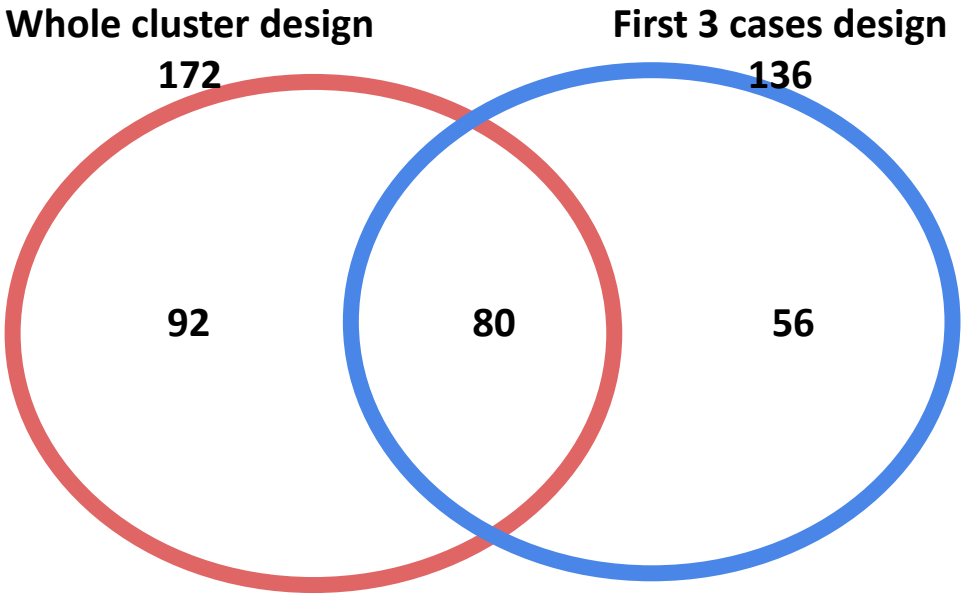
GEOCOVID Meeting

Presentation by Yangji Choi
2021.10.14

Sample inclusion

- 236 samples selected
- 9 samples missing
- 14 samples repeated

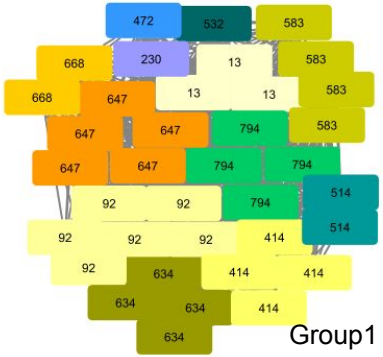
⇒ 227 samples



- Whole cluster design: Mar-Apr 2020
- First 3 cases design: Mar-Jun 2020

Whole cluster design (172)

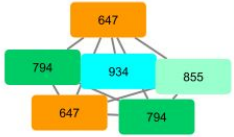
Network (SNP=0)



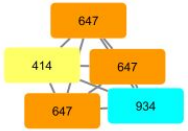
Group1

Group2

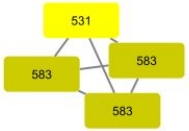
Group3



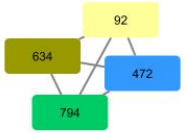
Group4



Group5

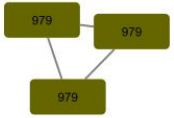


Group6



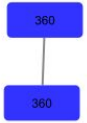
Group7

Group8



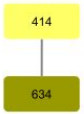
Group9

Group10

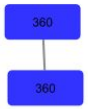


Group11

Group12

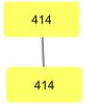


Group13



Group14

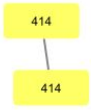
Group15



Group16

Group17

Group18



Group19

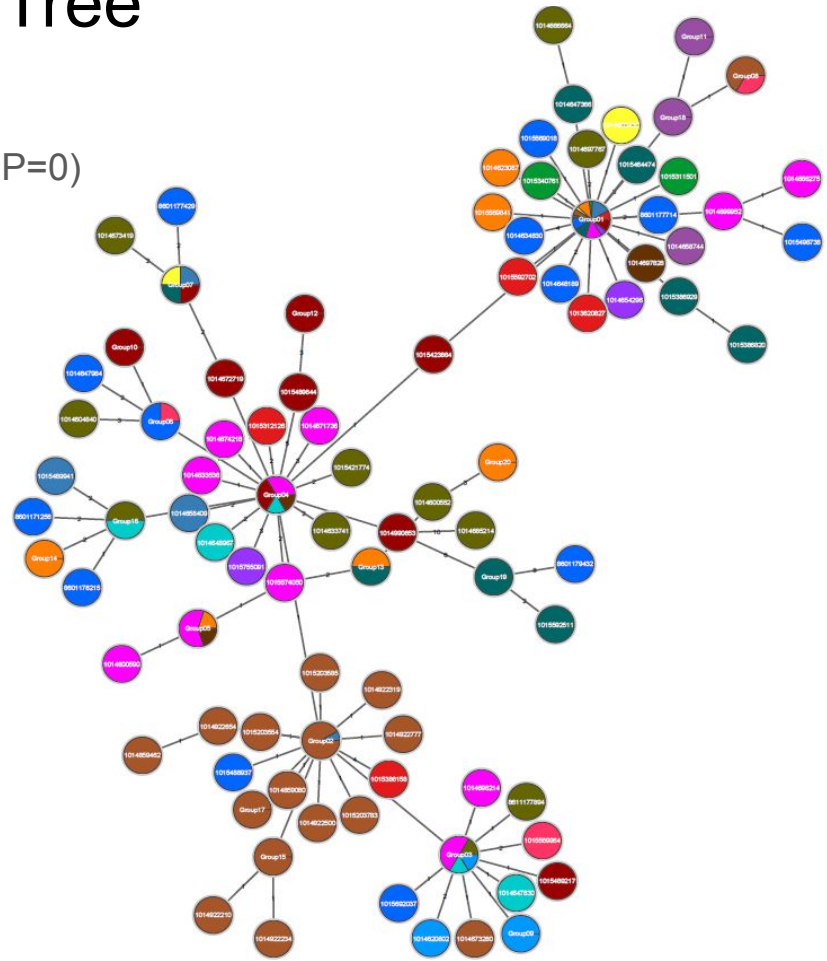
Group20

13	Lausanne (1000)
92	Lausanne (Epalinges)
230	Genolier
360	Servion
414	Lausanne (Le Mont)
472	Cossonay
514	Vallee de Joux
531	Lausanne (1004)
532	Morges
583	Lausanne (1005)
634	Lausanne (1007)
647	Lausanne (Cugy)
668	Yverdon les Bains
794	Nyon
855	Paudex
934	Oron
979	Lausanne (1007)

Minimum Spanning Tree

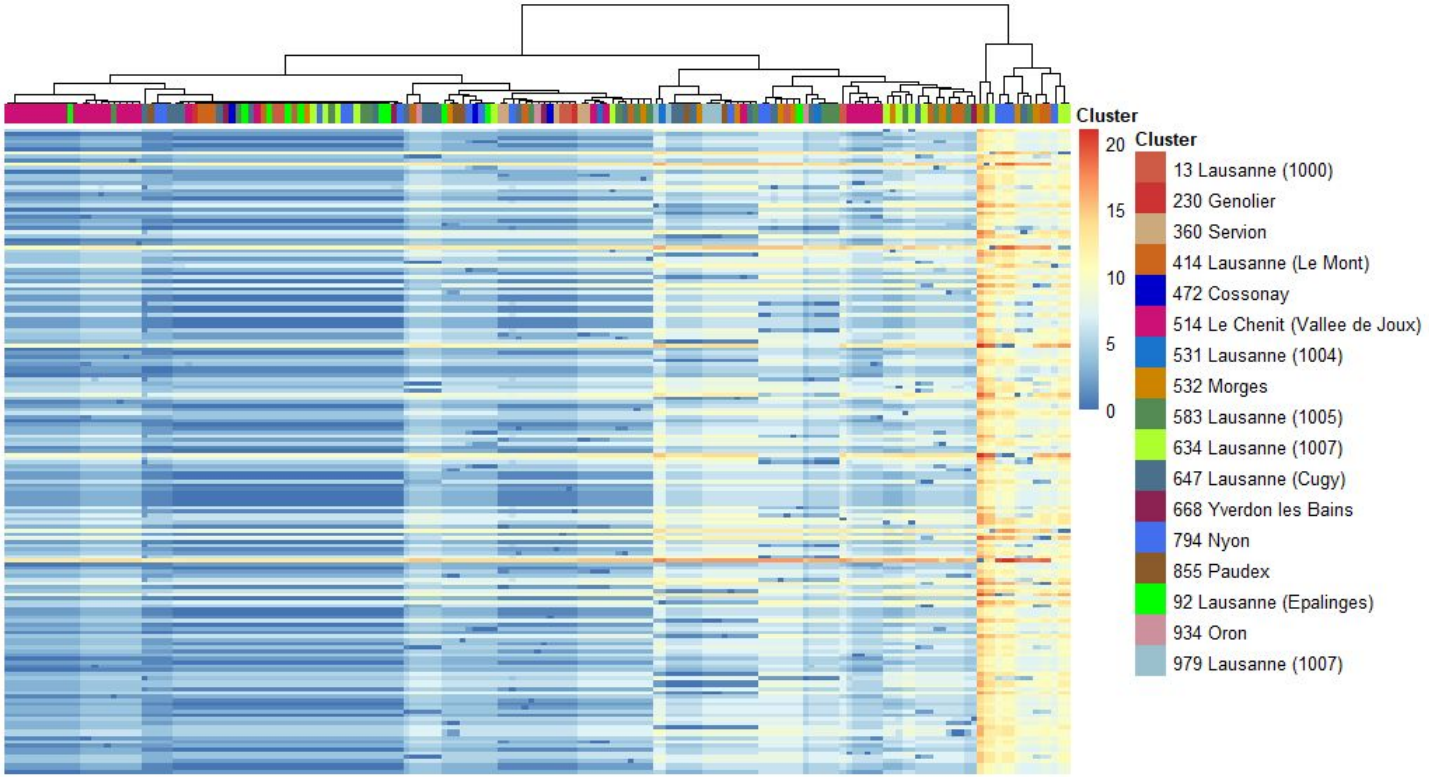
Whole cluster design (172)

Samples with identical sequence (SNP=0)
put into the same groups (nodes)

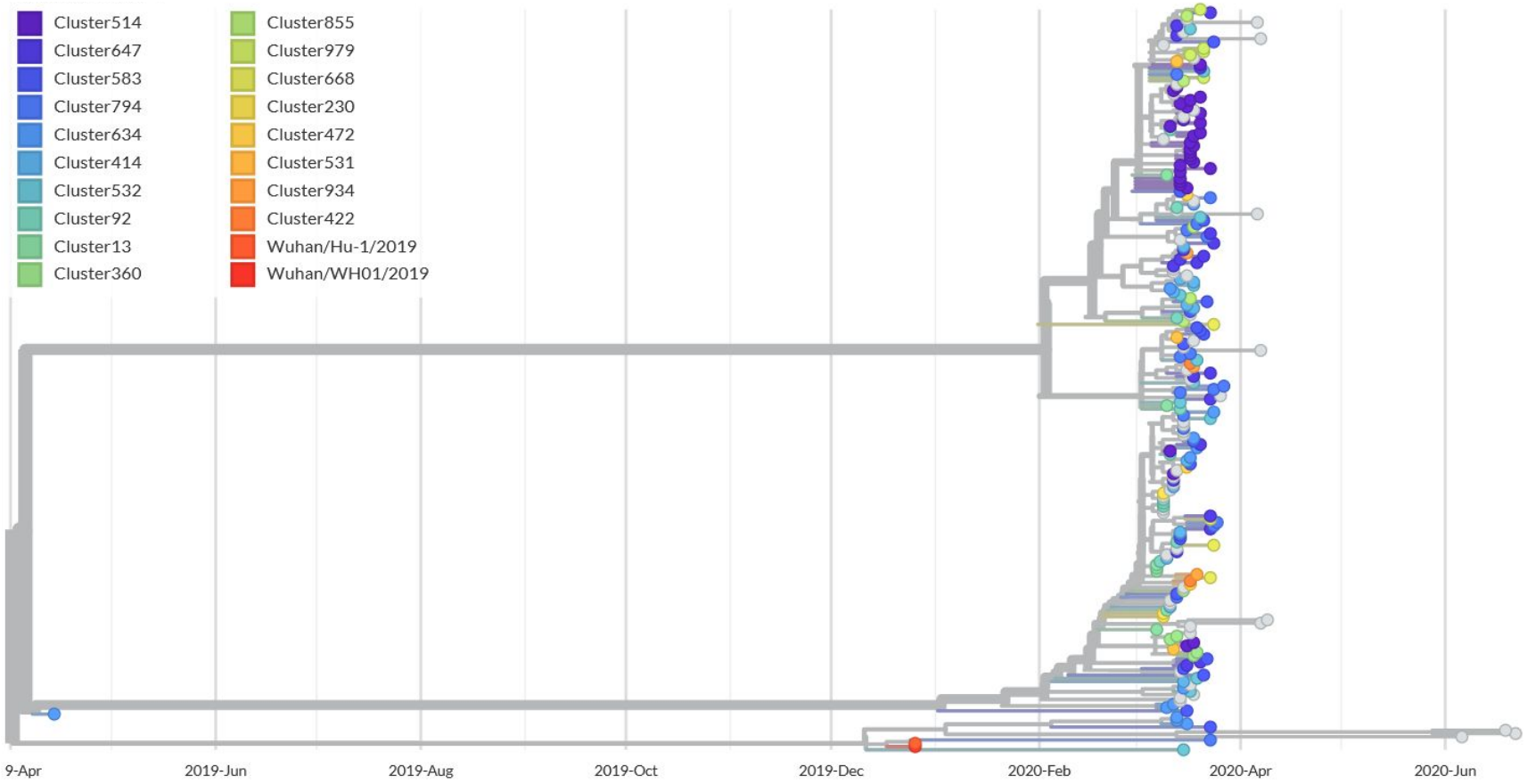


- 1 Lausanne (1000)
- 2 Lausanne (Epalinges)
- 3 Genolier
- 4 Servion
- 5 Lausanne (Le Mont)
- 6 Cossonay
- 7 Vallée de Joux
- 8 Lausanne (1004)
- 9 Morges
- 10 Lausanne (1005)
- 11 Lausanne (1007)
- 12 Lausanne (Cugy)
- 13 Yverdon les Bains
- 14 Nyon
- 15 Paudex
- 16 Oron
- 17 Lausanne (1007)

Hierarchical clustering based on SNP distance matrix

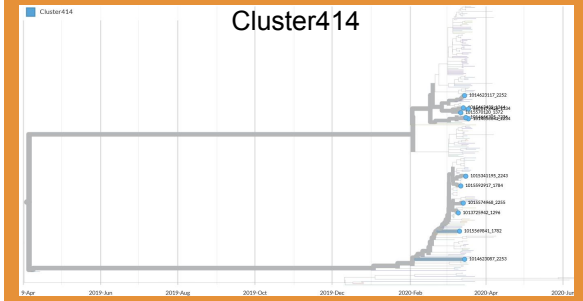


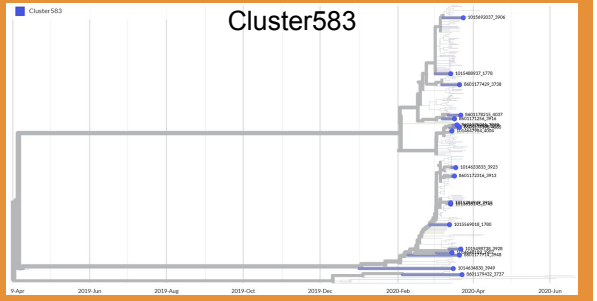
Phylogeny

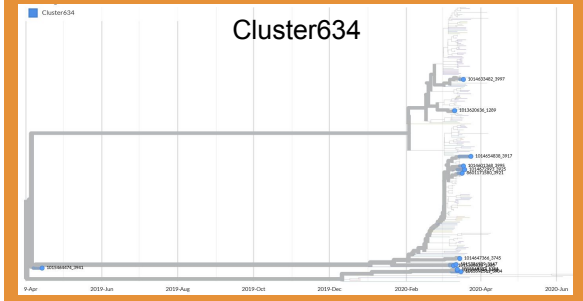

Cluster514
Cluster647
Cluster583
Cluster794
Cluster634
Cluster414
Cluster532
Cluster92
Cluster13
Cluster360
Cluster855
Cluster979
Cluster668
Cluster230
Cluster472
Cluster531
Cluster934
Cluster422
Wuhan/Hu-1/2019
Wuhan/WH01/2019
9-Apr
2019-Jun
2019-Aug
2019-Oct
2019-Dec
2020-Feb
2020-Apr
2020-Jun

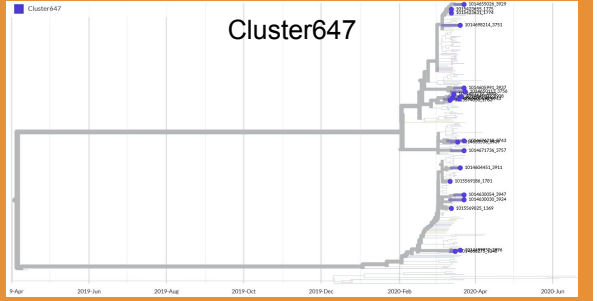
Phylogeny

Urban

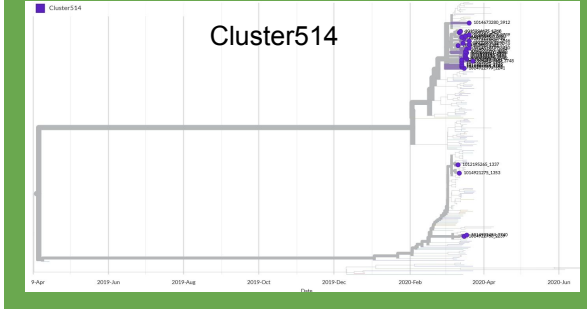


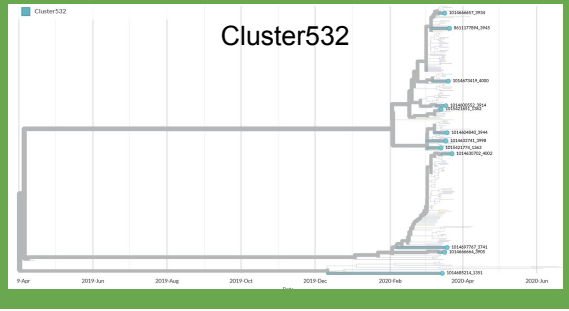


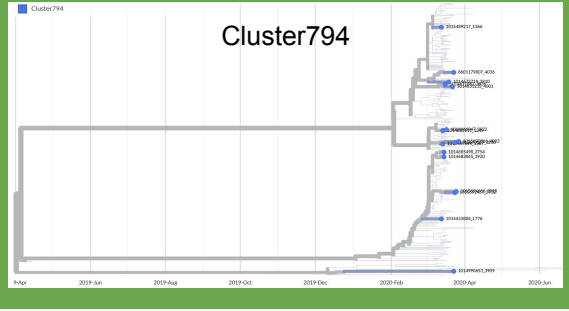




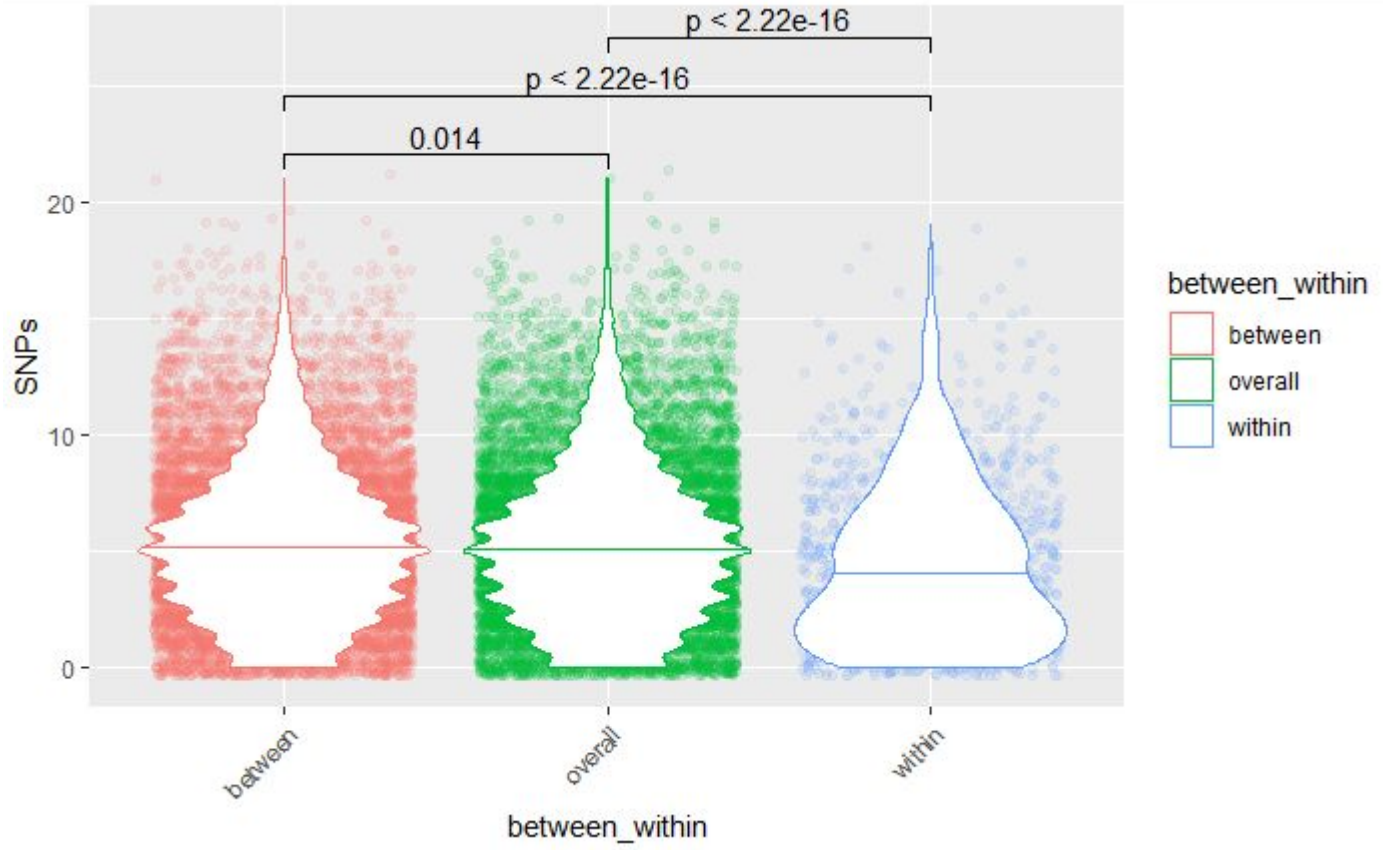
Rural



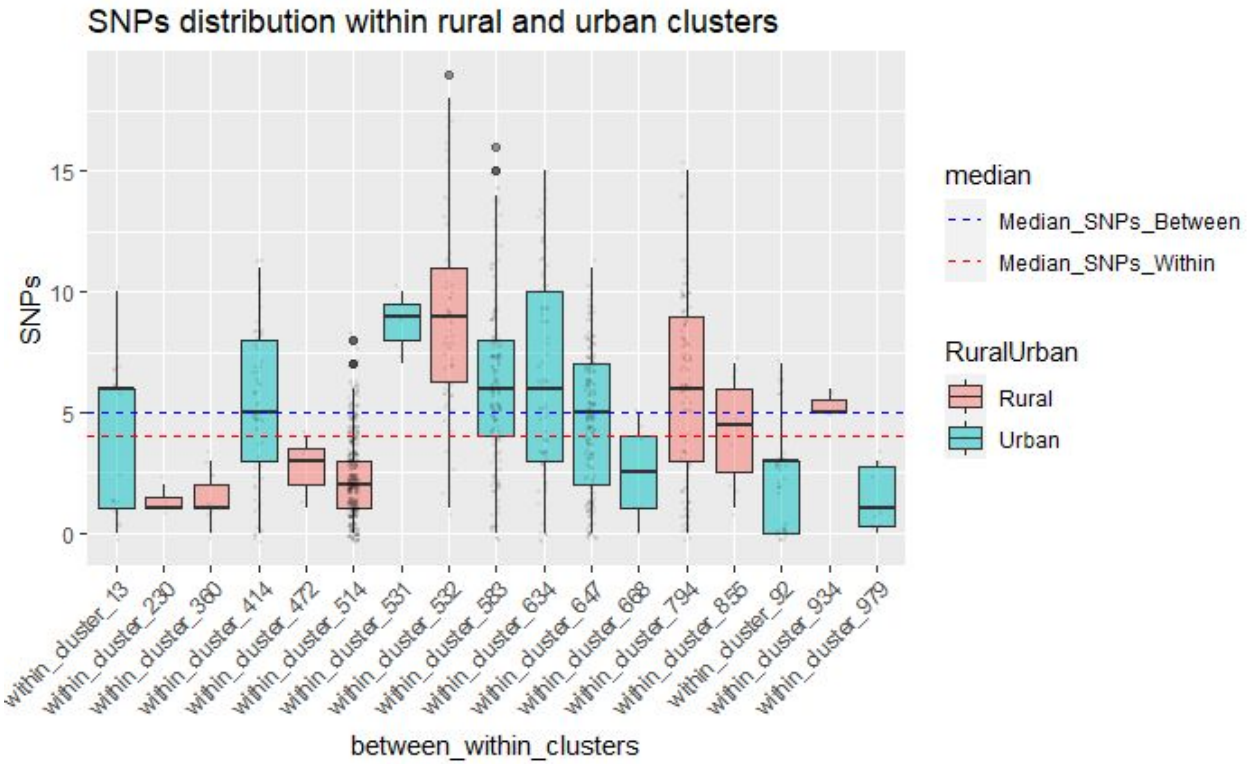




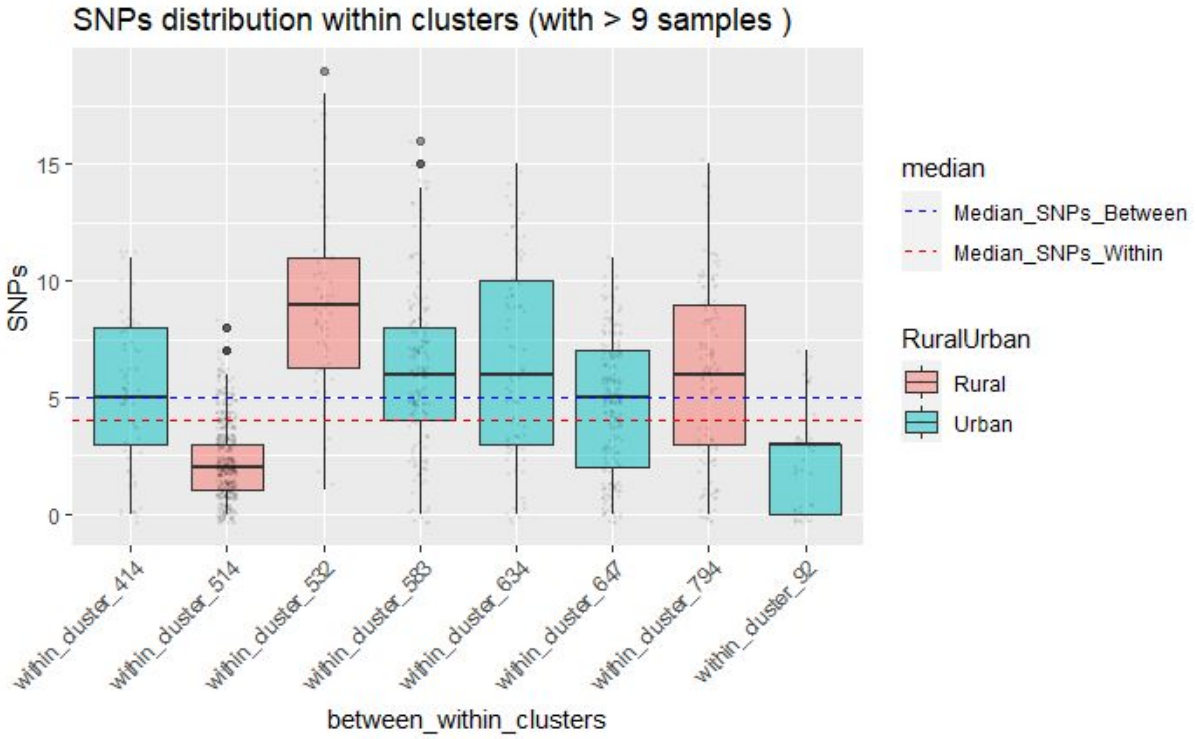
SNPs distribution between/within clusters



Rural vs Urban



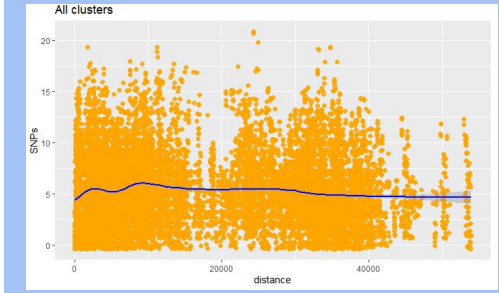
Rural vs Urban clusters with >9 samples



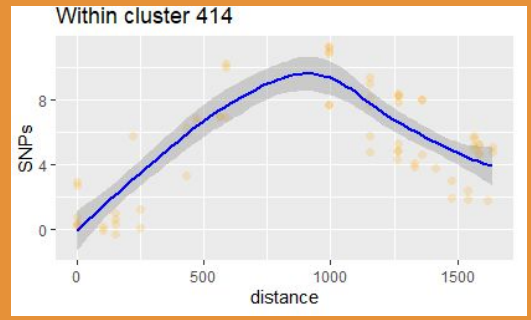
Whole cluster design (172)

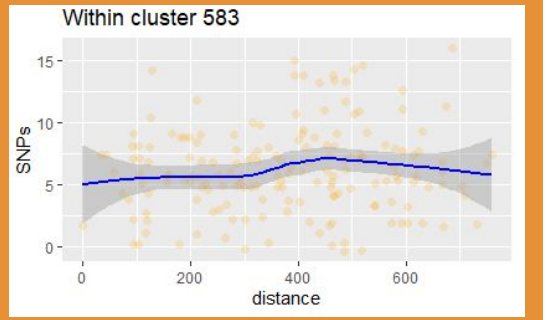
SNPs ~ geographical distance (m)

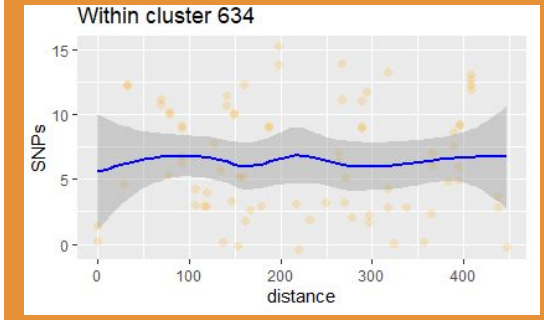
Overall

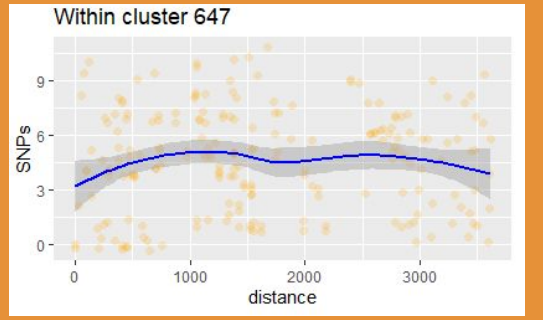


Urban

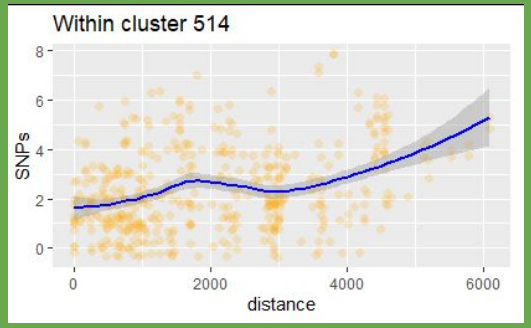


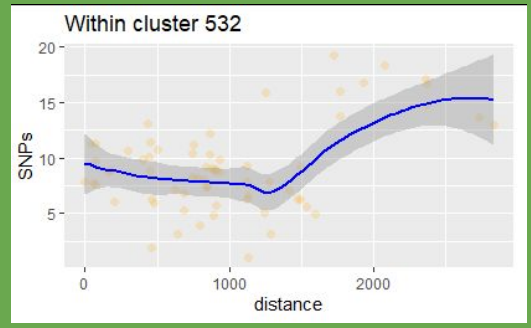


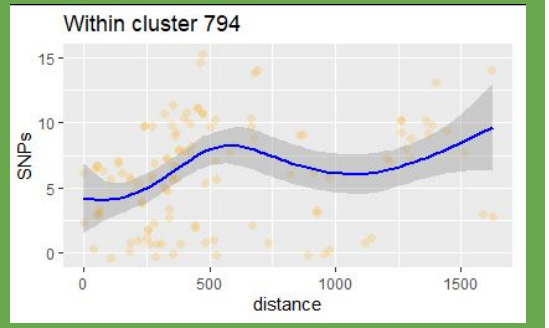




Rural



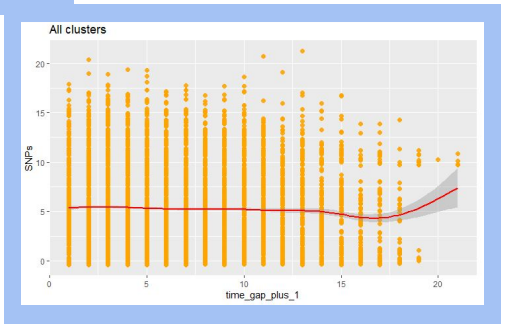




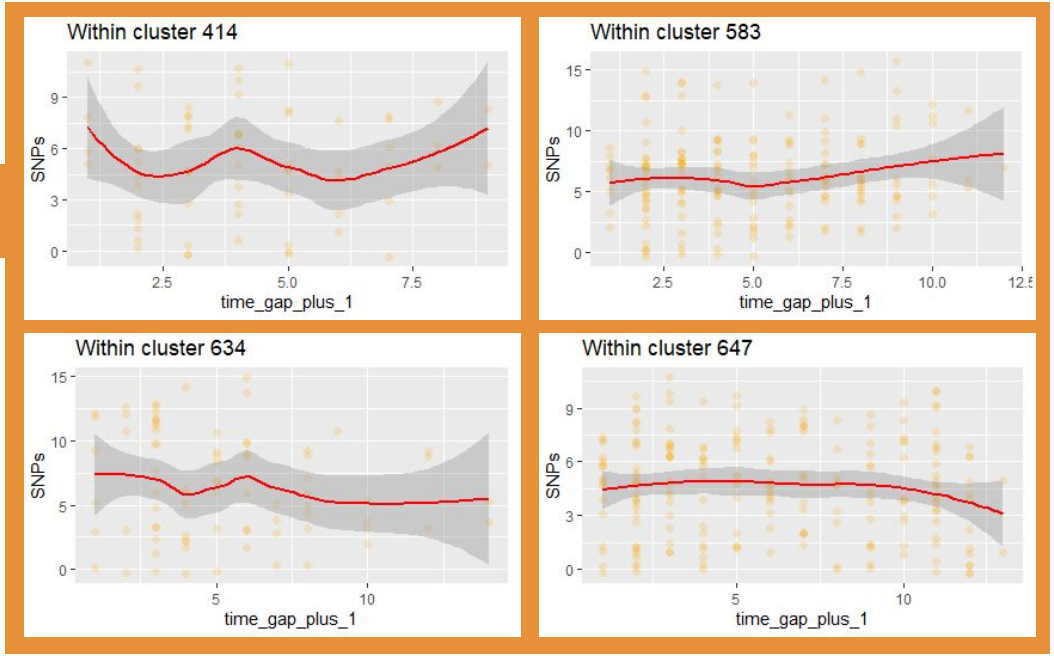
Whole cluster design (172)

SNPs ~ time (day)

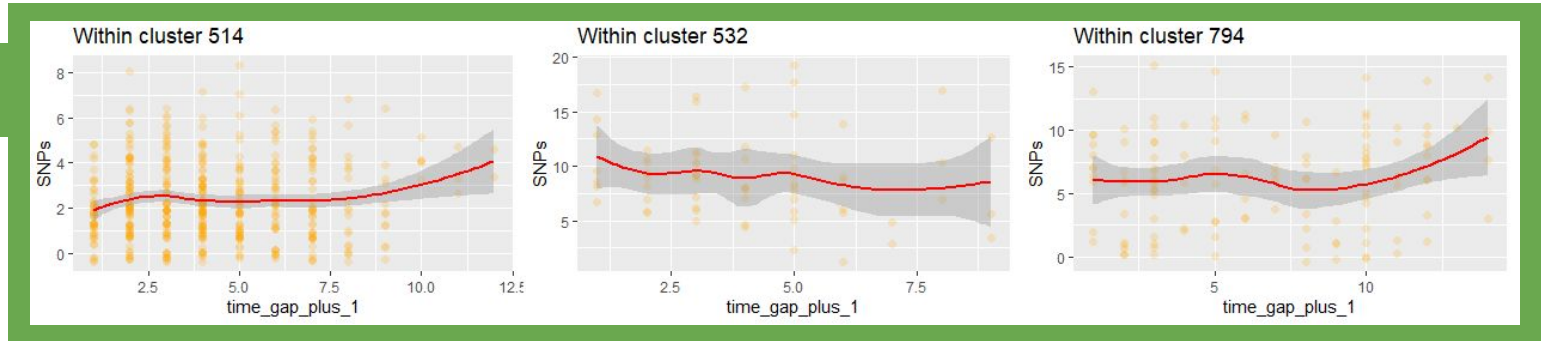
Overall



Urban



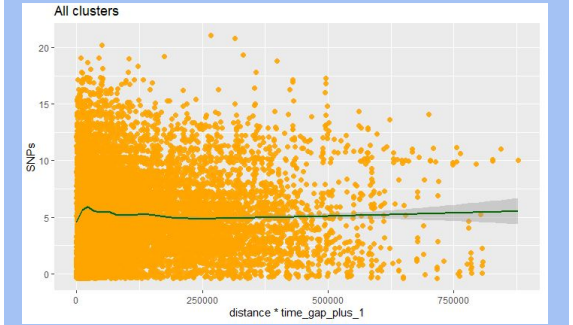
Rural



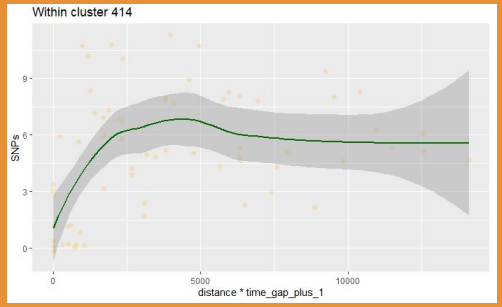
Whole cluster design (172)

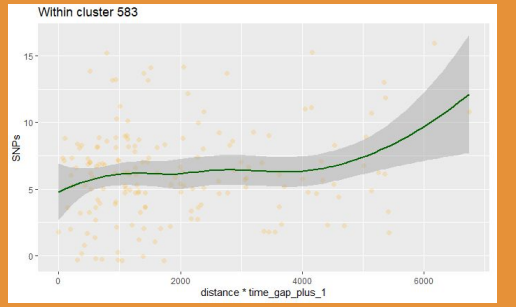
SNPs ~ distance*time

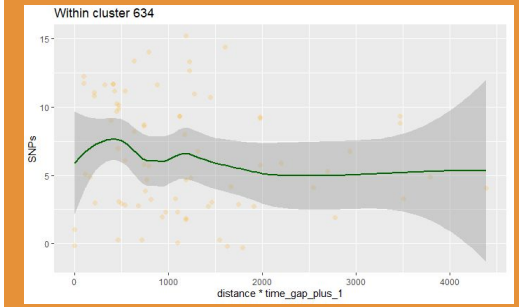
Overall

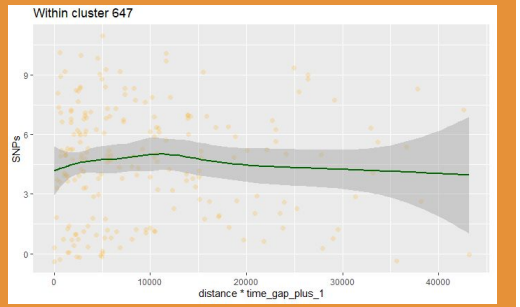


Urban

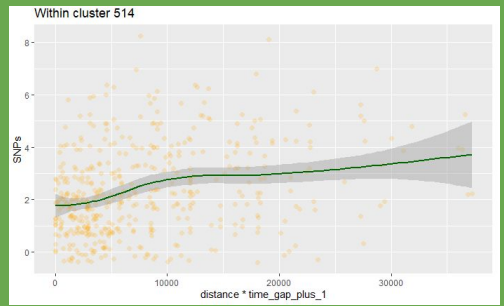


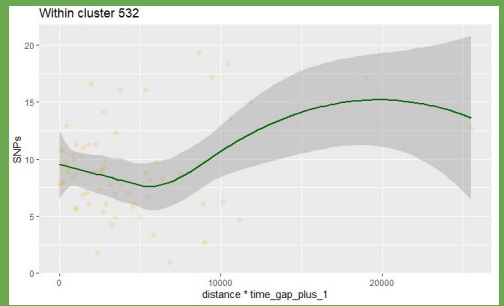


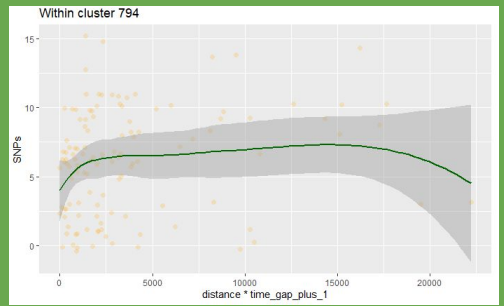




Rural



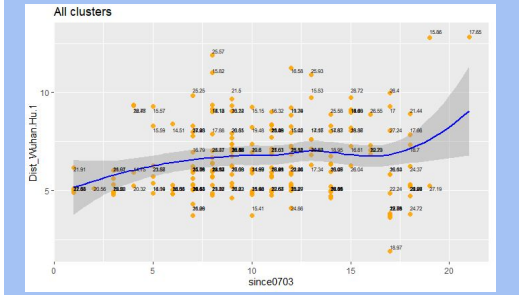




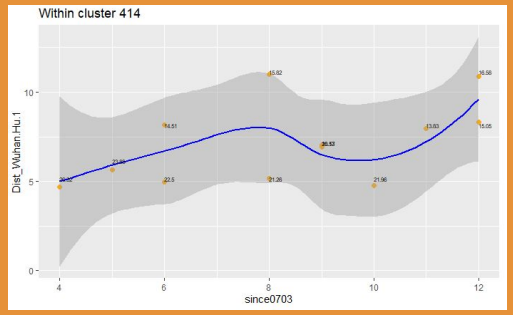
Whole cluster design (172)

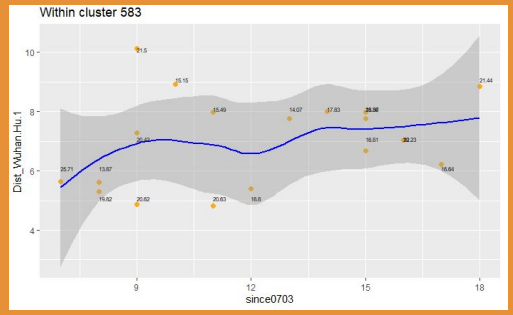
SNPs from Wuhan ~ time

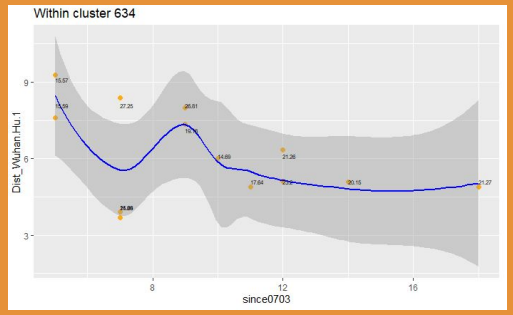
Overall

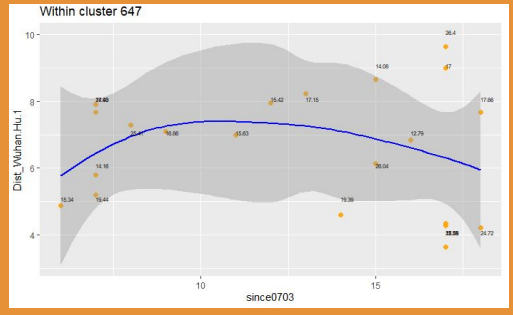


Urban

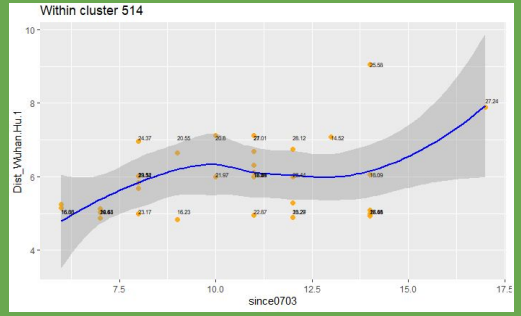


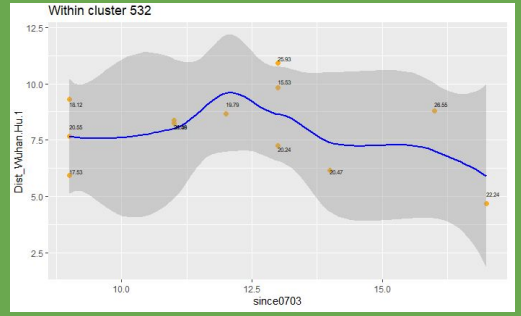


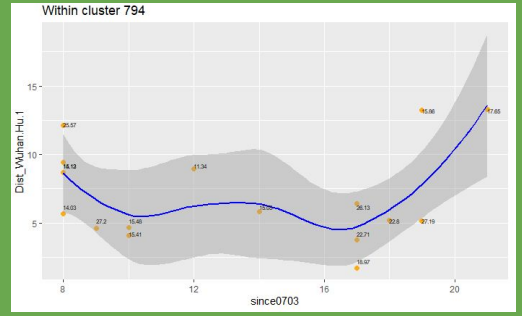




Rural

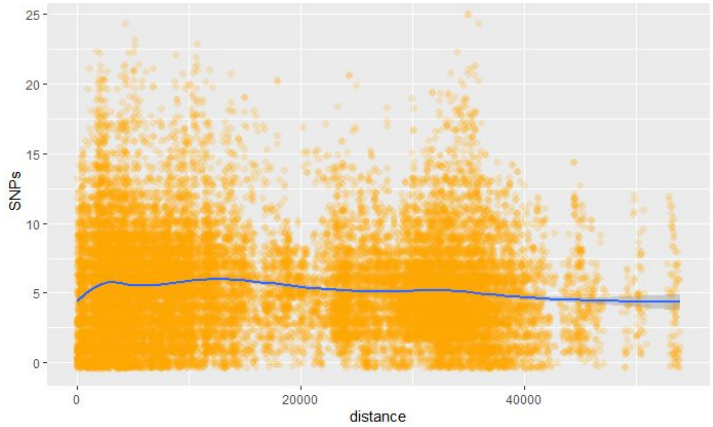




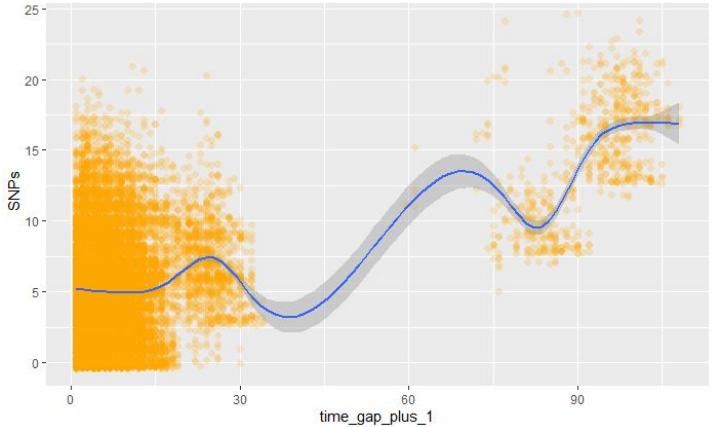


All samples (227)

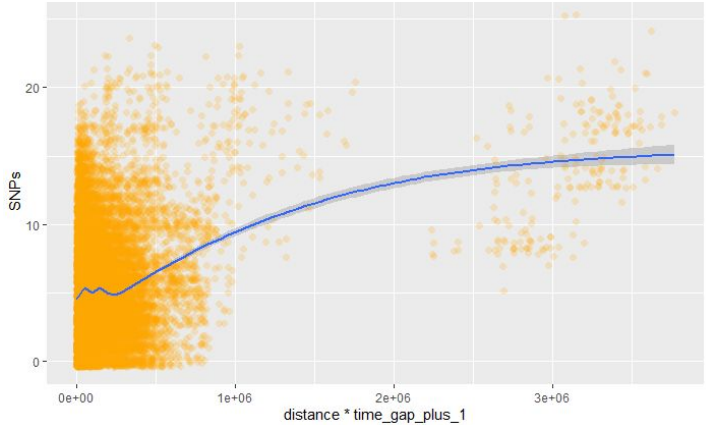
SNPs ~ distance



SNPs ~ time



SNPs ~ distance*time



Thanks