

# SARS-CoV-2 Evolution in Companion Animals

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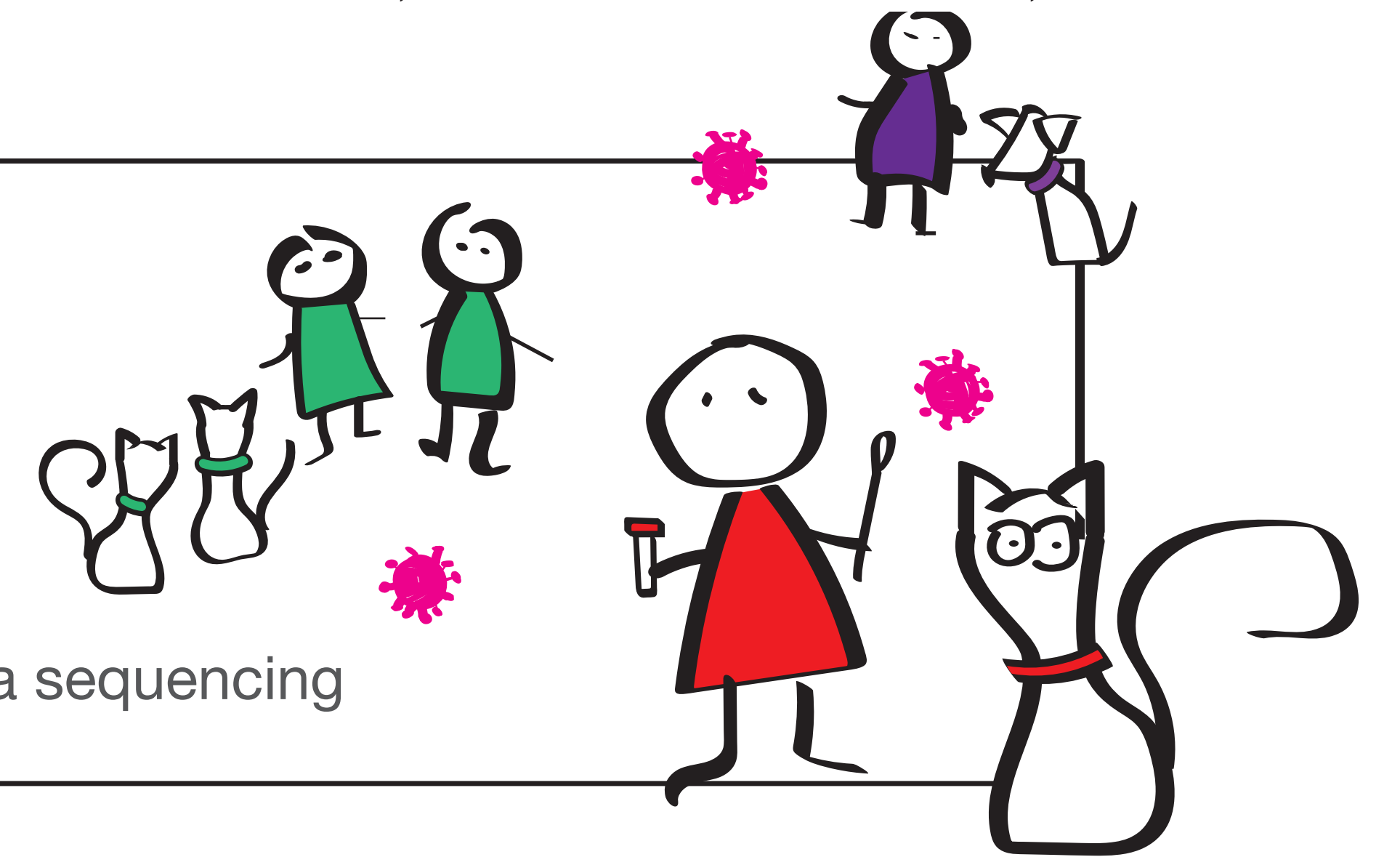
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## DATA

34 Swiss households  
34 cats, 15 dogs and 39 owners  
142 sequences + negative controls

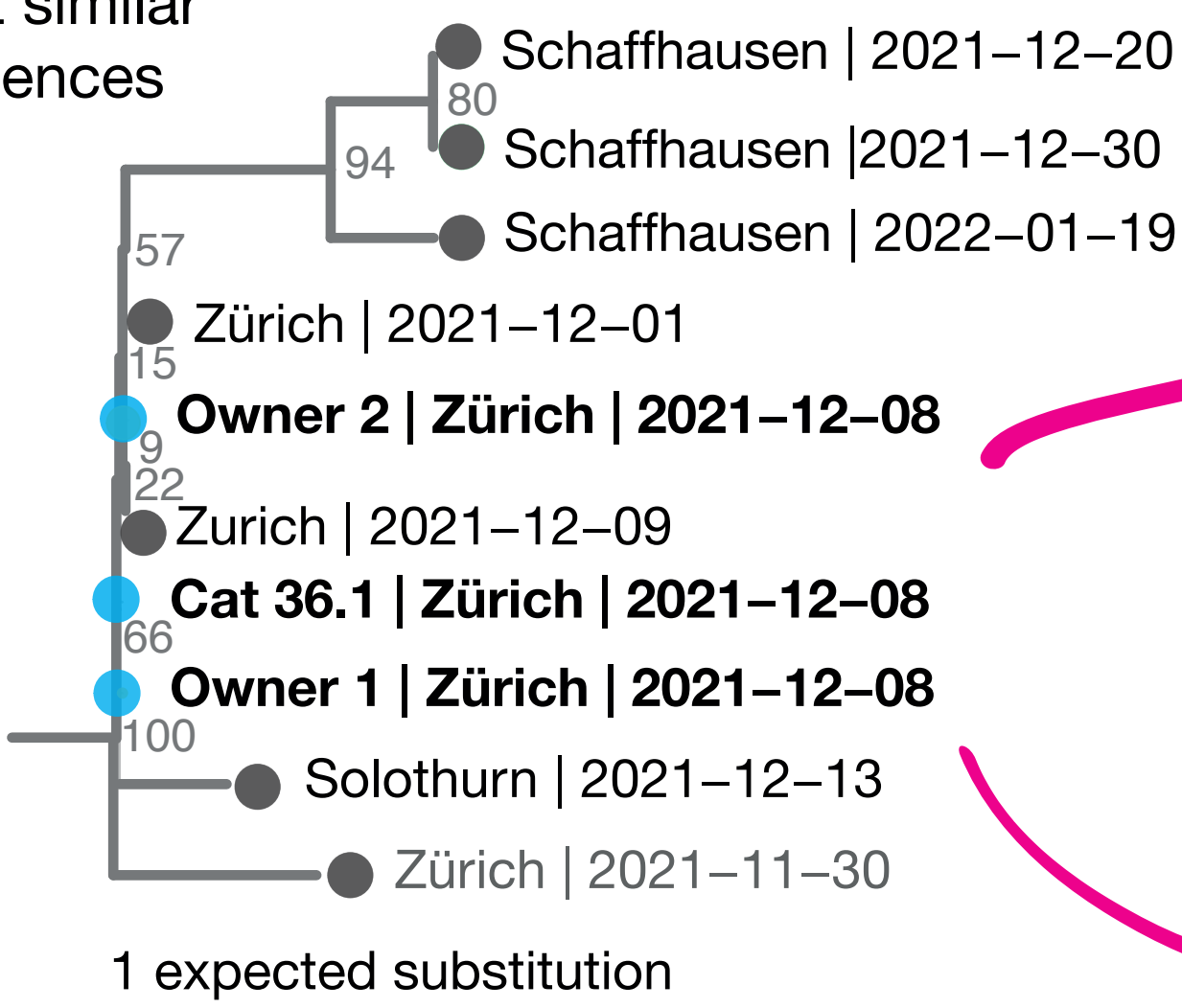
✂ Samples taken by owners  
Vetsuisse RT-qPCR and GFB ETH NGS Illumina sequencing



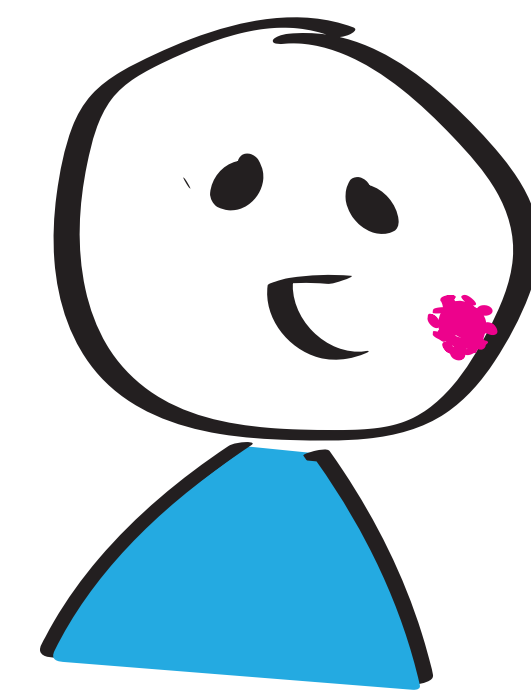
## OWNER TO ANIMAL TRANSMISSION

● Household 36 - AY.43

● Most similar sequences

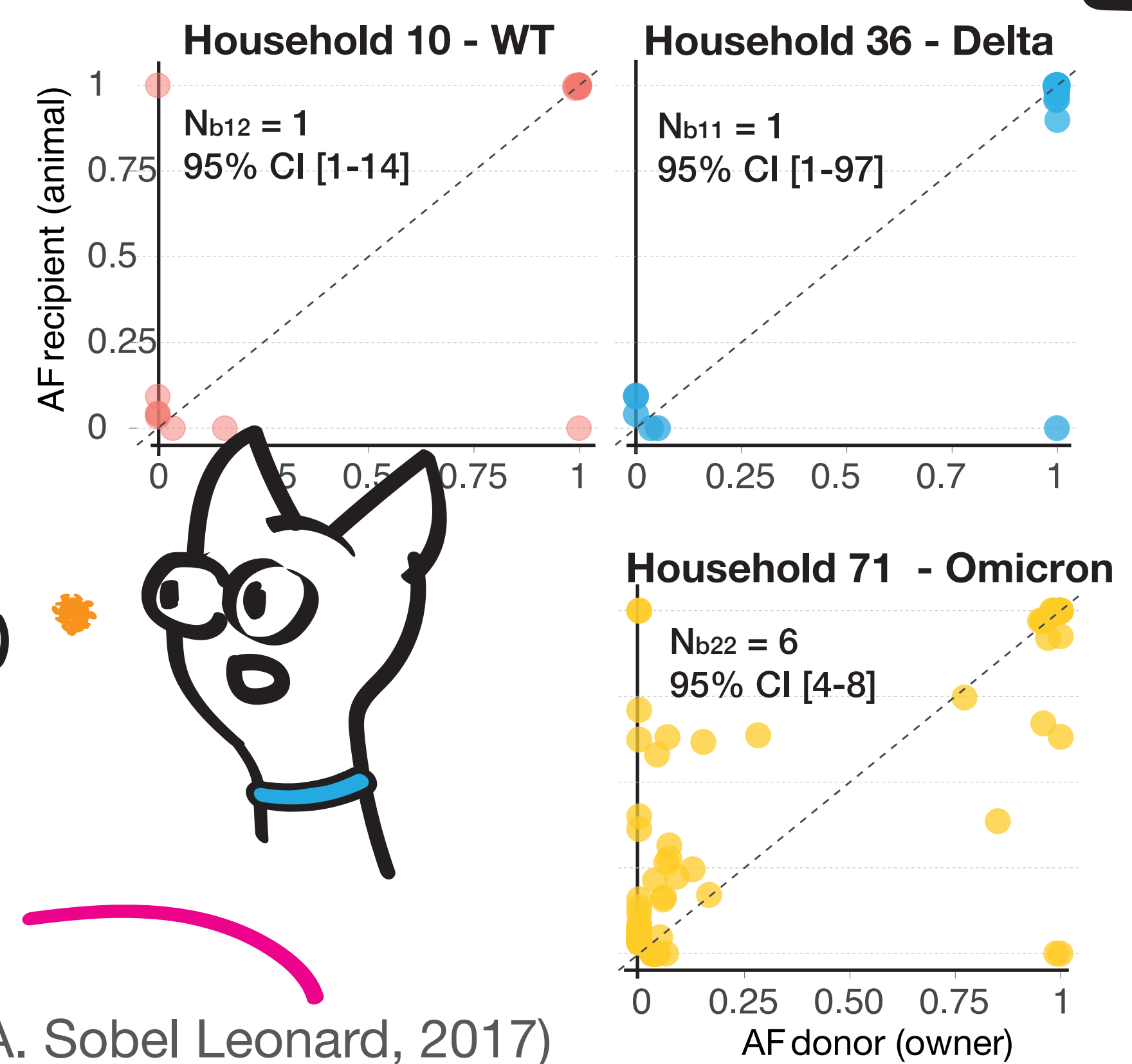


Consensus sequences owner-animal  
≈ identical or ≤ 3 SNVs differences



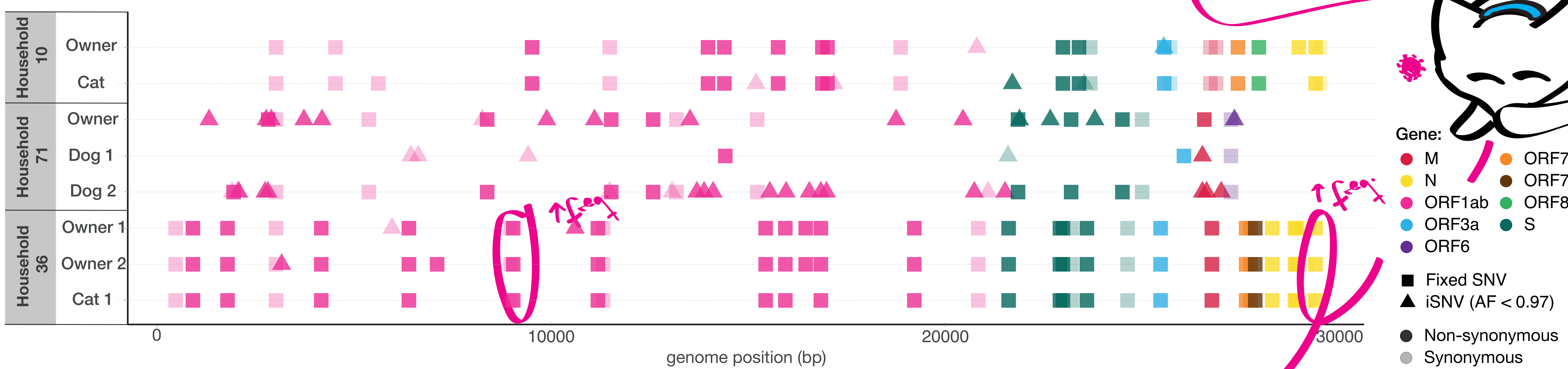
Bottleneck Size ( $N_b$ ) 1-6 ≈ similar to Human to Human transmission estimates

✂ Beta Binomial sampling Bottleneck estimation (A. Sobel Leonard, 2017)



✂ NGS data analysis: V-pipe  
ML tree: iqtree2

## WITHIN-HOST DIVERSITY IN COMPANION ANIMALS

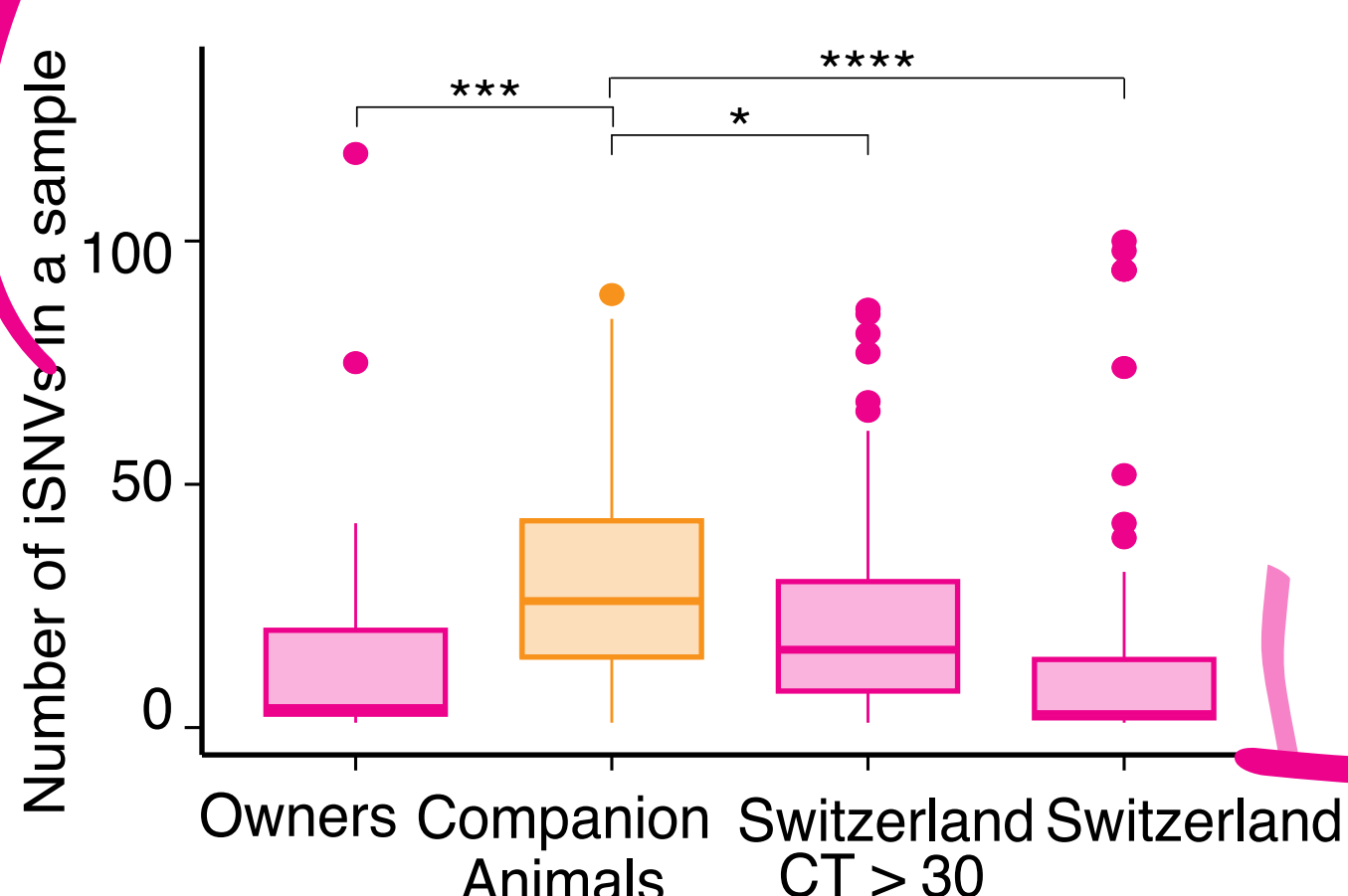


More iSNVs in companion animal samples than owner's, but the lower viral load ( $CT > 30$ ) could entail low sequencing quality/contamination

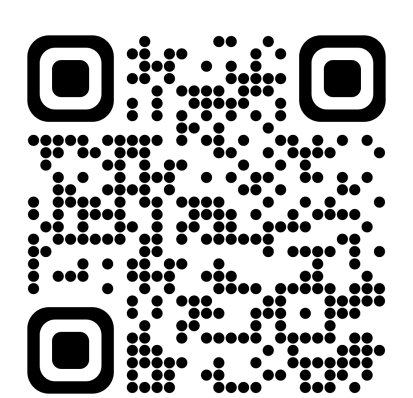
↑ Increased frequency of certain mutations (owner + animals) in comparison to Community

✂ SNV frequencies: LAPIS covSPECTRUM  
Pangolin and Nextclade

✂ Variant calling: LoFreq MAF 3% DP min. 100  
SNV annotation: Ensembl VEP



More about Delta within-household transmission and phylogenetics



## SUMMARY

NGS data supports owner - animal transmission, with small bottleneck size ≈ other Human to Human estimates (large household variability)

Larger ↑ within-host diversity in animals, (? related to low viral load) + animal serial samples

↑ Increased frequency of some SNVs in animals compared to human sequences

? fitness effect  
✂ MTMF Phylodynamic BD model development

