From DNA to actionable result. Right now

HYRAX BIOSCIENCES

Exatype: automated SARS-CoV-2 variant typing directly from NGS sequence data

The identification of SARS-CoV-2 variants that exhibit increased transmissibility and may impact vaccine efficacy has accelerated the need for global genomic surveillance of SARS-CoV-2.

While DNA sequencing provides the most comprehensive approach for characterising variants, the analysis and interpretation of sequence data at scale remains a challenge.

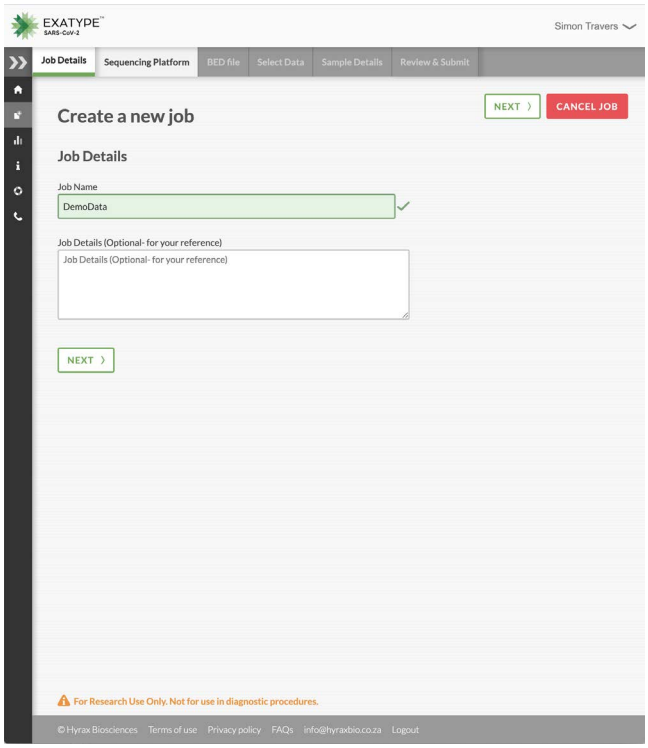
Hyrax Biosciences' Exatype platform provides fast, automated SARS-CoV-2 lineage/clade typing.

Exatype features:

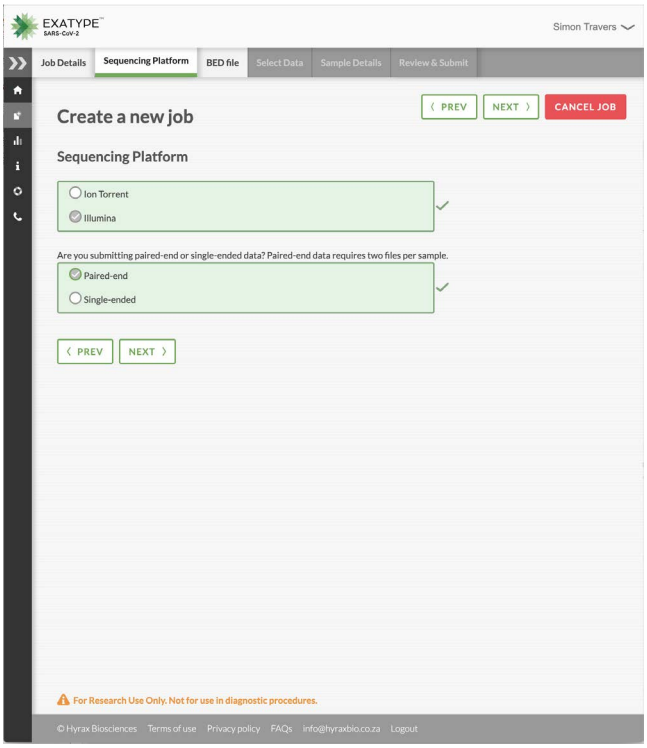
- Reports detected variants using both Pangolin lineages and Nextstrain clades nomenclature
- Analyses data from a range of sequencing platforms and can process data generated from any amplification protocol/assay
- Requires no expert training and no software needs to be installed
- Easily scaled with **parallel** processing in the cloud or through direct **integration** with sequencers and/or LIMS
- Is secure and complies with all necessary HIPAA requirements
- Uses algorithms with proven superior accuracy in read mapping and variant calling in viral data

Once you've set up an account, analysing your data is simple:

1. Name your job:

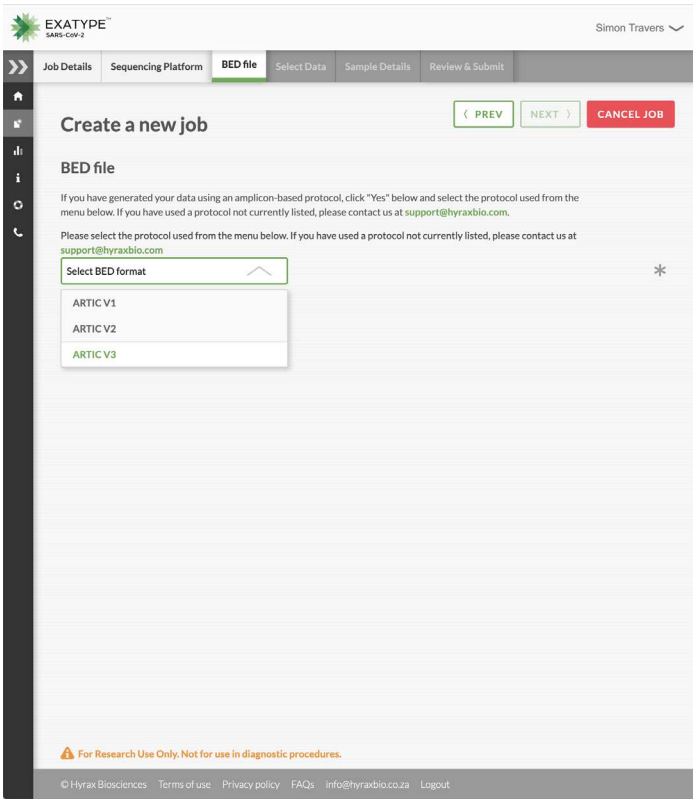


2. Select the sequencing platform:

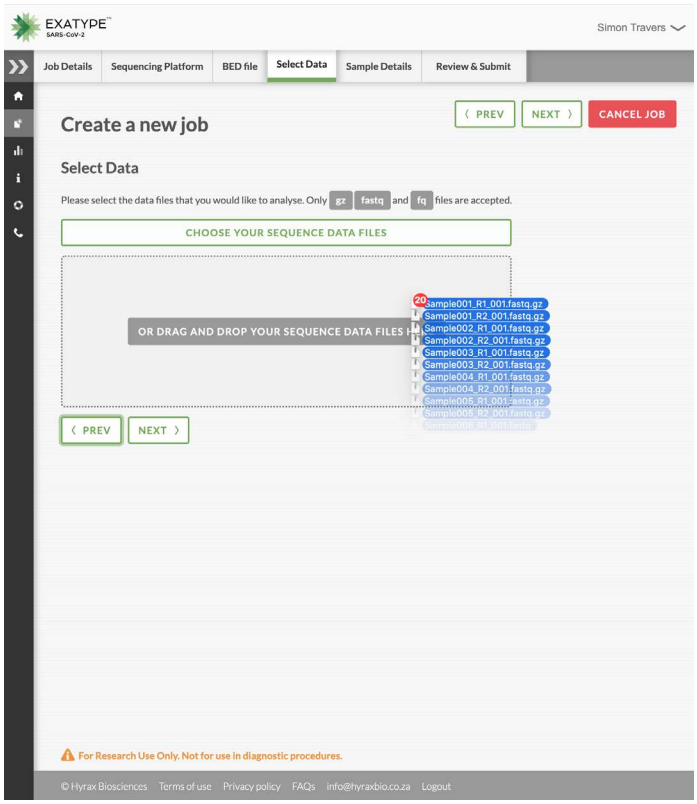


Exatype: Automated SARS-CoV-2 lineage/clade typing directly from raw NGS sequence data.

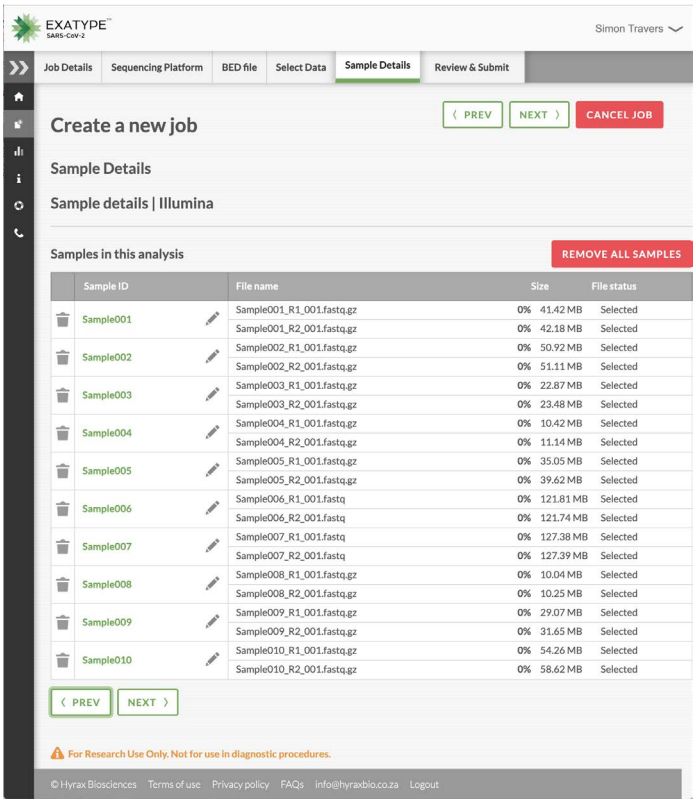
3. Select the assay used to generate the data:



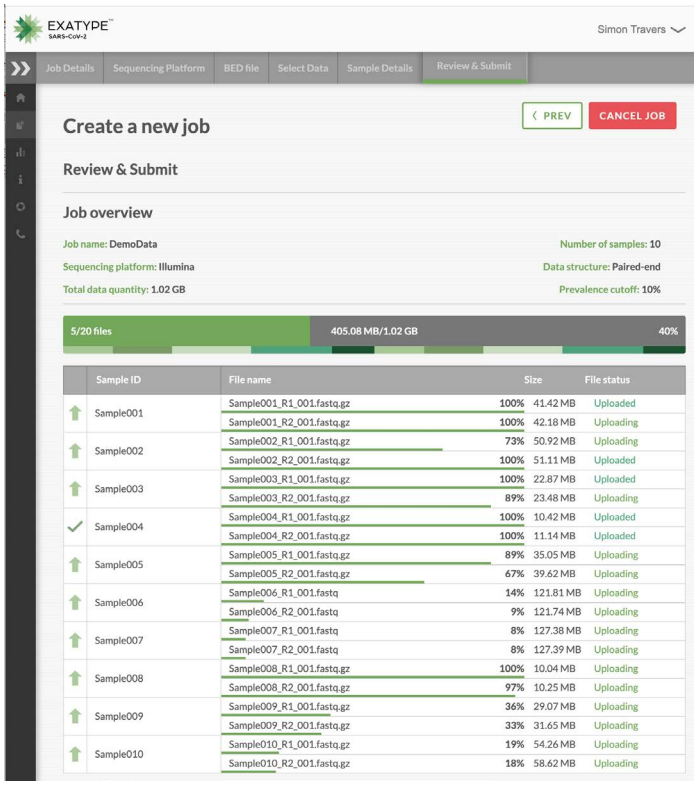
4. Drag and drop your fastq files into the browser:



5. Exatype automatically groups files for paired-end data and extracts sample names (you can edit these manually if you wish):

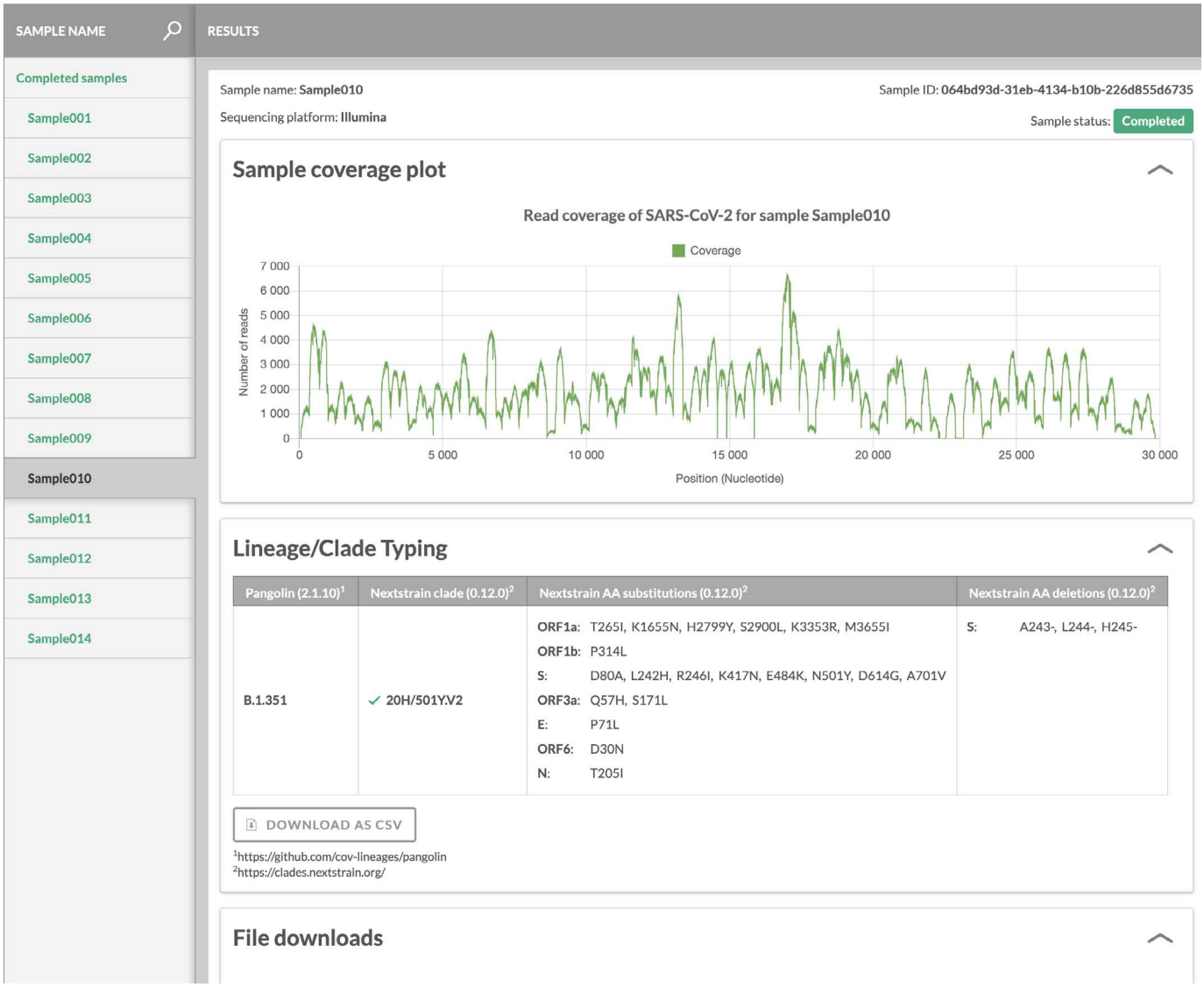


6. That's it! Click upload and walk away. You will receive an email once your analysis is complete:



Outputs

1. Explore per-sample results through the front-end:



2. Exatype uses both Pangolin lineages (cov-lineages.org) and Nextstrain clades (nextstrain.org) and outputs a table showing calls from each approach. It includes amino acid substitutions and deletions observed in each sample.

Sample	Pangolin (2.1.10)[1]	Nextstrain clade (0.12.0)[2]	Nextstrain AA substitutions (0.12.0)[2]	Nextstrain AA deletions (0.12.0)[2]
Sample003	B.1.338	✓ 20C	ORF1a: T265I, A2129V ORF1b: P314L S: D614G ORF3a: Q57H	None detected
Sample005	B.1	⚠ 20C	ORF1a: T265I, I1206K ORF1b: P314L, S2430R S: D614G ORF3a: Q57H	ORF1a: P1207-, K1208-, E1209-, E1210-, V1211-, K1212-
Sample011	P.1	✓ 20J/501Y.V3	ORF1a: S1188L, K1795Q, S2947N, A3523V ORF1b: P314L, E1264D S: L18F, T20N, P26S, D138Y, R190S, K417T, E484K, N501Y, D614G, H655Y, T1027I, V1176F ORF3a: S253P F8: E92K	ORF1a: S3675-, G3676-, F3677-

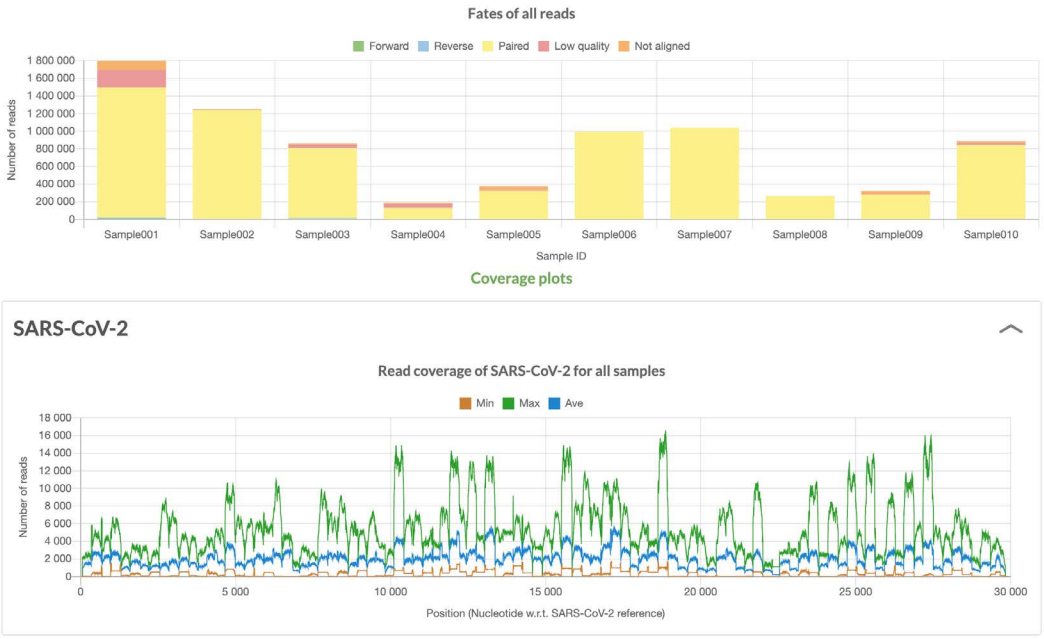
DOWNLOAD AS CSV

[1]https://github.com/cov-lineages/pangolin
[2]https://clades.nextstrain.org/

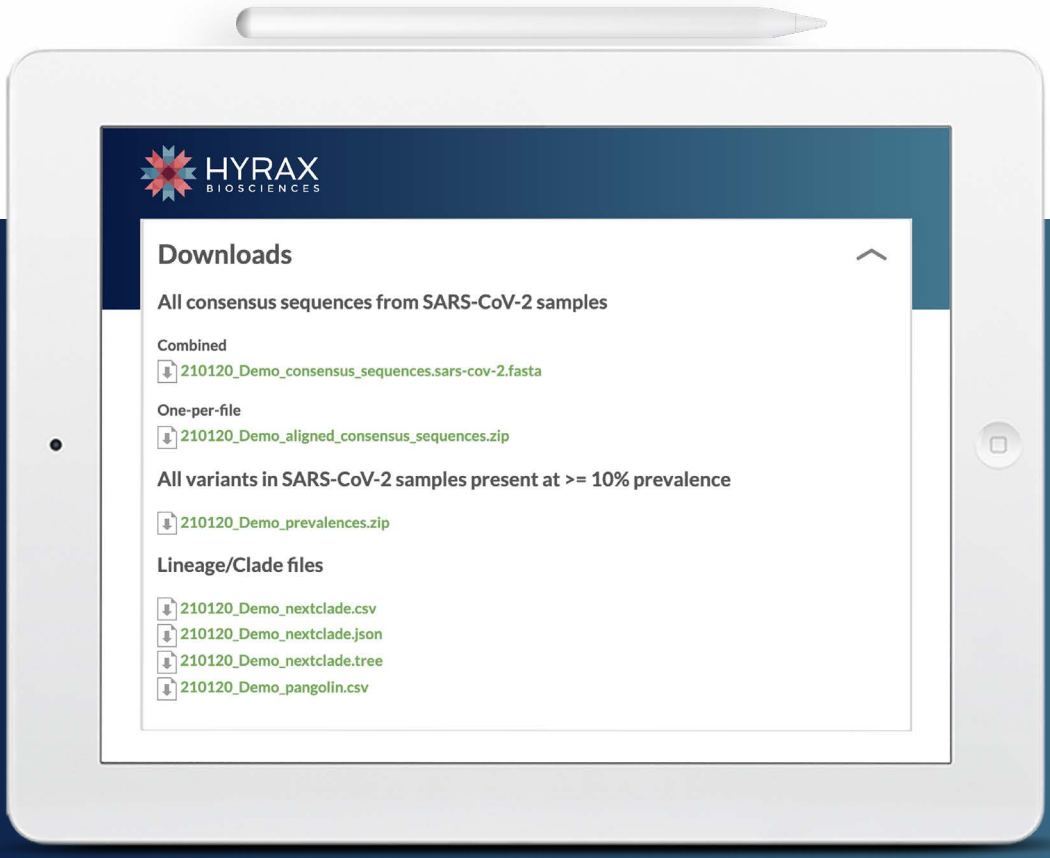
Sample011

- ✓ Missing data: Good
- ✓ Mixed sites: Good
- ✓ Private mutations: Good
- ✓ SNP clusters: Good

3. QC plots provide a valuable oversight of data quality:



4. A wide range of outputs in standardised formatting are available for download for further analysis or for publication of outputs to public repositories e.g. consensus sequences can be uploaded to GISAID:



How to get in touch

Visit sars-cov-2.exatype.com to sign up for a free account and upload your first sample.
Contact us at info@hyraxbio.com to discuss how we can provide companion software for your needs.