

新型コロナウイルスのNGS解析

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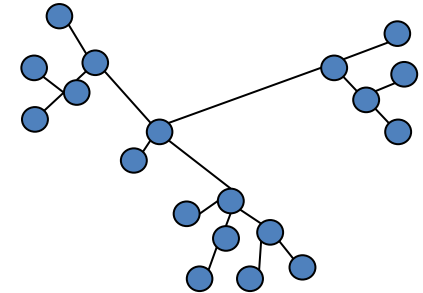
遺伝子型の決定

サンプル1・・・ TCGAGCTG
サンプル2・・・ TCGAGCAG
サンプル3・・・ TCCAGCTG
サンプル4・・・ TCGAGCTG
サンプル5・・・ TCGTGCTG

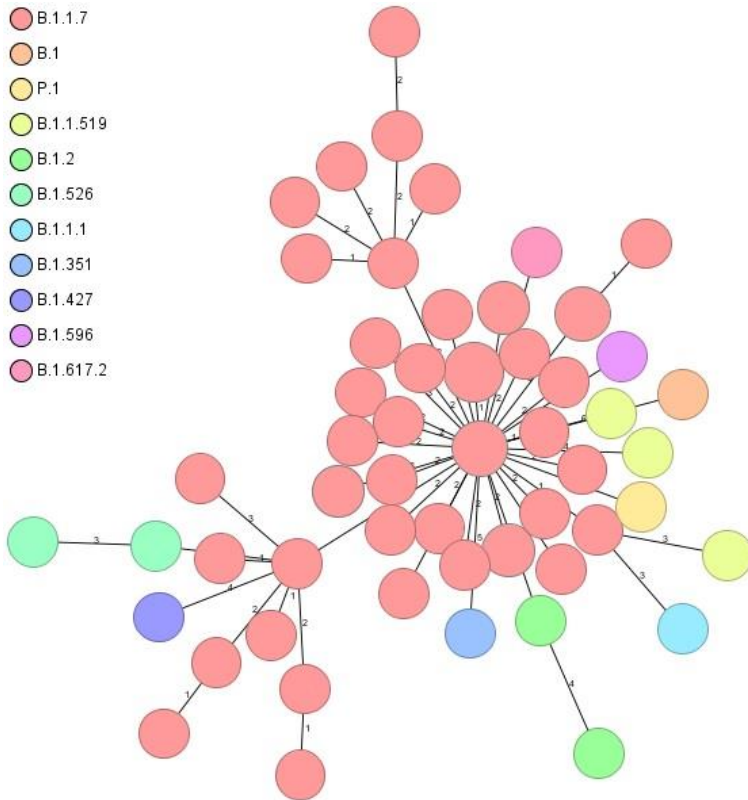
系統の分類

| | |
|-------|-----------|
| サンプル1 | B.1.1.7 |
| サンプル2 | B.1.2 |
| サンプル3 | B.1.1.519 |
| サンプル4 | B.1.1.7 |
| サンプル5 | B.1.427 |

クラスター解析



- 次世代シーケンサーを利用した、新型コロナウイルスの感染症サーベイランスにおけるデータ解析には、一般的なNGSのデータ処理に加え、ウイルスの系統解析や疫学解析などを行う必要がある
- Ridom社Ridom SeqSphere+では、NGSの生データから始まり、遺伝子変異の検出による遺伝子型の決定、PANGO lineageに基づいたウイルス系統の分類、さらにクラスター解析や系統樹解析を実行可能なワークフローが搭載されており、新型コロナウイルスのゲノム解析や疫学解析を簡単に行うことができる



■ Ridom SeqSphere+ のSARS-CoV-2関連機能

- SARS-CoV-2における重要な変異（N501Yなど）をまとめたテンプレートを搭載
- イルミナ tiled amplicon（ARTIC, AmpliSeqなど）パネル実験で得られたFASTQファイルに対応
- PANGO lineageに基づくウイルス型タイピング（B.1.1.7など）
- Minimum Spanning Treeによるクラスター解析や系統樹解析
- 変異テーブルやコンセンサス配列、BAMファイルの出力
- リードデータのクオリティーチェックとアダプタートリミング
- GISAID登録用ファイルの自動作成

Define Project
ゲノム、変異、系統データ
スキーマなどのダウンロード



FASTQ files from
sequencer or SRA

Assembling
De Novoアセンブル or
リファレンスマッピング

Typing
変異検出、PANGO系統
の分類

Analyze
Minimum Spanning
Tree、系統樹解析

- New Project**
Create a new 'species-specific' Project to hold Sample data
- Import Epi Metadata**
Import epi metadata from MS Excel and CSV files into Samples of a Project
- Process Assembled Genome Data**
Process and import assembled data from local files or from NCBI Genomes into Samples of a Project
- SRA**
Download FASTQ from SRA
Download FASTQ and metadata from NCBI SRA to be processed by a pipeline
- Logout & Start Pipeline Mode**
Configure and start non-interactive data assembling and processing pipelines
- Comparison Table**
Compare and visualize Sample data (e.g., phylogenetic trees, epi curve, maps)
- Search Samples**
Search Samples by Project, epi/genotyping data, or last modified date

Pipelineモード

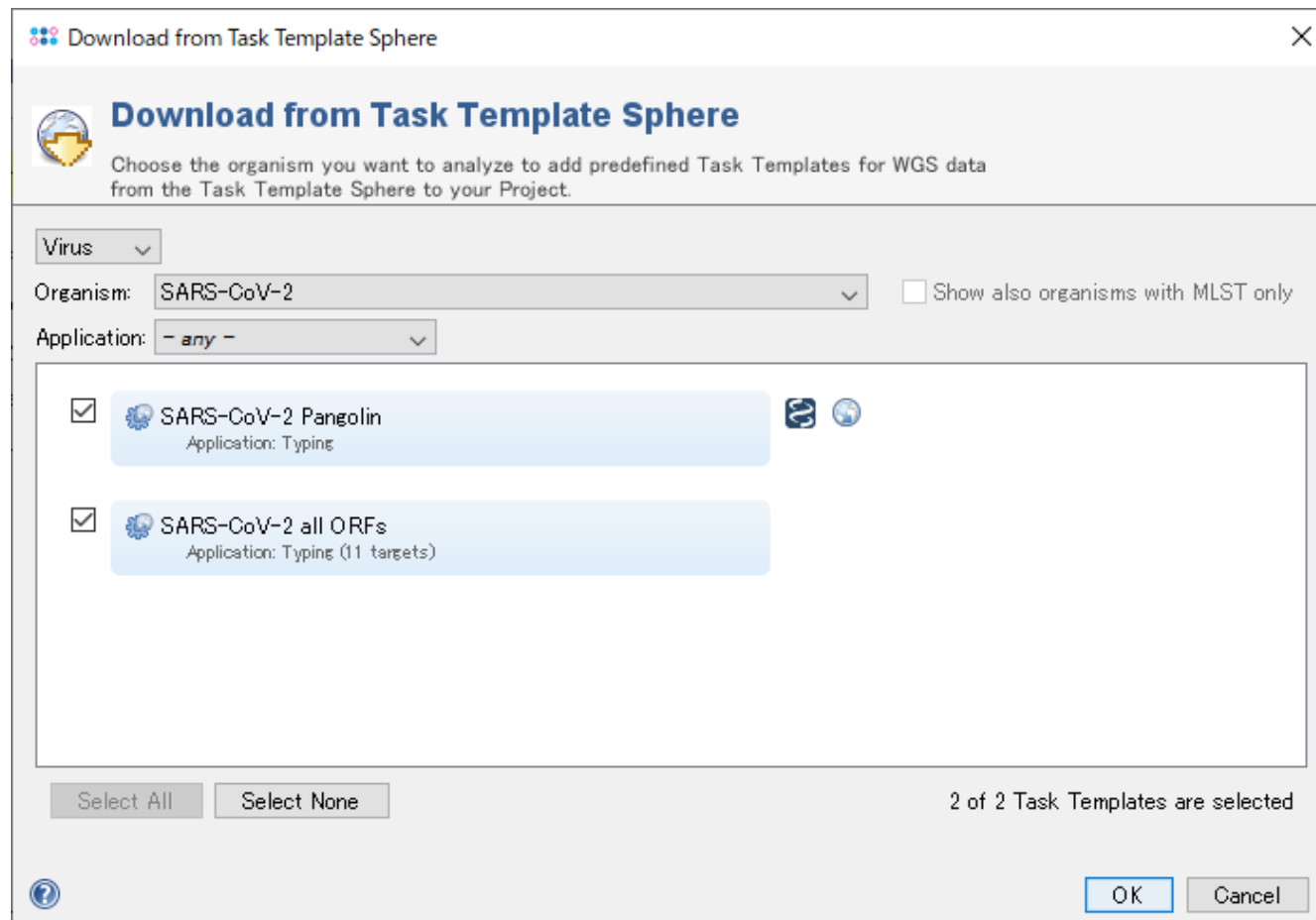
- サンプル（FASTQファイル）ごとに、AssemblingとTypingを一括で実行

Comparisonモード

- プロジェクト内全サンプルのタイピング結果の比較・解析

■ プロジェクトの作成

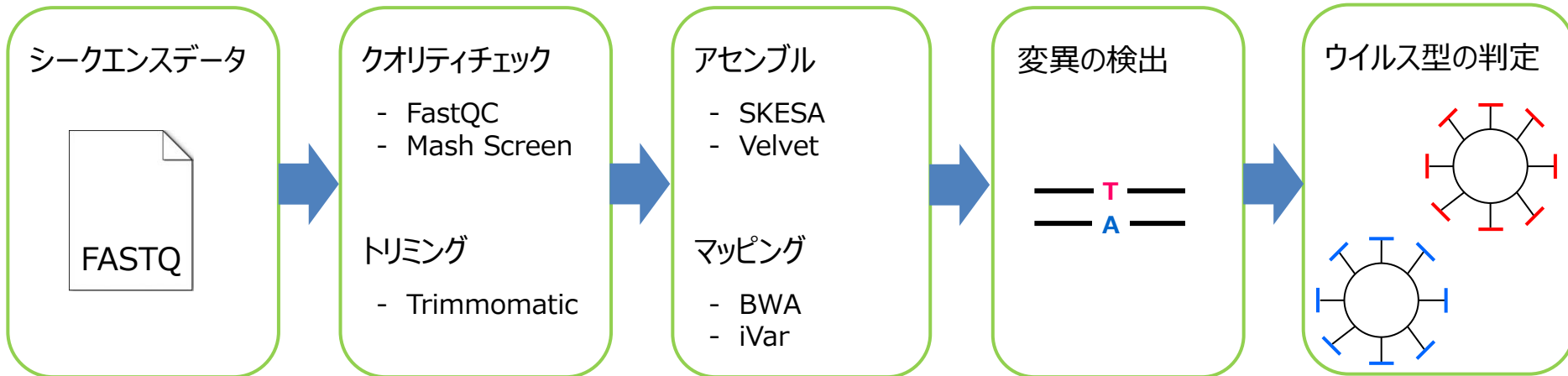
- 新型コロナウイルスのゲノムデータや、PANGO系統などの最新データのスキーマをダウンロード
- 細菌ゲノム解析の際は、薬剤耐性遺伝子や病原性因子データベースなどのスキーマも取得可能



■ スキーマに登録されている重要な変異

| Noteable Mutation | Example(s) | Gene | Start Genome Position | Start Gene Position | AA Number | Ref NT | Mutation NT | Ref AA | Mutation AA |
|-------------------|---|------|-----------------------|---------------------|-----------|--------|-------------------------|--------|-------------|
| S:S13I | B.1.429, B.1.427 | S | 21599 | 37 | 13 | AGT | ATT/ATC/ATA | S | I |
| S:69-70del | B.1.1.7, Cluster 5, B.1.525 | S | 21765 | 203 | 69-70 | TACATG | ----- | HV | -- |
| S:W152C | B.1.429, B.1.427 | S | 22016 | 454 | 152 | TGG | TGT/TGC | W | C |
| S:K417N | B.1.351 | S | 22811 | 1249 | 417 | AAG | AAT/AAC | K | N |
| S:K417T | P.1 | S | 22811 | 1249 | 417 | AAG | ACT/ACC/ACA/ACG | K | T |
| S:N440K | EPI_ISL_539744 | S | 22880 | 1318 | 440 | AAT | AAG/AAA | N | K |
| S:L452R | B.1.617, B.1.429, B.1.427 | S | 22916 | 1354 | 452 | CTG | CGG/CGT/CGC/CGA/AGA/AGG | L | R |
| S:Y453F | Cluster 5 | S | 22919 | 1357 | 453 | TAT | TTT/TTC | Y | F |
| S:477G | | S | 22991 | 1429 | 477 | AGC | GGT/GGC/GGA/GGG | S | G |
| S:477N | EPI_ISL_1061213 | S | 22991 | 1429 | 477 | AGC | AAC/AAT | S | N |
| S:E484K | B.1.351, P.1, P.2, P.3, B.1.525, B.1.1.7 with E484K | S | 23012 | 1450 | 484 | GAA | AAA/AAG | E | K |
| S:E484Q | B.1.617 | S | 23012 | 1450 | 484 | GAA | CAA/CAG | E | Q |
| S:N501Y | B.1.1.7, B.1.351, P.1, P.3 | S | 23063 | 1501 | 501 | AAT | TAT/TAC | N | Y |
| S:D614G | found in B.1 clade | S | 23402 | 1840 | 614 | GAT | GGT/GGC/GGA/GGG | D | G |
| S:P681H | B.1.1.7, B.1.1.207 | S | 23603 | 2041 | 681 | CCT | CAT/CAC | P | H |
| S:P681R | B.1.617 | S | 23603 | 2041 | 681 | CCT | CGT/CGC/CGA/CGG | P | R |
| S:A701V | B.1.526 | S | 23663 | 2101 | 701 | GCA | GTT/GTG/GTC/GTA | A | V |
| S:F888L | B.1.525 | S | 24224 | 2662 | 888 | TTT | CTT/CTC/CTA/CTG | F | L |

2021年6月現在



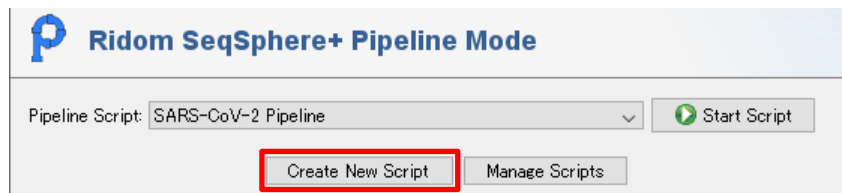
```
SeqSphere+ Pipeline: Lm ACCO demo
Whole Pipeline: Sample L14-10 (1/2)
Current Step: Assembling/Mapping reads...
Minimize to Tray Icon

07.06.16 17:10:08 Ridom SeqSphere+ 3.2.2-rc14_h_(2016-06) (workshoplivedemo)
07.06.16 17:10:08 Start Pipeline Script 'Lm ACCO demo'
07.06.16 17:10:08 Connecting server localhost
07.06.16 17:10:08 Login user: livedemo (host: LenovoZ70)
07.06.16 17:10:08 Found files for 2 Samples

07.06.16 17:10:08 Initialize Sample L14-10
07.06.16 17:10:08 Start processing files L14-10_1.fastq.gz, L14-10_2.fastq.gz
07.06.16 17:10:08 No Project acronym found
07.06.16 17:10:08 Using default Project for import: ACCO
07.06.16 17:10:09 Found existing Sample L14-10 in database
07.06.16 17:10:09 Start assembling with Velvet...
07.06.16 17:10:09 Velvet params: downsamples to 120x coverage, trim-quality: 30, trim-window-size: 20 bp
07.06.16 17:10:09 Trimming at 5' and 3' end until average quality is 30 in a window of 20 bases.
07.06.16 17:10:10 Trimmed 105277 bases.
07.06.16 17:10:10 Merging to interleaved read file.
07.06.16 17:10:10 Merging 2 files.
07.06.16 17:10:10 After processing, read files contain 2,220,847 bases in 9,900 reads (avg. read
```

■ Pipelineモード

- NGSシーケンスデータは、はじめにPipelineモードでデータ処理のワークフローを実行し、サンプルごとの遺伝子型データなどを取得する必要がある
- Ridom SeqSphere+には、NGSデータ処理に使われている様々なオープンソースのツールが組み込まれており、ツールの組み合わせなどを自由に選択が可能
- 複数のサンプルデータの一括処理が可能で、実行ログよりエラーや実行時間も確認が可能



■ クオリティチェック・トリミング設定

- Perform read data quality and adapter control (FastQC)
- Perform Illumina adapter trimming (Trimmomatic) if adapters found by FastQ...
- Perform contamination check (Mash Screen)
- Store read data and/or base qualities for targets with QC errors/warnings if available
- Continuous Mode: Run pipeline as continuous process that monitors the input sources for new files

■ アセンブル・マッピング設定

- Perform Assembling/Mapping for read files
- For 'Illumina': Tiled amplicon BWA+iVar (reference mappin... Settings...
- Seed Genome: NC_045512.2.gb Alternative Seed Genome...
- Expected Genome Size: 29.9 kbp

■ ファイル出力設定

- Assembly Result Files
- Do not keep aligned read files (ACE/BAM) in SeqSphere+
- Copy aligned read files (ACE/BAM) files to folder:
- Create sub-folder for each Project
- Export contig files (FASTA) to the folder

■ スクリプトの作成

- Pipelineモードでは、スクリプトを作成することによって、AssemblingとTypingの処理内容の設定を行う
- ほとんどの設定は、ソフトウェア上で対話形式で行い、項目を選択するだけで設定可能なため、簡単な操作で行うことができる
- 作成したスクリプトは、別サンプルの解析時に再利用したり、設定内容の編集も可能

パイプラインの解析結果

■ PANGO系統

SARS-CoV-2 Pangolin (SARS-CoV-2 ...)

Lineage: B.1.1.7

SARS-CoV-2 all ORFs (SARS-CoV-2 ...)

ORF 1ab: [Target](#) [Contig](#)

S: [Target](#) [Contig](#)

ORF 3a: [Target](#) [Contig](#)

E: [Target](#) [Contig](#)

M: [Target](#) [Contig](#)

ORF 6: [Target](#) [Contig](#)

ORF 7a: [Target](#) [Contig](#)

ORF 7b: [Target](#) [Contig](#)

ORF 8: [Target](#) [Contig](#)

N: [Target](#) [Contig](#)

ORF 10: [Target](#) [Contig](#)

Noteable Mutations:
S:69-70del, S:N501Y, S:P681H, S:D614G

■ 変異テーブル

| Target | VQ | AA Variant | Variant Type | Position | Abs. Position | Base Change (Ref:Var) | AA Change (Ref:Var) | Codon Number | Codon Effect | Var. Read Frequency | Total Coverage |
|---------|----|---------------|--------------|--------------|---------------|-----------------------|---------------------|--------------|-------------------|---------------------|----------------|
| ORF 1ab | ✓ | | SNP | 648 | 913 | C : T | | 216 | Silent | 100.0 % | 72 |
| ORF 1ab | ✓ | | SNP | 1,845 | 2,110 | C : T | | 615 | Silent | 100.0 % | 62 |
| ORF 1ab | ✓ | | SNP | 2,772 | 3,037 | C : T | | 924 | Silent | 100.0 % | 91 |
| ORF 1ab | ✓ | ORF 1a:T100I | SNP | 3,002 | 3,267 | C : T | T : I | 1,001 | Missense | 100.0 % | 154 |
| ORF 1ab | ✓ | ORF 1a:T1240I | SNP | 3,719 | 3,984 | C : T | T : I | 1,240 | Missense | 100.0 % | 151 |
| ORF 1ab | ✓ | ORF 1a:A1708D | SNP | 5,123 | 5,388 | C : A | A : D | 1,708 | Missense | 100.0 % | 70 |
| ORF 1ab | ✓ | | SNP | 5,721 | 5,986 | C : T | | 1,907 | Silent | 100.0 % | 74 |
| ORF 1ab | ✓ | ORF 1a:I2230T | SNP | 6,689 | 6,954 | T : C | I : T | 2,230 | Missense | 100.0 % | 111 |
| ORF 1ab | ✓ | ORF 1a:M2259I | SNP | 6,777 | 7,042 | G : T | M : I | 2,259 | Missense | 100.0 % | 108 |
| ORF 1ab | ✓ | | SNP | 9,930 | 10,195 | A : G | | 3,310 | Silent | 100.0 % | 143 |
| ORF 1ab | ✓ | deletion | DP | 11,023 | 11,288 | ----- : TCTGTTTT | | | In frame deletion | 95.6 % | 270 |
| ORF 1ab | ✓ | ORF 1b:P218L | SNP | 13,855 | 14,120 | C : T | P : L | 218 | Missense | 100.0 % | 144 |
| ORF 1ab | ✓ | ORF 1b:P314L | SNP | 14,143 | 14,408 | C : T | P : L | 314 | Missense | 100.0 % | 188 |
| ORF 1ab | ✓ | | SNP | 14,411 | 14,676 | C : T | | 403 | Silent | 100.0 % | 162 |
| ORF 1ab | ✓ | | SNP | 15,014 | 15,279 | C : T | | 604 | Silent | 100.0 % | 117 |
| ORF 1ab | ✓ | | SNP | 15,911 | 16,176 | T : C | | 903 | Silent | 100.0 % | 152 |
| ORF 1ab | ✓ | | SNP | 19,616 | 19,881 | C : T | | 2,138 | Silent | 100.0 % | 74 |
| S | ✓ | deletion | DP | 203 | 21,765 | ----- : TACATG | | | In frame dele... | 96.1 % | 128 |
| S | ✓ | deletion | DP | 429 | 21,991 | --- : TTA | | | In frame deletion | 92.3 % | 78 |
| S | ✓ | S:N501Y | SNP | 1,501 | 23,063 | A : T | N : Y | 501 | Missense | 100.0 % | 55 |
| S | ✓ | S:A570D | SNP | 1,709 | 23,271 | C : A | A : D | 570 | Missense | 100.0 % | 50 |
| S | ✓ | S:D614G | SNP | 1,841 | 23,403 | A : G | D : G | 614 | Missense | 100.0 % | 63 |
| S | ✓ | S:P681H | SNP | 2,042 | 23,604 | C : A | P : H | 681 | Missense | 100.0 % | 116 |
| S | ✓ | S:T716I | SNP | 2,147 | 23,709 | C : T | T : I | 716 | Missense | 100.0 % | 117 |
| S | ✓ | S:S982A | SNP | 2,944 | 24,506 | T : G | S : A | 982 | Missense | 100.0 % | 123 |
| S | ✓ | S:D1118H | SNP | 3,352 | 24,914 | G : C | D : H | 1,118 | Missense | 100.0 % | 130 |

■ QCデータ

| Reads Statistics | |
|--|---------------------|
| FastQC Per Base Sequence Quality (Forward Reads) | Completed |
| FastQC Per Base Sequence Quality (Reverse Reads) | Completed |
| FastQC Adapter Content | Completed |
| Avg. Coverage (Unassembled) | 208 |
| Avg. Read Length (Unassembled) | 163 |
| Read Count (Unassembled) | 38,040 |
| Read Base Count (Unassembled) | 6,234,025 |
| Assembly Statistics | |
| Genome Status | SRA |
| SRA Submission Center | TX-SARS-CoV-2 |
| SRA Run Accession | SRR14590433 |
| SRA Run Published | 2021-05-19 18:12:09 |
| GC-Content (Assembled) | 37.9 |
| Perc. Covered Genome | 99.14 % |
| Consensus Bases Below Coverage Threshold (Ns) | 127 |
| Consensus Bases with Non-N Ambiguity | 0 |
| Low Frequency Variants | 0 |
| Variants (genome wide) | 40 |
| Avg. Coverage (Assembled) | 114 |

■ Pipelineモード実行結果

- Pipelineモードの実行結果は、サンプル別に表示される
- 各サンプルのPANGO系統、検出された変異のテーブル、QCデータなどを確認可能
- これらデータは、ExcelやFASTA、PDFレポートなどでファイル出力も可能

コンティグ配列の確認

Contig: S (SARS-CoV-2 USA TX-DSHS-6425 2021) ...

Editing Mode, locked for other users

Ref.-seq. | SNP | MNP | DP | IP

Consensus: ...
Ref.-seq.: ...
Consensus AA: ...
Ref.-seq. AA: ...

Contig

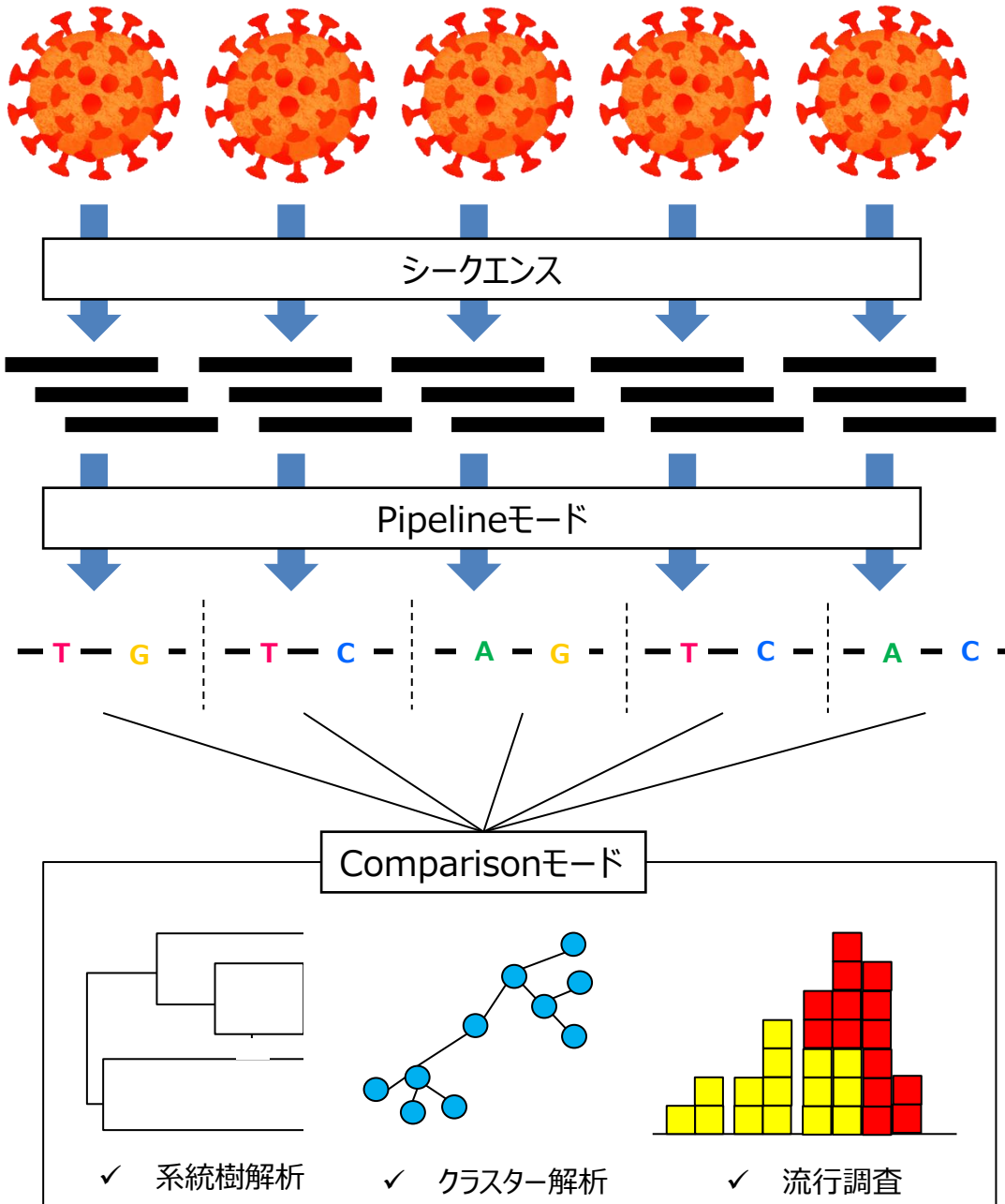
Consensus: ...
S: ...

Variants

| VQ | Known Var. | Variant Type | Position | Abs. Position | Area Position | Base Change (Ref:Var) | AA Change (Ref:Var) | Codon Number | Codon Effect | Var. Read Frequency | Total Coverage |
|----|------------|--------------|----------|---------------|---------------|-----------------------|---------------------|--------------|------------------|---------------------|----------------|
| ✓ | S:69-70del | DP | 203 | 21,765 | 203 | ----- : TACATG | | | In frame d... | 96.1 % | 128 |
| ✓ | S:N501Y | SNP | 1,501 | 23,063 | 1,501 | A : T | N : Y | 501 | Missense | 100.0 % | 55 |
| ✓ | S:D614G | SNP | 1,841 | 23,403 | 1,841 | A : G | D : G | 614 | Missense | 100.0 % | 63 |
| ✓ | S:P681H | SNP | 2,042 | 23,604 | 2,042 | C : A | P : H | 681 | Missense | 100.0 % | 116 |
| ✓ | | DP | 429 | 21,991 | 429 | --- : TTA | | | In frame dele... | 92.3 % | 78 |
| ✓ | | SNP | 1,709 | 23,271 | 1,709 | C : A | A : D | 570 | Missense | 100.0 % | 50 |
| ✓ | | SNP | 2,147 | 23,709 | 2,147 | C : T | T : I | 716 | Missense | 100.0 % | 117 |
| ✓ | | SNP | 2,944 | 24,506 | 2,944 | T : G | S : A | 982 | Missense | 100.0 % | 123 |
| ✓ | | SNP | 3,352 | 24,914 | 3,352 | G : C | D : H | 1,118 | Missense | 100.0 % | 130 |

■ 配列データの確認

- ターゲット遺伝子ごとに、リファレンスゲノム配列と、サンプルデータのコンセンサス配列を比較
- 配列データとともに変異テーブルも表示され、インタラクティブに操作が可能



■ Comparisonモード

- Pipelineモードで作成した、各サンプルごとの遺伝型データを統合して解析を行う
- 全サンプルのデータを俯瞰したり、疫学研究における統計解析やグラフ作成などが可能

Comparisonテーブル

Comparison Table: SARS-CoV-2 Test Project [unstored]
File Edit Data Columns Analysis Tools

| #Missing values | Avg. Coverage Procedure Detail | Perc. Covered Procedure Details | Sample ID Sample | Epi Info Source | Cluster/Outb Source | Collection Date Sample | Country of Source | City of Isol Source | ZIP of Isol Source | Lineage SARS-CoV-2 Pan | Noteable Mutations SARS-CoV-2 all ORFs:Variant Results | ORF1ab SARS-CoV-2 | S SARS-CoV-2 all O | ORF3a SARS-CoV |
|-----------------|-----------------------------------|------------------------------------|---------------------------------|--------------------|------------------------|---------------------------|----------------------|------------------------|-----------------------|---------------------------|---|----------------------|-----------------------|-------------------|
| 0 | 114 | 99.20 % | SARS-CoV-2 USA TX-DSHS-6398 ... | ? | ? | 2021/04/28 | USA | Texas | ? | B.1.1.519 | S:P681H, S:D614G | 17 | 12 | 1 |
| 0 | 118 | 99.20 % | SARS-CoV-2 USA TX-DSHS-6406 ... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.519 | S:P681H, S:D614G | 19 | 13 | 9 |
| 1 | 107 | 96.07 % | SARS-CoV-2 USA TX-DSHS-6424 ... | ? | ? | 2021/04/25 | USA | Texas | ? | B.1.1.519 | S:P681H, S:D614G | 27 | ?(N) | 1 |
| 0 | 77 | 99.13 % | SARS-CoV-2 USA TX-DSHS-6338 ... | ? | ? | 2021/04/22 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 2 | 2 | 1 |
| 0 | 88 | 99.16 % | SARS-CoV-2 USA TX-DSHS-6357 ... | ? | ? | 2021/04/20 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 5 | 2 | 1 |
| 0 | 87 | 99.13 % | SARS-CoV-2 USA TX-DSHS-6350 ... | ? | ? | 2021/04/22 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 4 | 4 | 1 |
| 0 | 81 | 99.16 % | SARS-CoV-2 USA TX-DSHS-6378 ... | ? | ? | 2021/04/23 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 11 | 9 | 1 |
| 0 | 84 | 99.03 % | SARS-CoV-2 USA TX-DSHS-6367 ... | ? | ? | 2021/04/15 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 9 | 2 | 1 |
| 0 | 127 | 99.14 % | SARS-CoV-2 USA TX-DSHS-6386 ... | ? | ? | 2021/04/24 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 9 | 2 | 1 |
| 0 | 126 | 99.03 % | SARS-CoV-2 USA TX-DSHS-6385 ... | ? | ? | 2021/04/24 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 12 | 2 | 1 |
| 0 | 119 | 99.14 % | SARS-CoV-2 USA TX-DSHS-6388 ... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 13 | 2 | 1 |
| 0 | 117 | 99.02 % | SARS-CoV-2 USA TX-DSHS-6391 ... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 14 | 2 | 6 |
| 0 | 132 | 99.14 % | SARS-CoV-2 USA TX-DSHS-6393 ... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 15 | 10 | 7 |
| 0 | 115 | 99.03 % | SARS-CoV-2 USA TX-DSHS-6394 ... | ? | ? | 2021/04/23 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 16 | 2 | 1 |
| 0 | 122 | 99.03 % | SARS-CoV-2 USA TX-DSHS-6410 ... | ? | ? | 2021/04/27 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 21 | 2 | 1 |
| 0 | 114 | 99.14 % | SARS-CoV-2 USA TX-DSHS-6408 ... | ? | ? | 2021/04/27 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 20 | 14 | 1 |
| 0 | 117 | 99.17 % | SARS-CoV-2 USA TX-DSHS-6411 ... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 22 | 2 | 1 |
| 0 | 124 | 99.03 % | SARS-CoV-2 USA TX-DSHS-6415 ... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 24 | 15 | 10 |
| 0 | 120 | 99.03 % | SARS-CoV-2 USA TX-DSHS-6412 ... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 23 | 2 | 1 |
| 0 | 114 | 99.14 % | SARS-CoV-2 USA TX-DSHS-6425 ... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D614G | 28 | 2 | 1 |
| 0 | 66 | 99.09 % | SARS-CoV-2 USA TX-DSHS-6363 ... | ? | ? | 2021/04/14 | USA | Texas | ? | B.1.2 | S:D614G | 7 | 7 | 5 |
| 0 | 91 | 99.20 % | SARS-CoV-2 USA TX-DSHS-6366 ... | ? | ? | 2021/04/15 | USA | Texas | ? | B.1.2 | S:D614G | 8 | 8 | 5 |
| 0 | 90 | 99.03 % | SARS-CoV-2 USA TX-DSHS-6346 ... | ? | ? | 2021/04/22 | USA | Texas | ? | B.1.351 | S:K417N, S:E484K, S:N501Y, S:D614G, S:A7... | 3 | 3 | 2 |
| 1 | 121 | 96.07 % | SARS-CoV-2 USA TX-DSHS-6418 ... | ? | ? | 2021/04/27 | USA | Texas | ? | B.1.427 | S:D614G, S:S13I, S:L452R | 25 | ?(N) | 11 |
| 1 | 81 | 99.17 % | SARS-CoV-2 USA TX-DSHS-6356 ... | ? | ? | 2021/04/20 | USA | Texas | ? | B.1.526 | S:E484K, S:D614G, S:A701V | ?(N) | 5 | 3 |
| 1 | 116 | 96.14 % | SARS-CoV-2 USA TX-DSHS-6399 ... | ? | ? | 2021/04/28 | USA | Texas | ? | B.1.526.3 | S:E484K, S:D614G, S:A701V | 18 | ?(N) | 3 |
| 0 | 125 | 99.09 % | SARS-CoV-2 USA TX-DSHS-6421 ... | ? | ? | 2021/04/20 | USA | Texas | ? | B.1.596 | S:D614G | 26 | 16 | 12 |
| 1 | 88 | 99.04 % | SARS-CoV-2 USA TX-DSHS-6362 ... | ? | ? | 2021/04/24 | USA | Texas | ? | B.1.617.2 | S:P681R, S:D614G, S:L452R | 6 | 6 | 4 |
| 1 | 90 | 98.99 % | SARS-CoV-2 USA TX-DSHS-6372 ... | ? | ? | 2021/04/24 | USA | Texas | ? | C.37 | S:69-70del, S:D614G | 10 | ?(failed) | 1 |
| 1 | 112 | 96.24 % | SARS-CoV-2 USA TX-DSHS-6396 ... | ? | ? | 2021/04/26 | USA | Texas | ? | P.1 | S:K417T, S:E484K, S:N501Y, S:D614G | ?(N) | 11 | 8 |

■ Comparisonテーブル

- プロジェクトの全サンプルのデータをまとめたテーブル
- PANGO系統や検出された重要な変異、ターゲット遺伝子の遺伝子型データなどを俯瞰的にみることが

Comparisonテーブル

Comparison Table: SNV Positions : SARS-CoV-2 Test Project

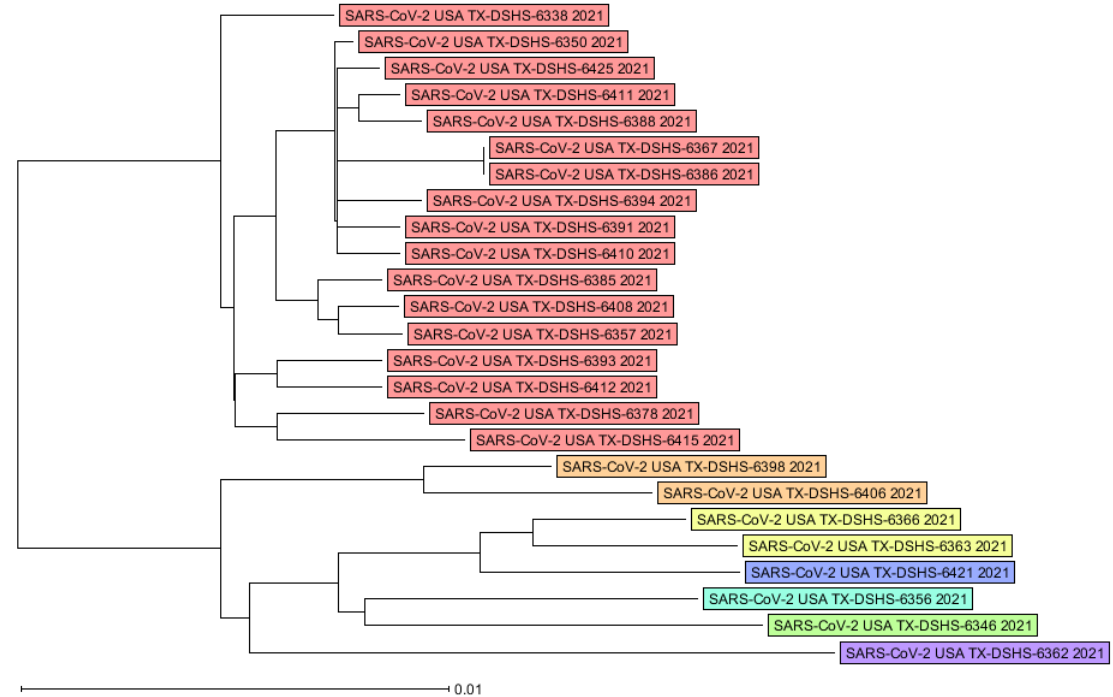
File Edit Data Columns Analysis Tools

| #Missing | Avg. C ₁ Procedure | Perc. C ₁ Procedure | Sample ID Sample | Epi Int Source | Cluster Source | Collection Sample | Count Source | City of Source | ZIP of Source | Lineage* SARS-CoV- | Noteable Mutations SARS-CoV-2 all DRFs: Variant Results | 322 ORF1 | 58 OF | 69 OF | 73 OF | 82 OF | 84 OF | 91 OF | 10 OF | 10 OF | 12 OF | 15 OF | 16 OF | 16 OF | 19 OF | 19 OF | 20 OF | 21 OF | 23 OF | 26 OF | 27 OF | 28 OF | 30 OF | 31 OF | | |
|----------|-------------------------------|--------------------------------|----------------------------|----------------|----------------|-------------------|--------------|----------------|---------------|-----------------------|--|----------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|-------|---|---|
| 0 | 114 | 99.20 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/28 | USA | Texas | ? | B.1.1.519 | S:P681H, S:D614G | T | C | G | T | C | T | C | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | A | T | |
| 0 | 118 | 99.20 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.519 | S:P681H, S:D614G | T | C | G | T | C | T | C | C | C | A | G | T | C | T | C | C | C | G | A | C | C | C | C | A | T |
| 879 | 107 | 96.07 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/25 | USA | Texas | ? | B.1.1.519 | S:P681H, S:D614G | T | C | G | T | C | T | C | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | T | A | T |
| 0 | 77 | 99.13 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/22 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 0 | 88 | 99.16 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/20 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 87 | 99.13 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/22 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 81 | 99.16 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/23 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | T | T | C | T | T | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 0 | 84 | 99.03 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/15 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | A | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 127 | 99.14 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/24 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | A | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 126 | 99.03 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/24 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | T | C | T | G | A | C | C | C | C | A | C |
| 0 | 119 | 99.14 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 117 | 99.02 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 132 | 99.14 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | A | C | C | C | G | A | C | C | C | C | A | C |
| 0 | 115 | 99.03 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/23 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | T | C | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 122 | 99.03 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/27 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | A | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 114 | 99.14 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/27 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 117 | 99.17 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 124 | 99.03 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 0 | 120 | 99.03 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 0 | 114 | 99.14 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | B.1.1.7 | S:69-70del, S:N501Y, S:P681H, S:D61... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | T | G | A | C | C | C | C | A | C |
| 0 | 66 | 99.09 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/14 | USA | Texas | ? | B.1.2 | S:D614G | T | T | G | T | C | T | C | T | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 0 | 91 | 99.20 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/15 | USA | Texas | ? | B.1.2 | S:D614G | T | C | G | T | C | T | C | T | T | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 0 | 90 | 99.03 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/22 | USA | Texas | ? | B.1.351 | S:K417N, S:E484K, S:N501Y, S:D614G,... | T | C | G | T | C | T | T | C | C | A | G | G | C | T | C | C | C | G | T | T | C | C | C | A | C |
| 878 | 121 | 96.07 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/27 | USA | Texas | ? | B.1.427 | S:D614G, S:S13I, S:L452R | T | C | G | T | T | C | T | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 1 | 81 | 99.17 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/20 | USA | Texas | ? | B.1.526 | S:E484K, S:D614G, S:A701V | ?(Y) | C | G | T | C | T | C | T | C | A | G | G | C | T | C | C | C | A | A | C | C | C | C | A | C |
| 880 | 116 | 96.14 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/28 | USA | Texas | ? | B.1.526.3 | S:E484K, S:D614G, S:A701V | T | C | G | T | C | T | C | T | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 0 | 125 | 99.09 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/20 | USA | Texas | ? | B.1.596 | S:D614G | T | C | G | T | C | T | C | T | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 12 | 88 | 99.04 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/24 | USA | Texas | ? | B.1.617.2 | S:P681R, S:D614G, S:L452R | T | C | G | T | C | T | C | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 957 | 90 | 98.99 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/24 | USA | Texas | ? | C.37 | S:69-70del, S:D614G | T | C | G | T | C | T | C | C | C | A | G | G | C | T | C | C | C | G | A | C | C | C | C | A | C |
| 851 | 112 | 96.24 % | SARS-CoV-2 USA TX-DSHS-... | ? | ? | 2021/04/26 | USA | Texas | ? | P.1 | S:K417T, S:E484K, S:N501Y, S:D614G | T | C | G | C | C | T | C | C | C | A | G | G | C | T | C | T | C | G | A | C | C | T | C | C | C |

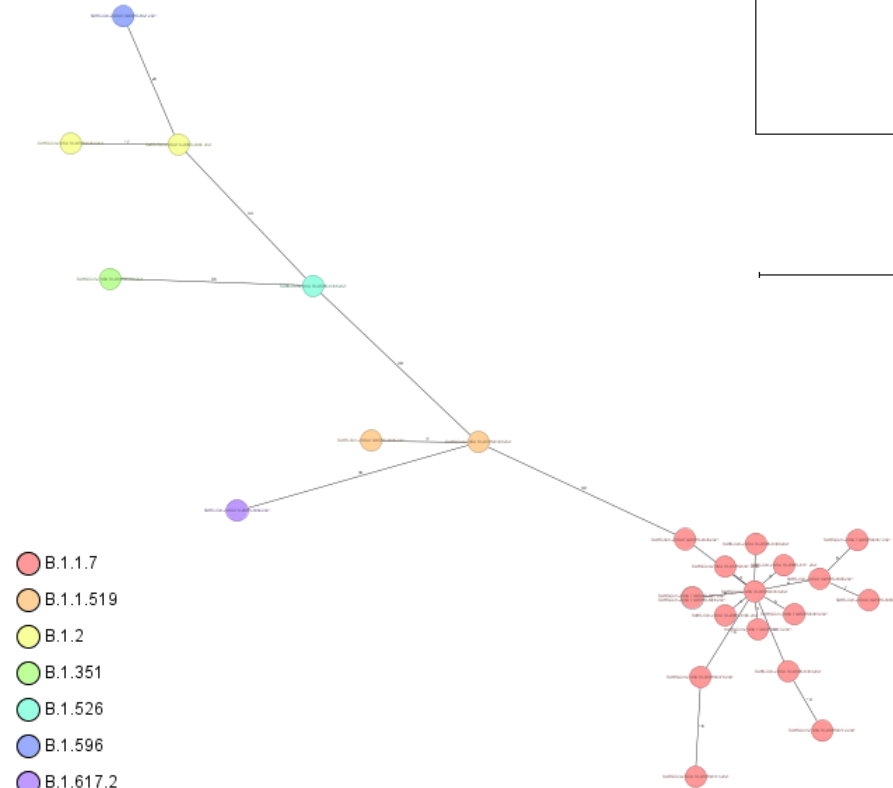
■ SNVデータを付与したComparisonテーブル

- 通常のComparisonテーブルにおける、ターゲット遺伝子の遺伝子型データをSNVデータに置き換えたもの
- この画面から系統樹やクラスター解析を実行すれば、サンプル間の距離をSNVに基づいた計算が可能

Neighbor Joining Tree



Minimum Spanning Tree



各種統計解析やグラフ作成

- Comparisonテーブル上でアイコンをクリックするだけで、系統樹やクラスター解析とグラフ作成が可能
- その他、サンプルのメタデータの情報を使って、Epi CurveやGeographical Mapなどの表示も可能

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