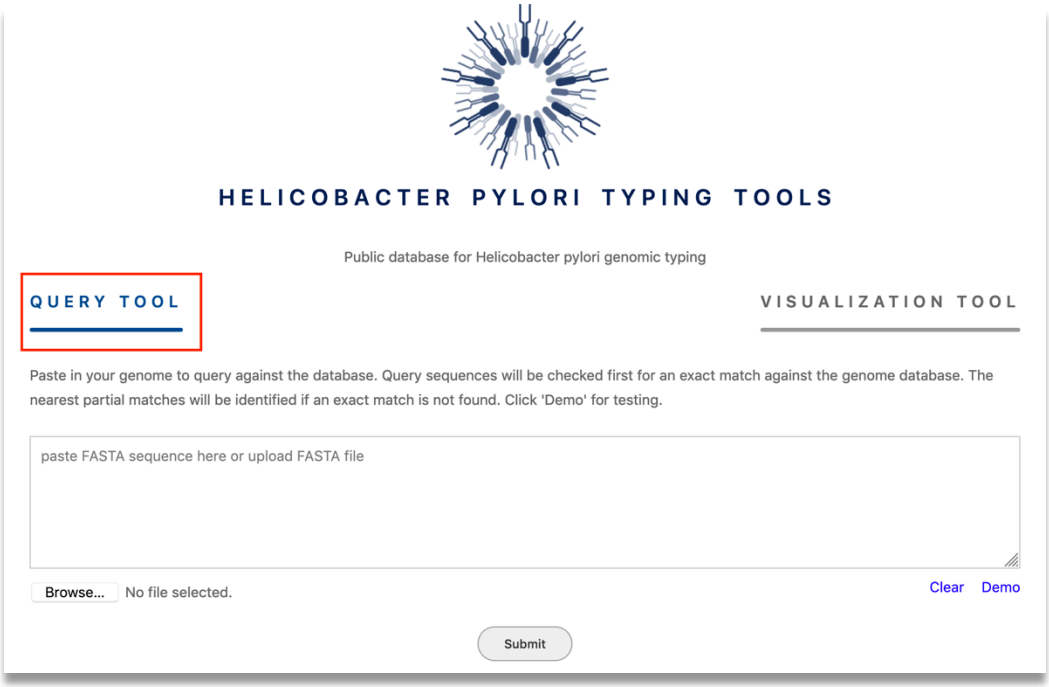
User instruction

Helicobactor pylori typing tool (HPTT) is a genomic typing method based on whole genome sequencing (WGS) data, which can facilitate genetic population analysis and epidemiological origin tracing. In our *H. pylori* typing website (https://db.cngb.org/HPTT/), two modules are available, including both genetic typing and geographic visualizing of the global *H. pylori* isolates. Here is the website instruction for users.

Homepage

You can see the brief introduction of our HPTT on the homepage of our website. Two modules were displayed at this page: the genomic typing tool of *H. pylori* ("QUERY TOOL") and the phylogeographic visualization tool of *H. pylori* ("VISUALIZATION TOOL").

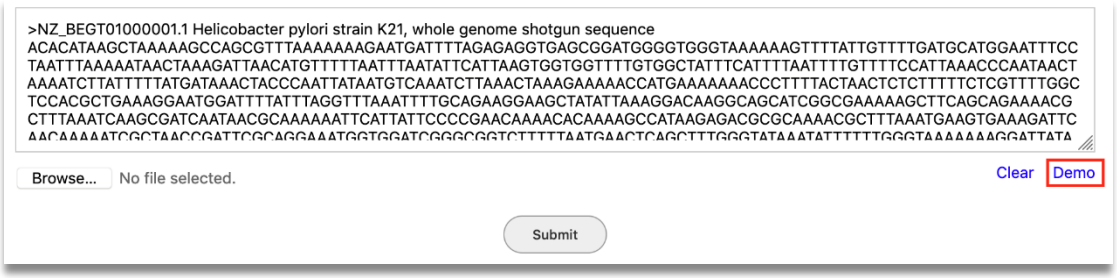


- Data compatibility

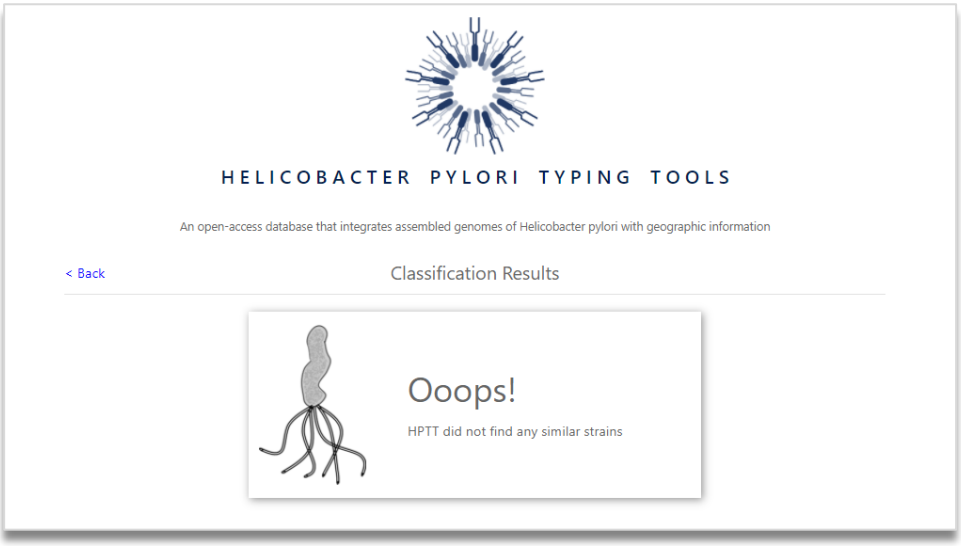
In order to achieve the best typing results, it is highly recommended to upload sequencing data generated by the MPS (Massive Parallel Sequencing) method. The common MPS platform includes MGI DNBSEQ® platform and Illumina® platform. General workflow for the MPS including sample pre-treatment, library preparation, sequencing and data analysis. Companies who doing MPS would offer the solutions for all steps, including reagent, instrument, etc.

- The genomic typing tool of *H. pylori*

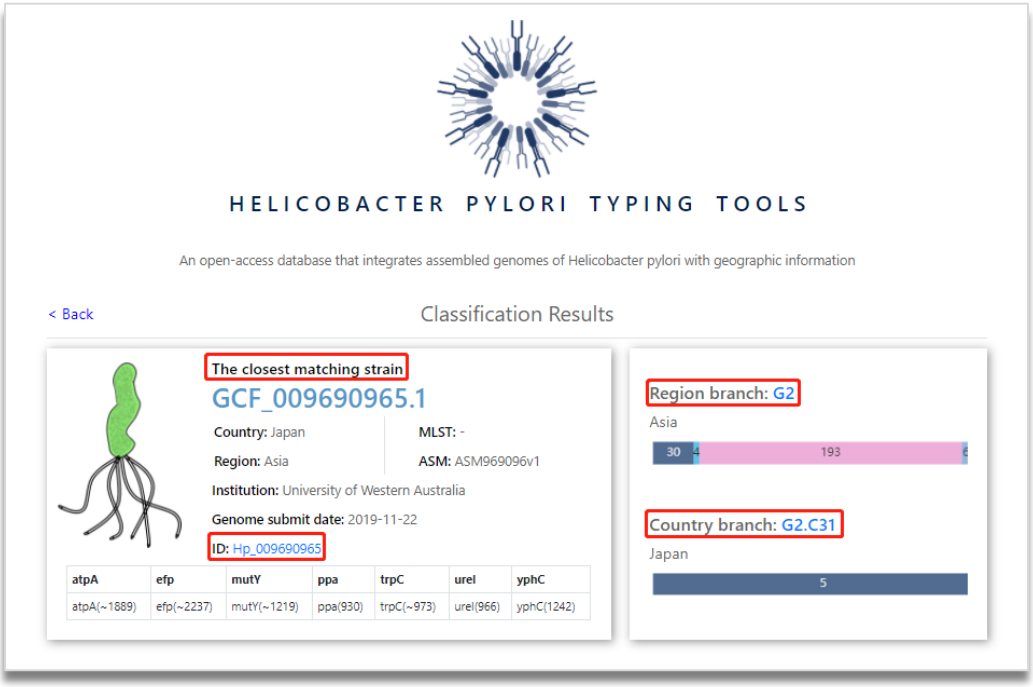
At the homepage of website, a tested demo genome is provided. Please see the screenshot below. Click the "Demo" button at the bottom right corner of the input box. It may take few seconds since the genome file is relatively large, and there might be a slight freeze during the loading. If the genome is entered incorrectly, click the "Clear" button just next to the "Demo" to clear the input box. For your own sequenced genome, you can either copy and paste in the input box or upload it by click the "Browse" button. After entering/ uploading the genome, click the "Submit" button to query against the database.



If your uploaded file is neither *H. pylori* nor sequenced by the second-generation sequencing technology, it might be reported as an error. You will need to check whether your genome fit our criteria.



You will get the typing results if it is successfully typed. Please see the image below. Firstly, the strain with the highest identity ("the closest matching strain") that is most similar to our database will be displayed, including region, country, MLST type, data release time, sequenced research institution, etc. Secondly, if the most similar bacterial species has a typing patterns in our database, it will be displayed on the right. If the corresponding types not completely refer to one continent/country of patterns in our database, the proportion of each continent/country will be displayed in different colours in the bar.



For the region and country groups in our database, each strain can be listed to the corresponding groups. In addition, you can easily access to the visualization tool and NCBI information page by clicking the link (letters in blue).

G2 Region Group List - 233 strains

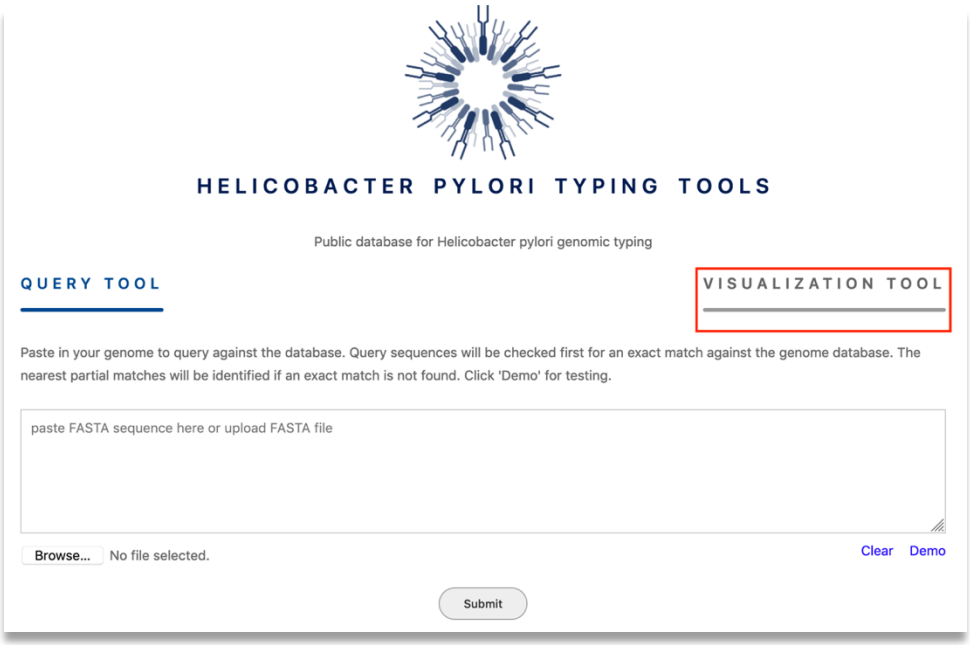
Group	Genome_id	Tip_id	Region	Country	Submit_date	MLST	Link(NCBI)
G2	GCF_000262655.1	Hp_000262655	Asia	China	2012-05-14	3039	more
G2	GCF_000287735.1	Hp_000287735	Asia	China	2013-02-23	2164	more
G2	GCF_000287755.1	Hp_000287755	Asia	China	2013-02-23	2128	more

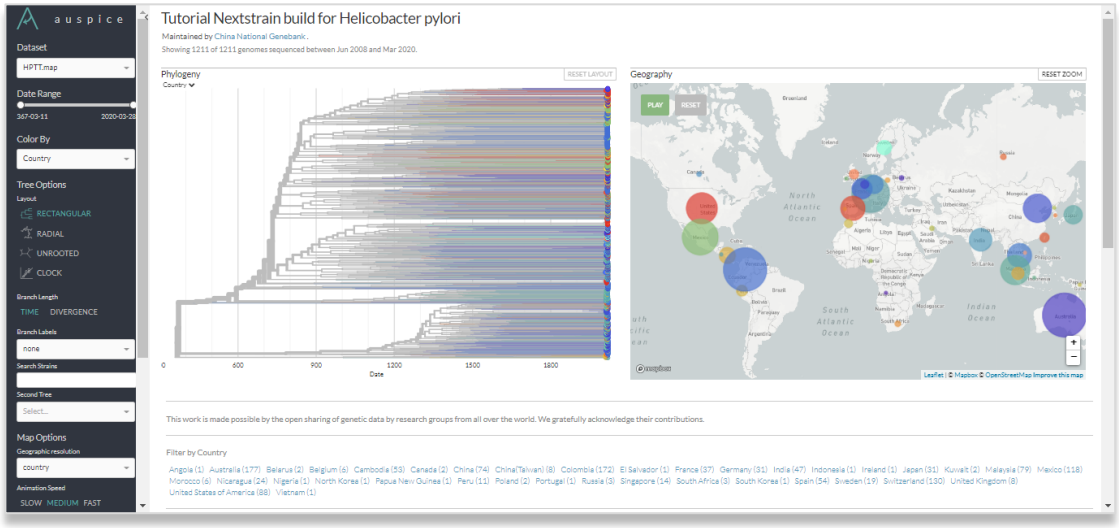
G2.C31 Country Group List - 5 strains

Group	Genome_id	Tip_id	Region	Country	Submit_date	MLST	Link(NCBI)
G2.C31	GCF_002357315.1	Hp_002357315	Asia	Japan	2017-01-17	-	more
G2.C31	GCF_002357415.1	Hp_002357415	Asia	Japan	2017-01-17	-	more
G2.C31	GCF_002357715.1	Hp_002357715	Asia	Japan	2017-01-17	-	more
G2.C31	GCF_002357775.1	Hp_002357775	Asia	Japan	2017-01-17	-	more
G2.C31	GCF_009690965.1	Hp_009690965	Asia	Japan	2019-11-22	-	more

- The visualization tool of *H. pylori*

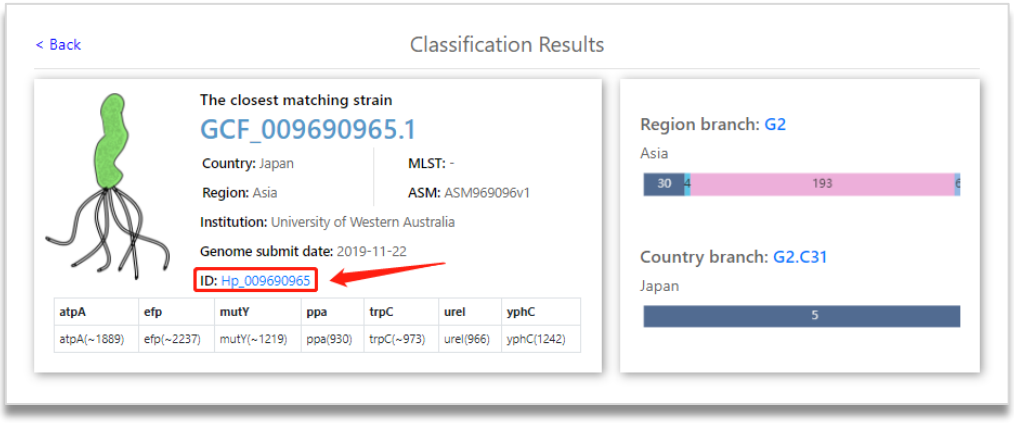
You can easily access to the visualization tool at the homepage by clicking the "VISUALIZATION TOOL" button. All the genomes in our database can be interacted and displayed in both phylogenetic relationships and geographic locations.

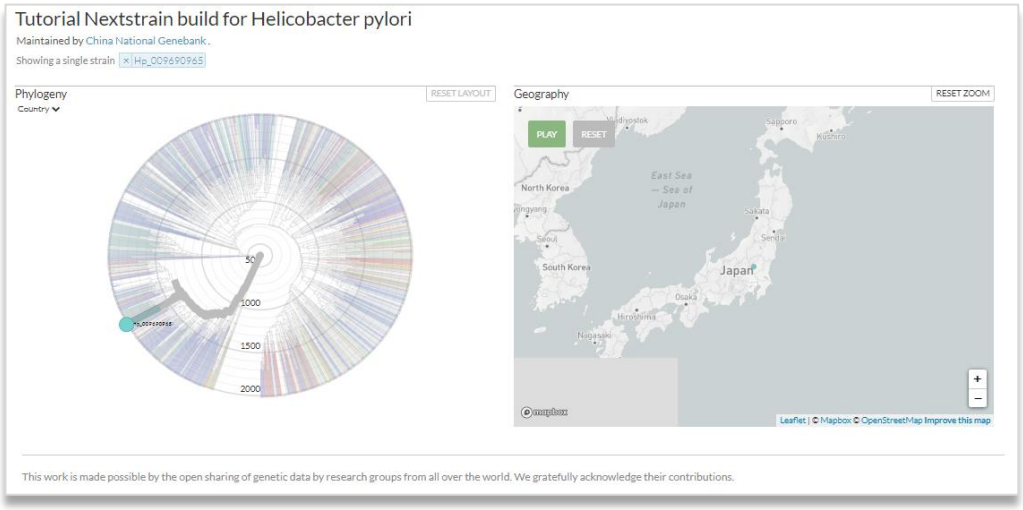




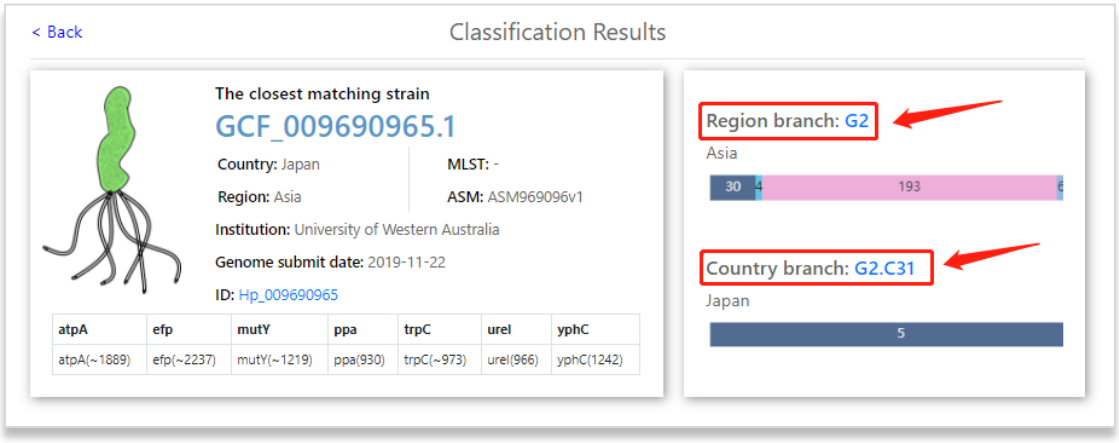
- The linking functions

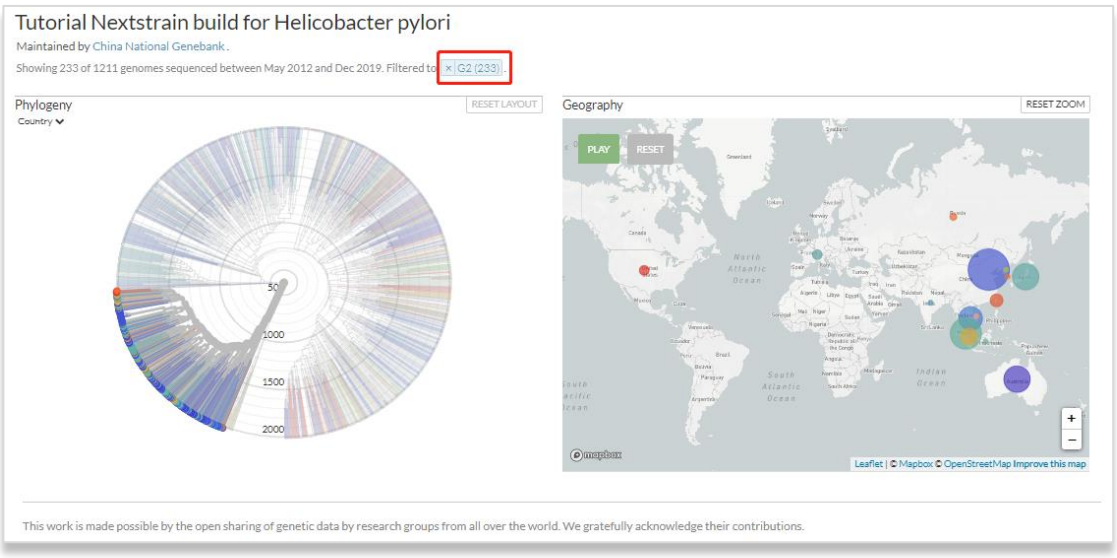
When the genome matched the data in our database, it is easily to see the geographic location by clicking ID.

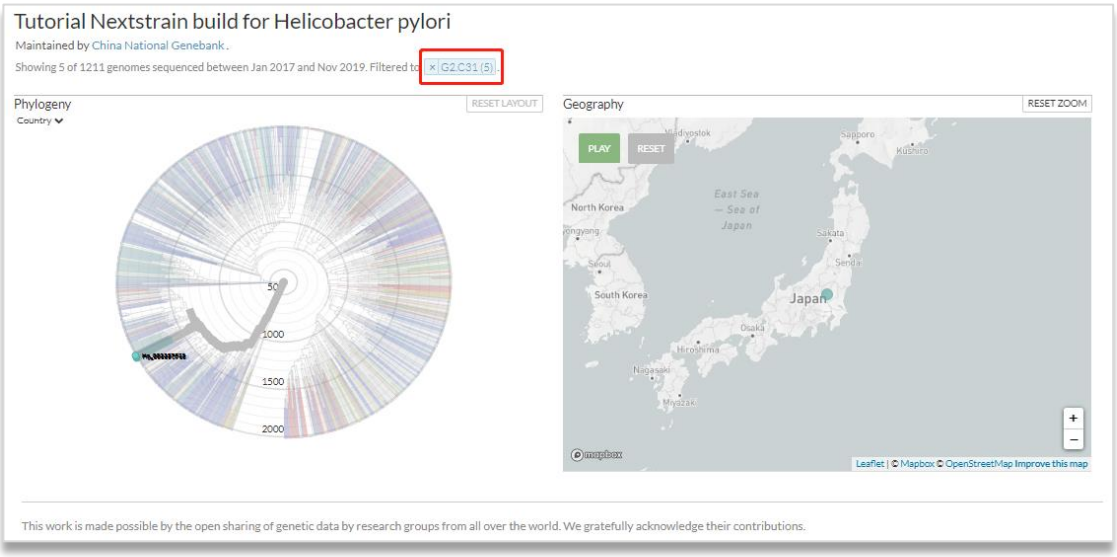




When the genome matched the data in our database, it is easily to see the phylogenetic relationship and geographic location by clicking the group ID (the letters in blue).




Tutorial Nextstrain build for Helicobacter pylori
Maintained by China National Genebank.
Showing 233 of 1211 genomes sequenced between May 2012 and Dec 2019. Filtered to × G2 (233).
Phylogeny
RESET LAYOUT
Country
50
1000
1500
2000
Geography
RESET ZOOM
PLAY
RESET
Leaflet | © Mapbox © OpenStreetMap Improve this map
This work is made possible by the open sharing of genetic data by research groups from all over the world. We gratefully acknowledge their contributions.


Tutorial Nextstrain build for Helicobacter pylori
Maintained by China National Genebank.
Showing 5 of 1211 genomes sequenced between Jan 2017 and Nov 2019. Filtered to × G2.C31 (5).
Phylogeny
RESET LAYOUT
Country
50
1000
1500
2000
Geography
RESET ZOOM
PLAY
RESET
North Korea
South Korea
Japan
Leaflet | © Mapbox © OpenStreetMap Improve this map
This work is made possible by the open sharing of genetic data by research groups from all over the world. We gratefully acknowledge their contributions.