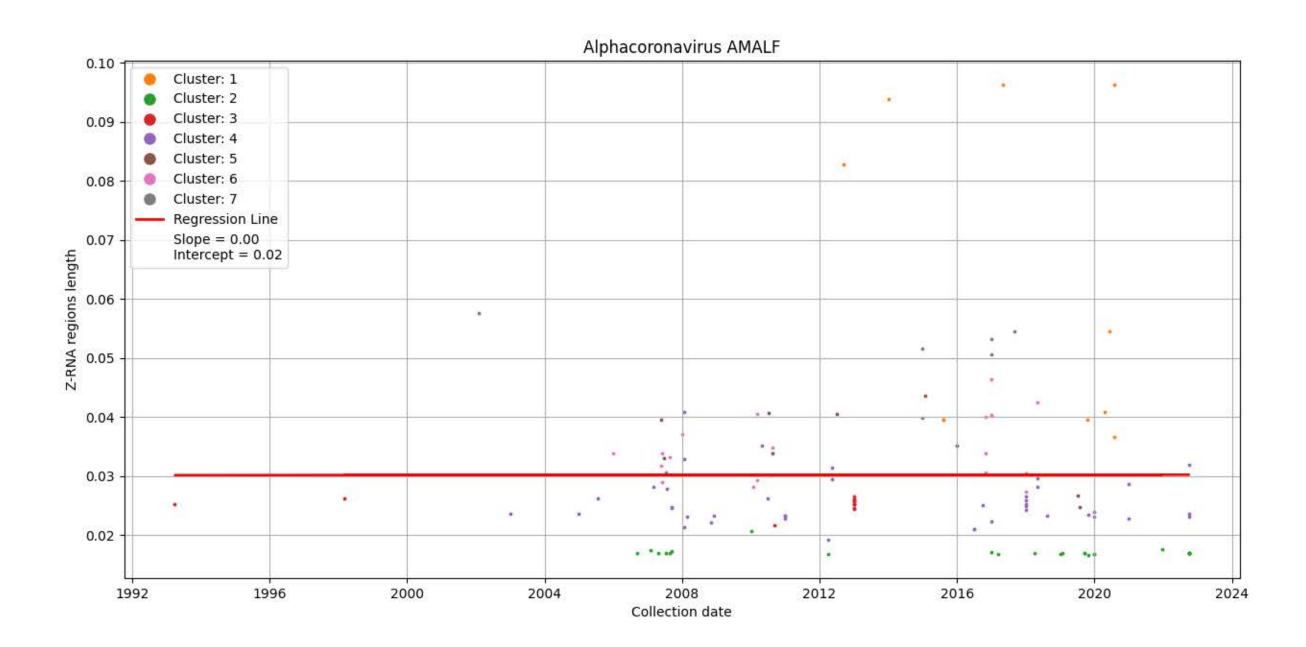
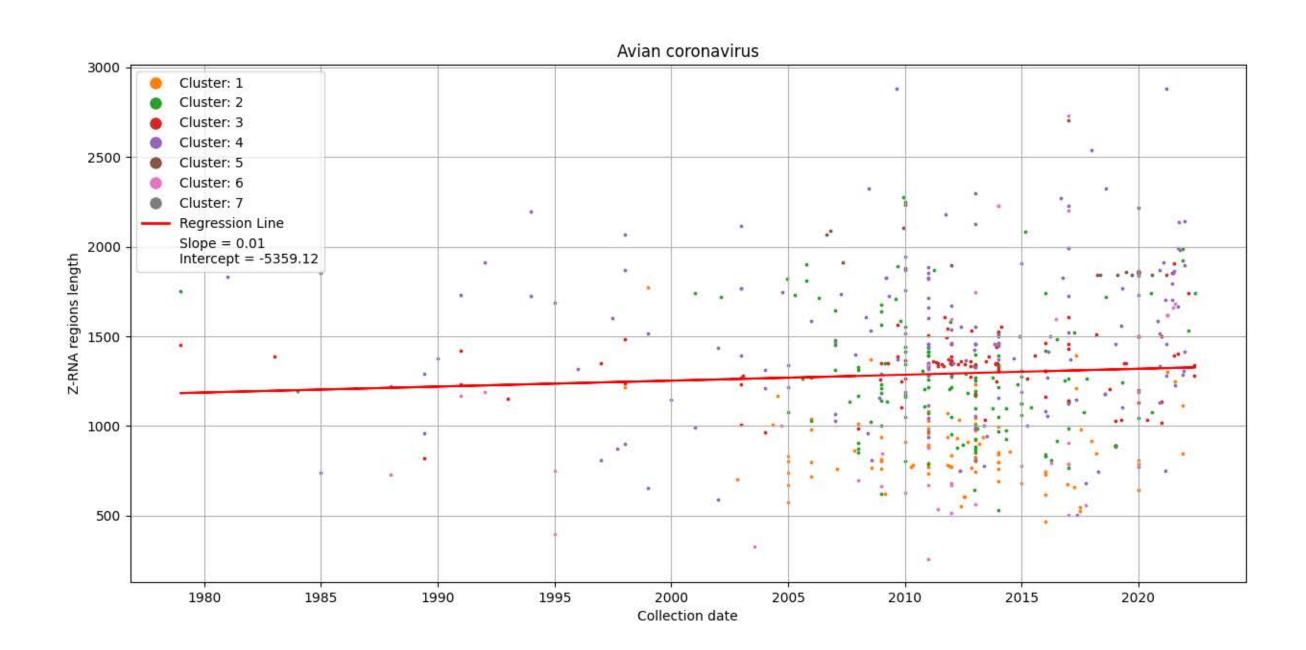
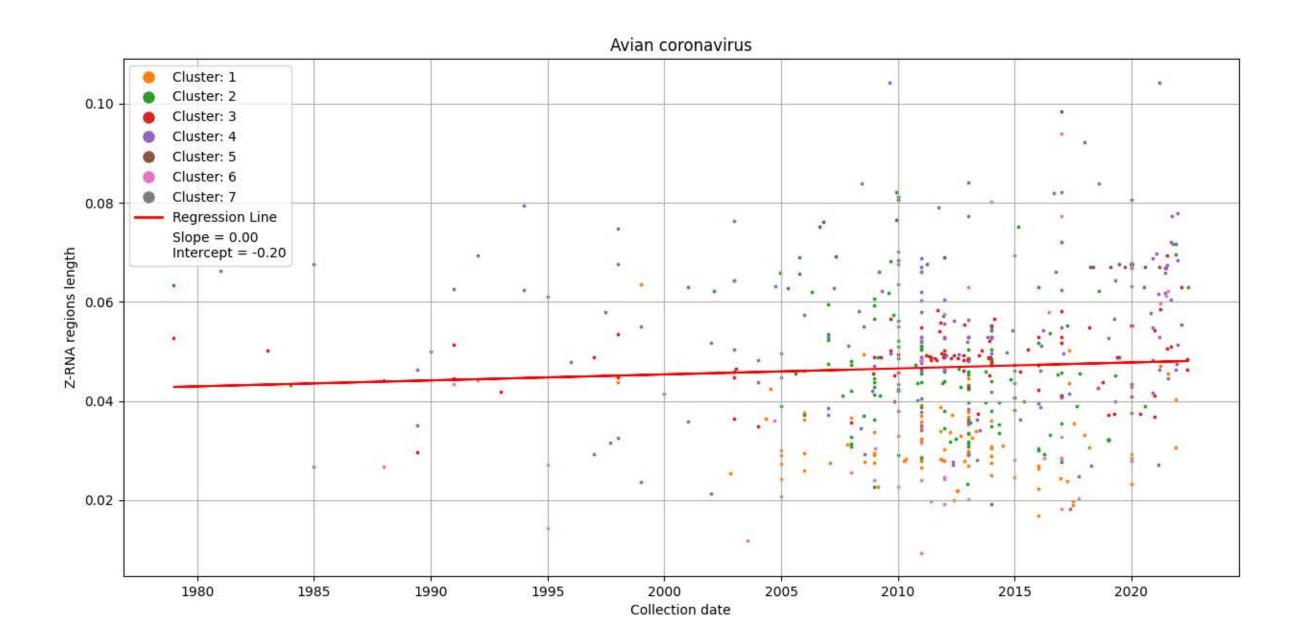


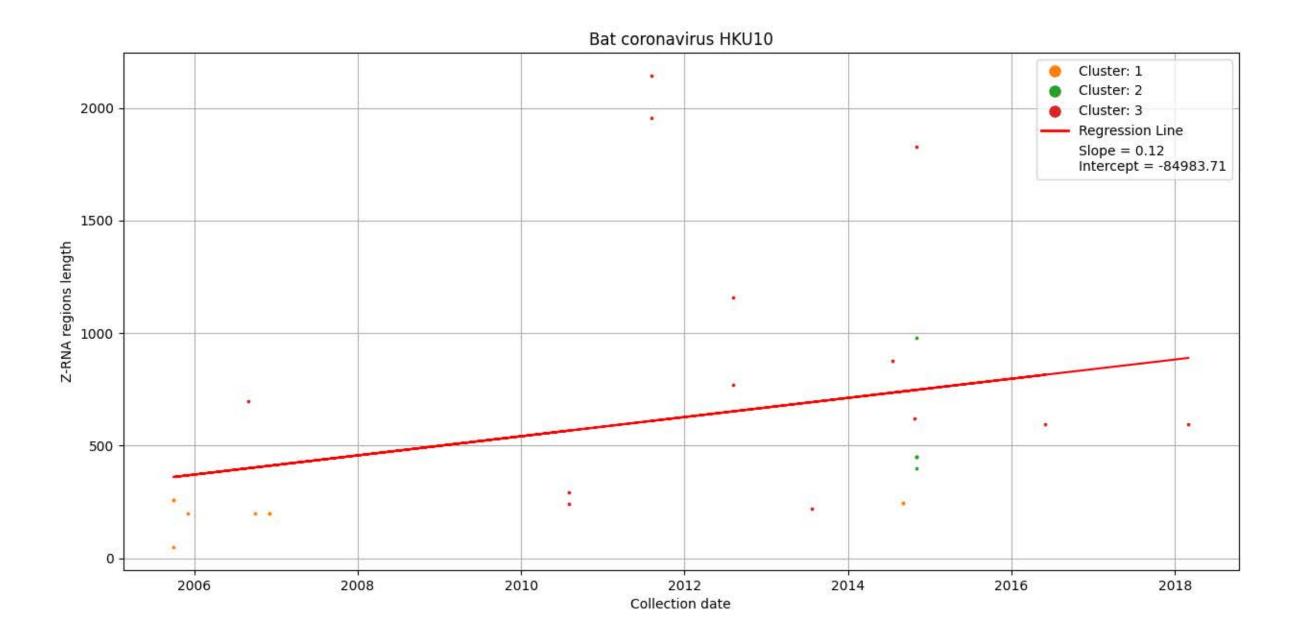
Alphacoronavirus AMALF Cluster: 1 Cluster: 2 Cluster: 3 Cluster: 4 2500 -Cluster: 5 Cluster: 6 Cluster: 7 Regression Line Slope = 0.002000 Intercept = 718.06 Z-RNA regions length 1500 . .. 1000 500 1992 1996 2000 2004 2008 2012 2016 2020 2024

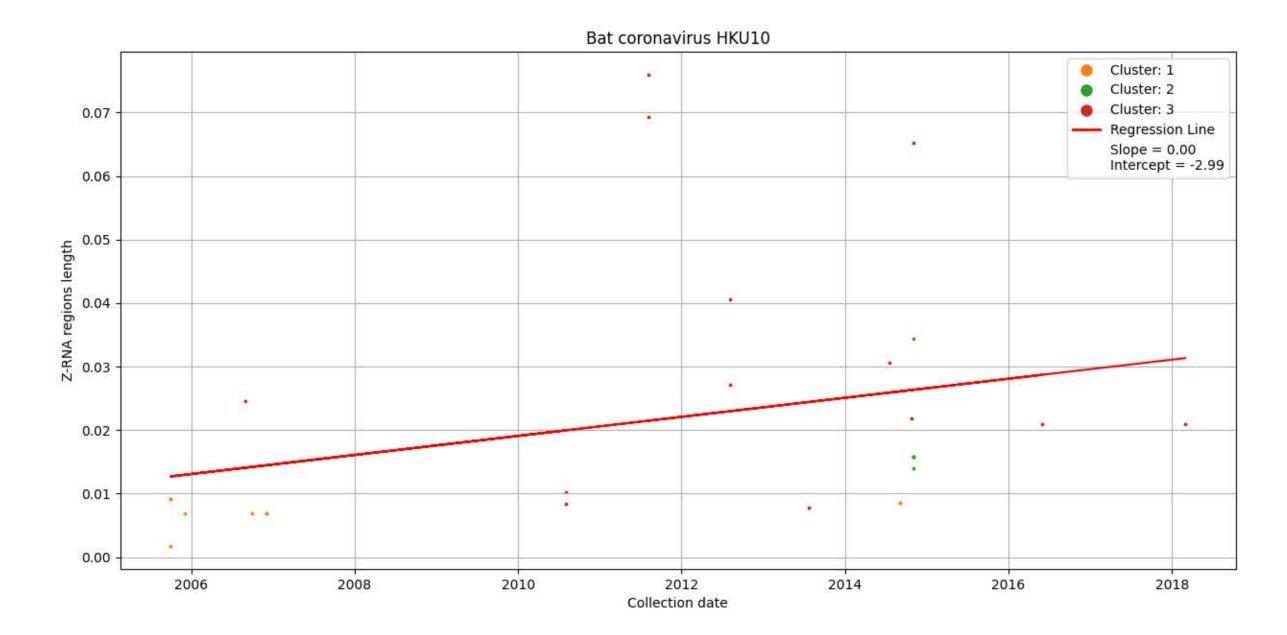
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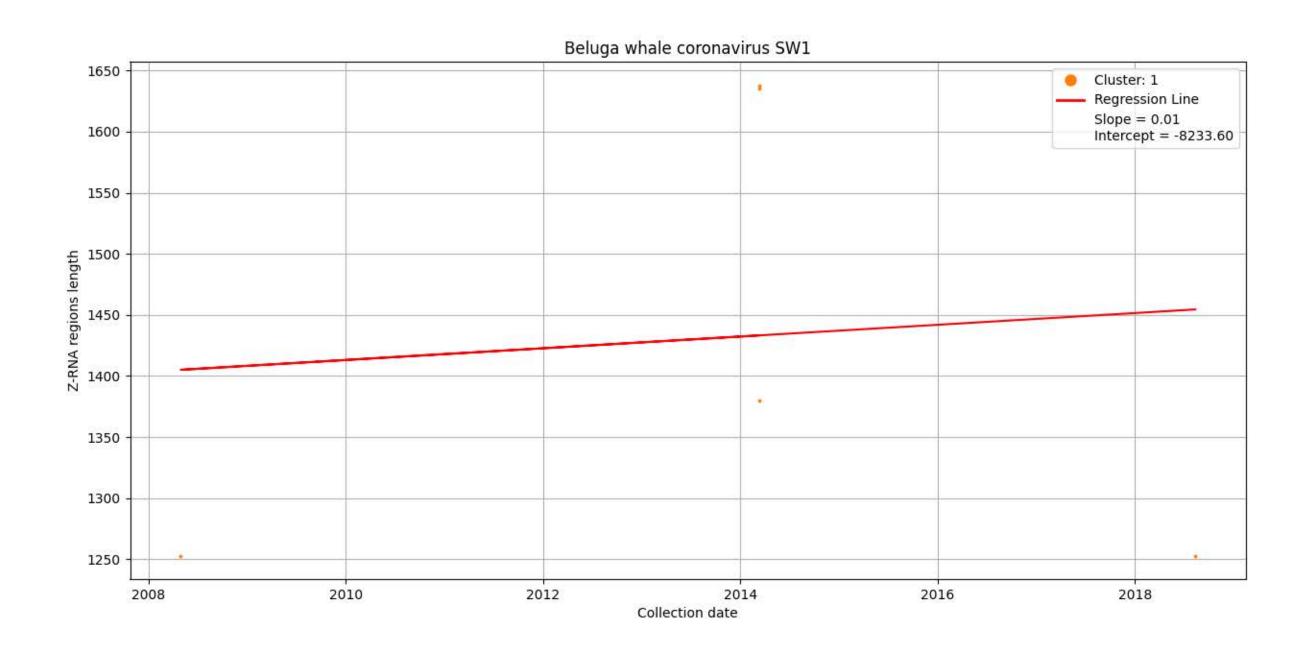


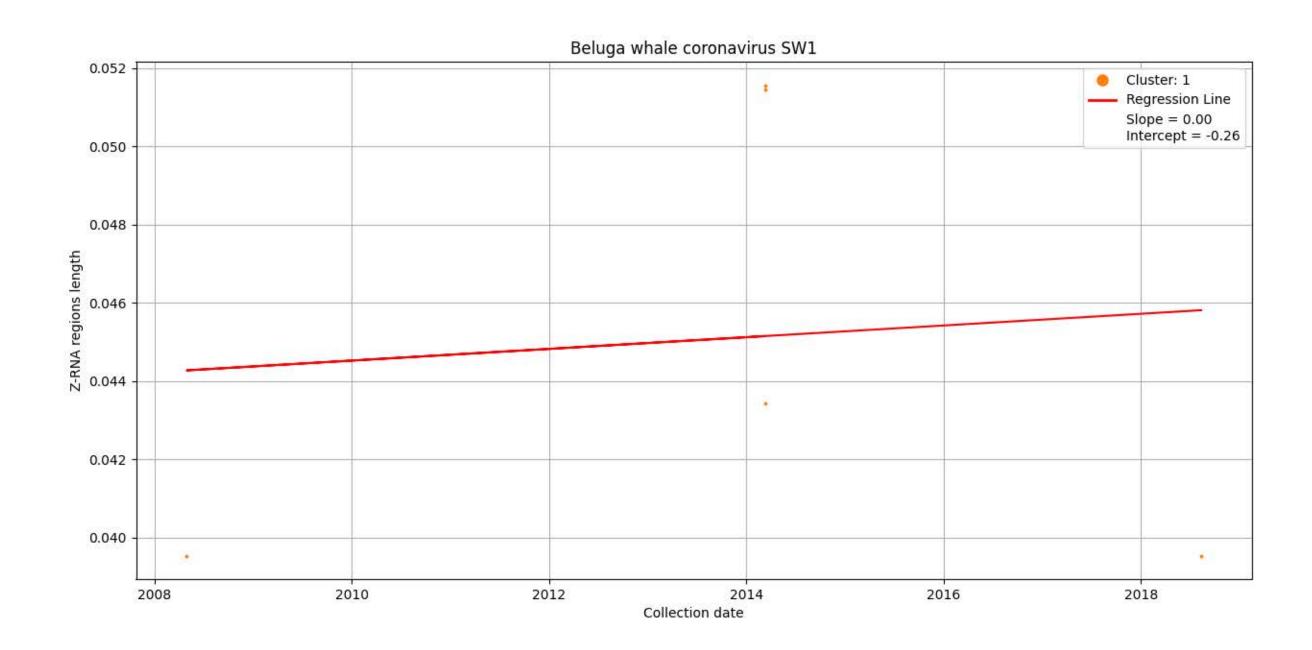


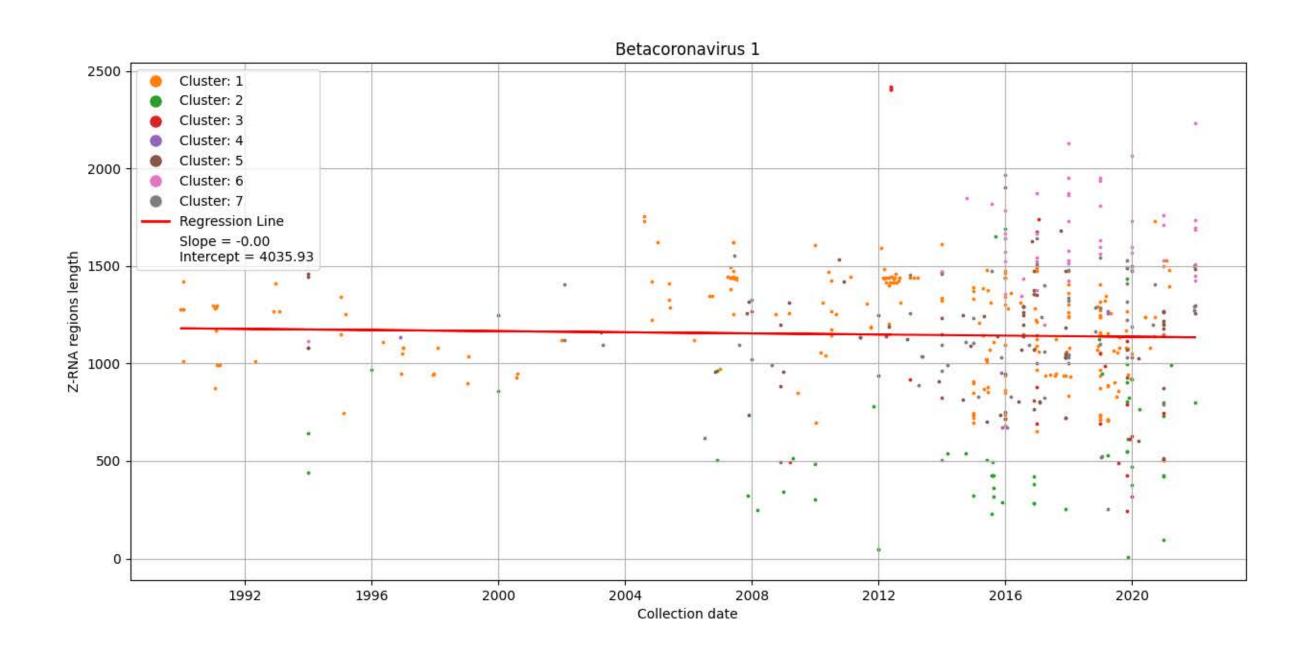


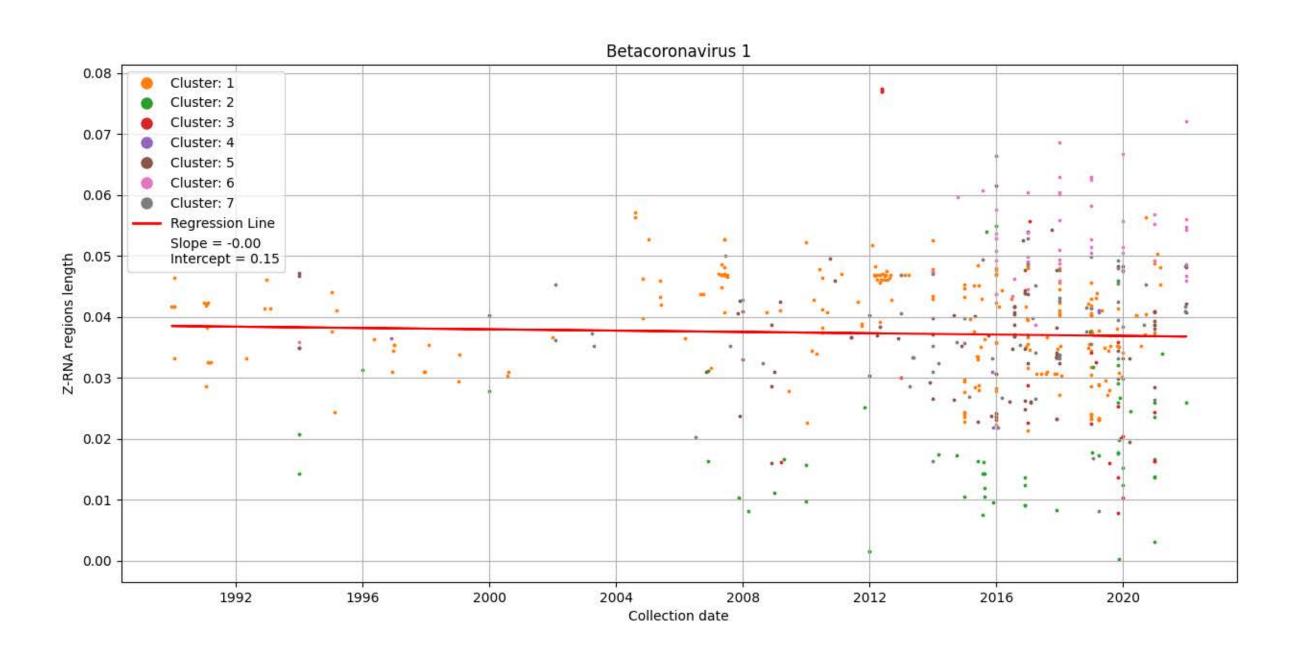


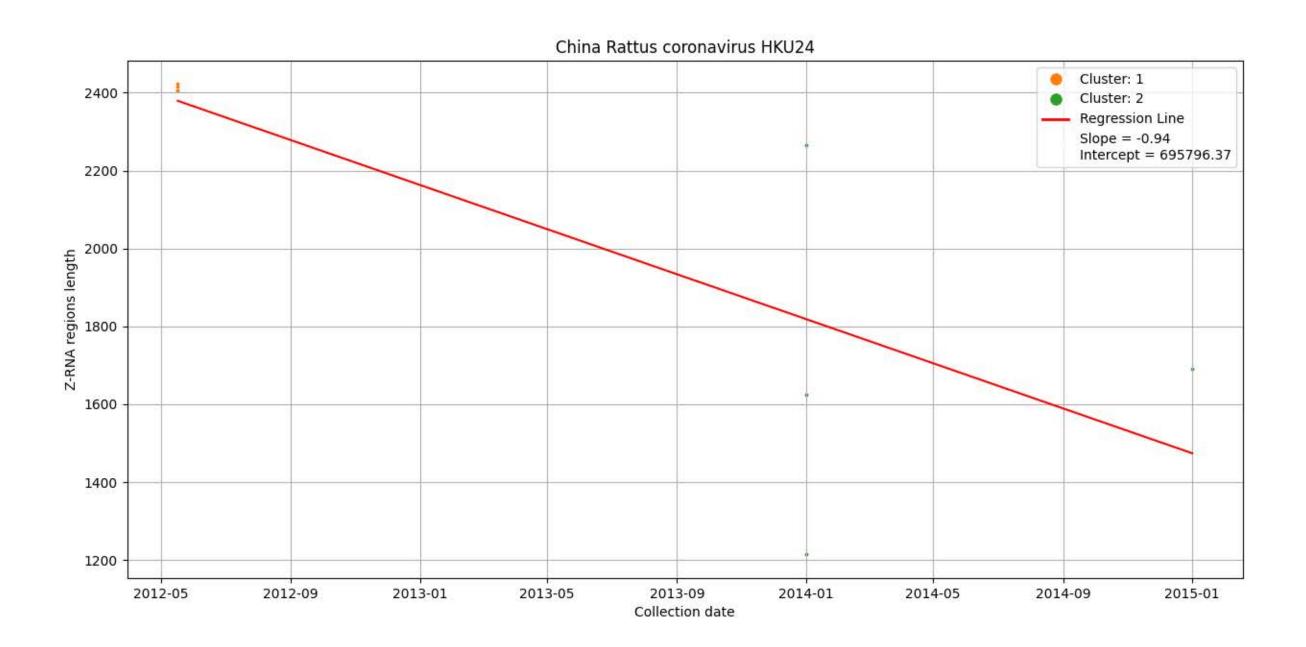


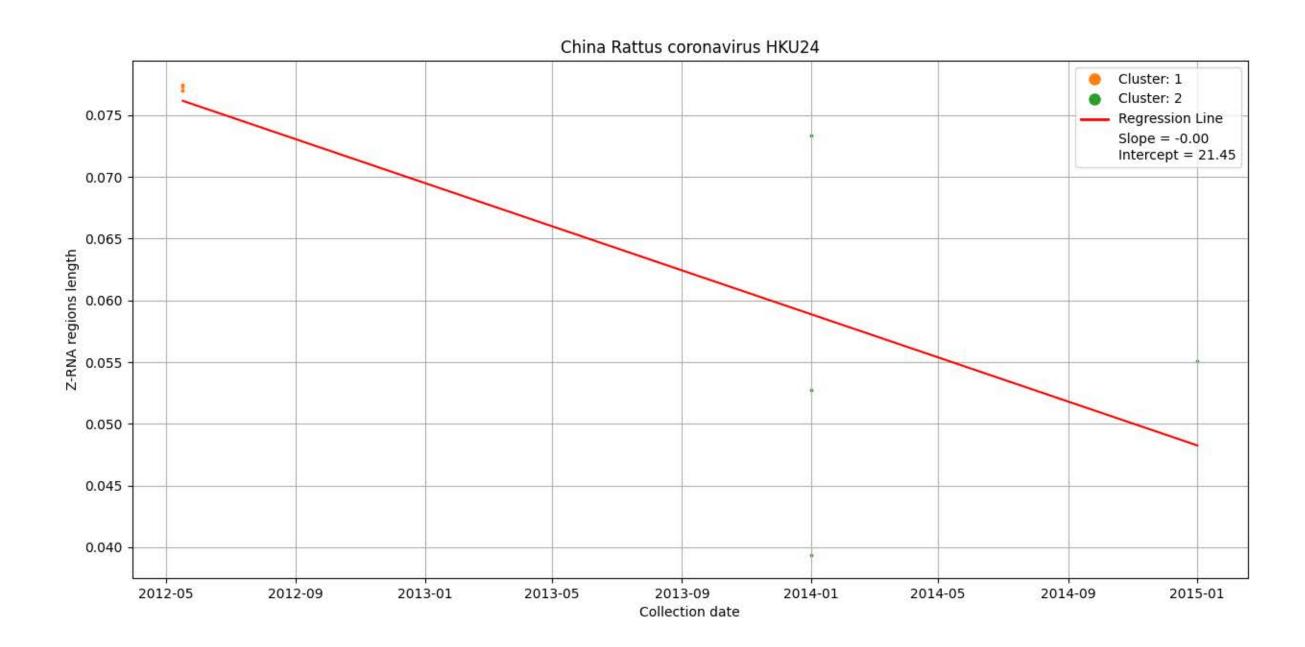


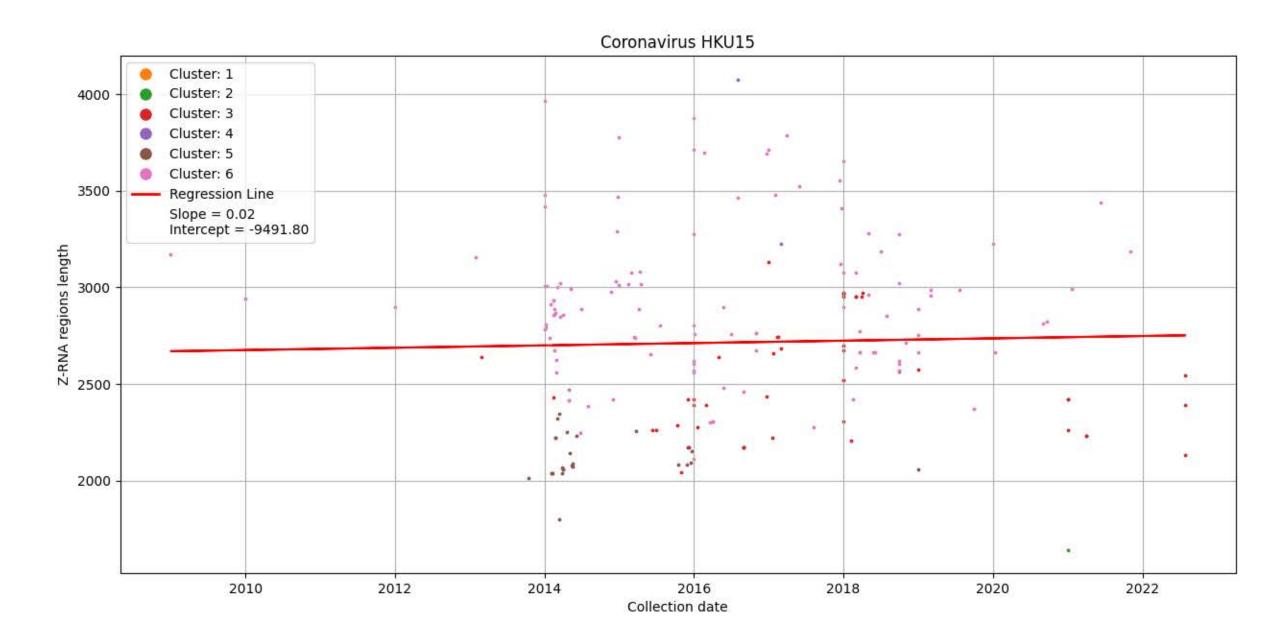


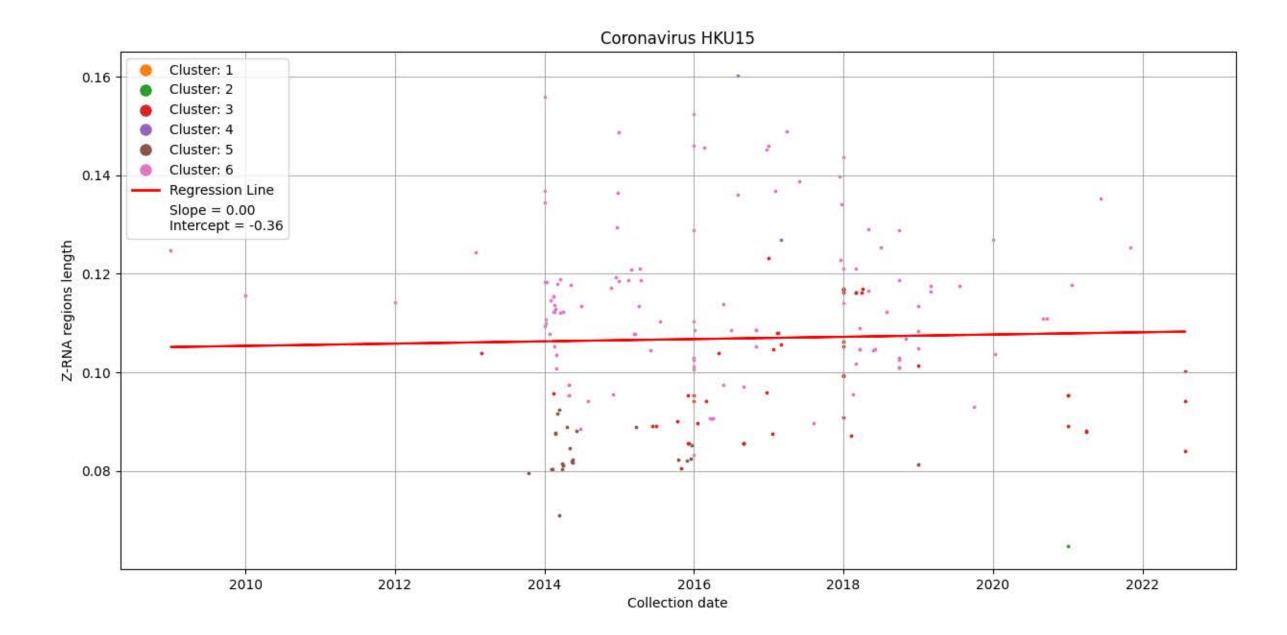




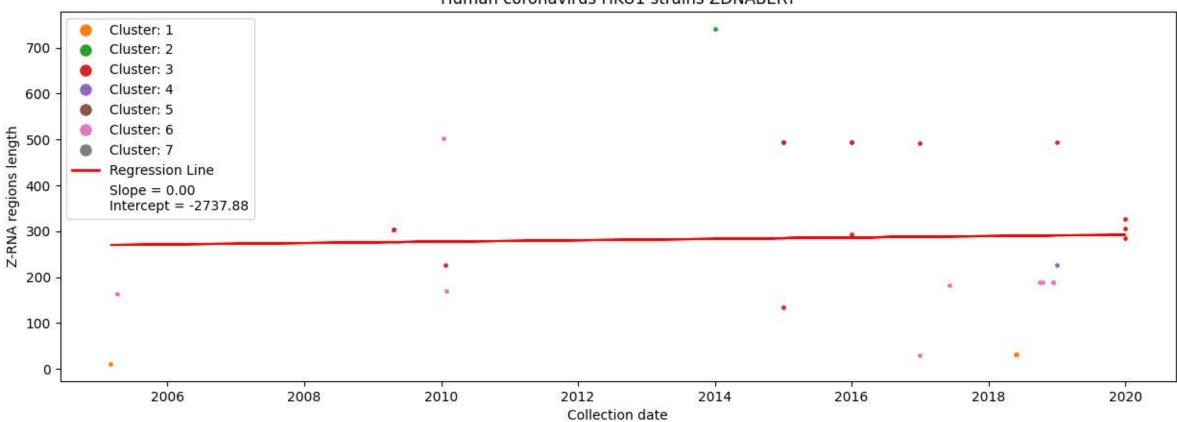




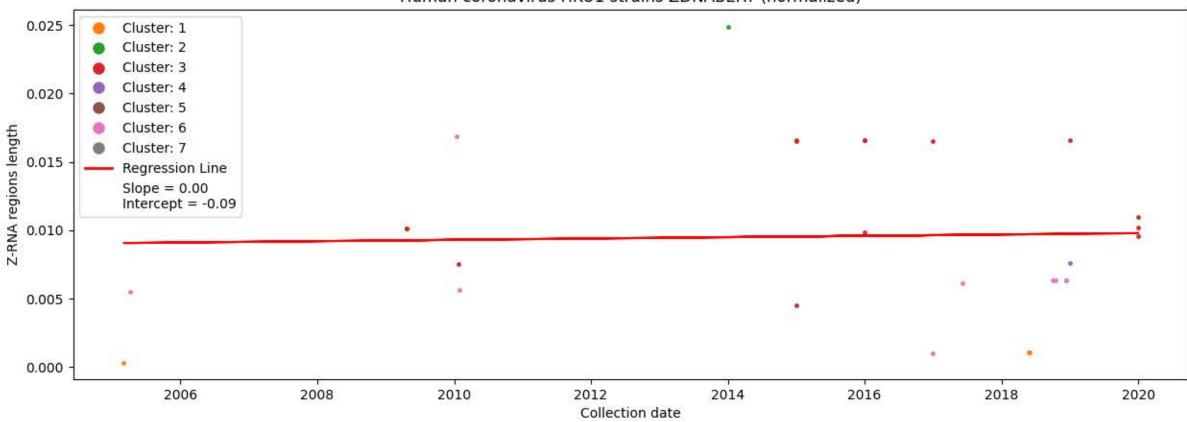




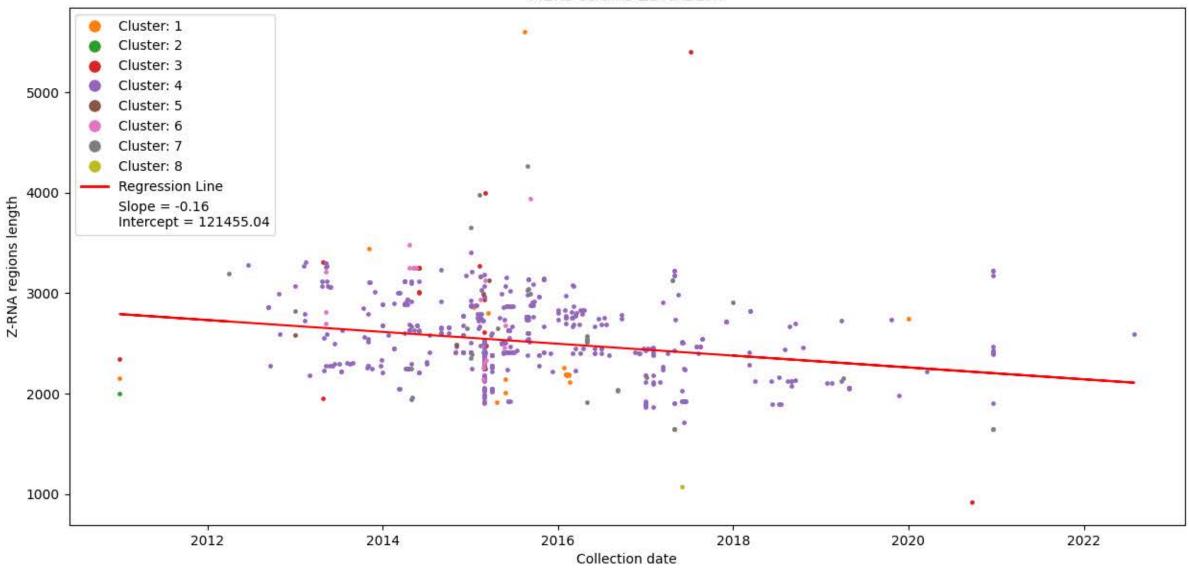
Human coronavirus HKU1 strains ZDNABERT

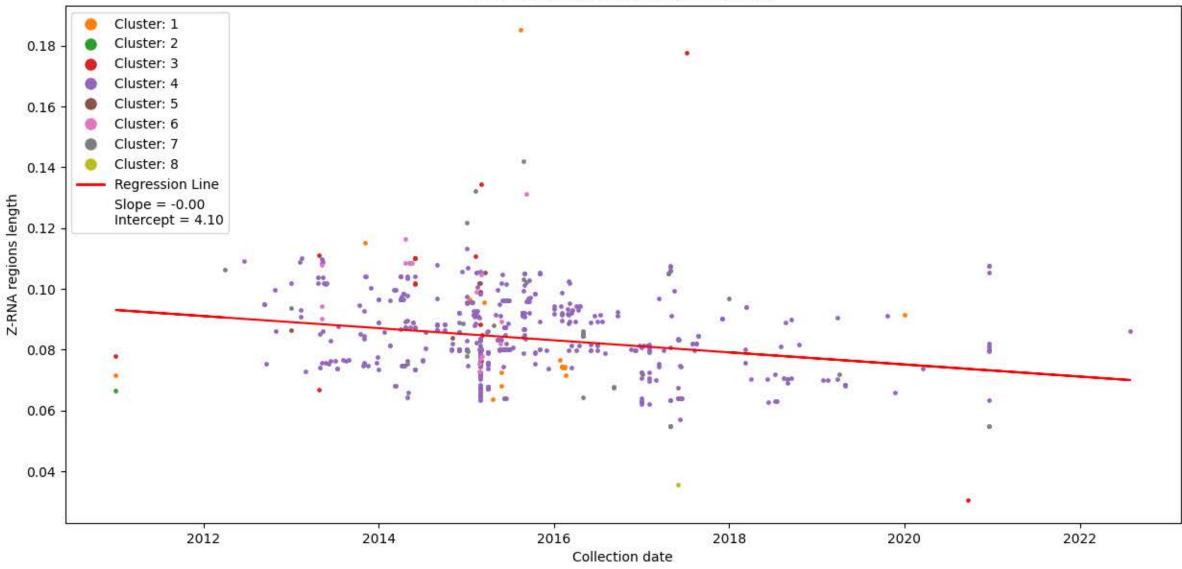


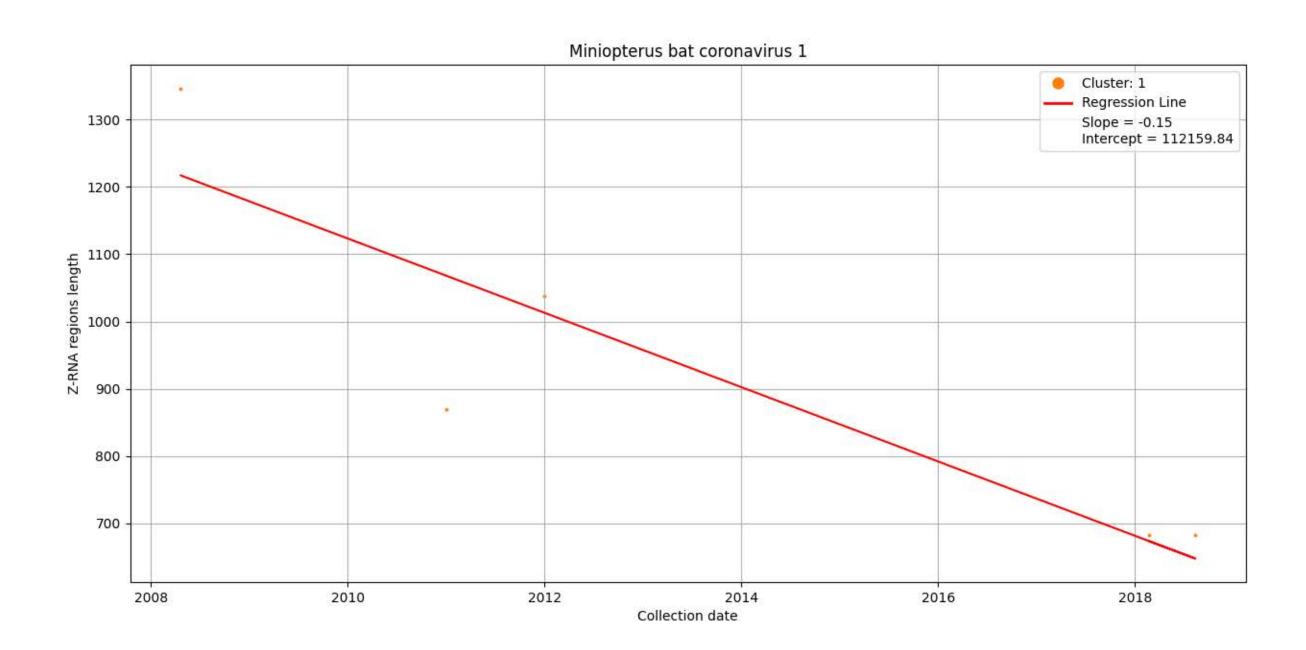
Human coronavirus HKU1 strains ZDNABERT (normalized)

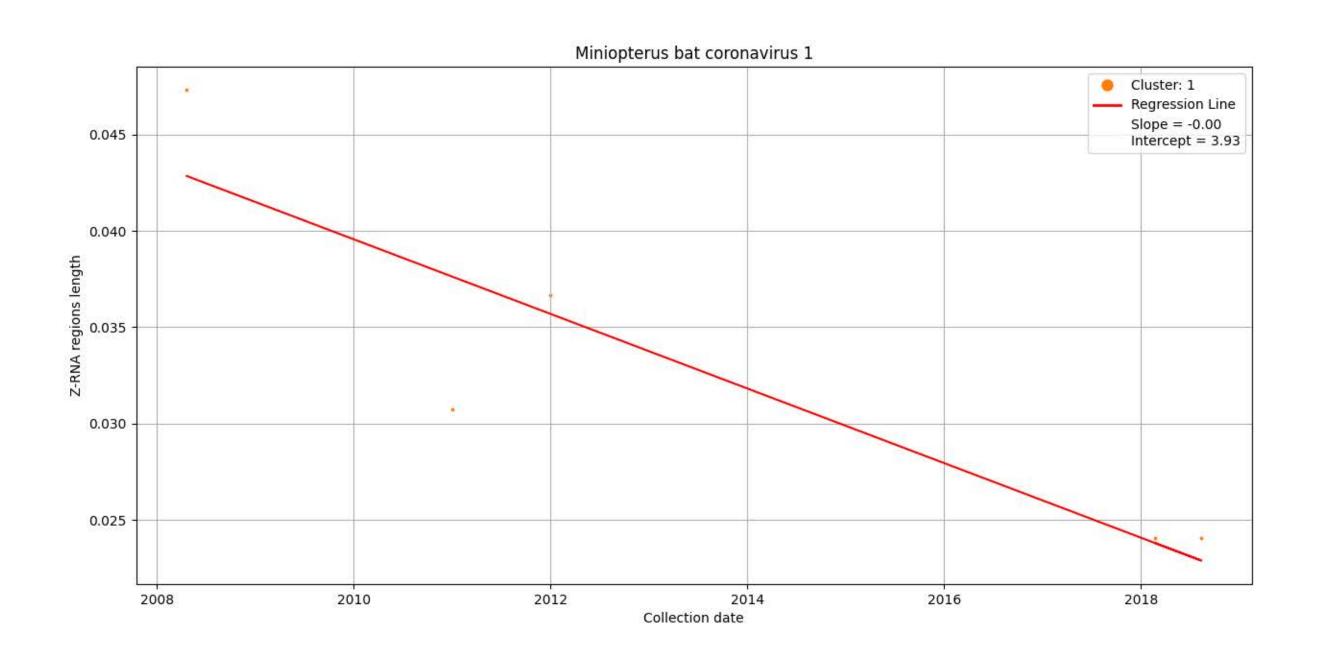


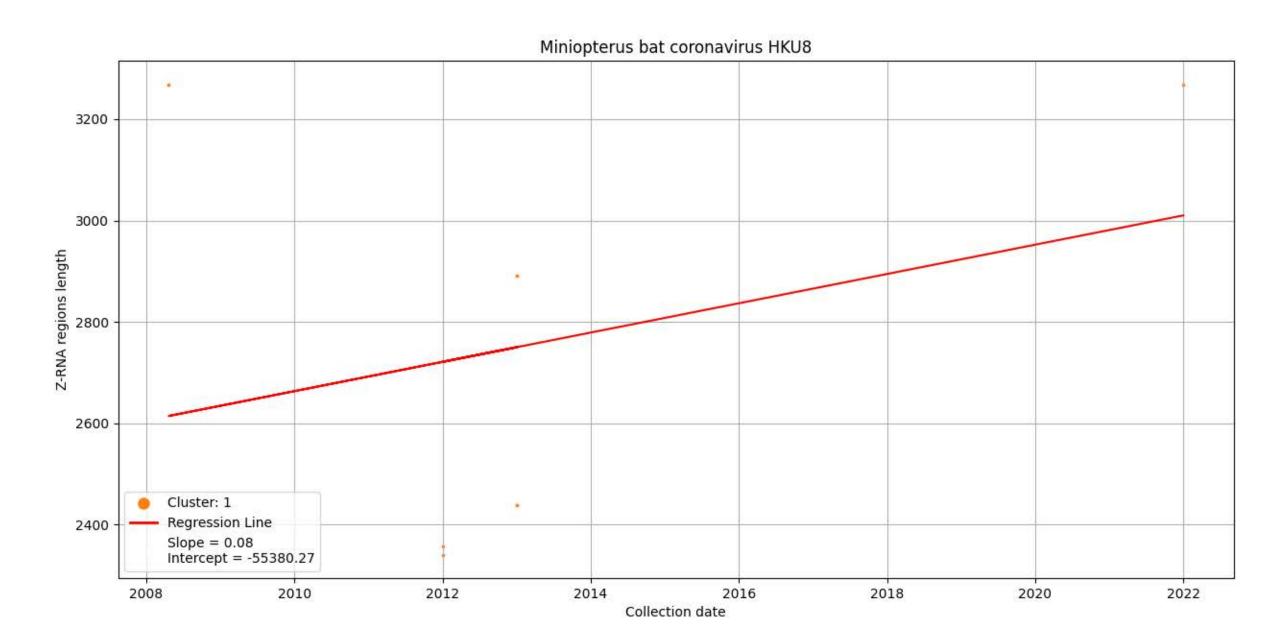
MERS strains ZDNABERT

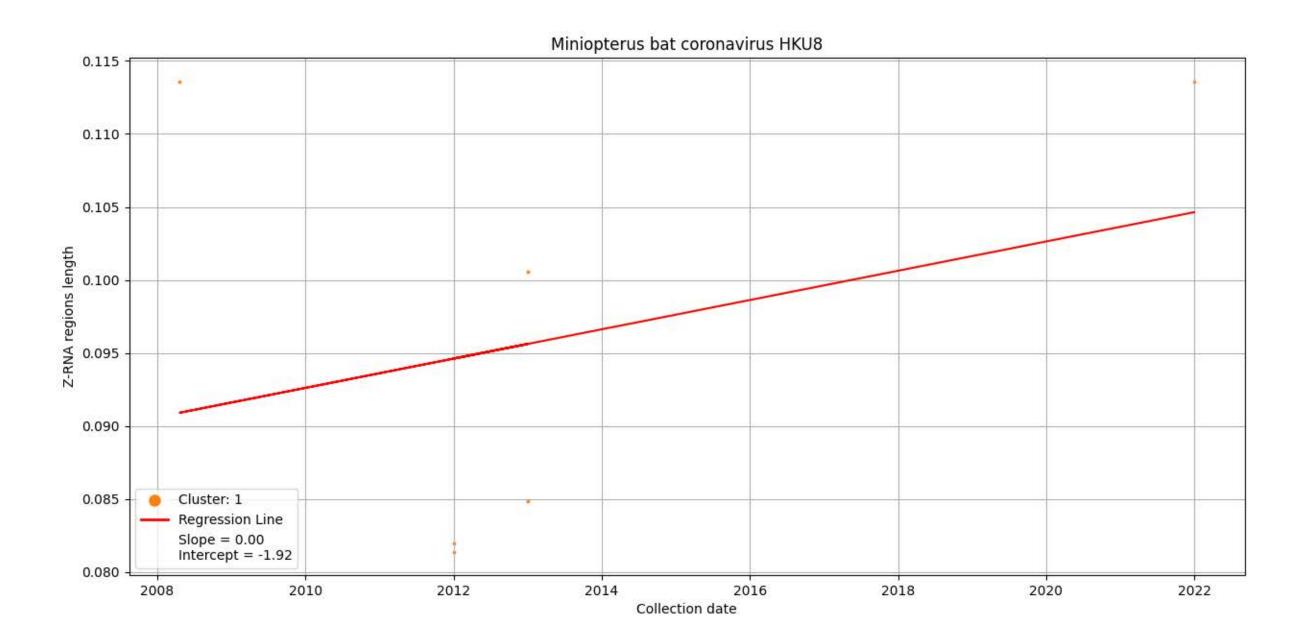


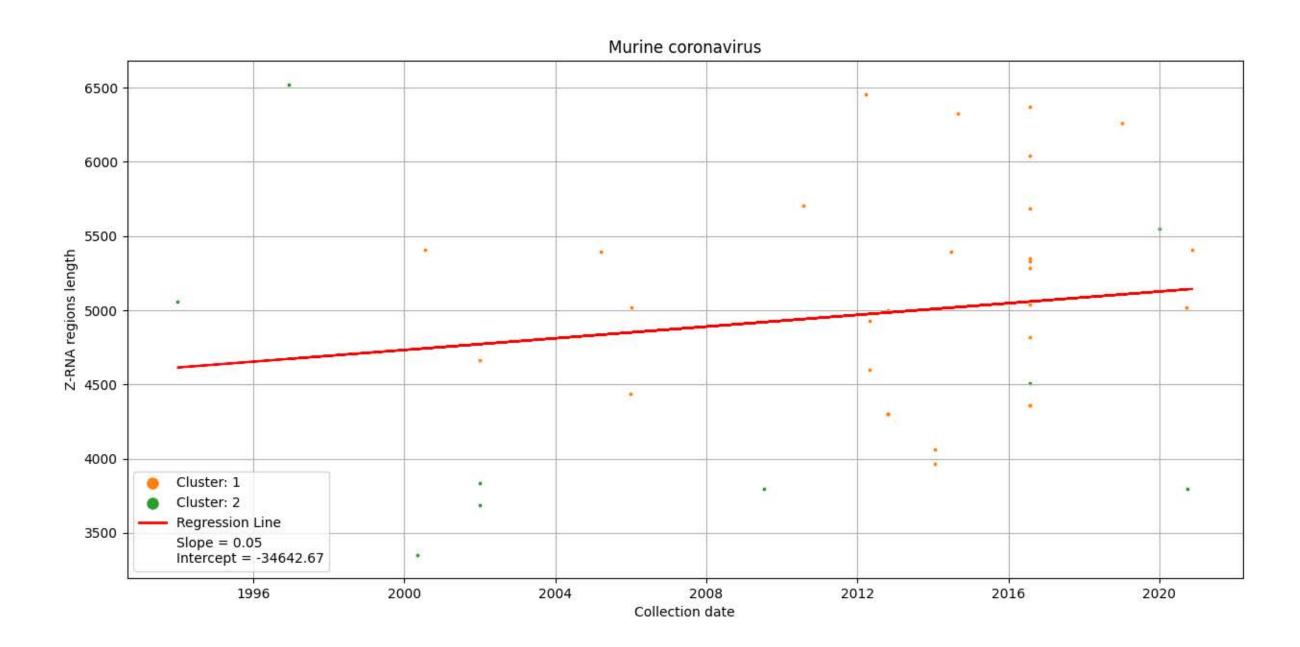


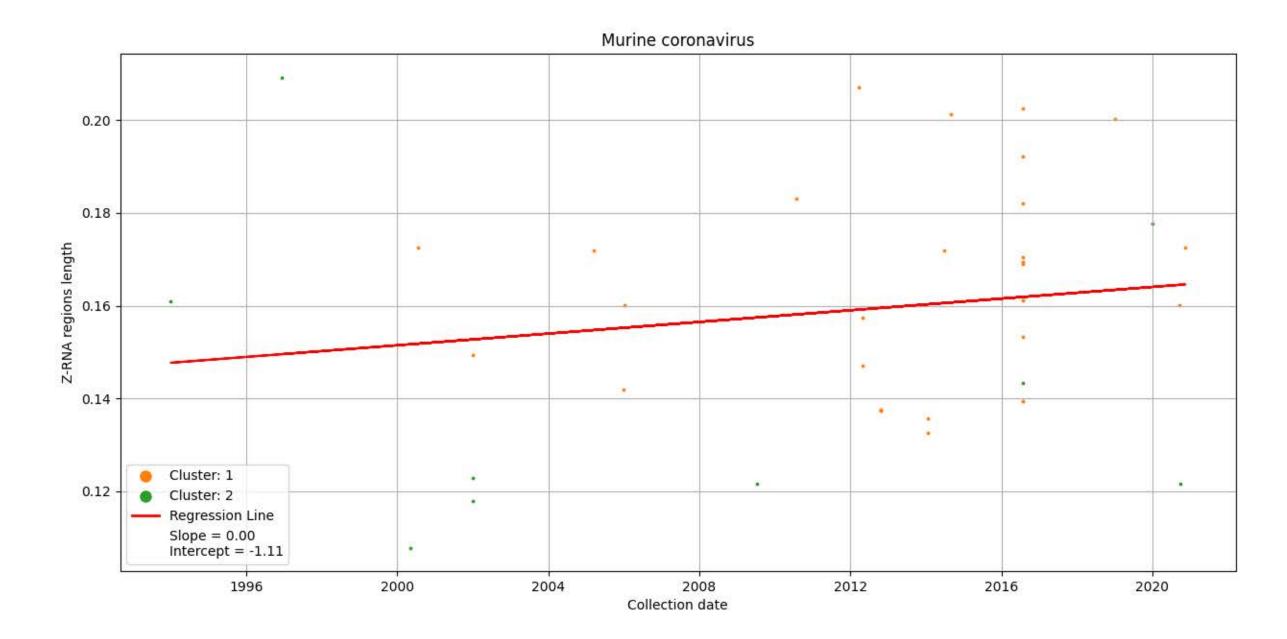


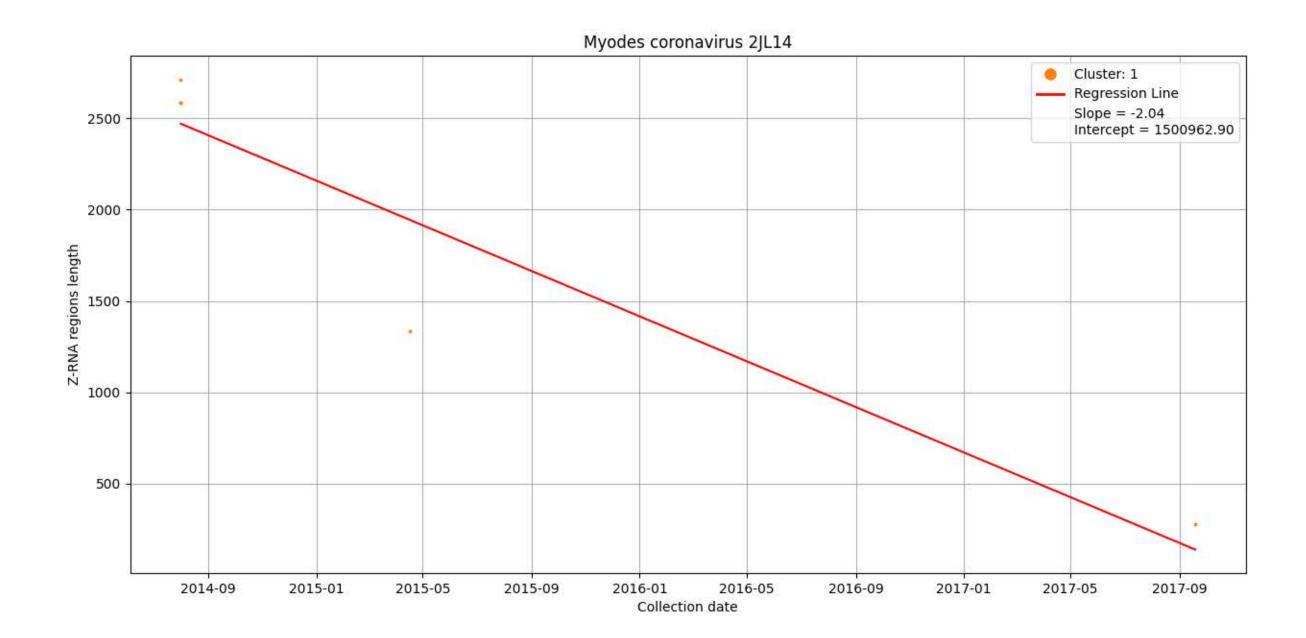


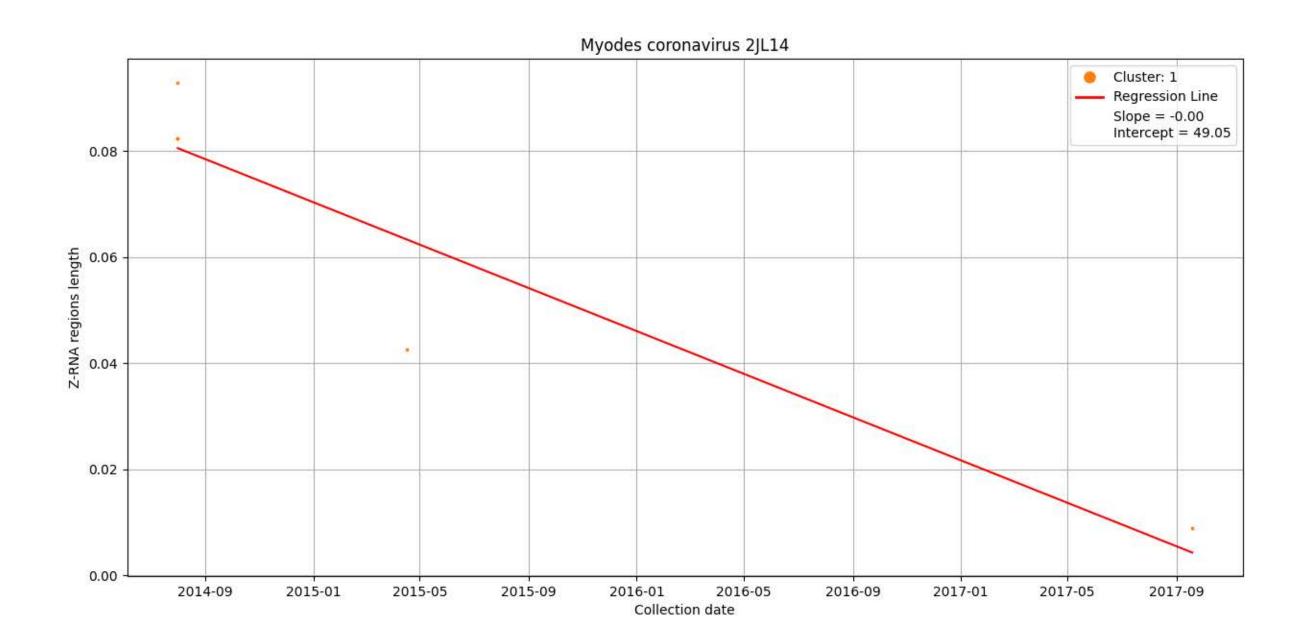




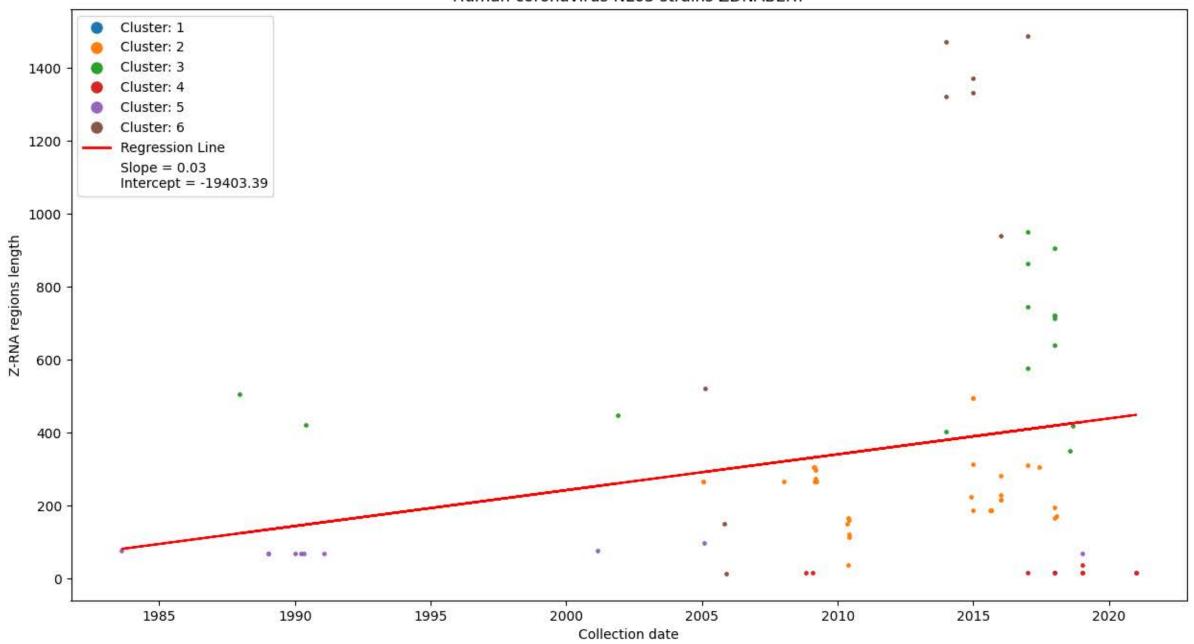




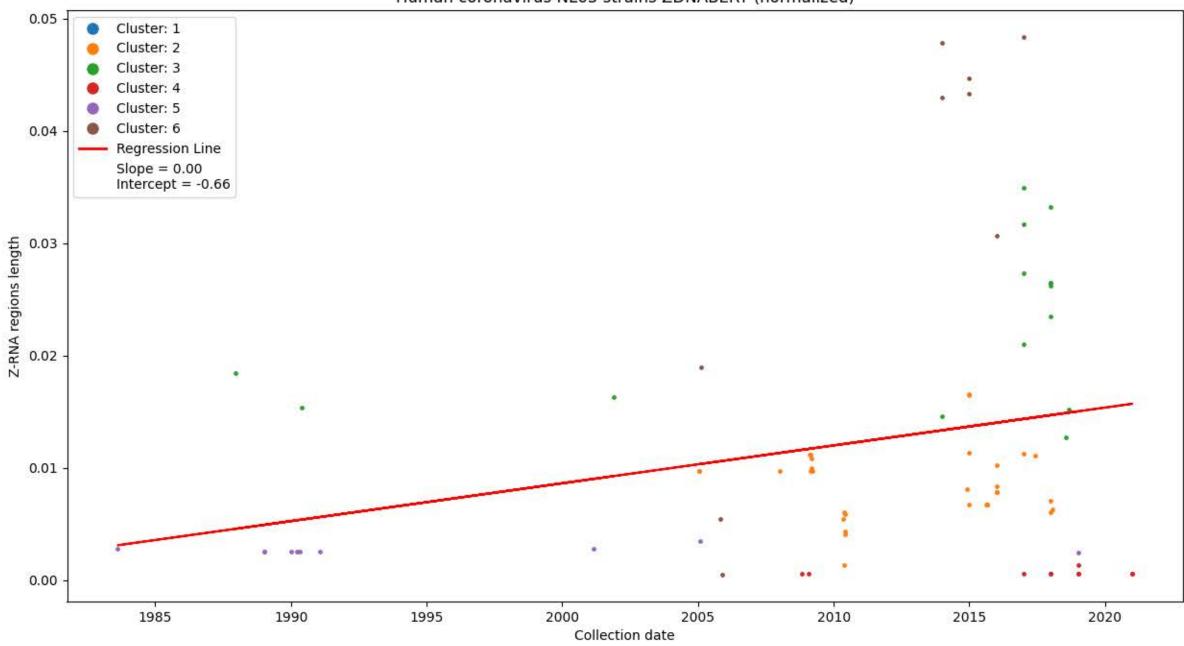




Human coronavirus NL63 strains ZDNABERT



Human coronavirus NL63 strains ZDNABERT (normalized)



NL63-related bat coronavirus strain BtKYNL63-9b Cluster: 1 Regression Line Slope = -3.174500 Intercept = 2326186.99 4000 Z-RNA regions length 3000 2500 2000 2008-10 2009-01 2009-04 2009-07 2010-01 2010-04 2010-07 2009-10 Collection date

NL63-related bat coronavirus strain BtKYNL63-9b Cluster: 1 Regression Line 0.16 Slope = -0.00 Intercept = 82.19 0.14 Z-RNA regions length 0.12 0.10 0.08 2008-10 2009-01 2009-04 2009-07 2009-10 2010-01 2010-04 2010-07 Collection date

Pipistrellus bat coronavirus HKU5 Cluster: 1 Cluster: 2 Regression Line Slope = -0.09 Intercept = 73003.69 Z-RNA regions length Collection date

Pipistrellus bat coronavirus HKU5 Cluster: 1 Cluster: 2 Regression Line Slope = -0.00 Intercept = 2.38 0.20 Z-RNA regions length 0.10 0.05 2008 2010 2012 2014 2016 2018 2020 2022

Collection date

