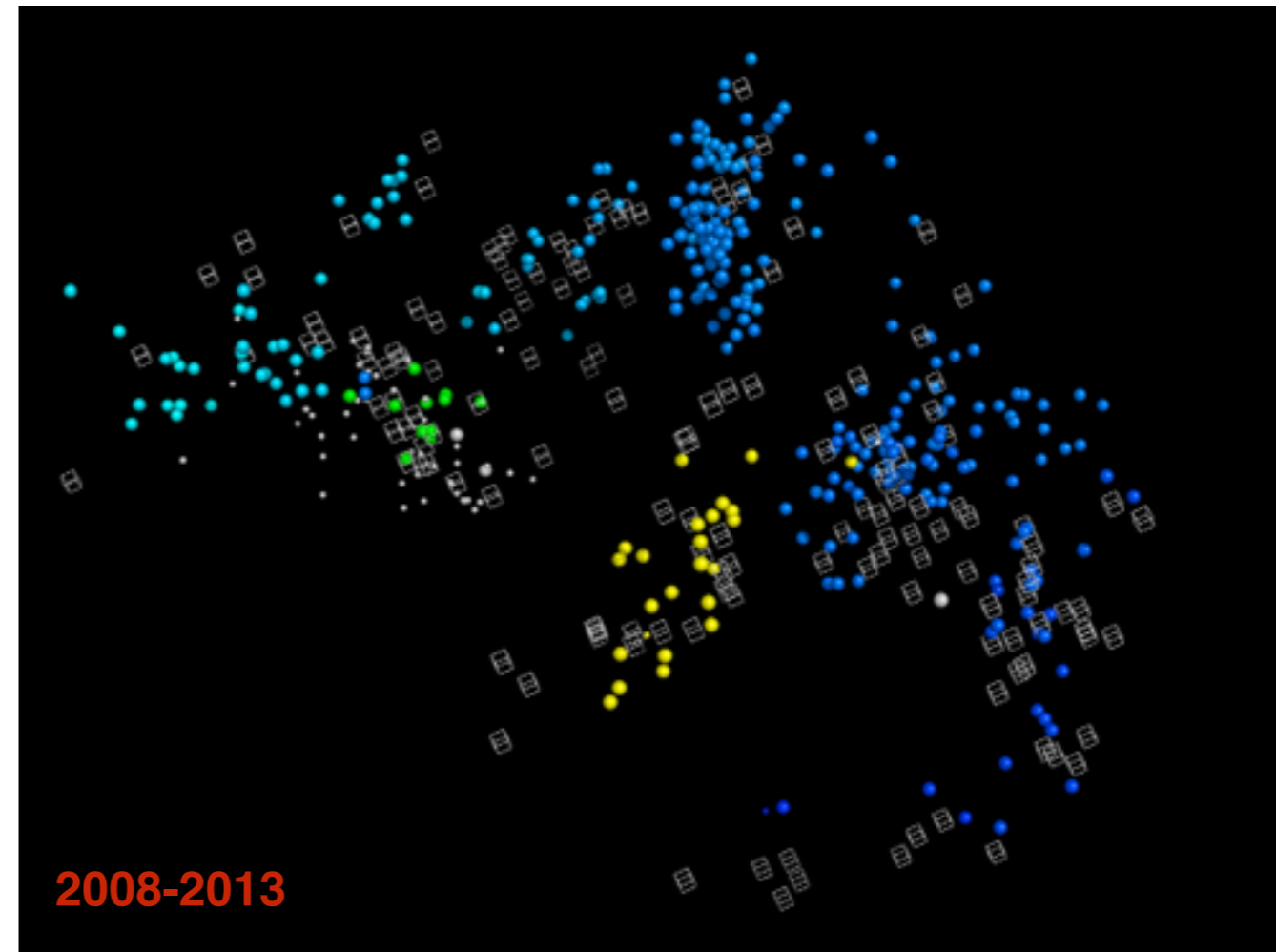
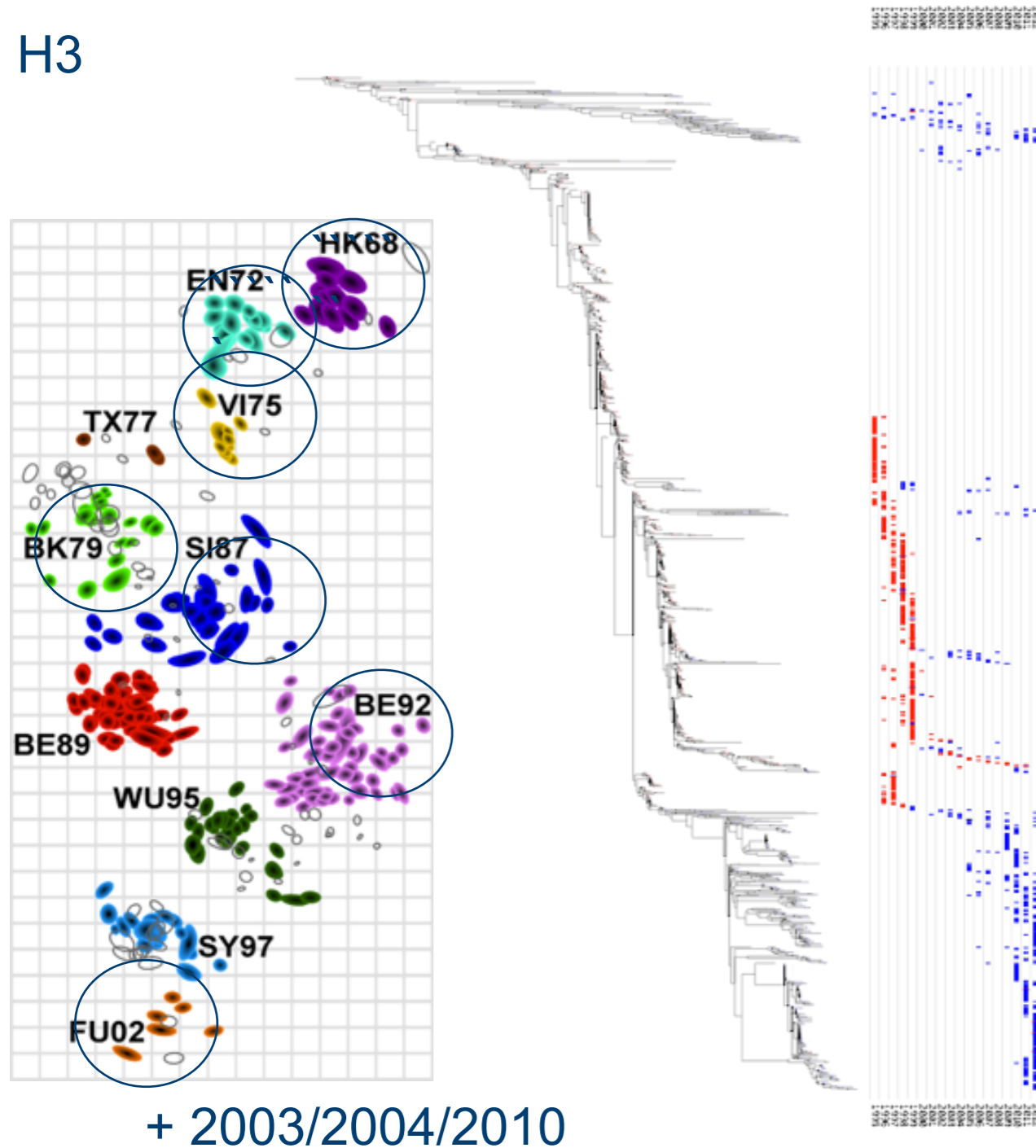
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H3



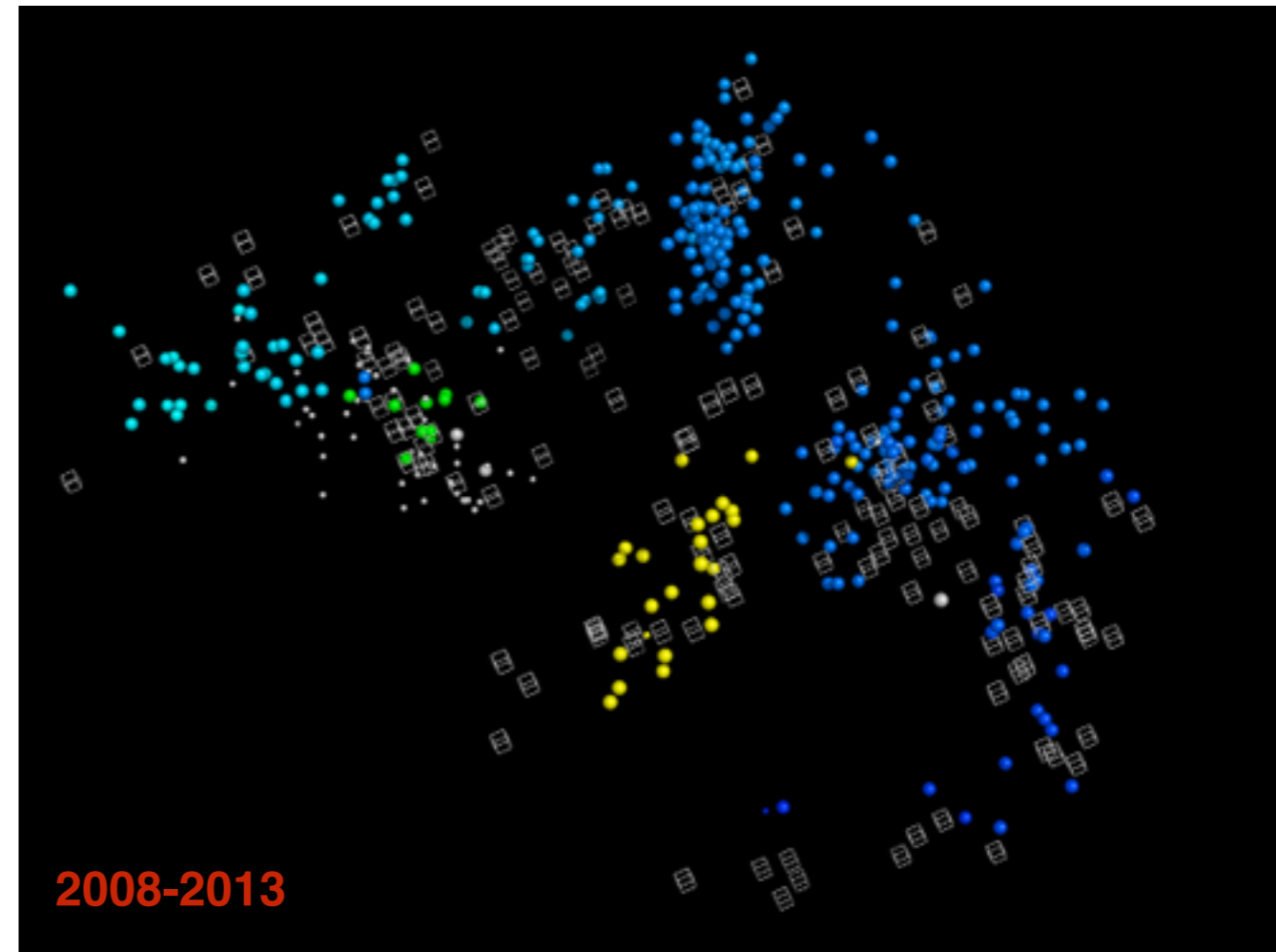
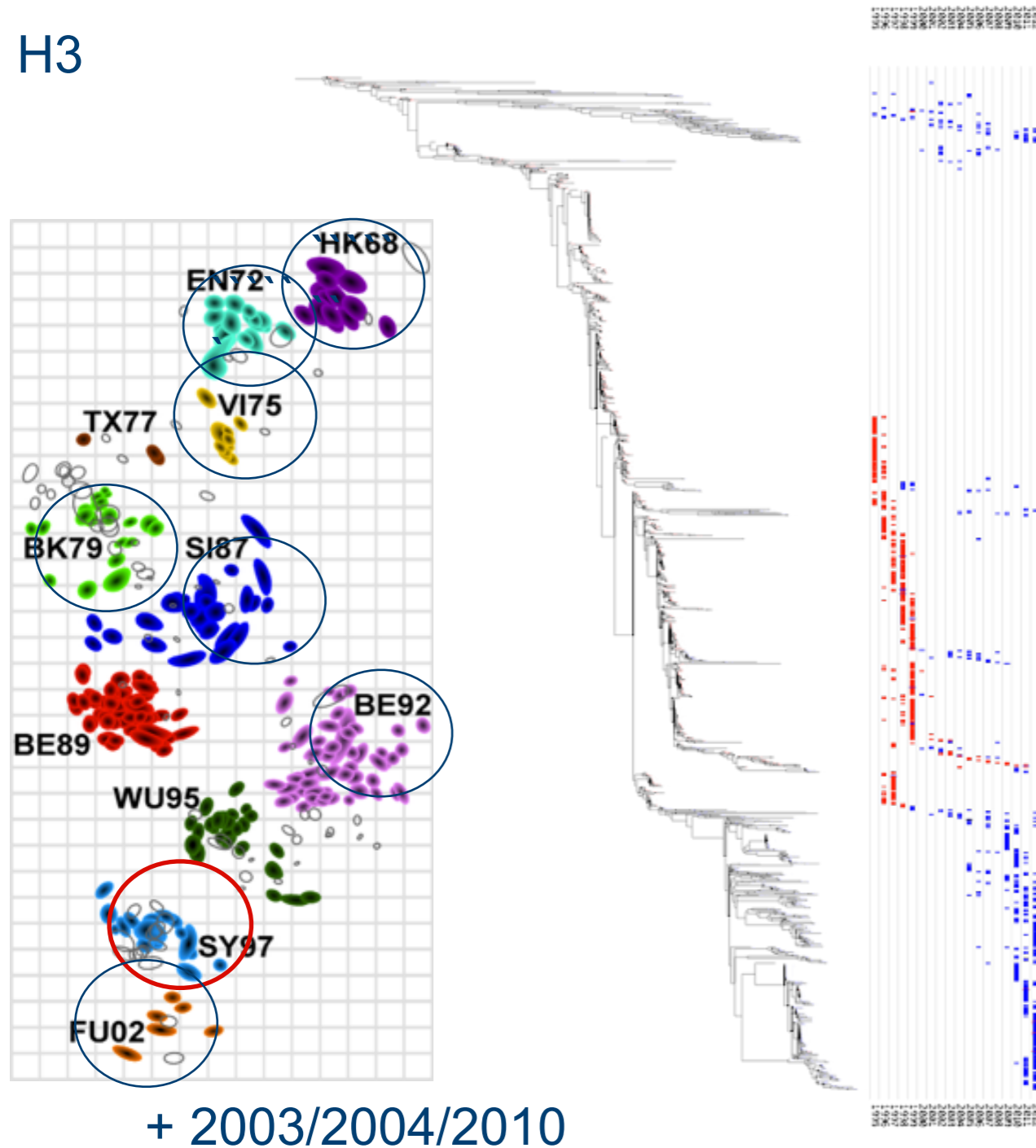
Human and swine influenza A viruses: H3

H3



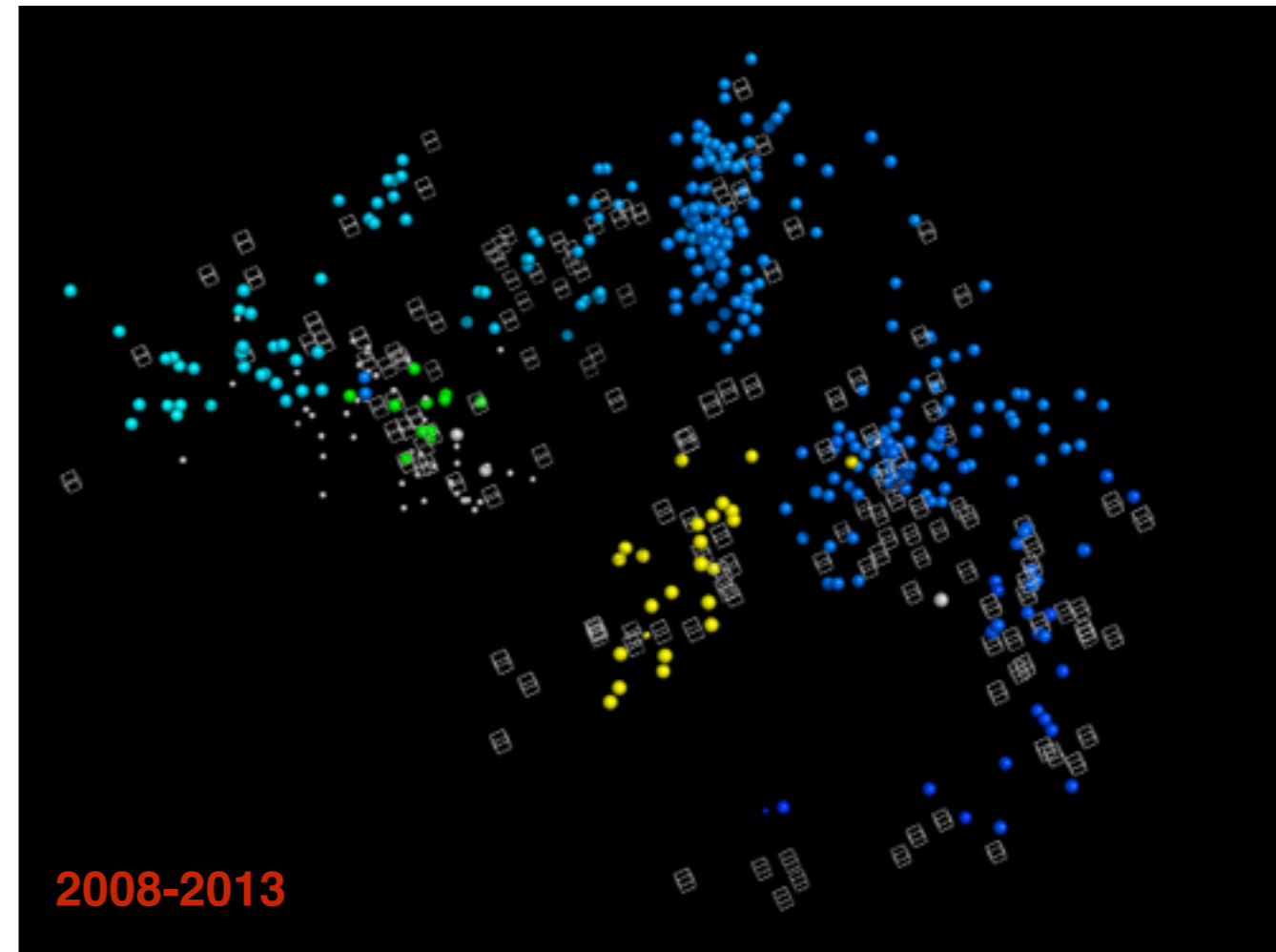
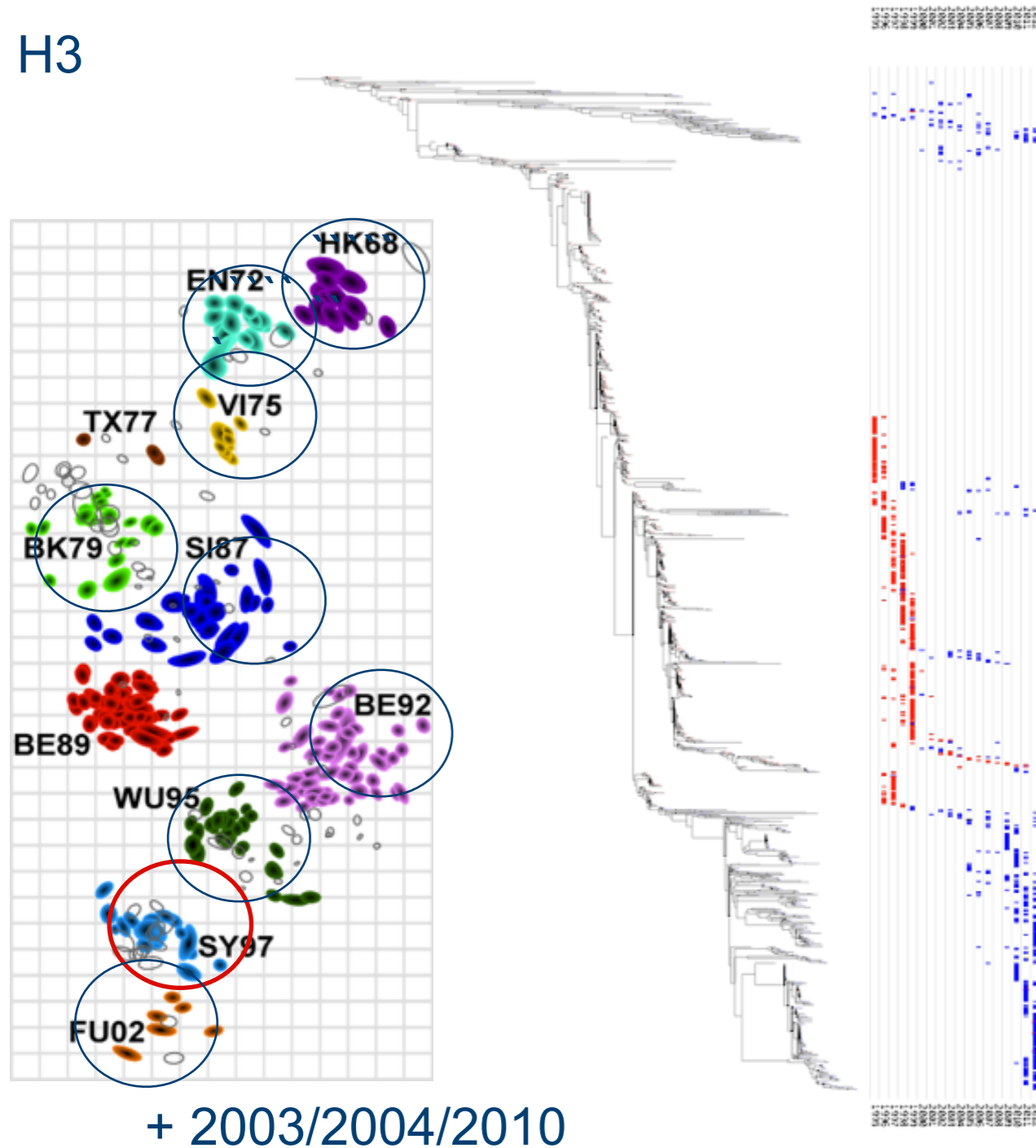
Human and swine influenza A viruses: H3

H3

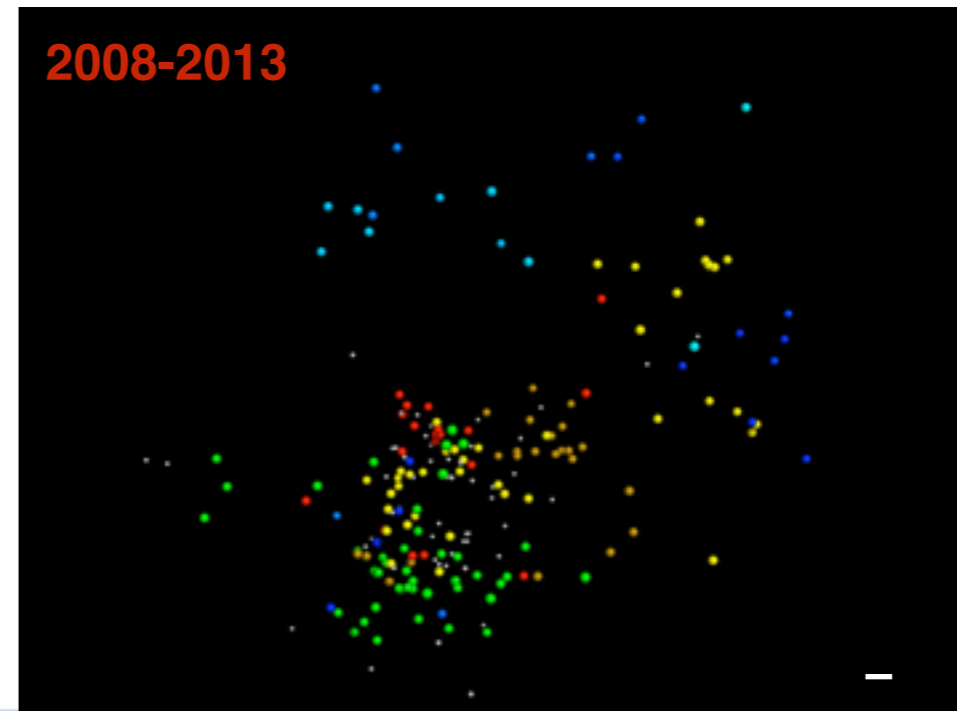
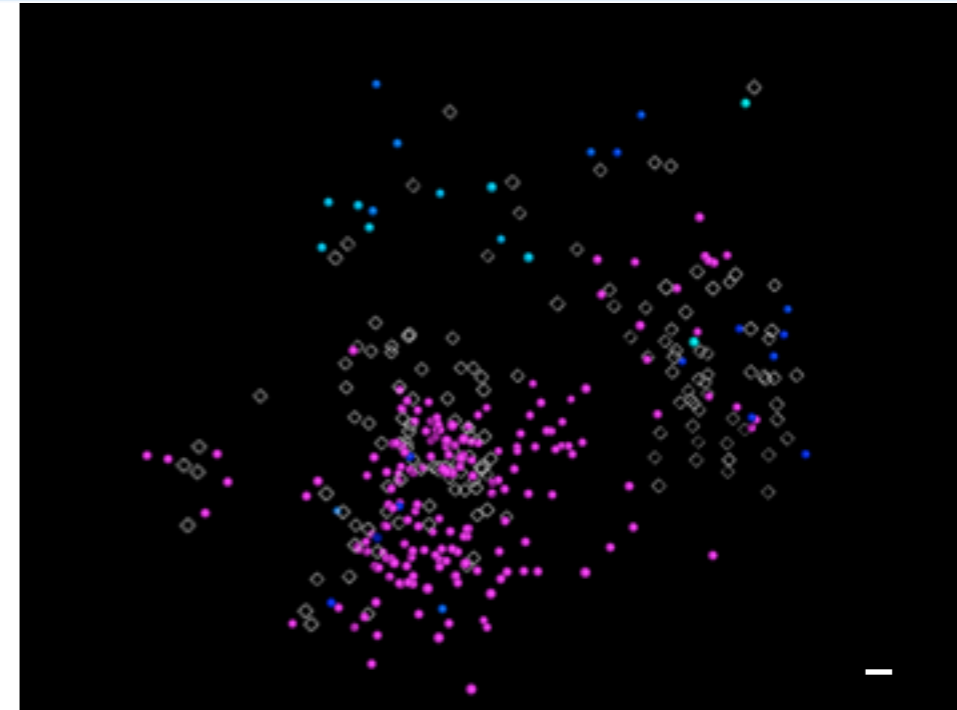
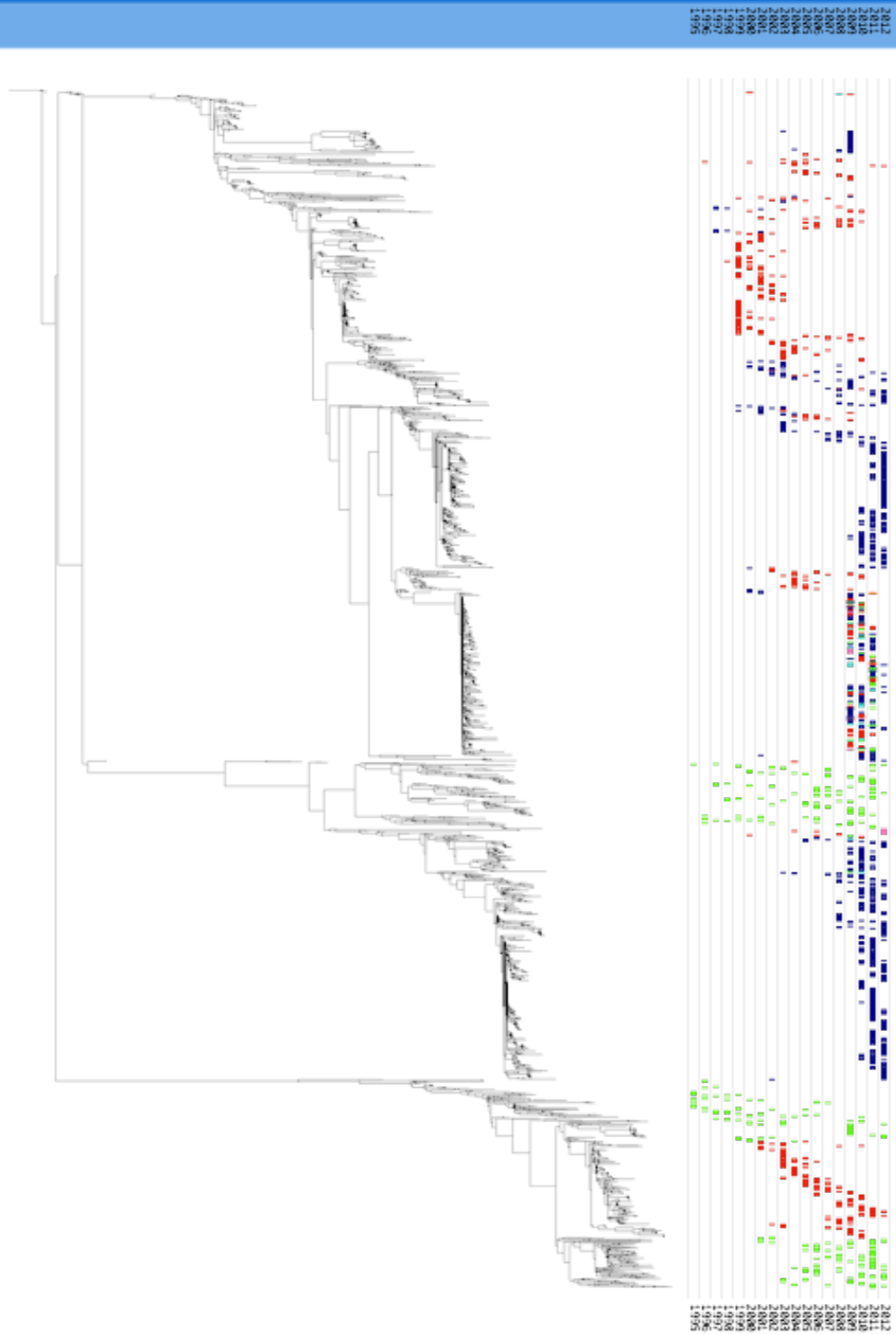


Human and swine influenza A viruses: H3

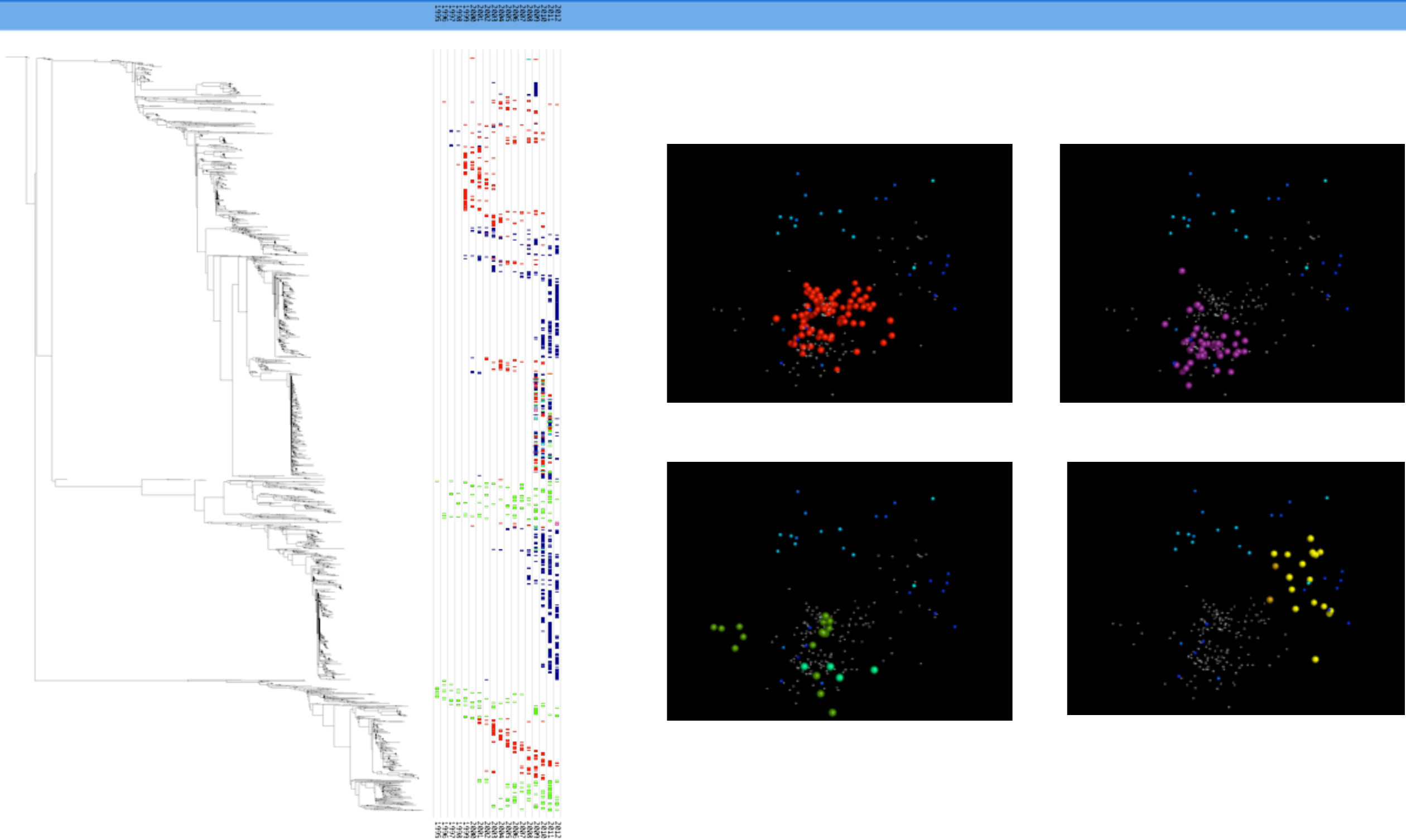
H3



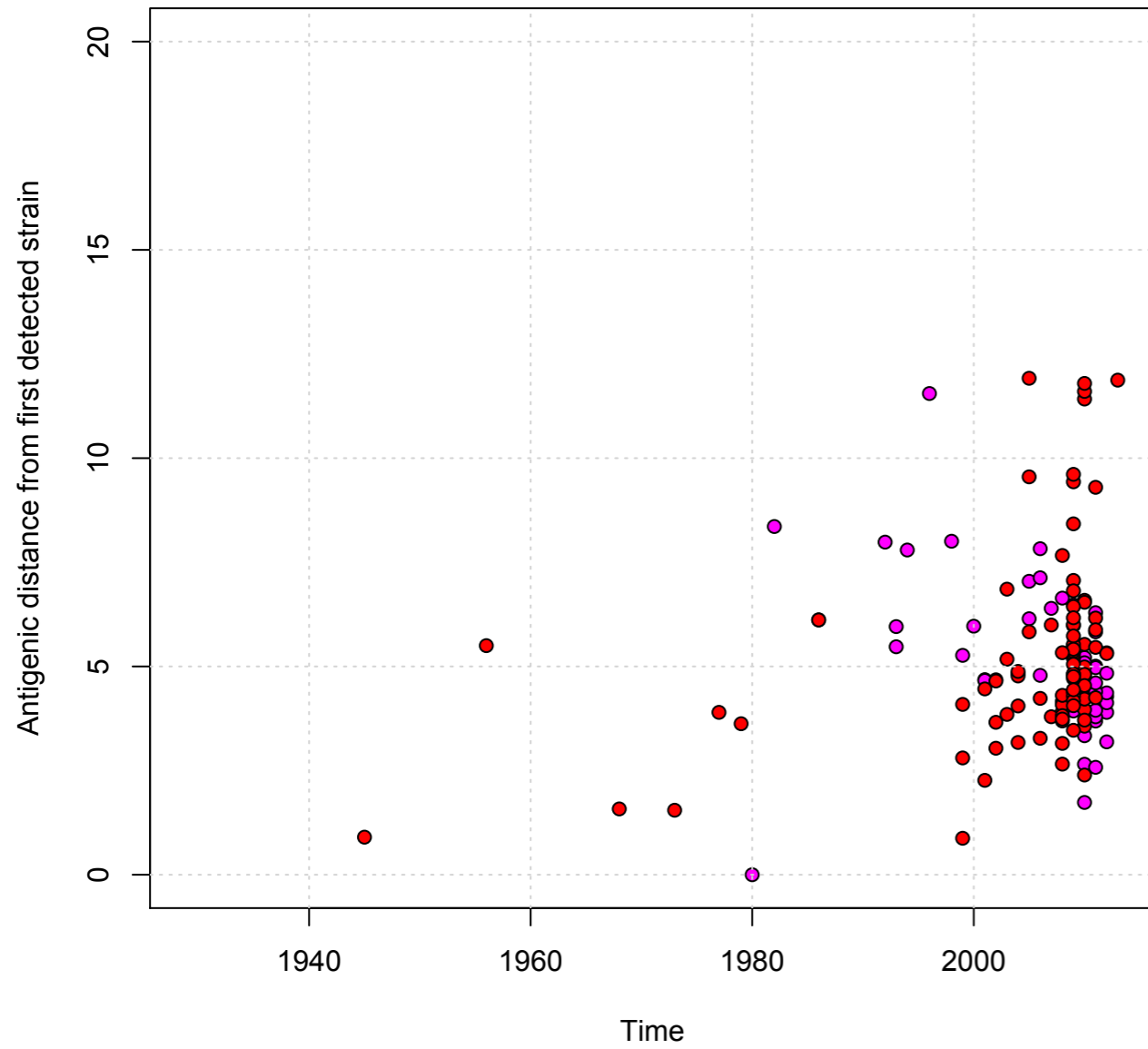
Human and swine influenza A viruses: H1



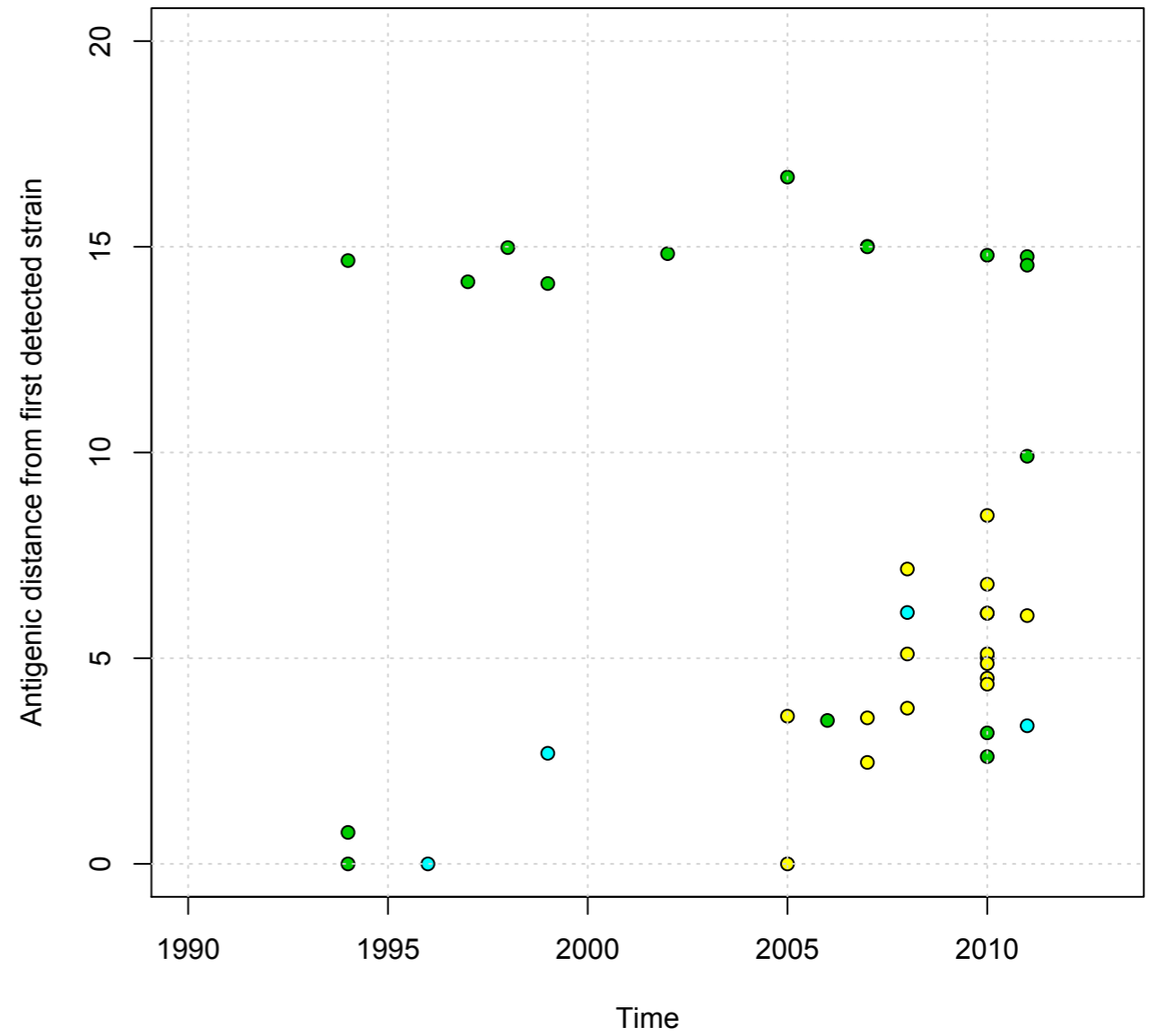
Evolution by introduction



Avian and Classical



human H1 seasonal





Discussion

Comments on the results???

**Publication: next steps a) human serum panel
b) which journal if no serum panel data**

**Long term benefit to surveillance and animal/public health?
Do we need to advocate for global risk assessment mechanism/
continuous antigenic monitoring as well as sequence data?**

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