findNeighbour3 monitor

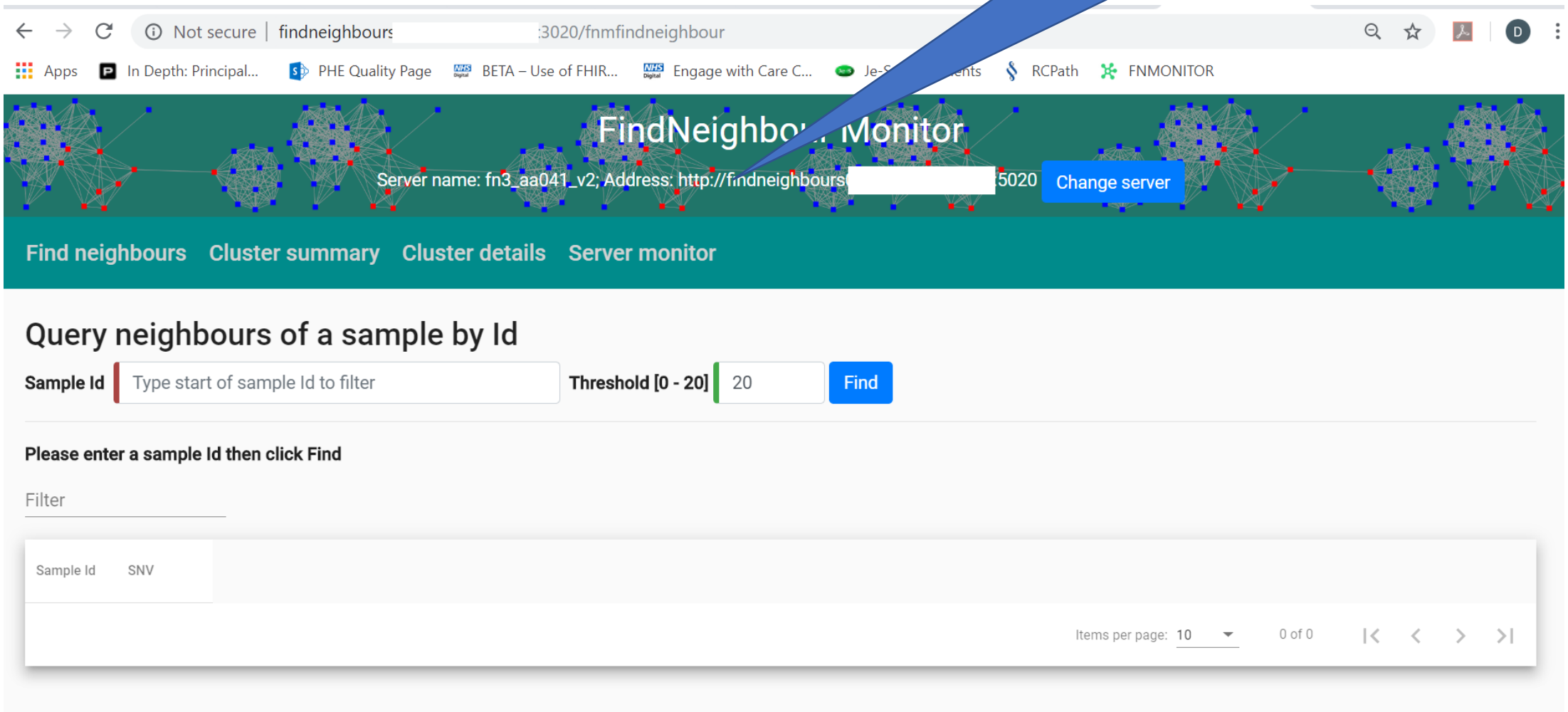
A front end for the findNeighbour3 server

V1.0 2019-07-07

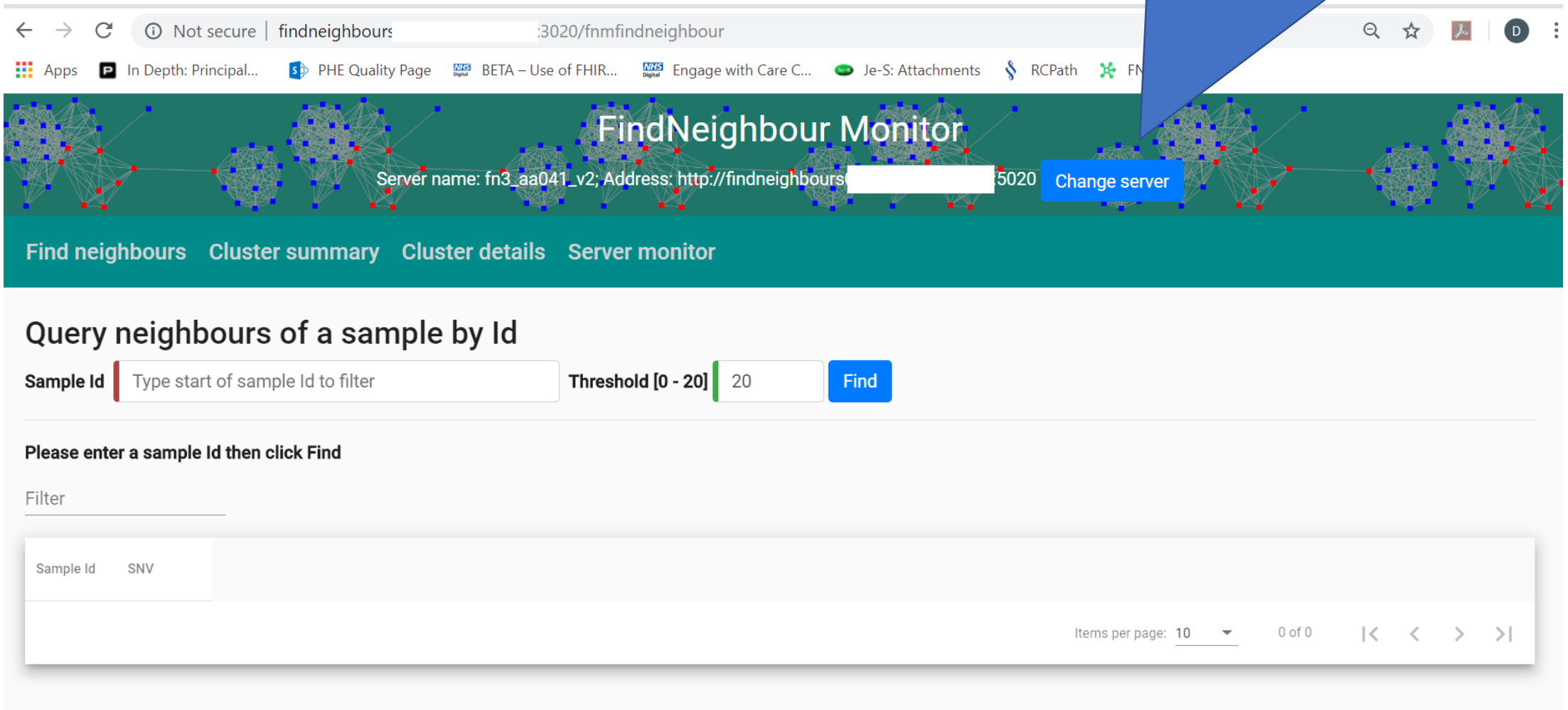
Launching the monitor

- Running a docker image is the easiest method
- See github for details

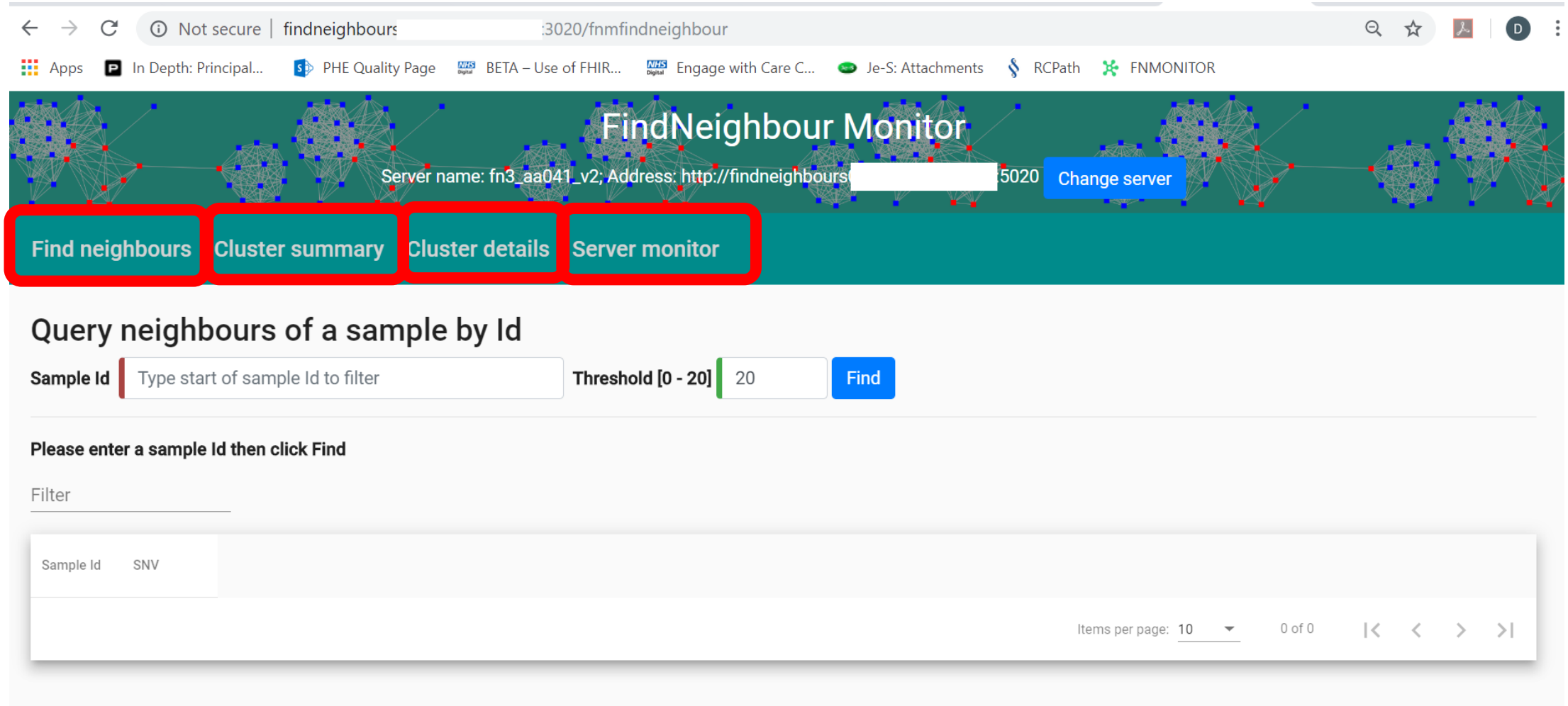
The monitor communicates with a findNeighbour3 server. You have to tell the monitor which findNeighbour server to talk to. One monitor can communicate with one findNeighbour server at at time.



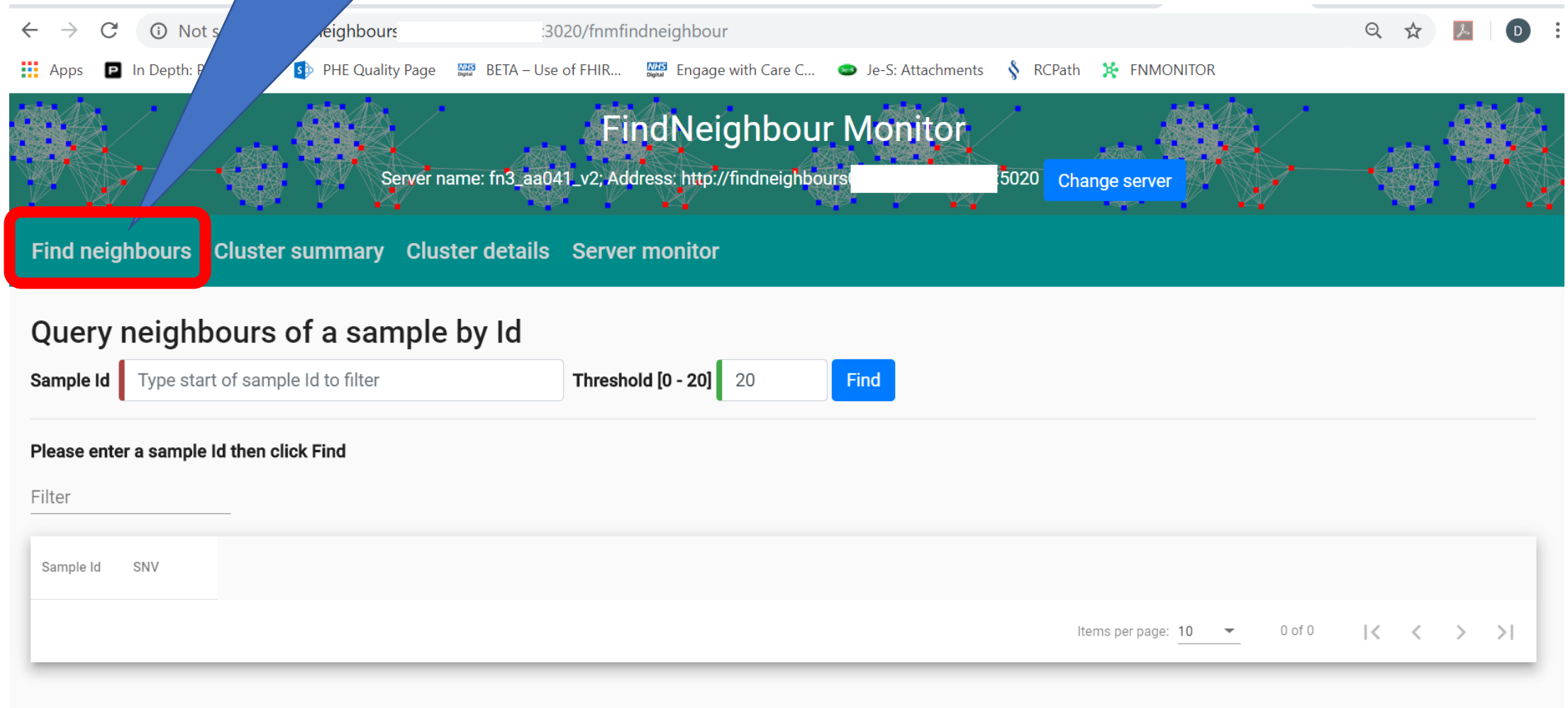
You can change the findNeighbour3 server the monitor communicates with. On startup, you will be asked for a findNeighbour3 server url.
The URL of our server has been redacted and replaced with a white box.



There are four main sections to the UI



This tab allows you to search for samples and their neighbours



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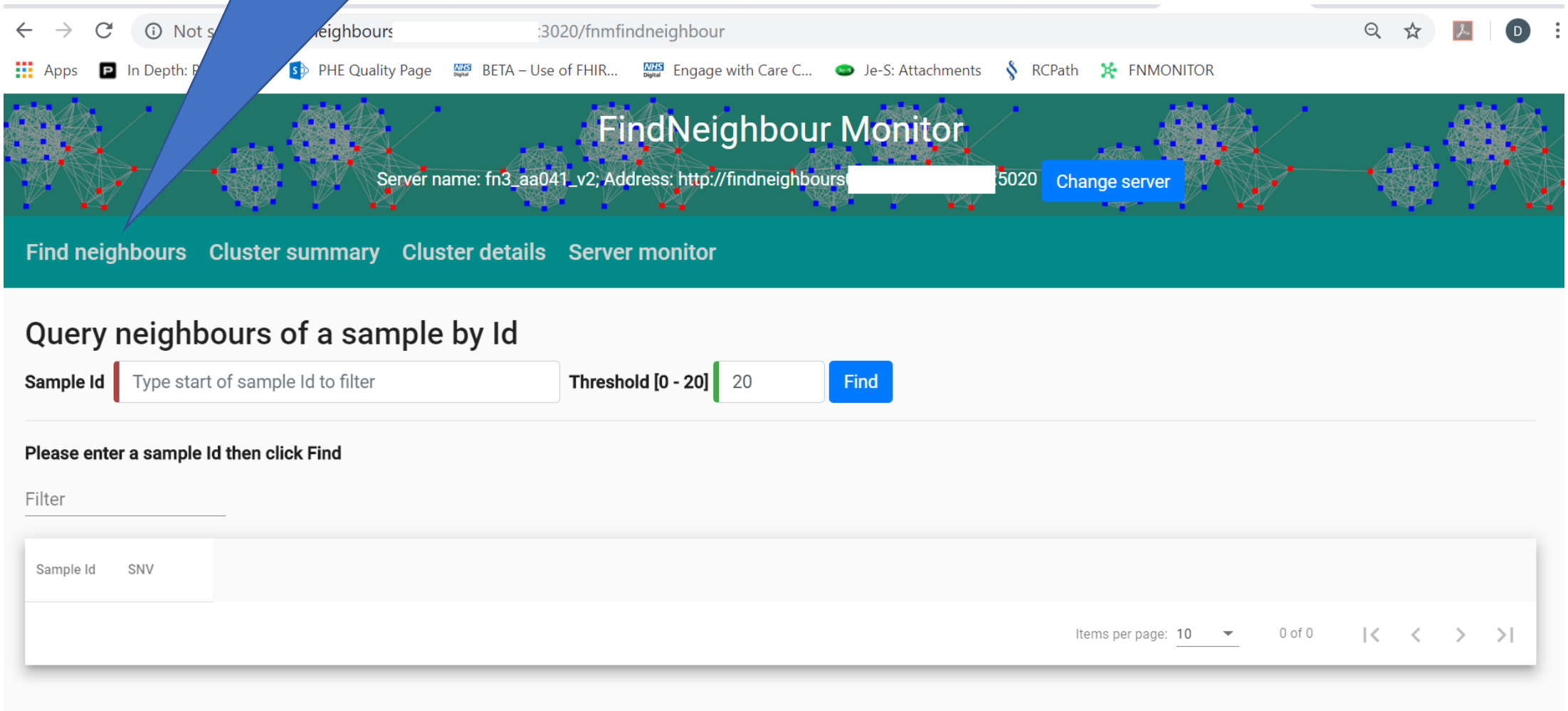
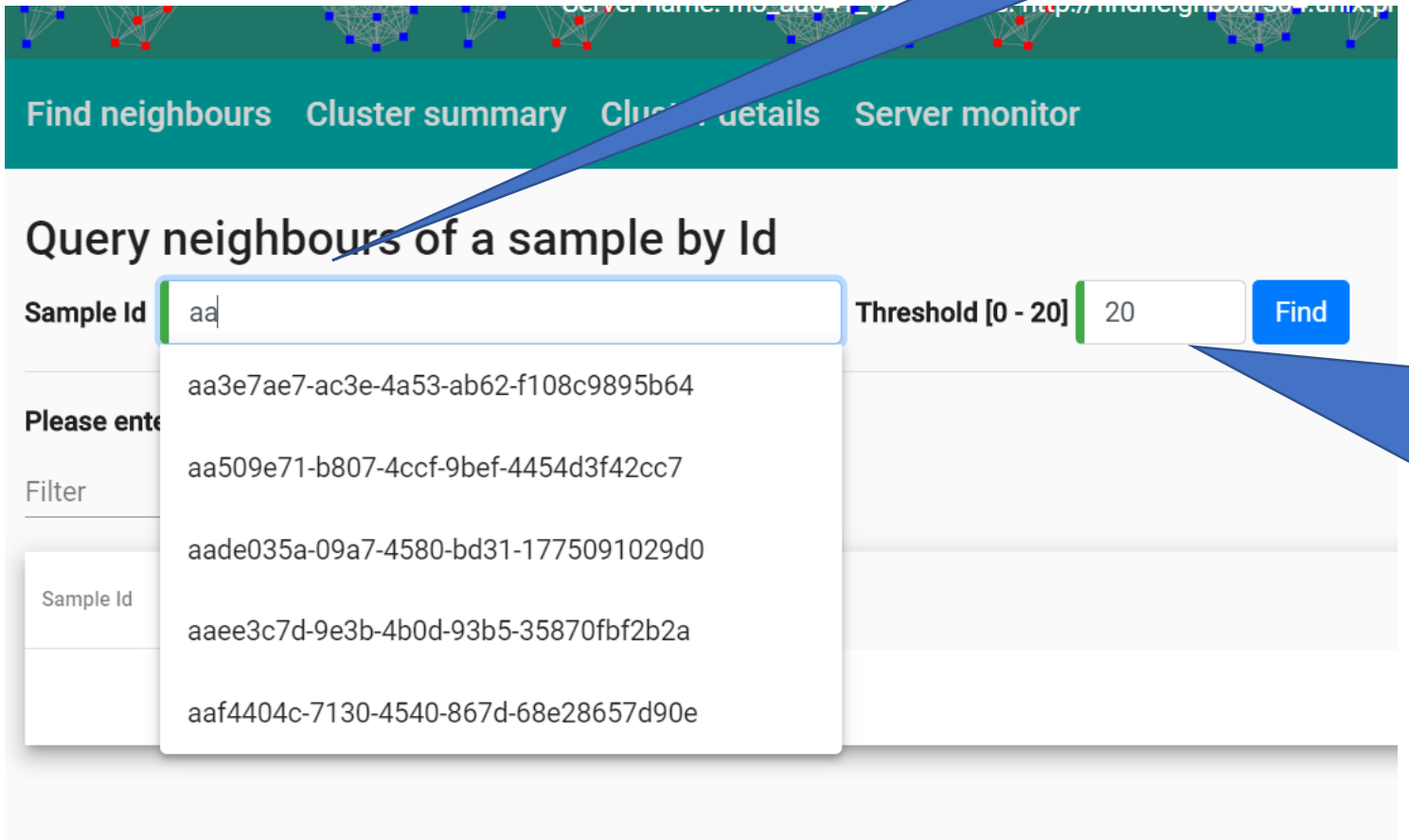
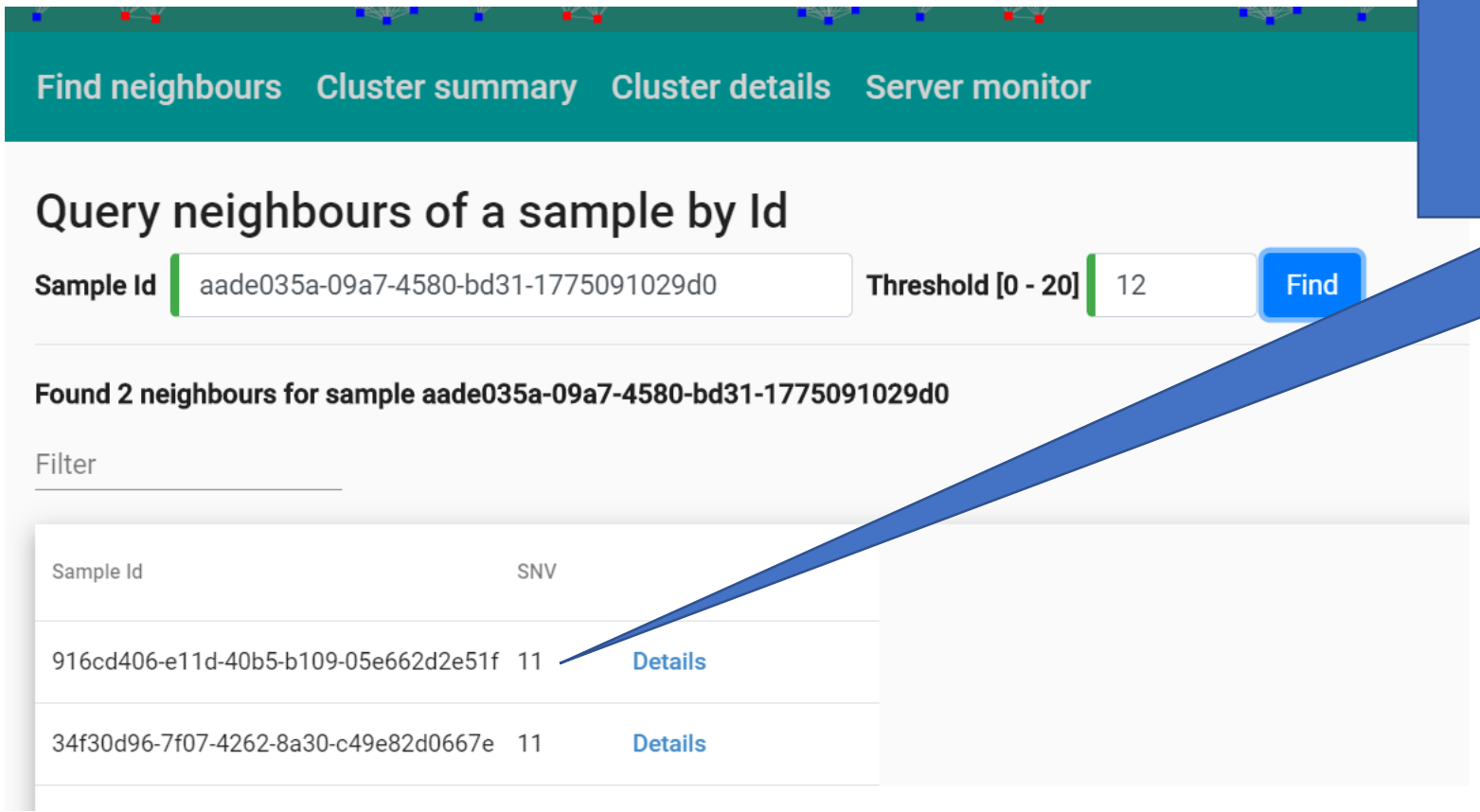


Enter the sample id and an autocomplete box appears

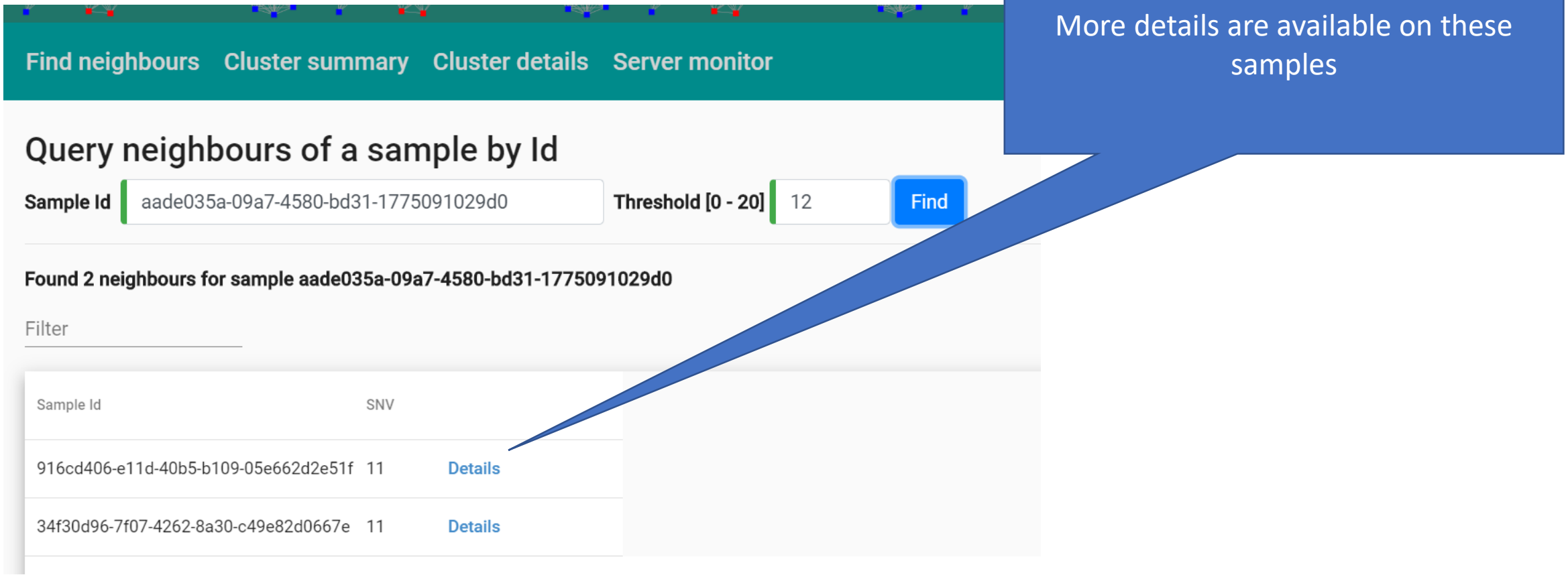


You can elect to find samples with less than a SNP distance from the sample.

The maximum distance allowed depends on the server configuration: the SNPCEILING entry in the config file tells the server the maximum SNP distance between samples to store.

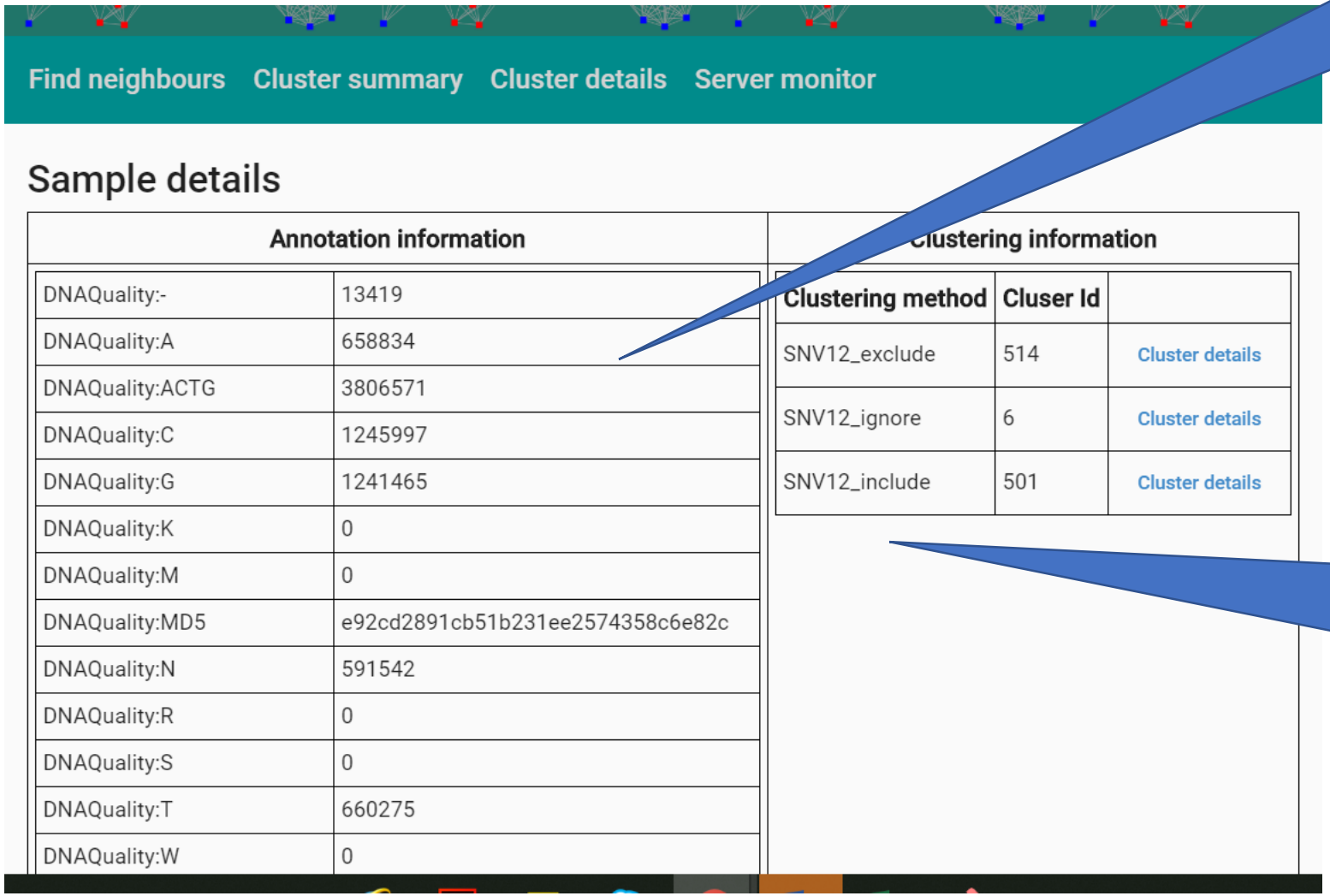


2 samples found within 12 SNP

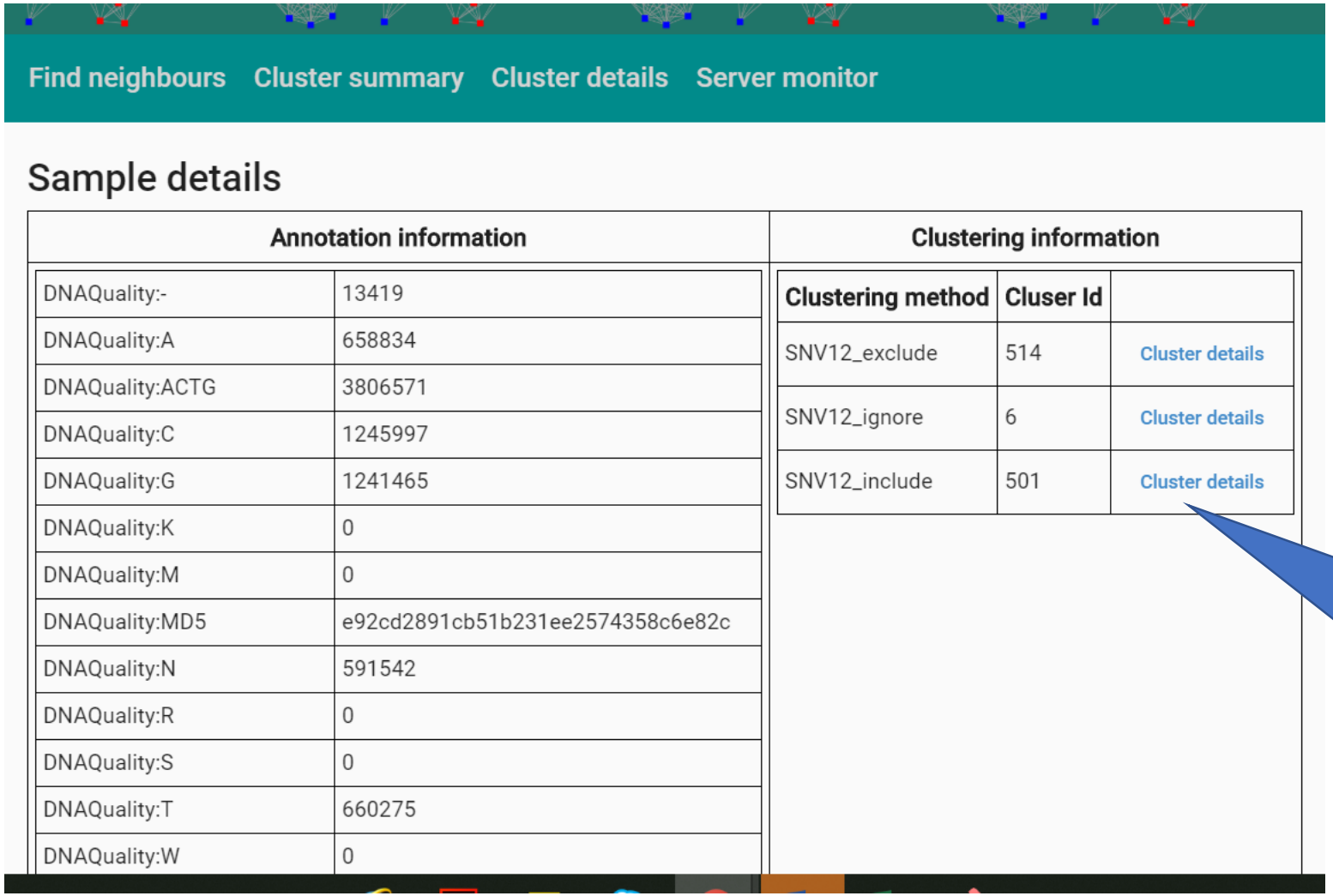


More details are available on these samples

Number of positions with particular bases, and similar technical data

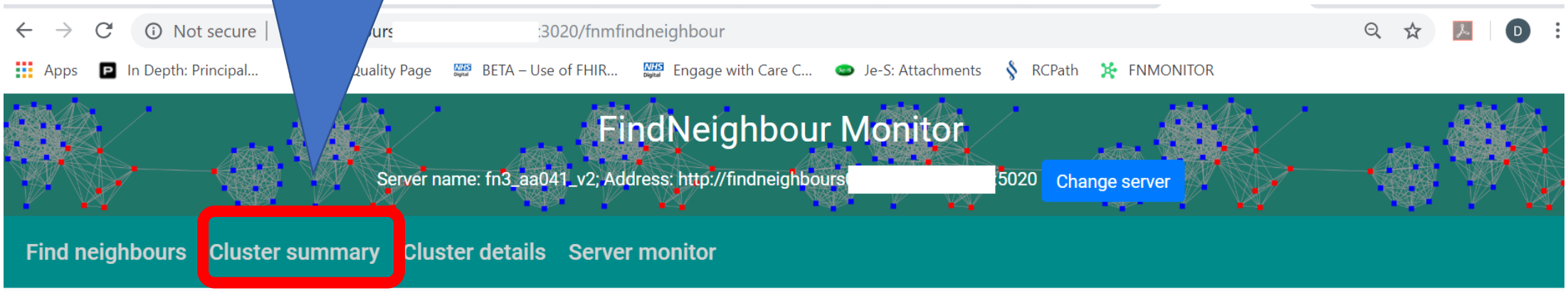


If the server is configured to build clusters of similar sequences, the clustering methods used (in this case, three different methods are in use) and cluster ids are shown.



This link will bring up a view of the cluster

Details of clusters can be searched for by number



Query neighbours of a sample by Id

Sample Id Type start of sample Id to filter **Threshold [0 - 20]** 20 Find

Please enter a sample Id then click Find

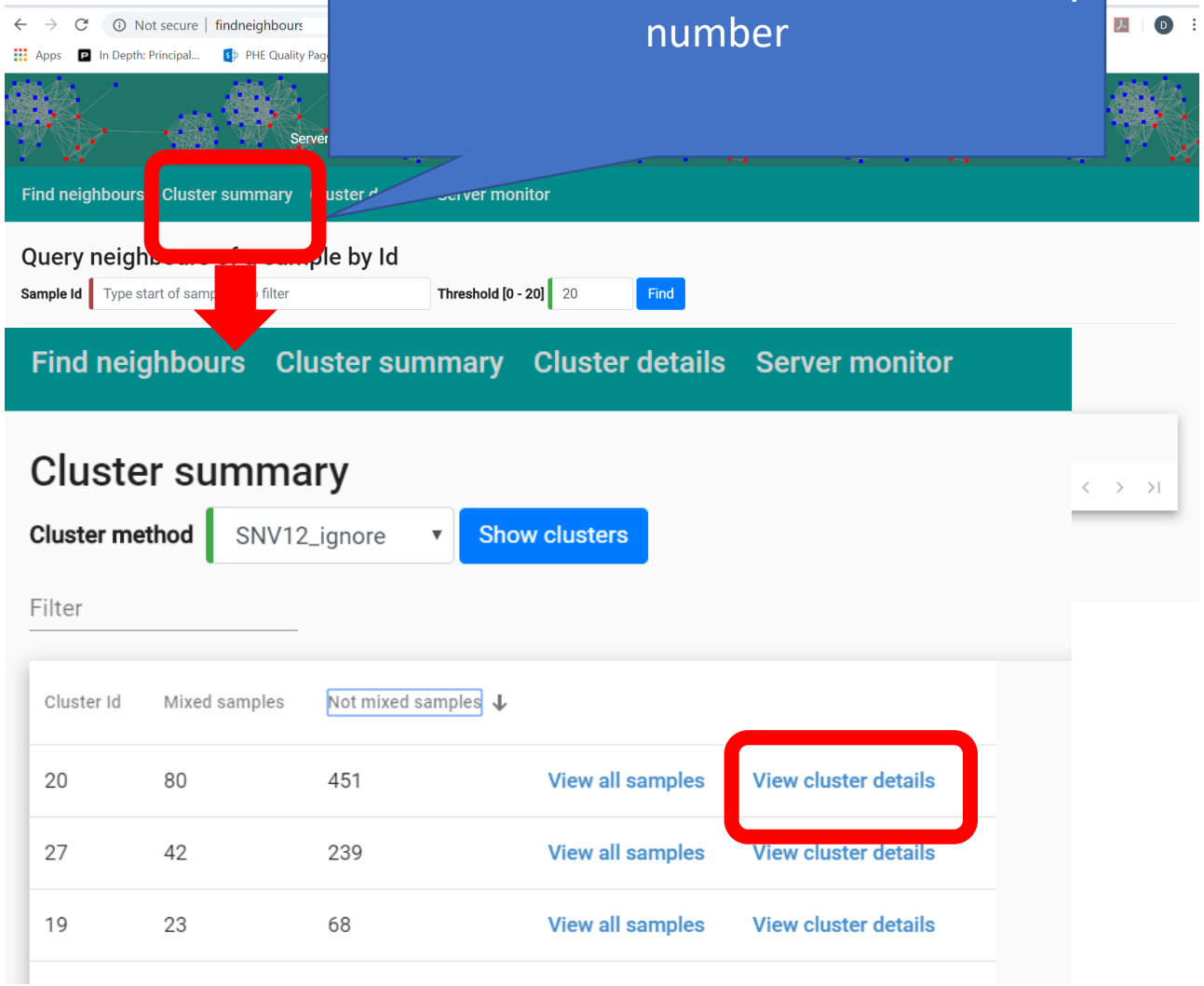
Filter

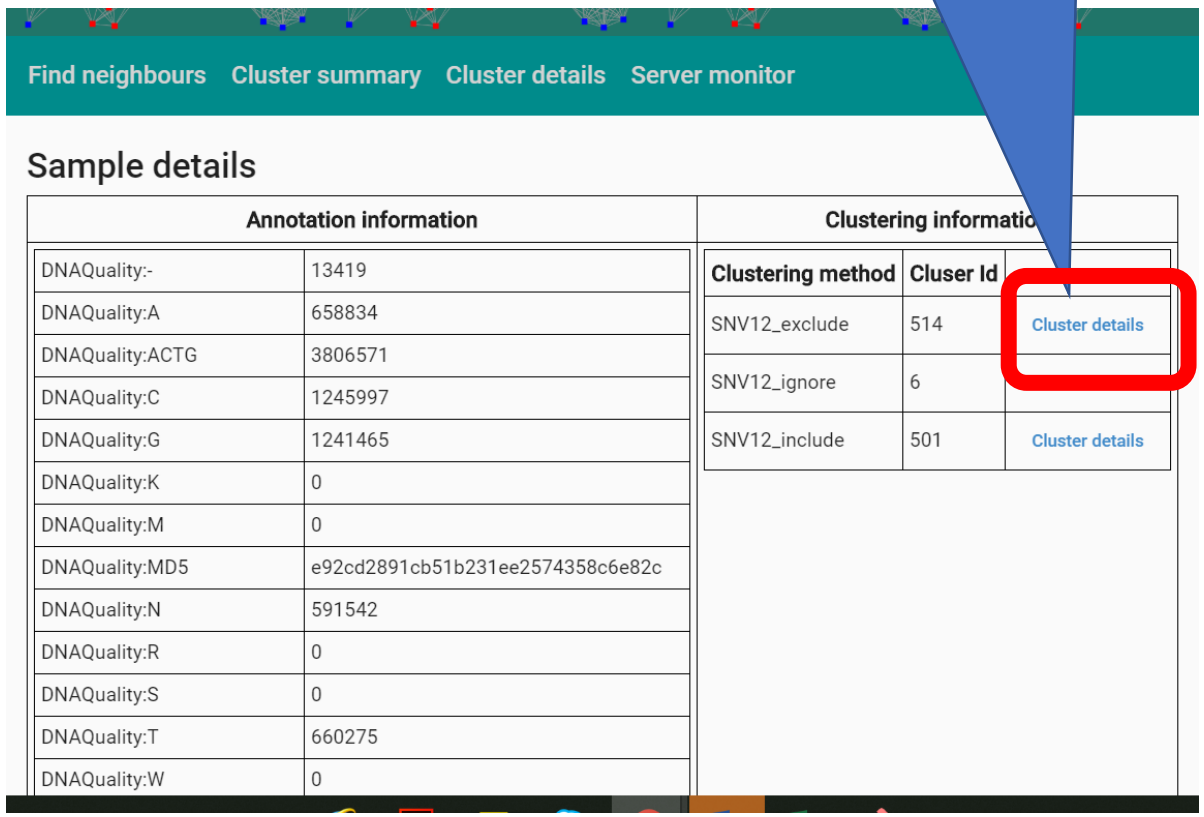
Sample Id	SNV

Items per page: 10 0 of 0

Details of clusters can be searched for by number

Or from the sample details page





Four formats of the cluster view are available. This is a tabular format

Find neighbours | Cluster summary | Cluster details | Server monitor

Cluster method SNV12_exclude **Cluster** 514 **Output format** json-records View

Filter

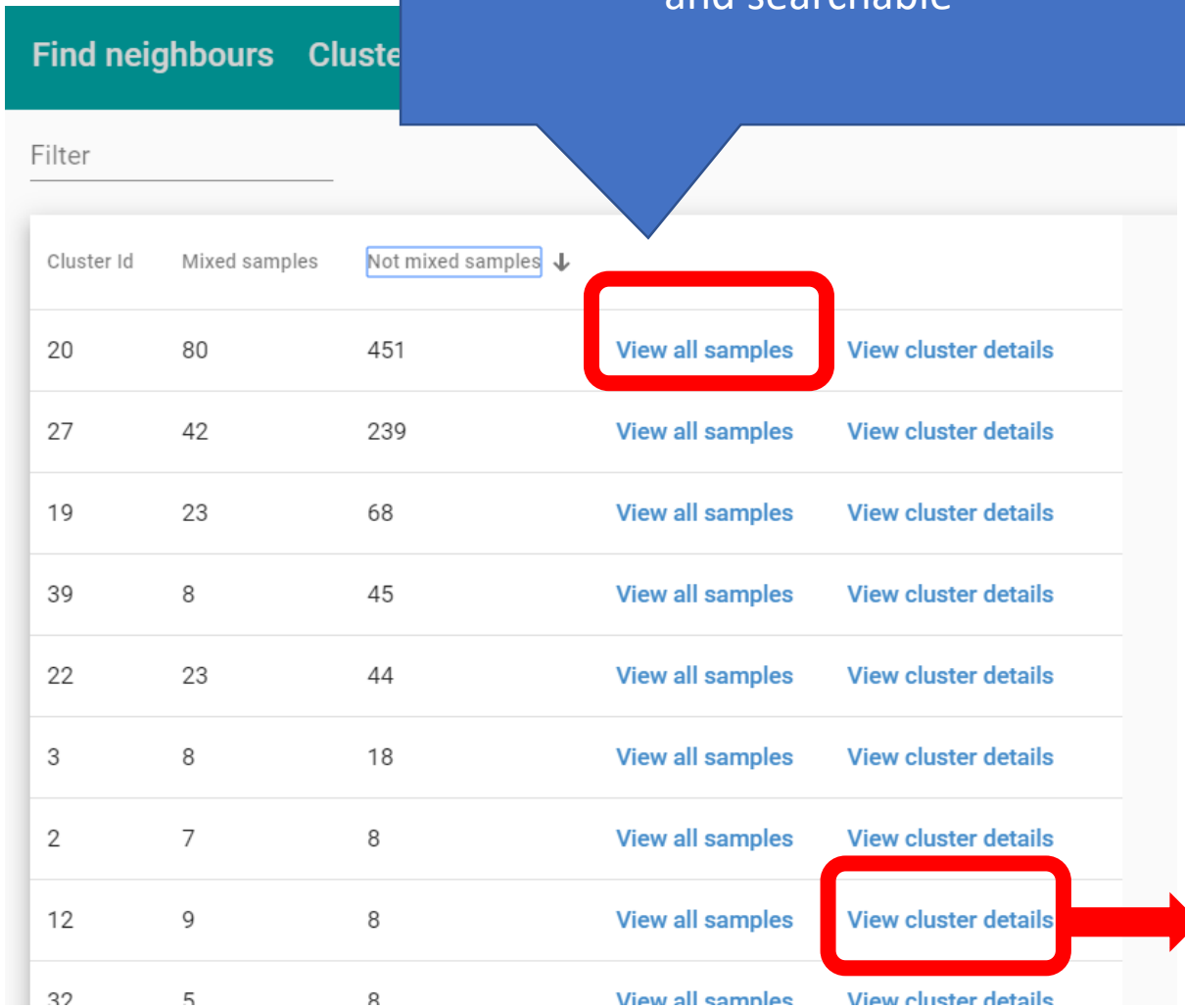
Show aligned sequence Download data as Excel

Sample Id	Aligned sequence length	AlignN	AllN	AlignM	AllM	Align N_or_M	All N_or_M	Expected Proportion1	Expected Proportion2	Expected Proportion3	Expected Proportion4	What Tested	Observed Proportion	P Value1	P Value2	P Value3	P Value4	
35b71dfb-22d2-468b-8914-201e58a3e1f7	45	1	43649	0	0	1	43649	0.0098	0.0099	0.0099	0.0444	N	0.0222	0.3589	0.0000	0.3607	0.8707	Details
7abe0fce-15b7-4cd2-a730-044badd67e5c	45	3	43363	0	0	3	43363	0.0098	0.0098	0.0098	0.0444	N	0.0667	0.0099	0.0000	0.0099	0.3233	Details
916cd406-e11d-40b5-b109-05e662d2e51f	45	3	48382	0	0	3	48382	0.0098	0.0110	0.0110	0.0444	N	0.0667	0.0099	0.0000	0.0133	0.3233	Details
aade035a-09a7-4580-bd31-1775091029d0	45	2	45812	0	0	2	45812	0.0098	0.0104	0.0104	0.0444	N	0.0444	0.0725	0.0000	0.0796	0.6001	Details
d8f5b886-50d3-4875-a813-3f332a7206e3	45	2	44929	0	0	2	44929	0.0098	0.0102	0.0102	0.0444	N	0.0444	0.0725	0.0000	0.0770	0.6001	Details
e08de9b4-2cb3-4066-865c-4fd50537b937	45	2	41805	0	0	2	41805	0.0098	0.0095	0.0095	0.0444	N	0.0444	0.0725	0.0000	0.0680	0.6001	Details

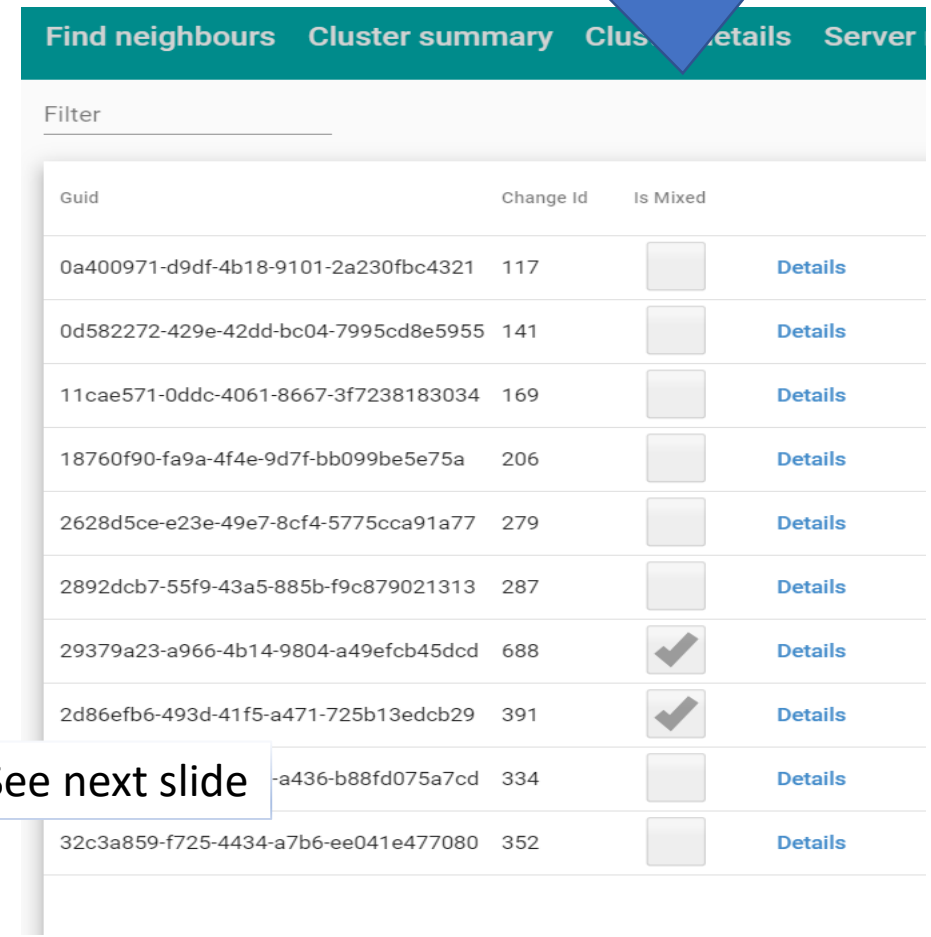
Items per page: 10 1 - 6 of 6

The grid (as with other grids) is sortable and searchable

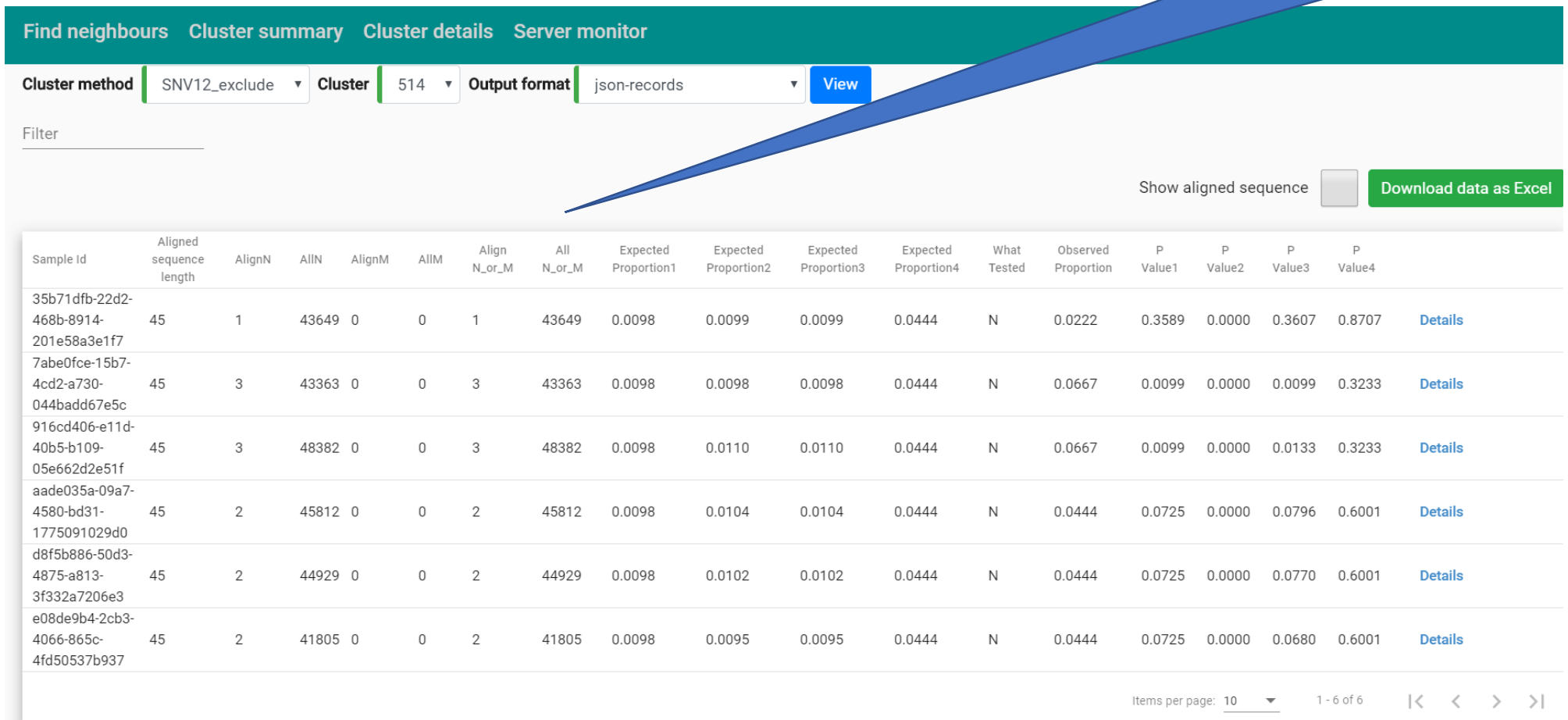
Ticks indicate the server detects this sample as mixed



See next slide

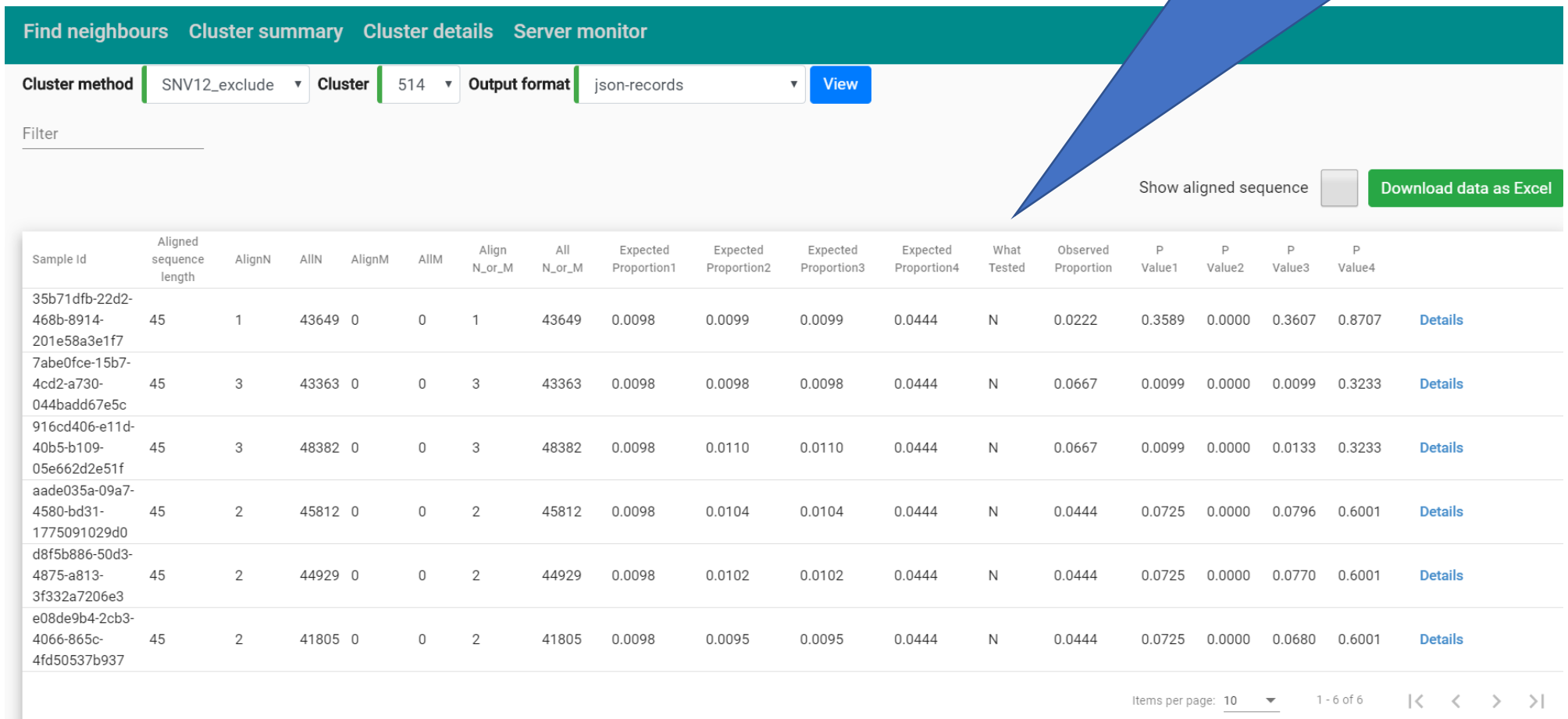


The length of the alignment (sites which vary between the members of the cluster) is shown along with the number of N (unknown) and M (mixed) bases



Sample Id	Aligned sequence length	AlignN	AllN	AlignM	AllM	Align N_or_M	All N_or_M	Expected Proportion1	Expected Proportion2	Expected Proportion3	Expected Proportion4	What Tested	Observed Proportion	P Value1	P Value2	P Value3	P Value4	
35b71dfb-22d2-468b-8914-201e58a3e1f7	45	1	43649	0	0	1	43649	0.0098	0.0099	0.0099	0.0444	N	0.0222	0.3589	0.0000	0.3607	0.8707	Details
7abe0fce-15b7-4cd2-a730-044badd67e5c	45	3	43363	0	0	3	43363	0.0098	0.0098	0.0098	0.0444	N	0.0667	0.0099	0.0000	0.0099	0.3233	Details
916cd406-e11d-40b5-b109-05e662d2e51f	45	3	48382	0	0	3	48382	0.0098	0.0110	0.0110	0.0444	N	0.0667	0.0099	0.0000	0.0133	0.3233	Details
aade035a-09a7-4580-bd31-1775091029d0	45	2	45812	0	0	2	45812	0.0098	0.0104	0.0104	0.0444	N	0.0444	0.0725	0.0000	0.0796	0.6001	Details
d8f5b886-50d3-4875-a813-3f332a7206e3	45	2	44929	0	0	2	44929	0.0098	0.0102	0.0102	0.0444	N	0.0444	0.0725	0.0000	0.0770	0.6001	Details
e08de9b4-2cb3-4066-865c-4fd50537b937	45	2	41805	0	0	2	41805	0.0098	0.0095	0.0095	0.0444	N	0.0444	0.0725	0.0000	0.0680	0.6001	Details

The statistical approach to detection of mixed sequences involves comparing the number of Ns, Ms, or Ns/Ms with an expectation. The choice is determined in the server config file



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7abe0fce-15b7-4cd2-a730-044badd67e5c	45	3	43363	0	0	3	43363	0.0098	0.0098	0.0098	0.0444	N	0.0667	0.0099	0.0000	0.0099	0.3233	Details
916cd406-e11d-40b5-b109-05e662d2e51f	45	3	48382	0	0	3	48382	0.0098	0.0110	0.0110	0.0444	N	0.0667	0.0099	0.0000	0.0133	0.3233	Details
aade035a-09a7-4580-bd31-1775091029d0	45	2	45812	0	0	2	45812	0.0098	0.0104	0.0104	0.0444	N	0.0444	0.0725	0.0000	0.0796	0.6001	Details
d8f5b886-50d3-4875-a813-3f332a7206e3	45	2	44929	0	0	2	44929	0.0098	0.0102	0.0102	0.0444	N	0.0444	0.0725	0.0000	0.0770	0.6001	Details
e08de9b4-2cb3-4066-865c-4fd50537b937	45	2	41805	0	0	2	41805	0.0098	0.0095	0.0095	0.0444	N	0.0444	0.0725	0.0000	0.0680	0.6001	Details

Four statistics are provided, each testing the number of ‘what tested’ bases exceeds an expectation

Find neighbours | Cluster summary | Cluster details | Server monitor

Cluster method: SNV12_exclude | Cluster: 514 | Output format: json-records | View

Filter

Sh aligned sequence | Download data as Excel

Sample Id	Aligned sequence length	AlignN	AllN	AlignM	AllM	Align N_or_M	All N_or_M	Expected Proportion1	Expected Proportion2	Expected Proportion3	Expected Proportion4	What Tested	Observed Proportion	P Value1	P Value2	P Value3	P Value4	
35b71dfb-22d2-468b-8914-201e58a3e1f7	45	1	43649	0	0	1	43649	0.0098	0.0099	0.0099	0.0444	N	0.0222	0.3589	0.0000	0.3607	0.8707	Details
7abe0fce-15b7-4cd2-a730-044badd67e5c	45	3	43363	0	0	3	43363	0.0098	0.0098	0.0098	0.0444	N	0.0667	0.0099	0.0000	0.0099	0.3233	Details
916cd406-e11d-40b5-b109-05e662d2e51f	45	3	48382	0	0	3	48382	0.0098	0.0110	0.0110	0.0444	N	0.0667	0.0099	0.0000	0.0133	0.3233	Details
aade035a-09a7-4580-bd31-1775091029d0	45	2	45812	0	0	2	45812	0.0098	0.0104	0.0104	0.0444	N	0.0444	0.0725	0.0000	0.0796	0.6001	Details
d8f5b886-50d3-4875-a813-3f332a7206e3	45	2	44929	0	0	2	44929	0.0098	0.0102	0.0102	0.0444	N	0.0444	0.0725	0.0000	0.0770	0.6001	Details
e08de9b4-2cb3-4066-865c-4fd50537b937	45	2	41805	0	0	2	41805	0.0098	0.0095	0.0095	0.0444	N	0.0444	0.0725	0.0000	0.0680	0.6001	Details

Items per page: 10 | 1 - 6 of 6

The sequence can be shown

Find neighbours | Cluster summary | Cluster details | Server monitor

Cluster method: SNV12_exclude | Cluster: 514 | Output format: json-records | View

Filter

Show aligned sequence | Download data as Excel

Sample Id	Aligned sequence length	AlignN	AllN	AlignM	AllM	Align N_or_M	All N_or_M	Expected Proportion1	Expected Proportion2	Expected Proportion3	Expected Proportion4	What Tested	Observed Proportion	P Value1	P Value2	P Value3	P Value4	
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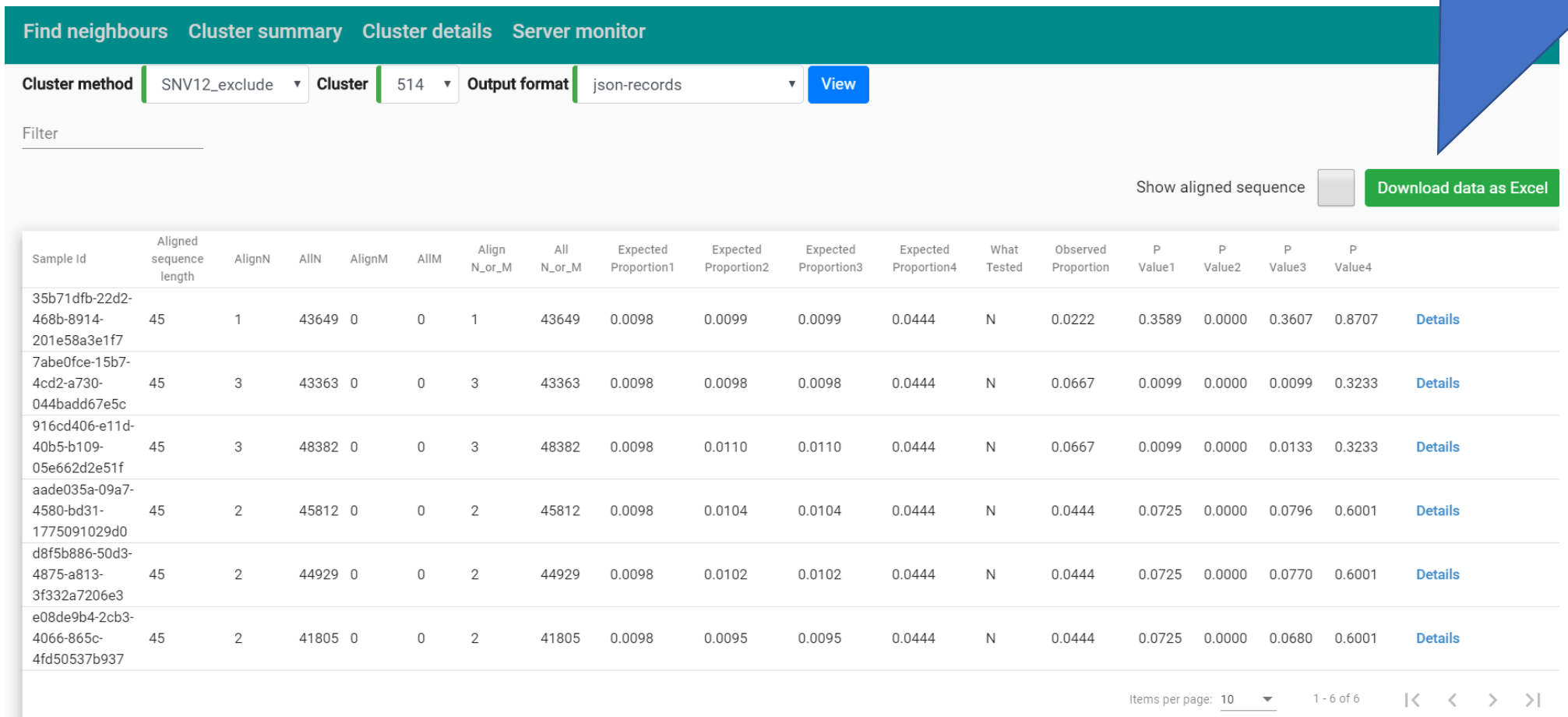
aade035a-09a7-4580-bd31-1775091029d0	45	2	45812	0	0	2	45812	0.0098	0.0104	0.0104	0.0444	N	0.0444	0.0725	0.0000	0.0796	0.6001	Details
d8f5b886-50d3-4875-a813-3f332a7206e3	45	2	44929	0	0	2	44929	0.0098	0.0102	0.0102	0.0444	N	0.0444	0.0725	0.0000	0.0770	0.6001	Details
e08de9b4-2cb3-4066-865c-4fd50537b937	45	2	41805	0	0	2	41805	0.0098	0.0095	0.0095	0.0444	N	0.0444	0.0725	0.0000	0.0680	0.6001	Details

Items per page: 10 | 1 - 6 of 6

The content of the table displayed can be downloaded



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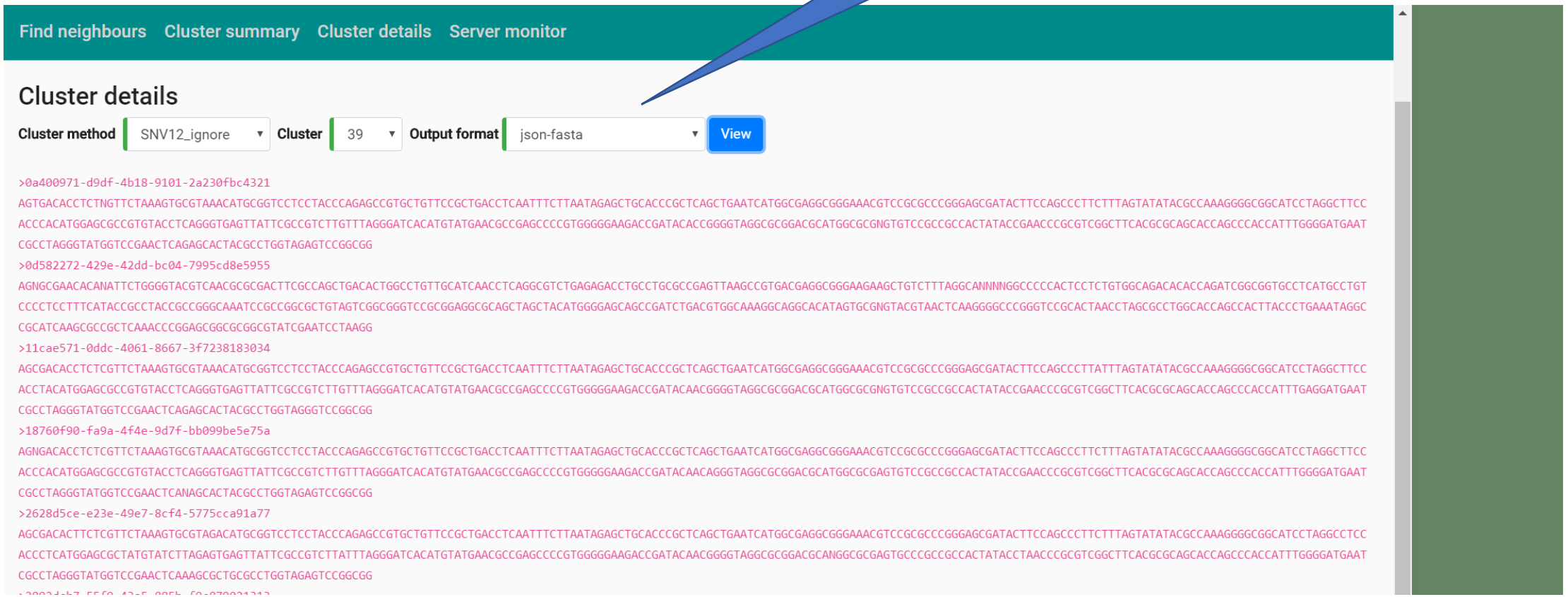
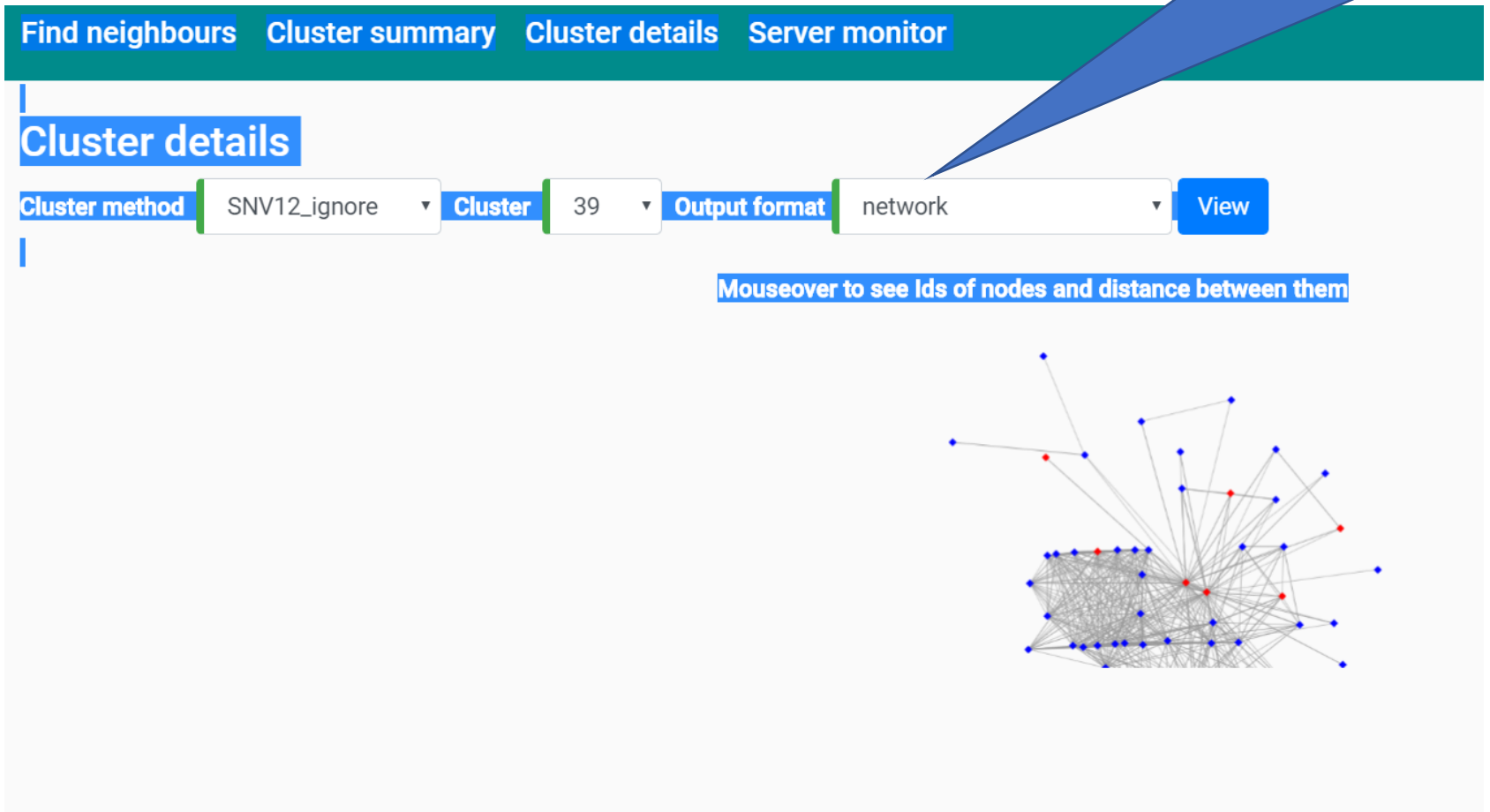
916cd406-e11d-40b5-b109-05e662d2e51f	45	3	48382	0	0	3	48382	0.0098	0.0110	0.0110	0.0444	N	0.0667	0.0099	0.0000	0.0133	0.3233	Details
aade035a-09a7-4580-bd31-1775091029d0	45	2	45812	0	0	2	45812	0.0098	0.0104	0.0104	0.0444	N	0.0444	0.0725	0.0000	0.0796	0.6001	Details
d8f5b886-50d3-4875-a813-3f332a7206e3	45	2	44929	0	0	2	44929	0.0098	0.0102	0.0102	0.0444	N	0.0444	0.0725	0.0000	0.0770	0.6001	Details
e08de9b4-2cb3-4066-865c-4fd50537b937	45	2	41805	0	0	2	41805	0.0098	0.0095	0.0095	0.0444	N	0.0444	0.0725	0.0000	0.0680	0.6001	Details

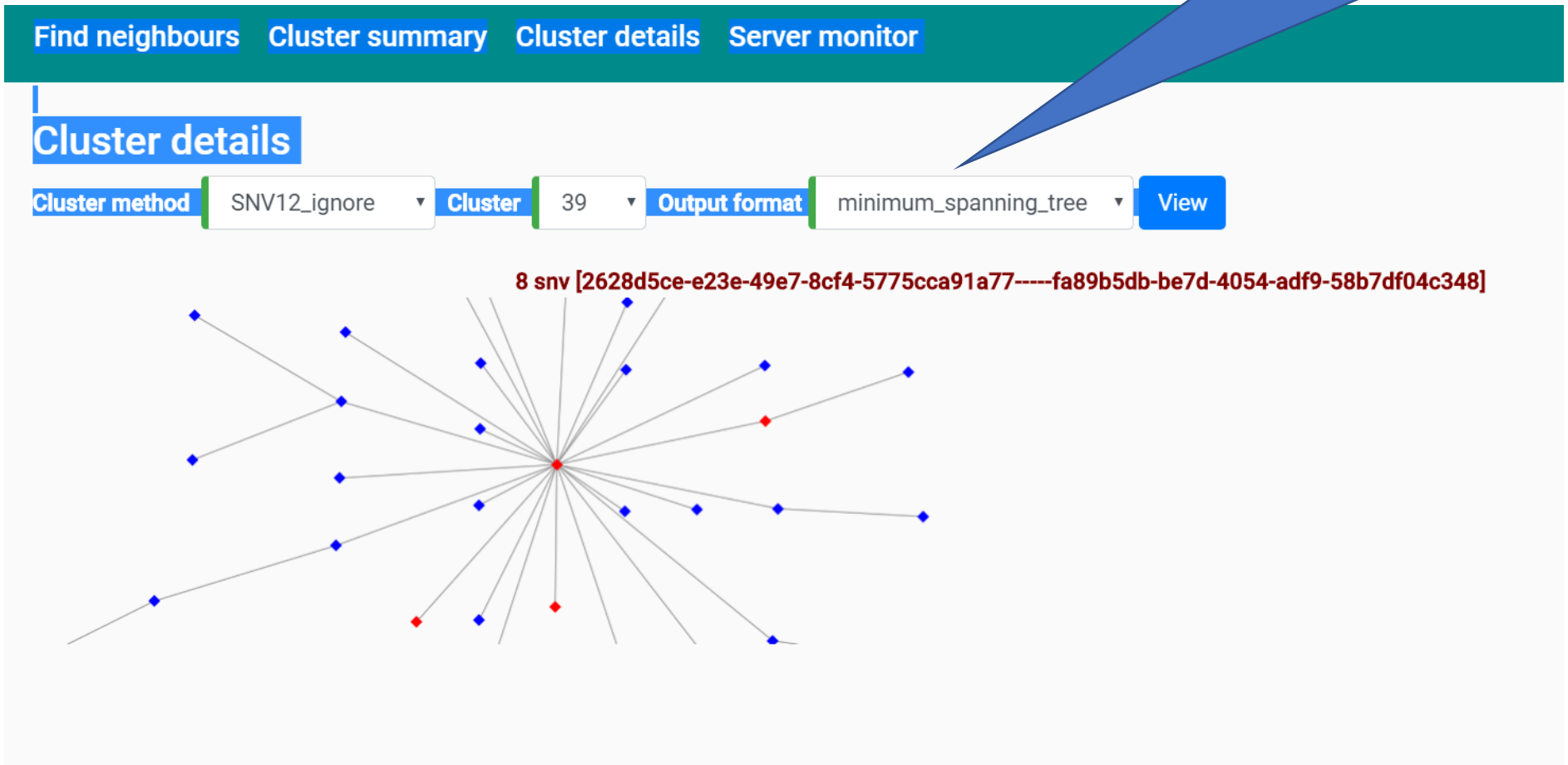
Shows multisequence alignment of positions varying between samples



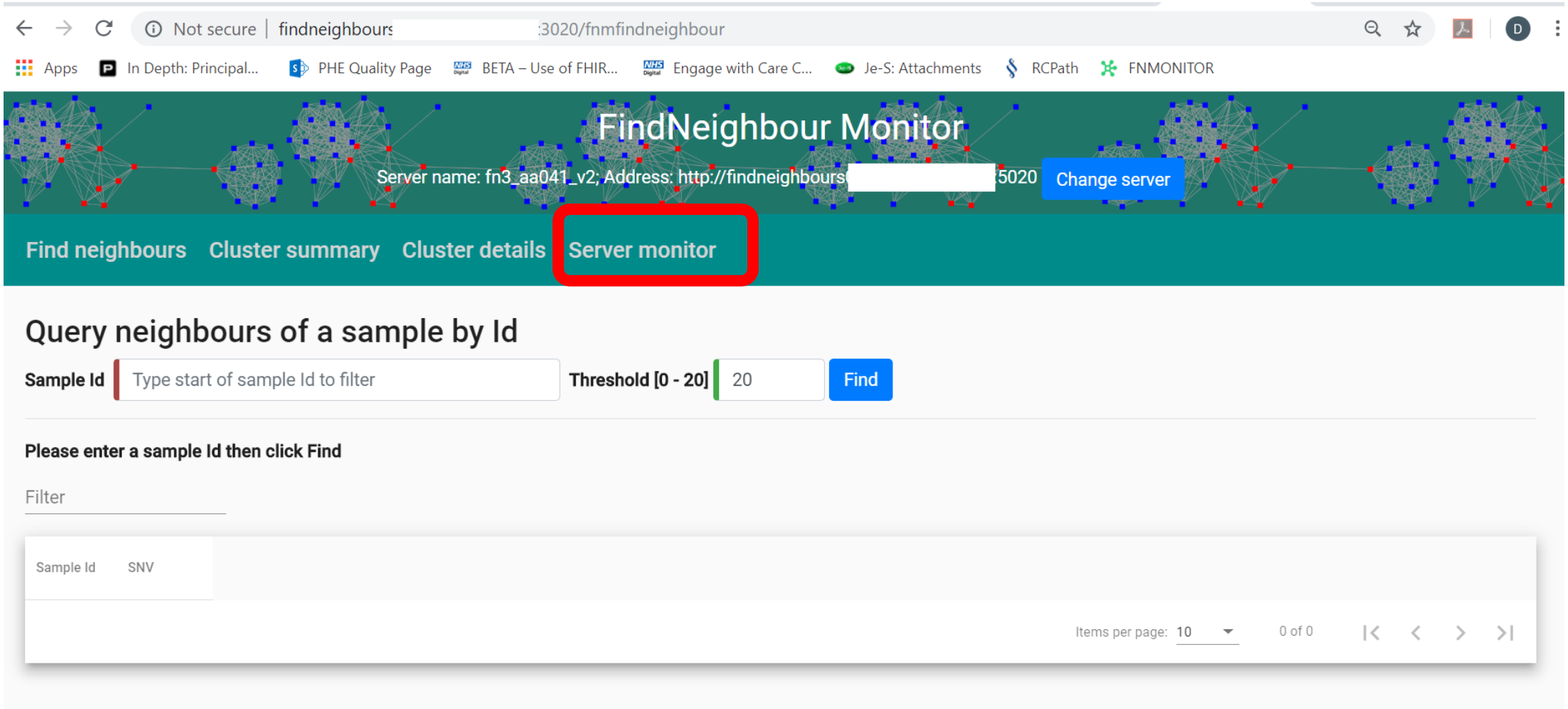
Shows all edges between samples less than the cutoff SNPCEILING set for the server. Mixed samples are coloured red



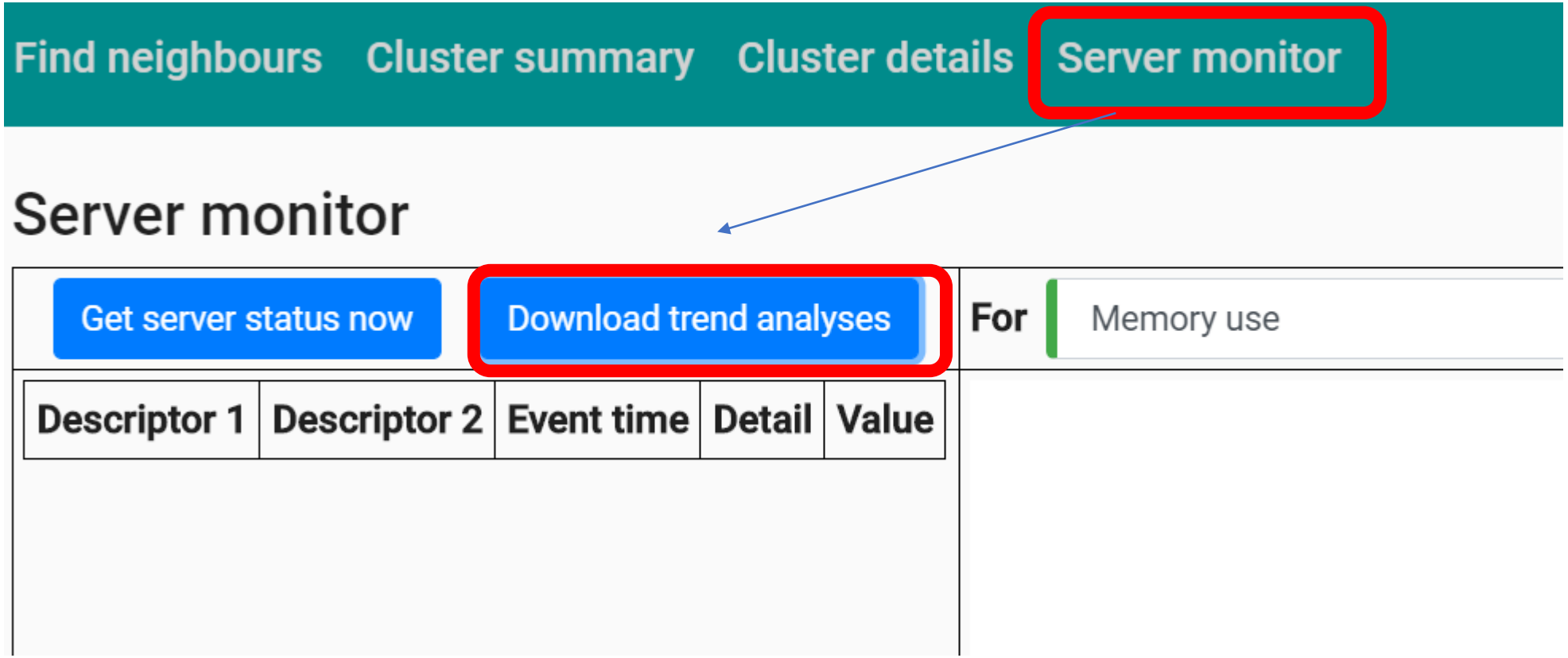
Shows a minimal spanning tree for an undirected graph with sequences as nodes and SNP distances as weighted edges. Mixed samples are coloured red



The server's status, RAM etc can be viewed



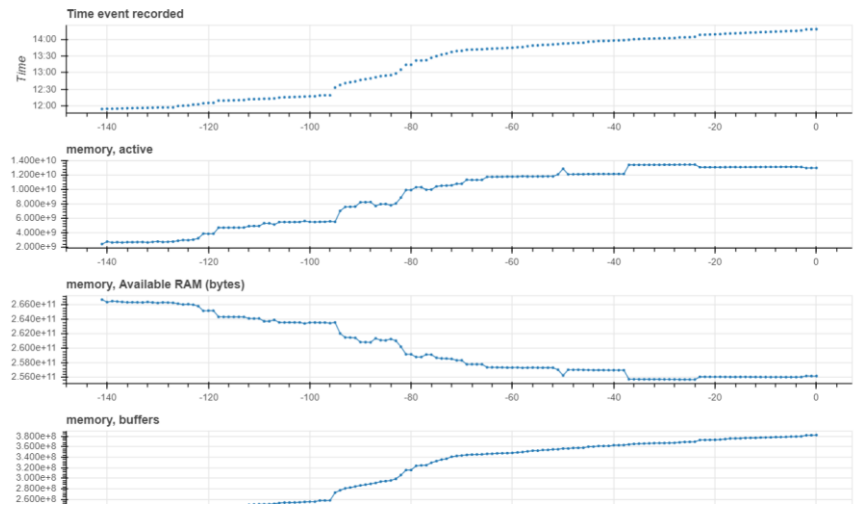
Server status



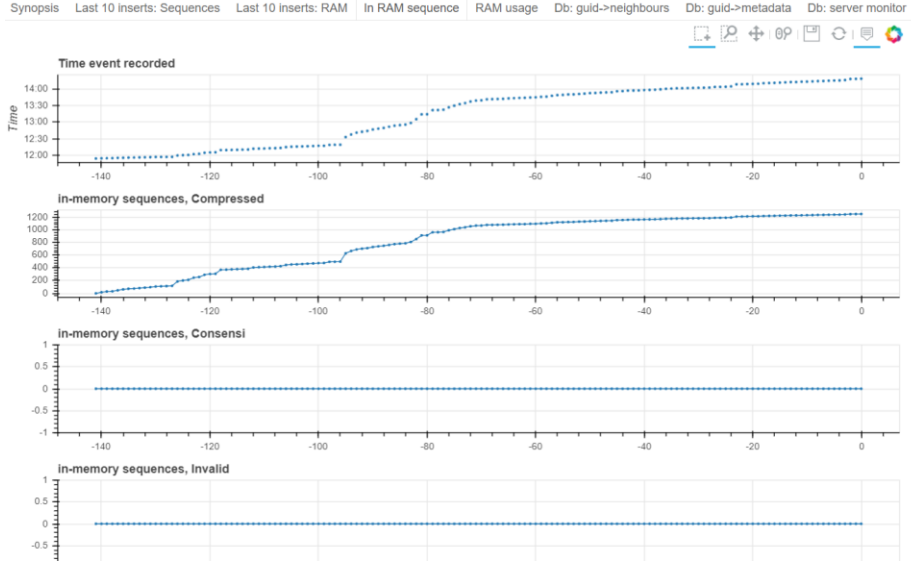
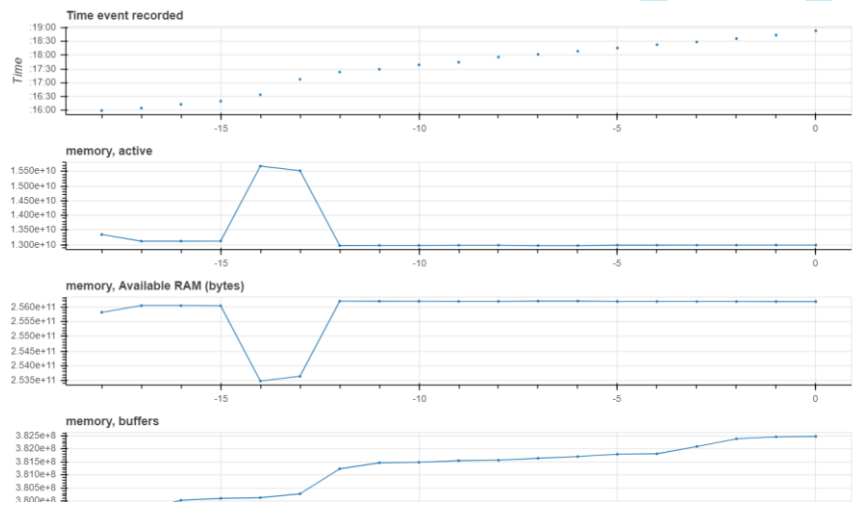
Synopsis | Last 10 inserts: Sequences | Last 10 inserts: RAM | In RAM sequence | RAM usage | Db: guid->neighbours | Db: guid->metadata | Db: server monitor | Log tail

#	Description	Value
0	Server URL	127.0.0.1
1	Server Port	5020
2	Server Description	A server operating in on localhost for a demo project using AA041 cluster data
3	Time report generated	2019-07-06T21:22:38.225491
4	memory, active	12984623104
5	memory, Available RAM (bytes)	256185987072
6	memory, buffers	382476288
7	memory, cached	12468269056
8	memory, Free RAM (bytes)	245597335552
9	memory, inactive	10998583296
10	memory, Percent RAM Used	5.3
11	memory, shared	1212416
12	memory, slab RAM (bytes)	615301120
13	memory, Total system (bytes)	270487711744
14	memory, Used RAM (bytes)	12039630848
15	in-memory sequences, Compressed	1252
16	in-memory sequences, Consensi	0
17	in-memory sequences, Invalid	0
18	in-memory sequences, Recompressed	0
19	in-memory sequences, Seqs	1252
20	Note: this data is based on the most recent server status report, which was at	2019-07-05T14:18:53.058663

Synopsis | Last 10 inserts: Sequences | Last 10 inserts: RAM | In RAM sequence | RAM usage | Db: guid->neighbours | Db: guid->metadata | Db: server monitor | Log tail



Synopsis | Last 10 inserts: Sequences | Last 10 inserts: RAM | In RAM sequence | RAM usage | Db: guid->neighbours | Db: guid->metadata | Db: server monitor | Log tail



Synopsis | Last 10 inserts: Sequences | Last 10 inserts: RAM | In RAM sequence | RAM usage | Db: guid->neighbours | Db: guid->metadata | Db: server monitor | Log tail