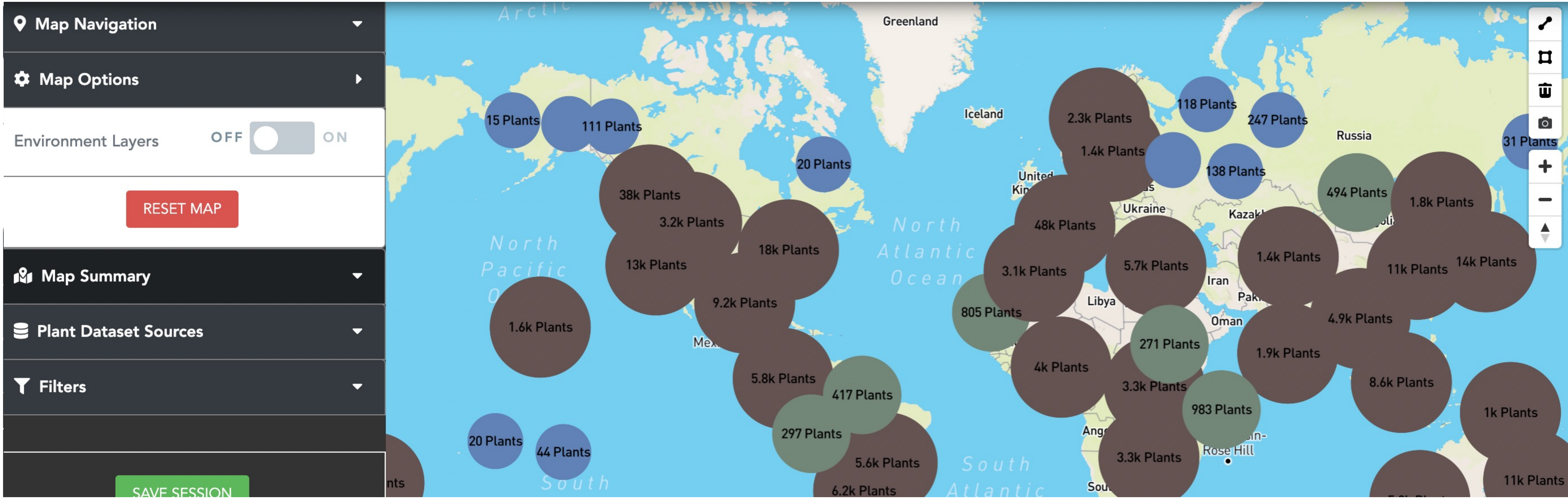
AG2PI WORKSHOP | JULY 12, 2023

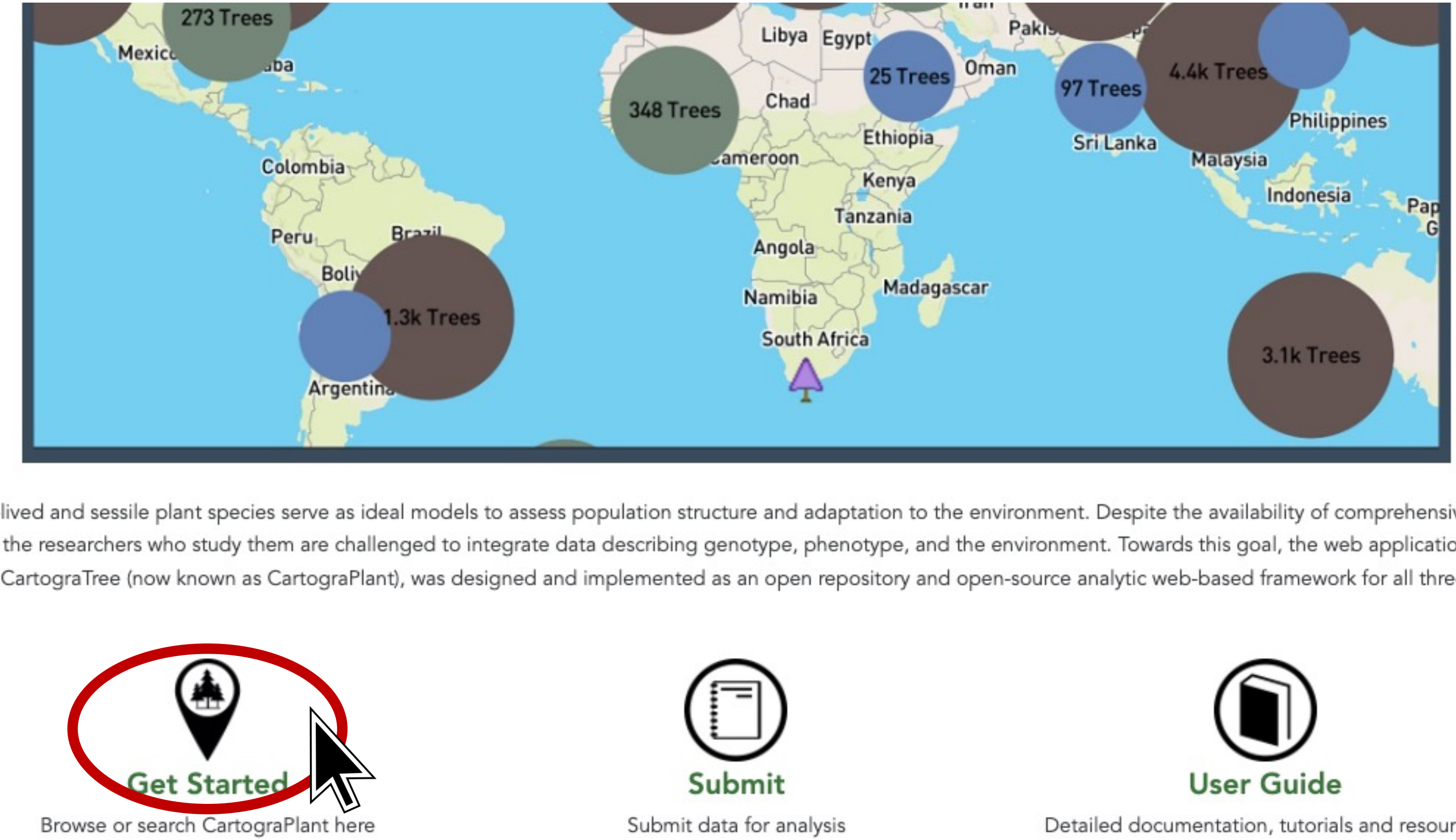
Analytics with CartograPlant (GWAS and GEA): Demo


Environment Layers OFF ON

Irene Cobo Simón, PhD.
Postdoctoral Research Associate/Postdoctoral Fellow
University of Connecticut/Institute of Forest Science (ICIFOR-INIA, CSIC), Spain

CSIC
CONSEJO SUPERIOR DE INVESTIGACIONES CIENTÍFICAS
INIA
Instituto Nacional de Investigación y Tecnología Agraria y Alimentaria
UCONN
UNIVERSITY OF CONNECTICUT

CARTOGRAPLANT WEBSITE



Long-lived and sessile plant species serve as ideal models to assess population structure and adaptation to the environment. Despite the availability of comprehensive data, the researchers who study them are challenged to integrate data describing genotype, phenotype, and the environment. Towards this goal, the web application CartograTree (now known as CartograPlant), was designed and implemented as an open repository and open-source analytic web-based framework for all three.

Get Started
Browse or search CartograPlant here

Submit
Submit data for analysis

User Guide
Detailed documentation, tutorials and resources

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/

INTERFACE AND DATA VISUALIZATION

Environment Layers OFF ON

Number of Plants	239363	SEL ALL
Selected Plants	0	
Species count	424	
Publications Count	307	
Number of Layers	0	

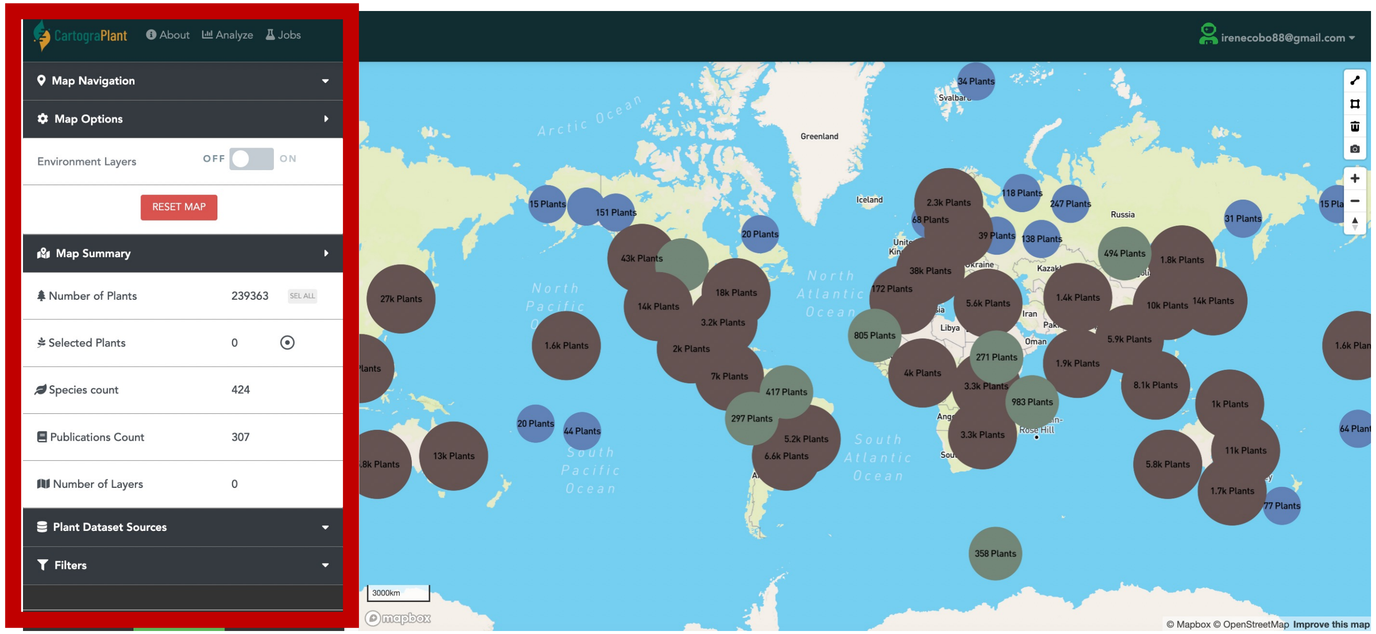
https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/

INTERFACE AND DATA VISUALIZATION

LEFT PANEL

The action panel from which users can interact with the map and the plants. It is located at the left of the screen



Environment Layers OFF ON

Number of Plants 239363

Selected Plants 0

Species count 424

Publications Count 307

Number of Layers 0

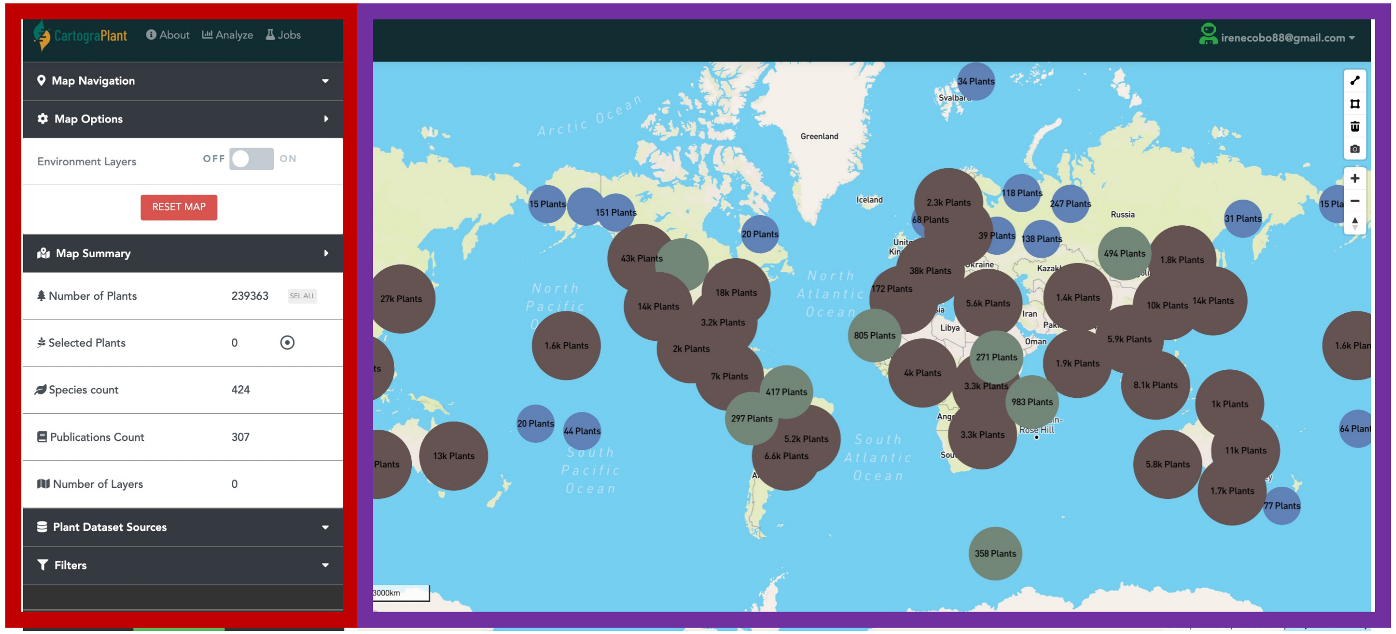
https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/

INTERFACE AND DATA VISUALIZATION

LEFT PANEL

The **action panel** from which users can interact with the map and the plants. It is located at the left of the screen



Environment Layers OFF ON

Number of Plants 239363 SEL ALL

Selected Plants 0

Species count 424

Publications Count 307

Number of Layers 0

RIGHT PANEL

An **interactive map**, showing the plants and the environmental layers that were selected on the left panel

https://cartograplant.org/

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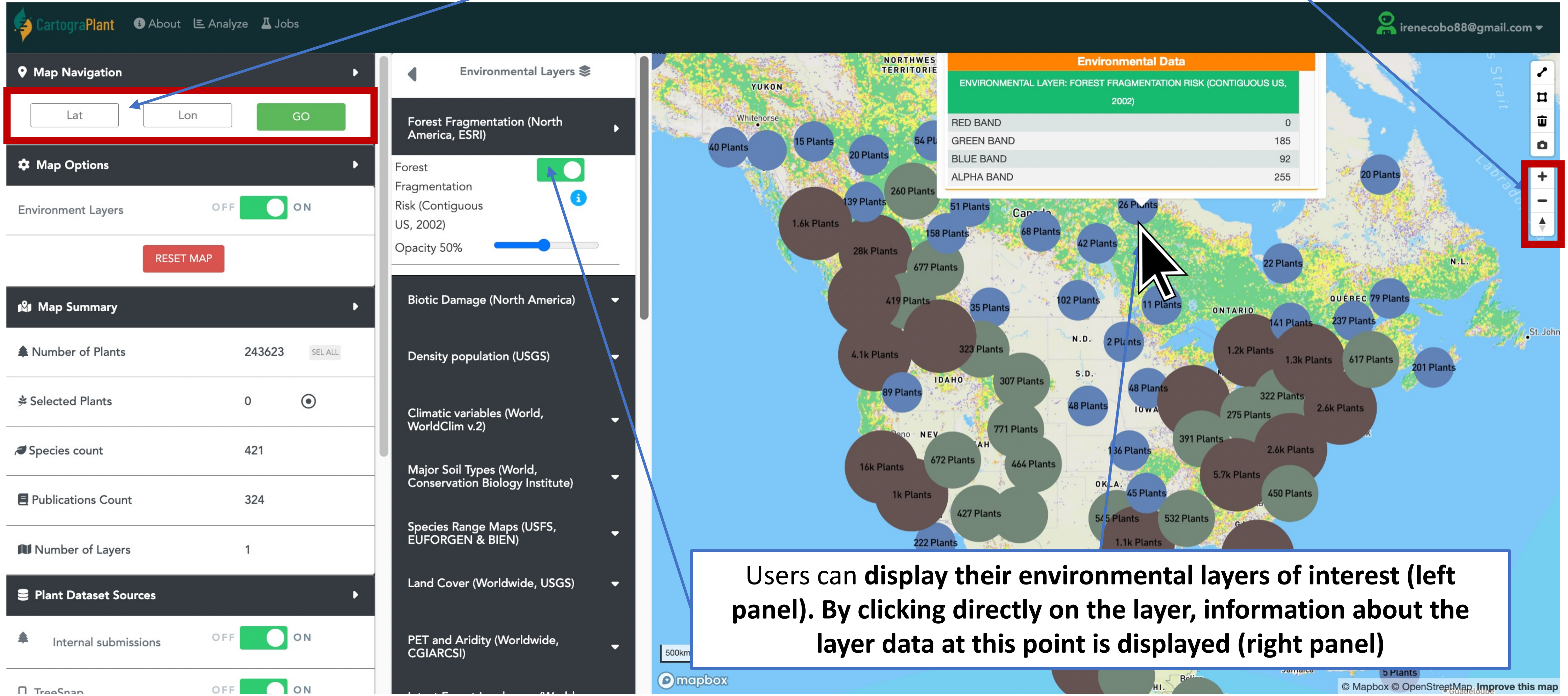
INTERFACE AND DATA VISUALIZATION

Users can **navigate** on the map by using the **zoom buttons** or by **typing the coordinates of interest**



Environment Layers OFF ON

Number of Plants	243623
Selected Plants	0
Species count	421
Publications Count	324
Number of Layers	1

Internal submissions OFF ON

TreeSnap OFF ON

Forest Fragmentation Risk (Contiguous US, 2002)

Opacity 50%

ENVIRONMENTAL LAYER: FOREST FRAGMENTATION RISK (CONTIGUOUS US, 2002)

RED BAND	0
GREEN BAND	185
BLUE BAND	92
ALPHA BAND	255

Users can **display their environmental layers of interest (left panel). By clicking directly on the layer, information about the layer data at this point is displayed (right panel)**

https://cartograplant.org/

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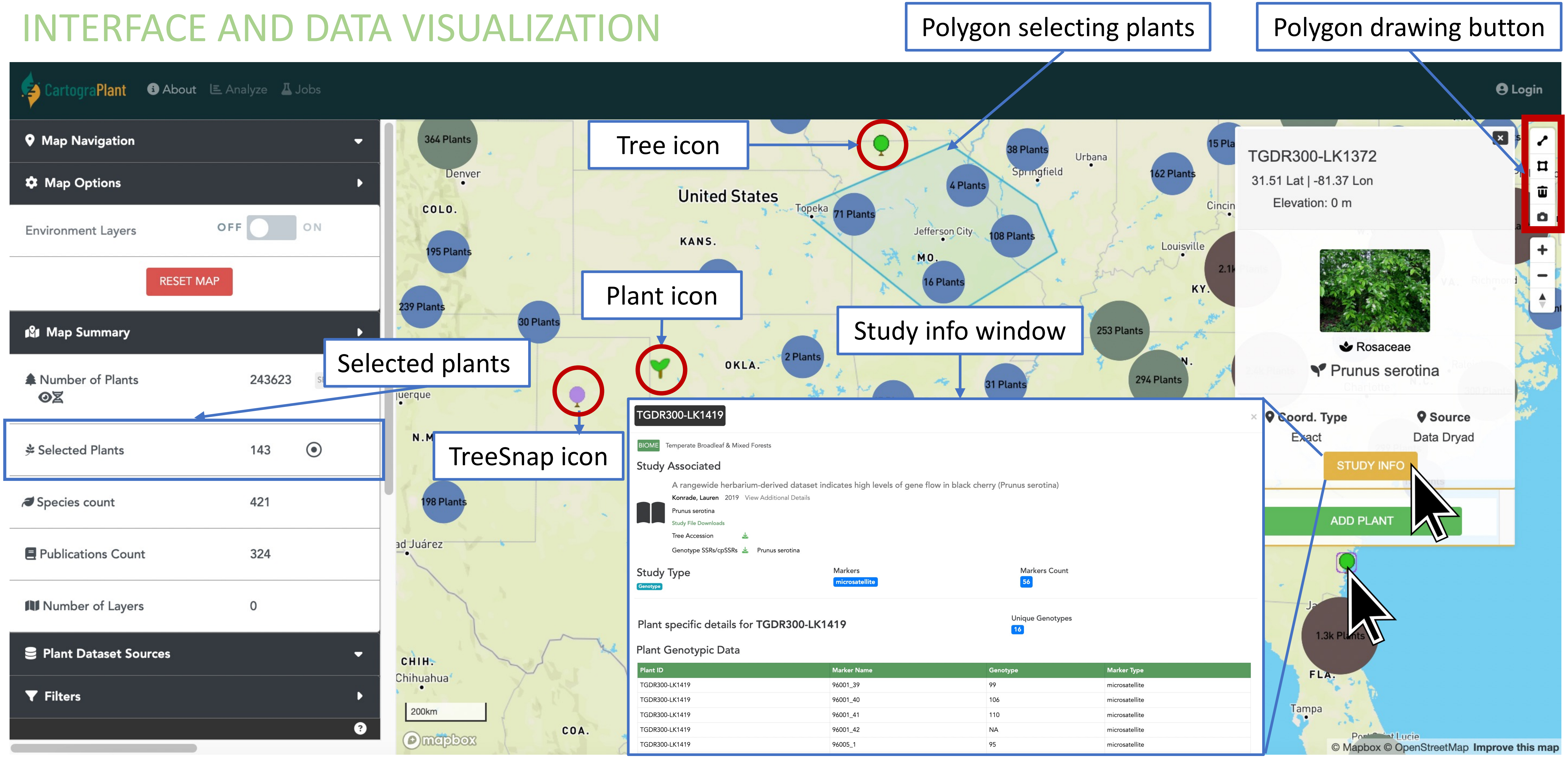
INTERFACE AND DATA VISUALIZATION



Number of Plants	243623
Selected Plants	143
Species count	421
Publications Count	324
Number of Layers	0

TGDR300-LK1372

31.51 Lat | -81.37 Lon

Elevation: 0 m

Rosaceae

Prunus serotina

Coord. Type: Exact

Source: Data Dryad

TGDR300-LK1419

BIOME Temperate Broadleaf & Mixed Forests

Study Associated

A rangewide herbarium-derived dataset indicates high levels of gene flow in black cherry (Prunus serotina)

Konrade, Lauren 2019 View Additional Details

Prunus serotina

Study File Downloads

Tree Accession

Genotype SSRs/cpSSRs Prunus serotina

Study Type: Genotype

Markers: microsatellite

Markers Count: 56

Plant specific details for **TGDR300-LK1419**

Unique Genotypes: 16

Plant Genotypic Data

Plant ID	Marker Name	Genotype	Marker Type
TGDR300-LK1419	96001_39	99	microsatellite
TGDR300-LK1419	96001_40	106	microsatellite
TGDR300-LK1419	96001_41	110	microsatellite
TGDR300-LK1419	96001_42	NA	microsatellite
TGDR300-LK1419	96005_1	95	microsatellite

https://cartograplant.org/

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INTERFACE AND DATA VISUALIZATION

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/

Number of Plants	243623
Selected Plants	0
Species count	421
Publications Count	324
Number of Layers	0

Internal submissions OFF [✓ ON]
TreeSnap OFF [✓ ON]
Direct submissions OFF [✓ ON]
BIEN [✓ OFF] ON
WFID [✓ OFF] ON

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

https://cartograplant.org/

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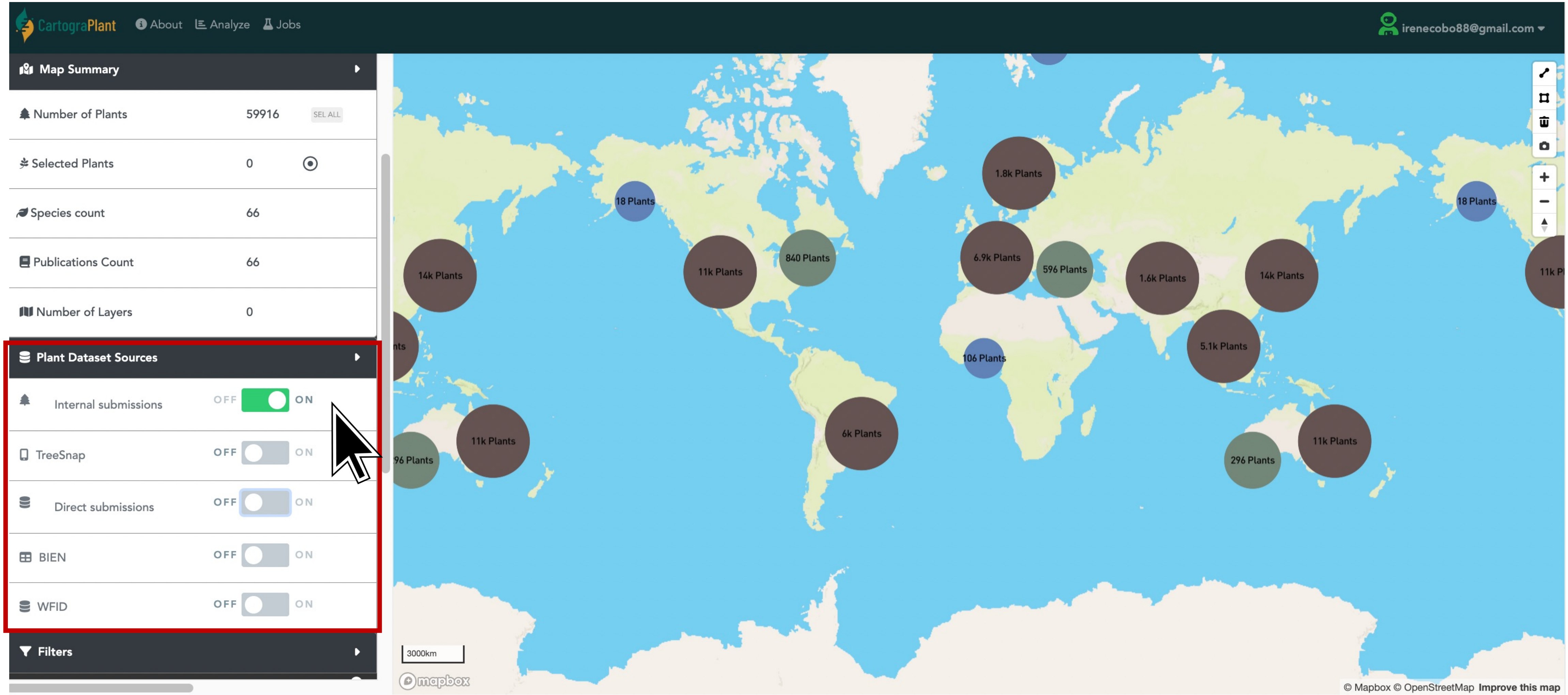

Number of Plants 59916

Selected Plants 0

Species count 66

Publications Count 66

Number of Layers 0

Internal submissions OFF ● ON

TreeSnap ● OFF ON

Direct submissions ● OFF ON

BIEN ● OFF ON

WFID ● OFF ON

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

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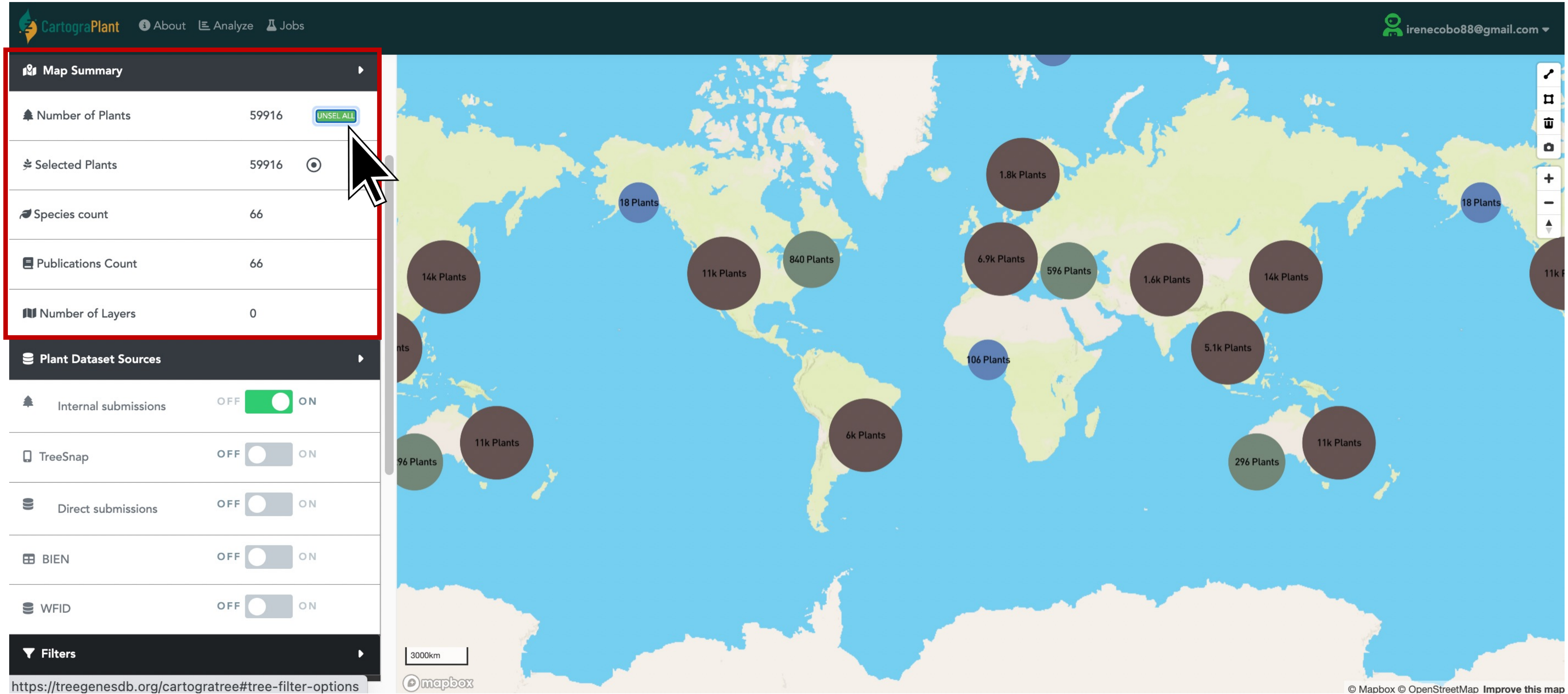

Number of Plants 59916

Selected Plants 59916

Species count 66

Publications Count 66

Number of Layers 0

Internal submissions OFF ON

TreeSnap OFF ON

Direct submissions OFF ON

BIEN OFF ON

WFID OFF ON

https://treegenesdb.org/cartogratree#tree-filter-options

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

https://cartograplant.org/

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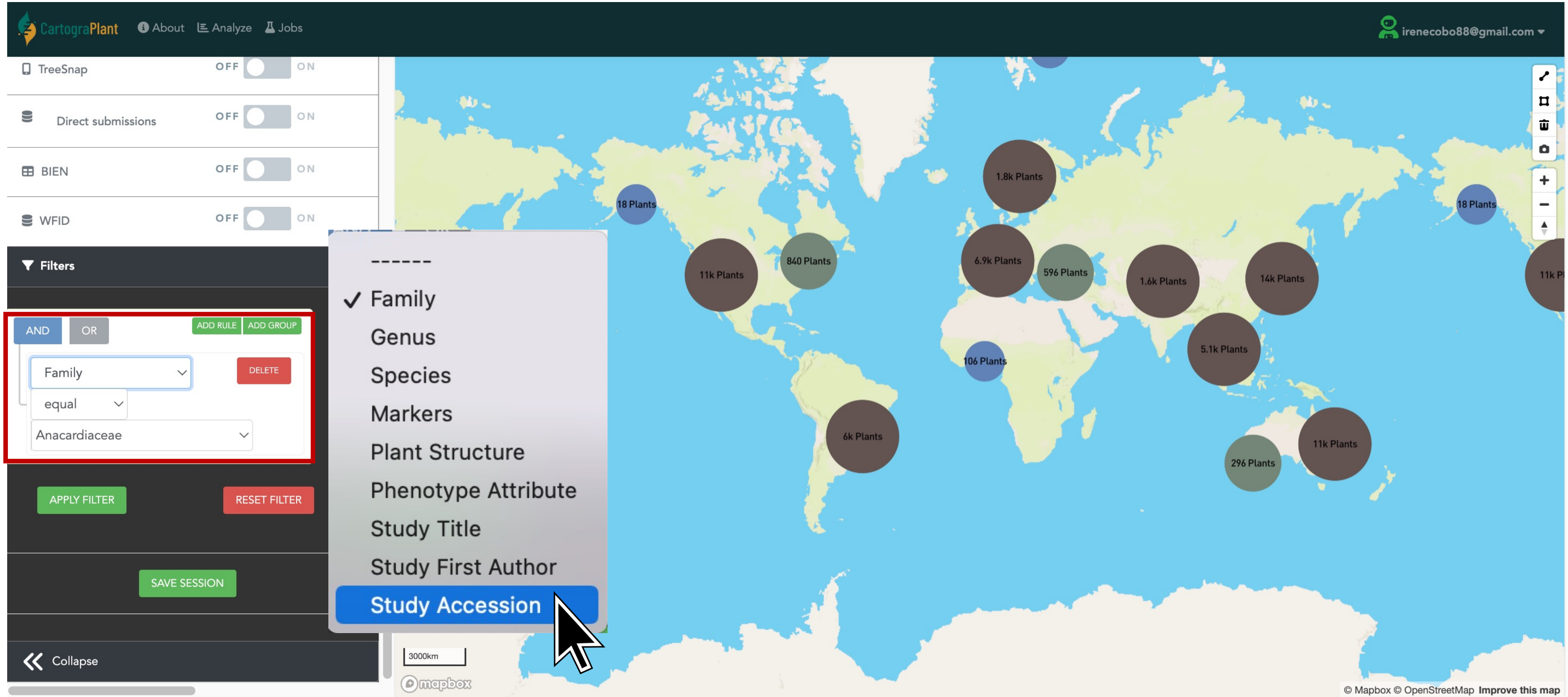

Family

equal

Anacardiaceae

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

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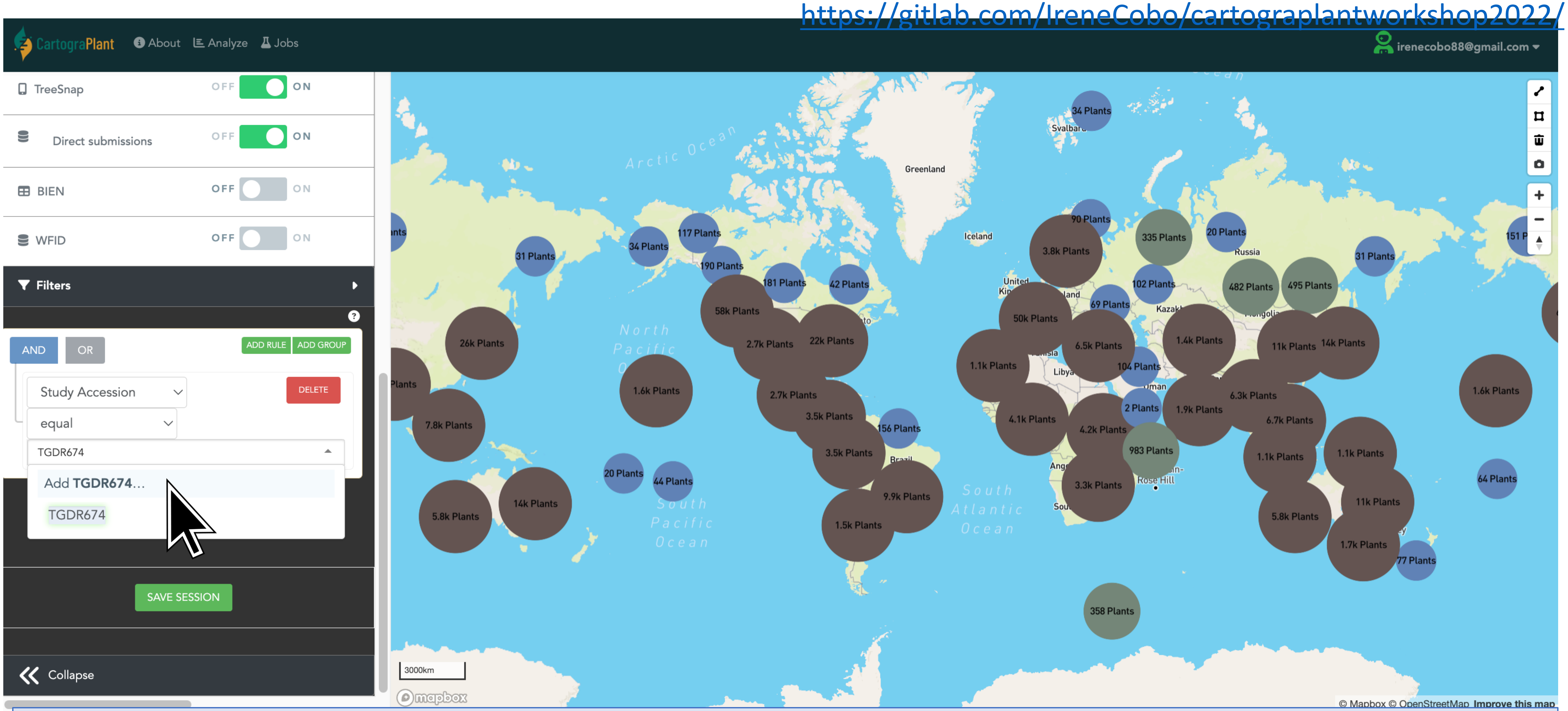


TreeSnap OFF ● ON

Direct submissions OFF ● ON

BIEN ○ OFF ON

WFID ○ OFF ON

Study Accession

equal

TGDR674

Add TGDR674...

TGDR674

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/

TreeSnap: ON

Direct submissions: ON

BIEN: OFF

WFID: OFF

Study Accession
equal
TGDR674

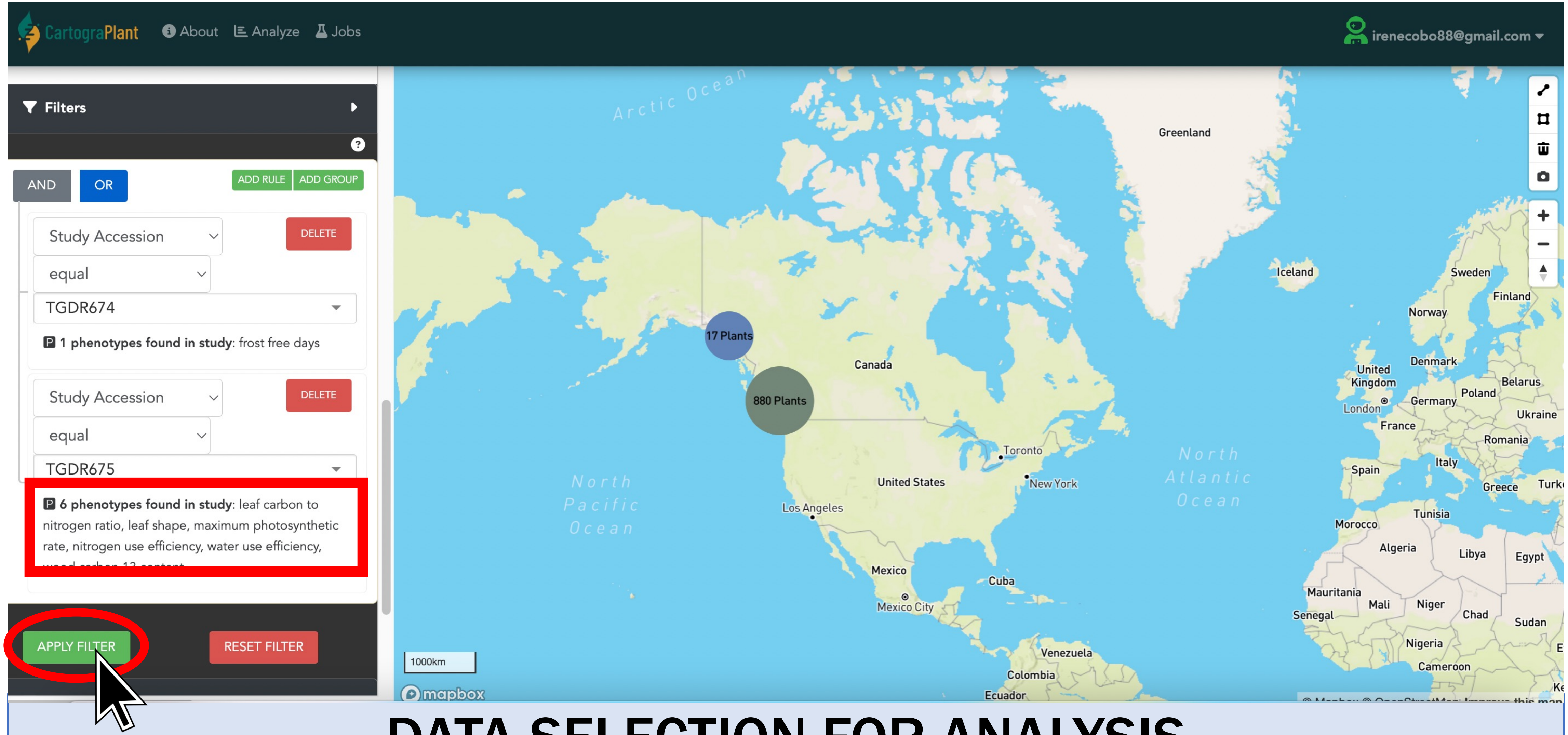
1 phenotypes found in study: frost free days

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Study Accession
equal
TGDR674

1 phenotypes found in study: frost free days

Study Accession
equal
TGDR675

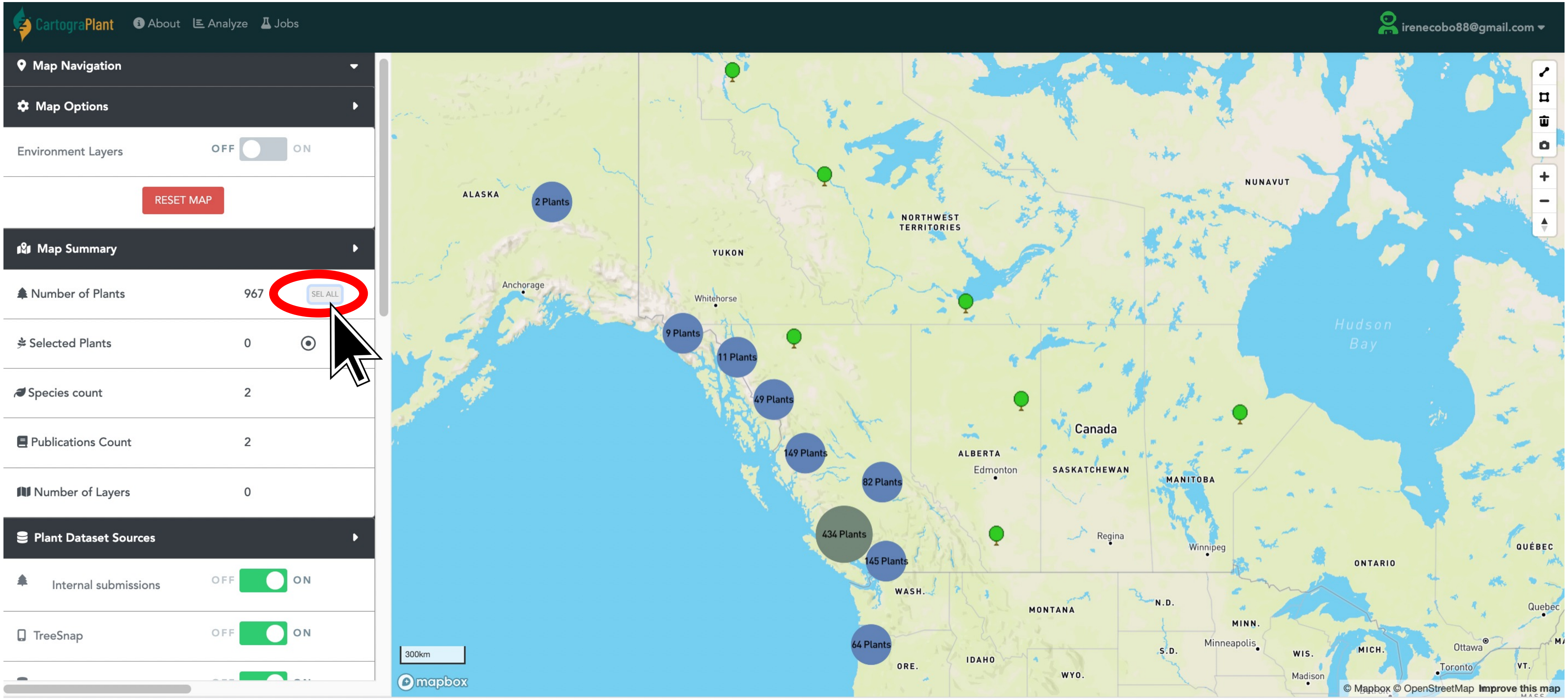
6 phenotypes found in study: leaf carbon to nitrogen ratio, leaf shape, maximum photosynthetic rate, nitrogen use efficiency, water use efficiency, wood carbon 13 content

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Environment Layers OFF ON

Number of Plants	967	SEL ALL
Selected Plants	0	⊙
Species count	2	
Publications Count	2	
Number of Layers	0	

Internal submissions OFF ON

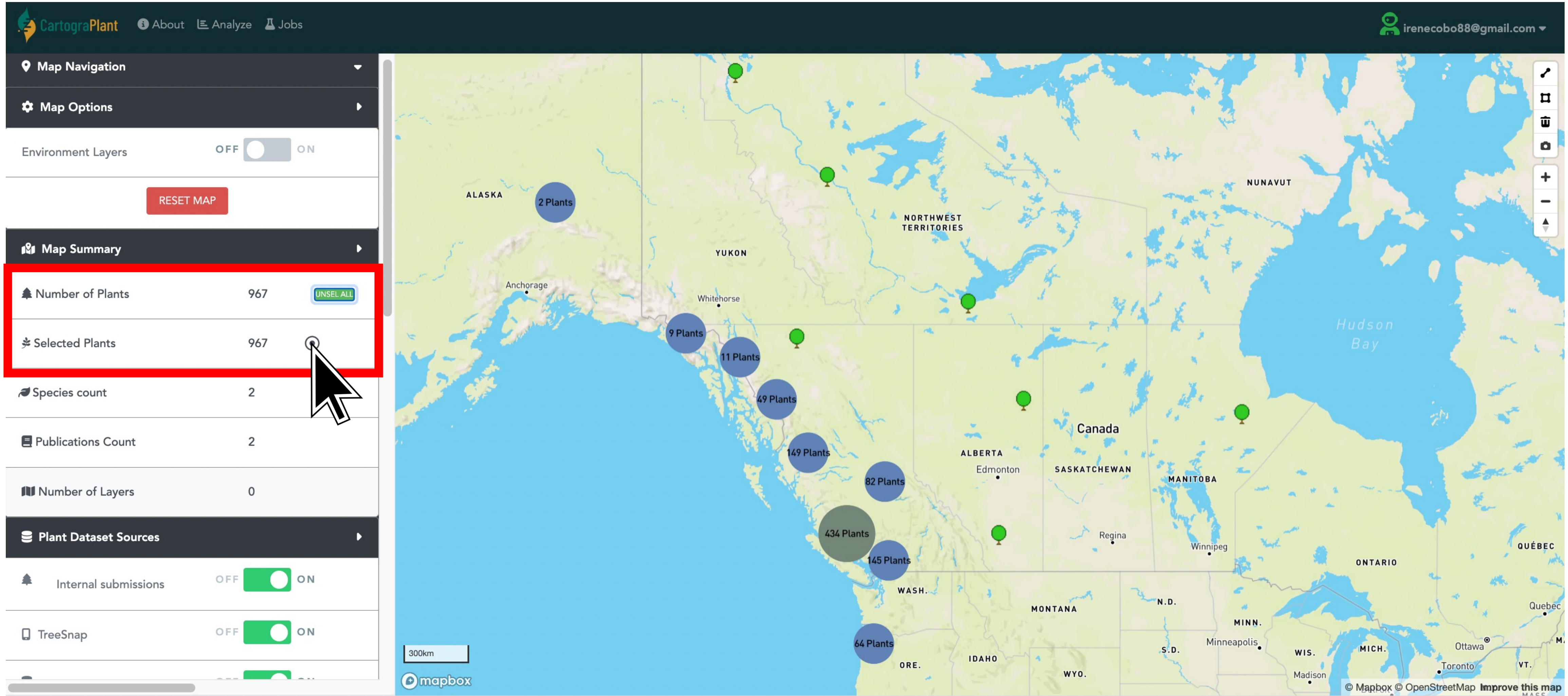
TreeSnap OFF ON

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

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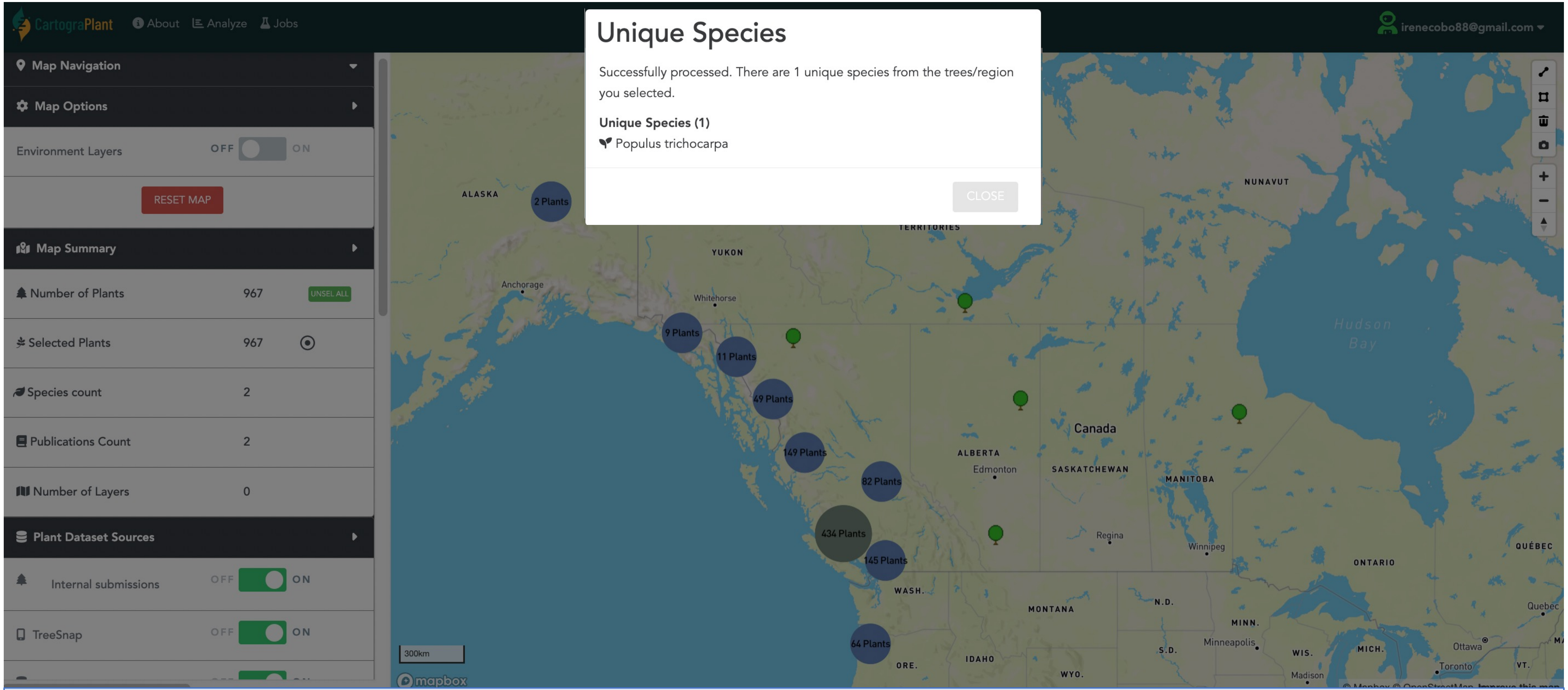

Unique Species

Successfully processed. There are 1 unique species from the trees/region you selected.

Unique Species (1)

Populus trichocarpa

Environment Layers OFF ON

Number of Plants 967

Selected Plants 967

Species count 2

Publications Count 2

Number of Layers 0

Internal submissions OFF ON

TreeSnap OFF ON

DATA SELECTION FOR ANALYSIS

INTERFACE AND DATA VISUALIZATION

https://cartograplant.org/

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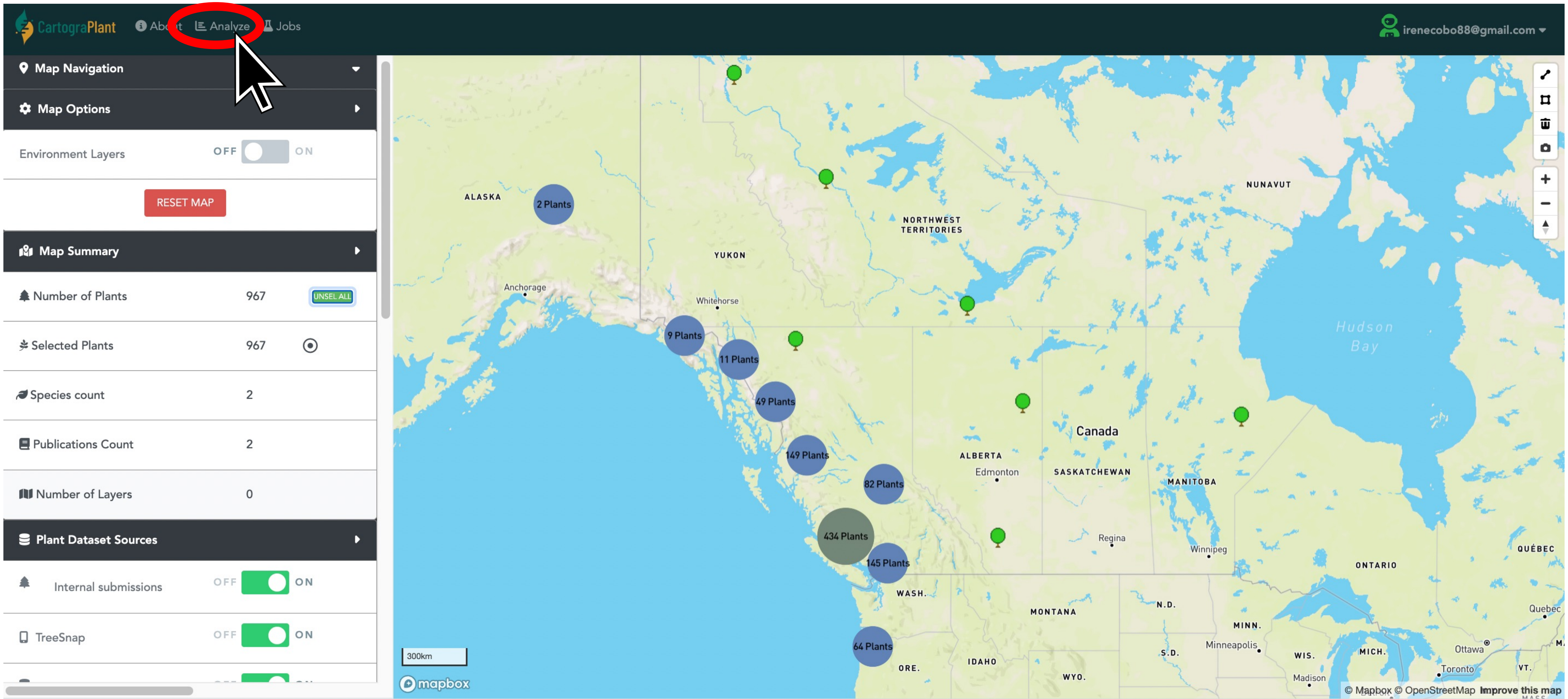

Environment Layers	OFF ○ ON	
Number of Plants	967	UNSEL ALL
Selected Plants	967	◉
Species count	2	
Publications Count	2	
Number of Layers	0	
Internal submissions	OFF ● ON	
TreeSnap	OFF ● ON	

DATA SELECTION FOR ANALYSIS

DATA ANALYSIS

https://cartograplant.org/

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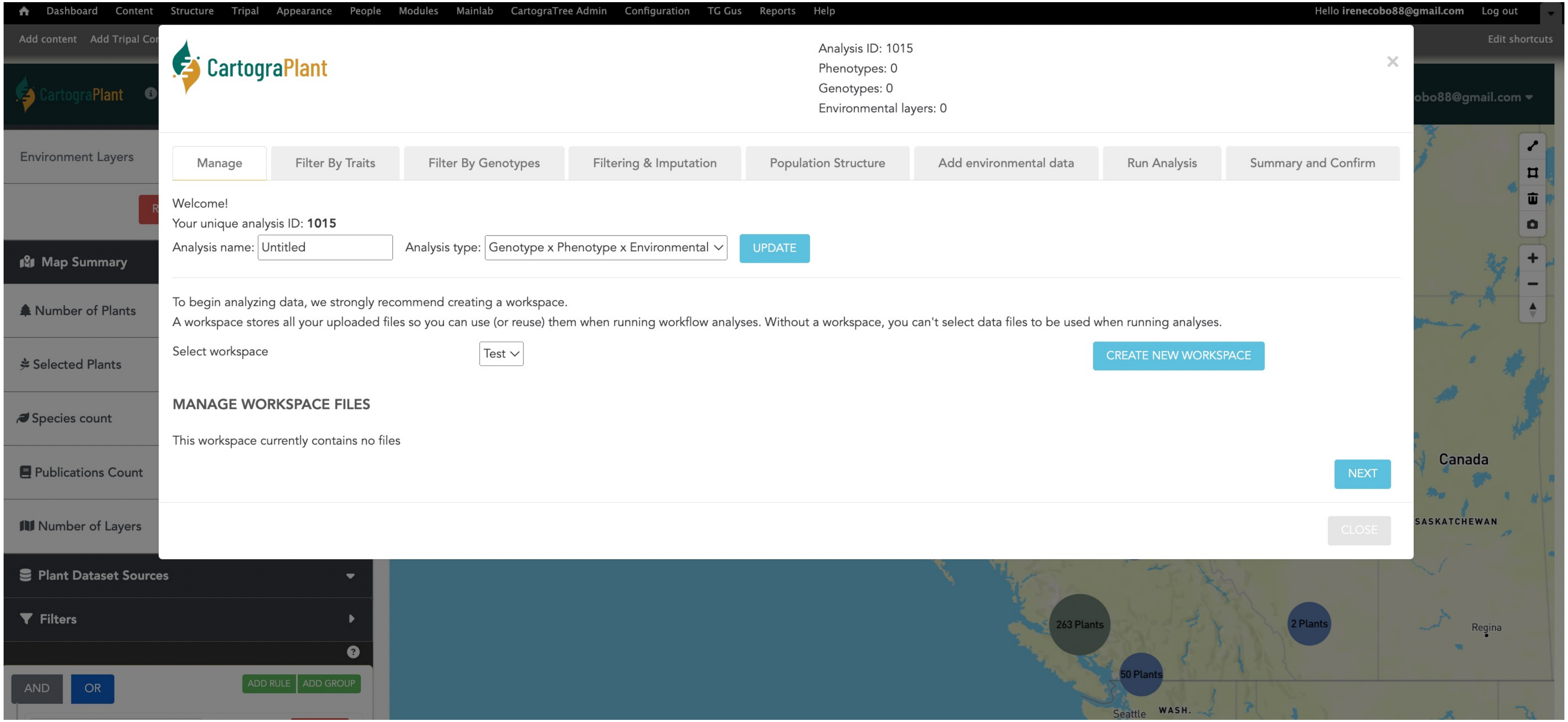

Analysis ID: 1015
Phenotypes: 0
Genotypes: 0
Environmental layers: 0

Welcome!
Your unique analysis ID: **1015**
Analysis name: Untitled
Analysis type: Genotype x Phenotype x Environmental

To begin analyzing data, we strongly recommend creating a workspace.
A workspace stores all your uploaded files so you can use (or reuse) them when running workflow analyses. Without a workspace, you can't select data files to be used when running analyses.

Select workspace: Test

MANAGE WORKSPACE FILES

This workspace currently contains no files

DATA ANALYSIS: WORKSPACE CREATION

DATA ANALYSIS

https://cartograplant.org/

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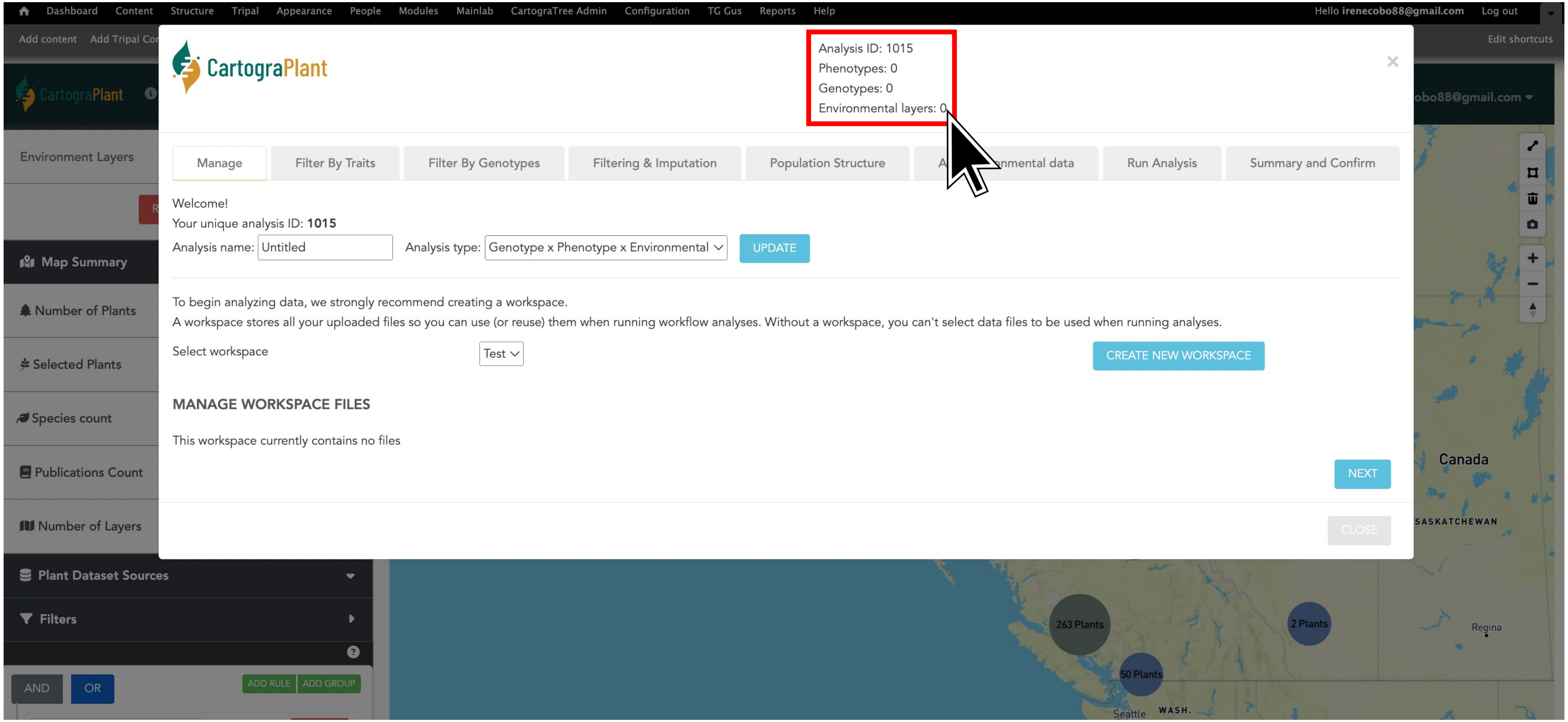

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DATA ANALYSIS: WORKSPACE CREATION

DATA ANALYSIS

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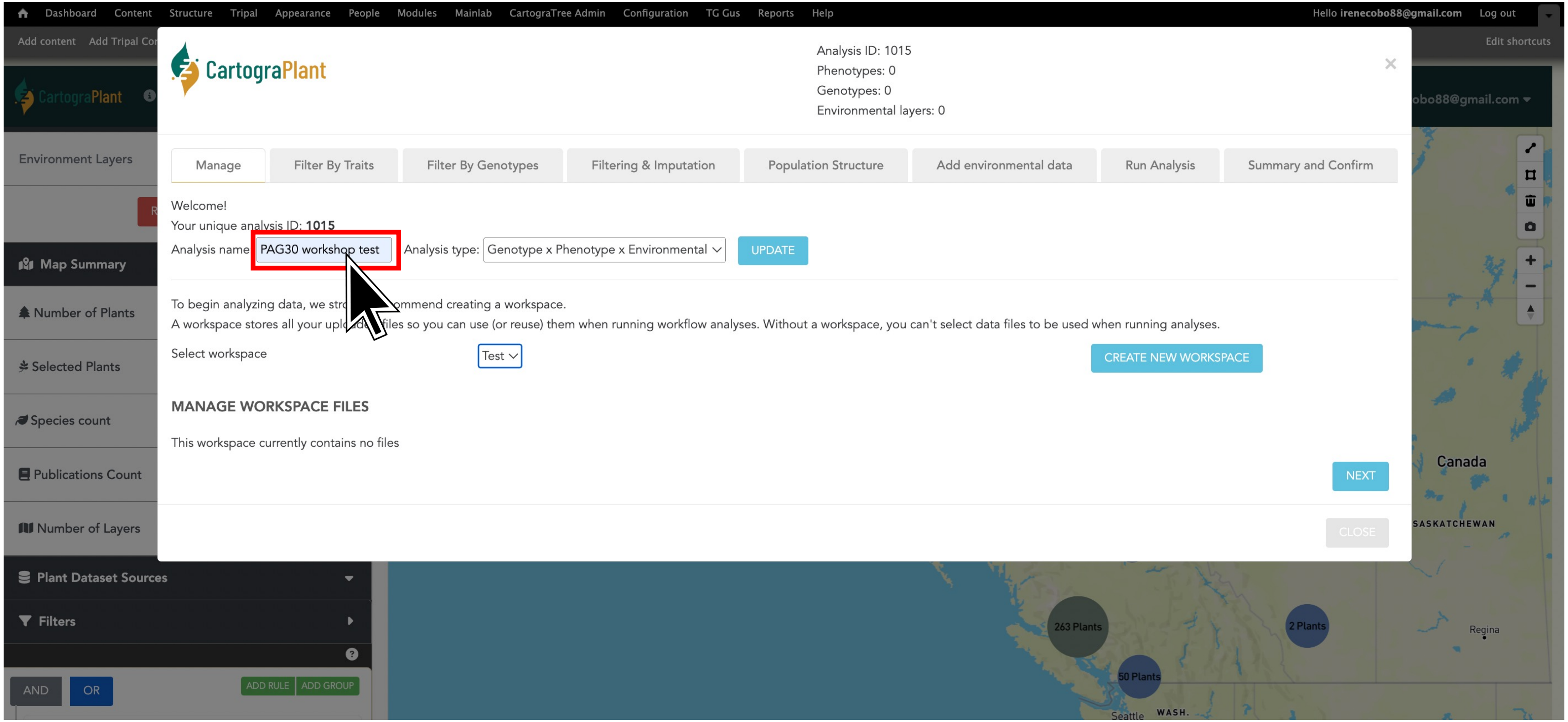


Analysis ID: 1015
Phenotypes: 0
Genotypes: 0
Environmental layers: 0

Welcome!
Your unique analysis ID: **1015**

Analysis name: PAG30 workshop test
Analysis type: Genotype x Phenotype x Environmental

To begin analyzing data, we str mmend creating a workspace.
A workspace stores all your upl files so you can use (or reuse) them when running workflow analyses. Without a workspace, you can't select data files to be used when running analyses.

Select workspace: Test

MANAGE WORKSPACE FILES

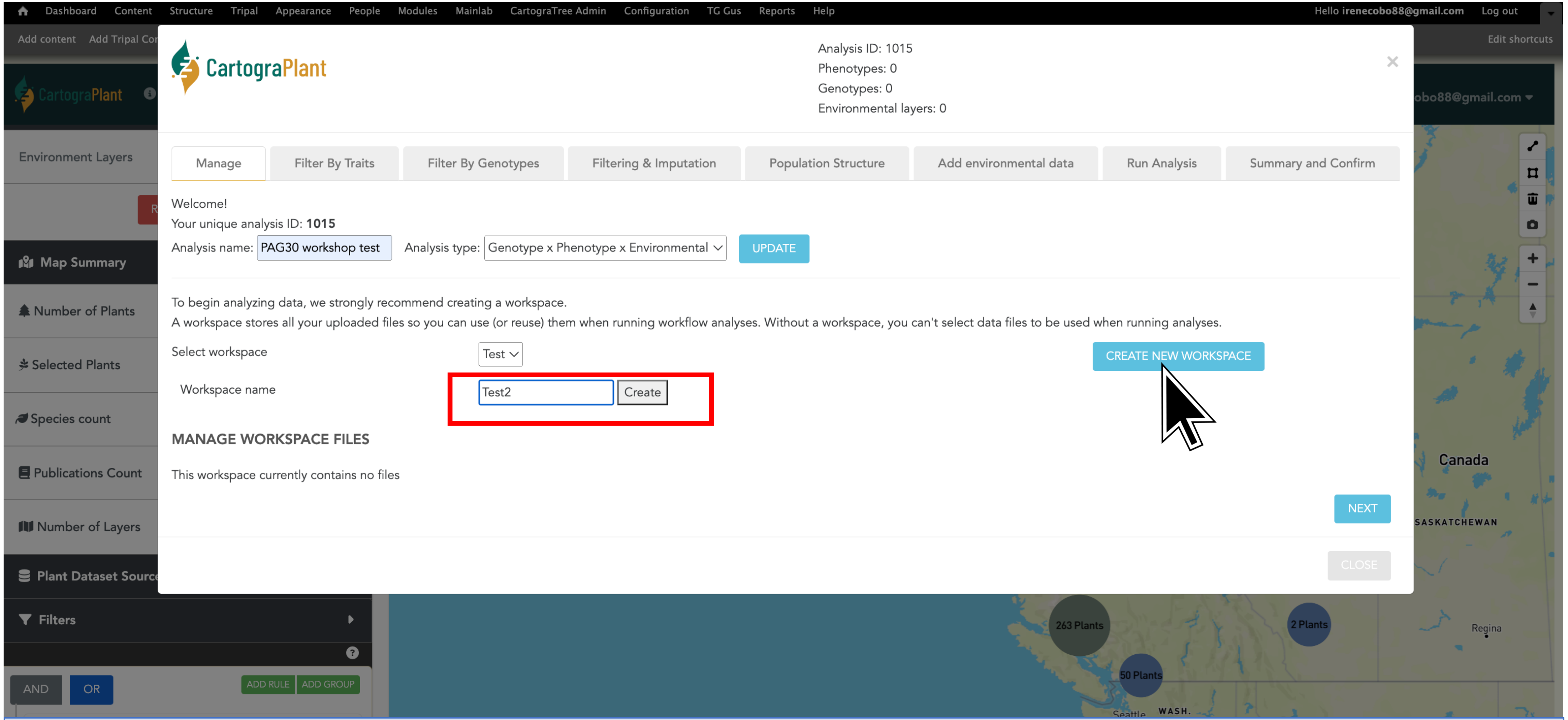
This workspace currently contains no files

DATA ANALYSIS: WORKSPACE CREATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1015
Phenotypes: 0
Genotypes: 0
Environmental layers: 0

Welcome!
Your unique analysis ID: **1015**
Analysis name: PAG30 workshop test
Analysis type: Genotype x Phenotype x Environmental

To begin analyzing data, we strongly recommend creating a workspace.
A workspace stores all your uploaded files so you can use (or reuse) them when running workflow analyses. Without a workspace, you can't select data files to be used when running analyses.

Select workspace: Test
Workspace name: Test2

MANAGE WORKSPACE FILES

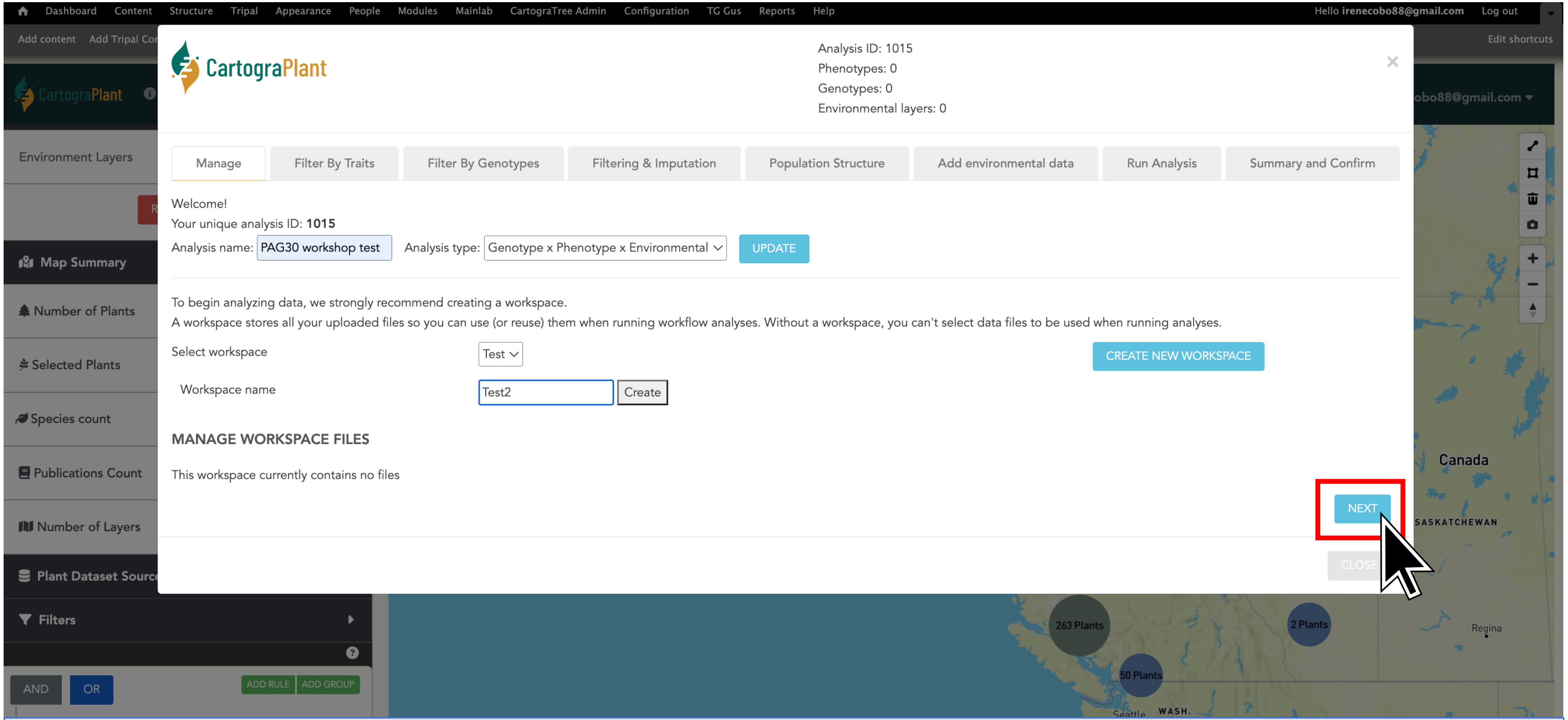
This workspace currently contains no files

DATA ANALYSIS: WORKSPACE CREATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1015
Phenotypes: 0
Genotypes: 0
Environmental layers: 0

Welcome!
Your unique analysis ID: **1015**
Analysis name: PAG30 workshop test
Analysis type: Genotype x Phenotype x Environmental

To begin analyzing data, we strongly recommend creating a workspace.
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Select workspace: Test
Workspace name: Test2

MANAGE WORKSPACE FILES

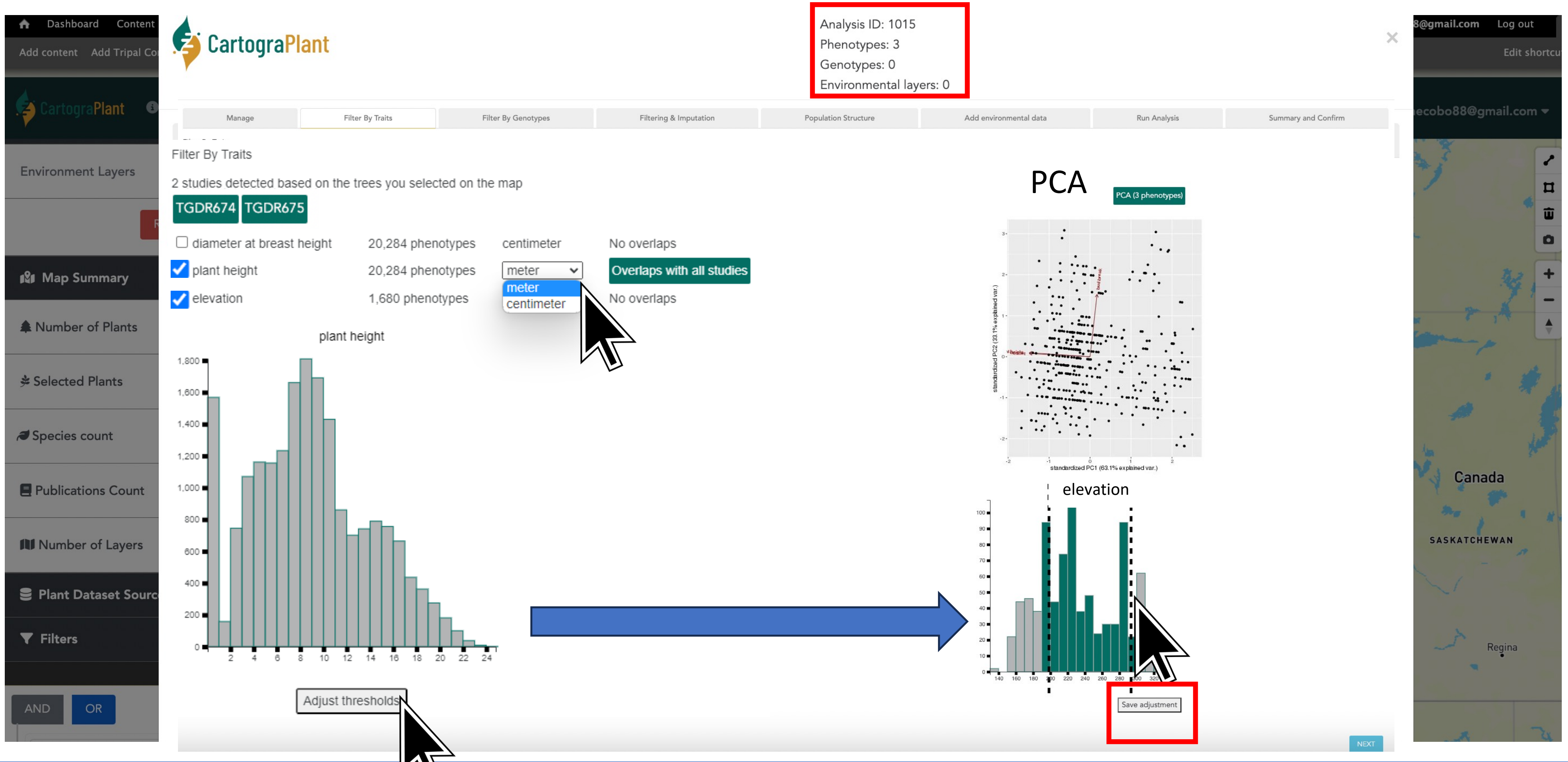
This workspace currently contains no files

DATA ANALYSIS: WORKSPACE CREATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1015
Phenotypes: 3
Genotypes: 0
Environmental layers: 0

Filter By Traits

2 studies detected based on the trees you selected on the map

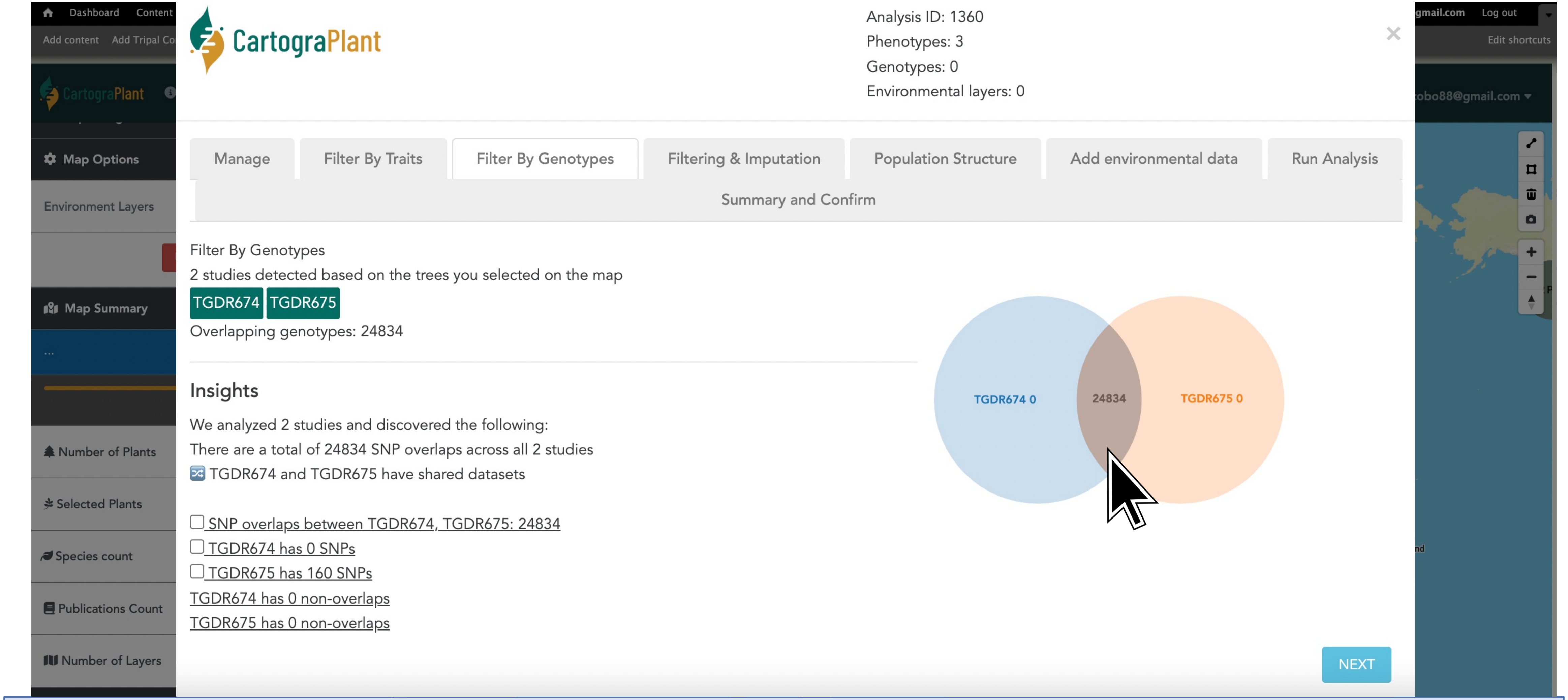
☐ diameter at breast height	20,284 phenotypes	centimeter	No overlaps
☑ plant height	20,284 phenotypes	meter	Overlaps with all studies
☑ elevation	1,680 phenotypes		No overlaps

DATA ANALYSIS: PHENOTYPIC TRAITS SELECTION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1360
Phenotypes: 3
Genotypes: 0
Environmental layers: 0

Filter By Genotypes
2 studies detected based on the trees you selected on the map
TGDR674 TGDR675
Overlapping genotypes: 24834

Insights

We analyzed 2 studies and discovered the following:
There are a total of 24834 SNP overlaps across all 2 studies
TGDR674 and TGDR675 have shared datasets

☐ SNP overlaps between TGDR674, TGDR675: 24834
☐ TGDR674 has 0 SNPs
☐ TGDR675 has 160 SNPs
TGDR674 has 0 non-overlaps
TGDR675 has 0 non-overlaps

DATA ANALYSIS: GENOTYPIC DATA SELECTION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

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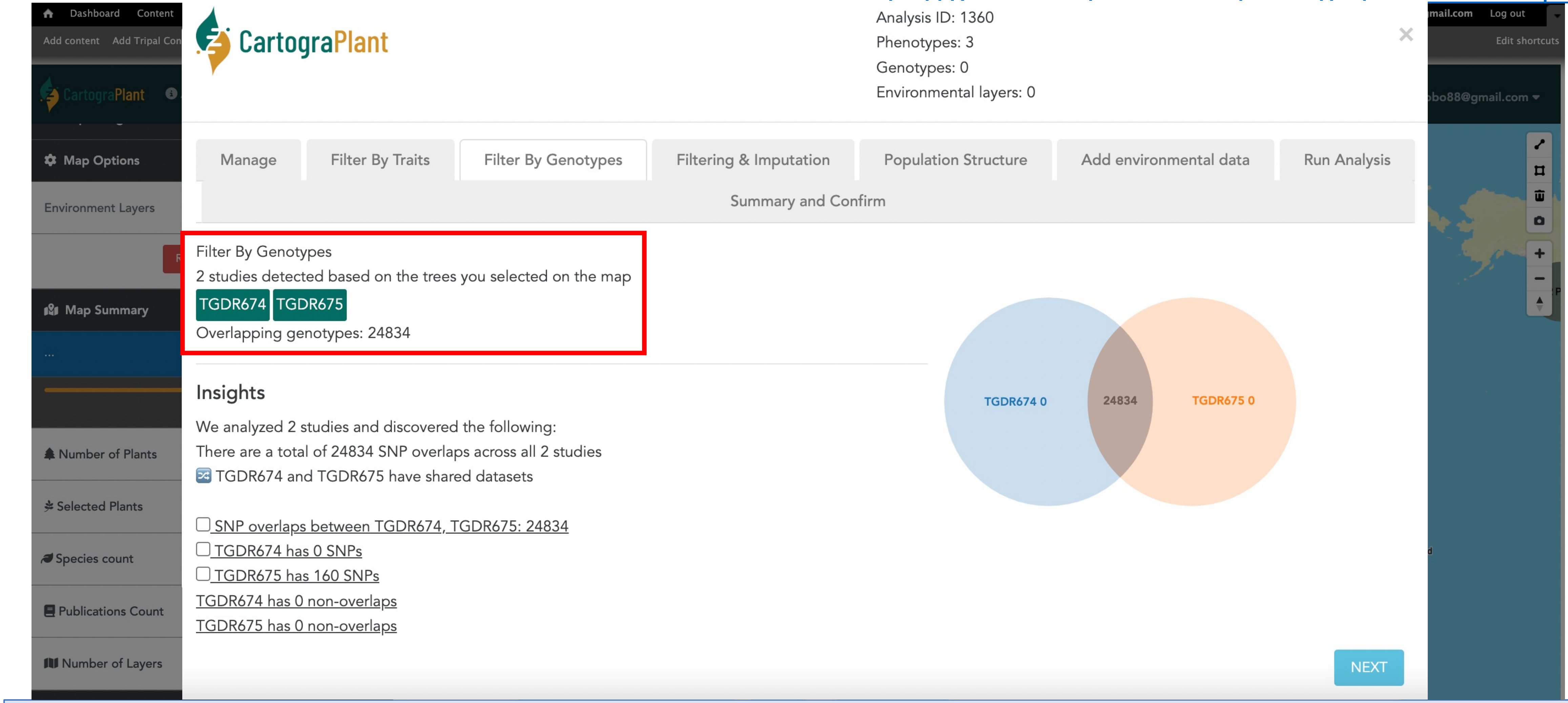

Analysis ID: 1360
Phenotypes: 3
Genotypes: 0
Environmental layers: 0

Filter By Genotypes
2 studies detected based on the trees you selected on the map
TGDR674 TGDR675
Overlapping genotypes: 24834

Insights

We analyzed 2 studies and discovered the following:
There are a total of 24834 SNP overlaps across all 2 studies
TGDR674 and TGDR675 have shared datasets

☐ SNP overlaps between TGDR674, TGDR675: 24834
☐ TGDR674 has 0 SNPs
☐ TGDR675 has 160 SNPs
TGDR674 has 0 non-overlaps
TGDR675 has 0 non-overlaps

DATA ANALYSIS: GENOTYPIC DATA SELECTION/VISUALIZATION

DATA ANALYSIS

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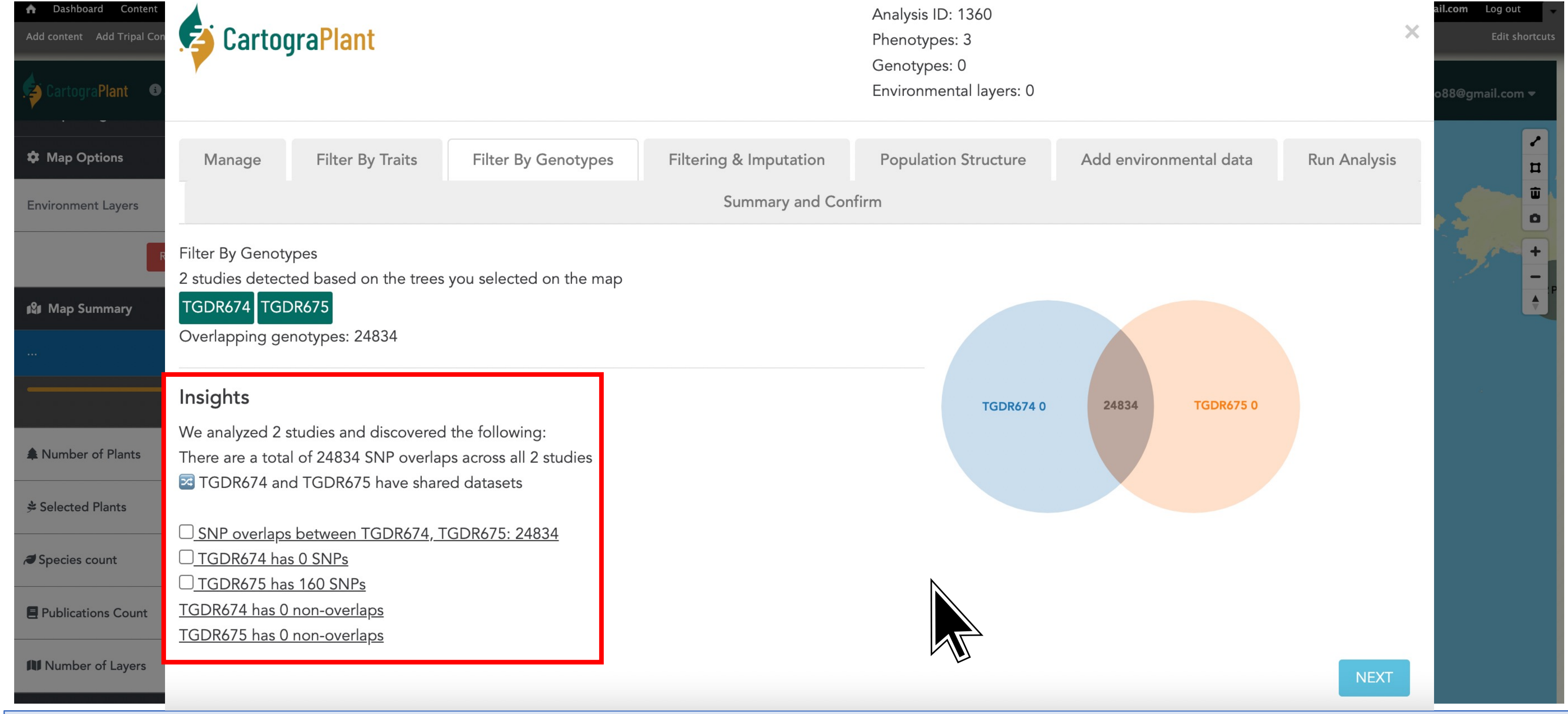
https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1360
Phenotypes: 3
Genotypes: 0
Environmental layers: 0

Filter By Genotypes

2 studies detected based on the trees you selected on the map

TGDR674 TGDR675

Overlapping genotypes: 24834

Insights

We analyzed 2 studies and discovered the following:
There are a total of 24834 SNP overlaps across all 2 studies
TGDR674 and TGDR675 have shared datasets

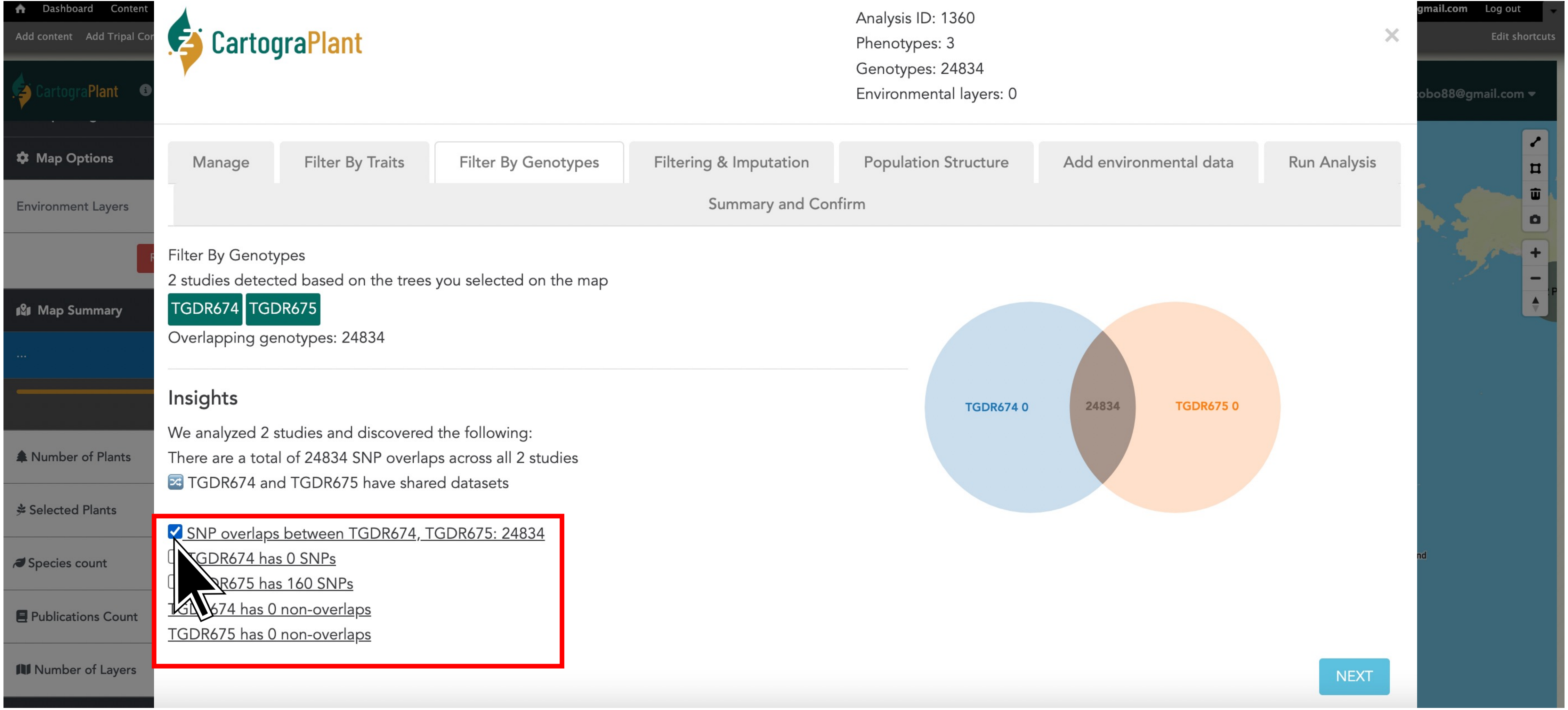
☐ SNP overlaps between TGDR674, TGDR675: 24834
☐ TGDR674 has 0 SNPs
☐ TGDR675 has 160 SNPs
TGDR674 has 0 non-overlaps
TGDR675 has 0 non-overlaps

DATA ANALYSIS: GENOTYPIC DATA SELECTION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1360
Phenotypes: 3
Genotypes: 24834
Environmental layers: 0

Filter By Genotypes
2 studies detected based on the trees you selected on the map
TGDR674 TGDR675
Overlapping genotypes: 24834

Insights

We analyzed 2 studies and discovered the following:
There are a total of 24834 SNP overlaps across all 2 studies
🔀 TGDR674 and TGDR675 have shared datasets

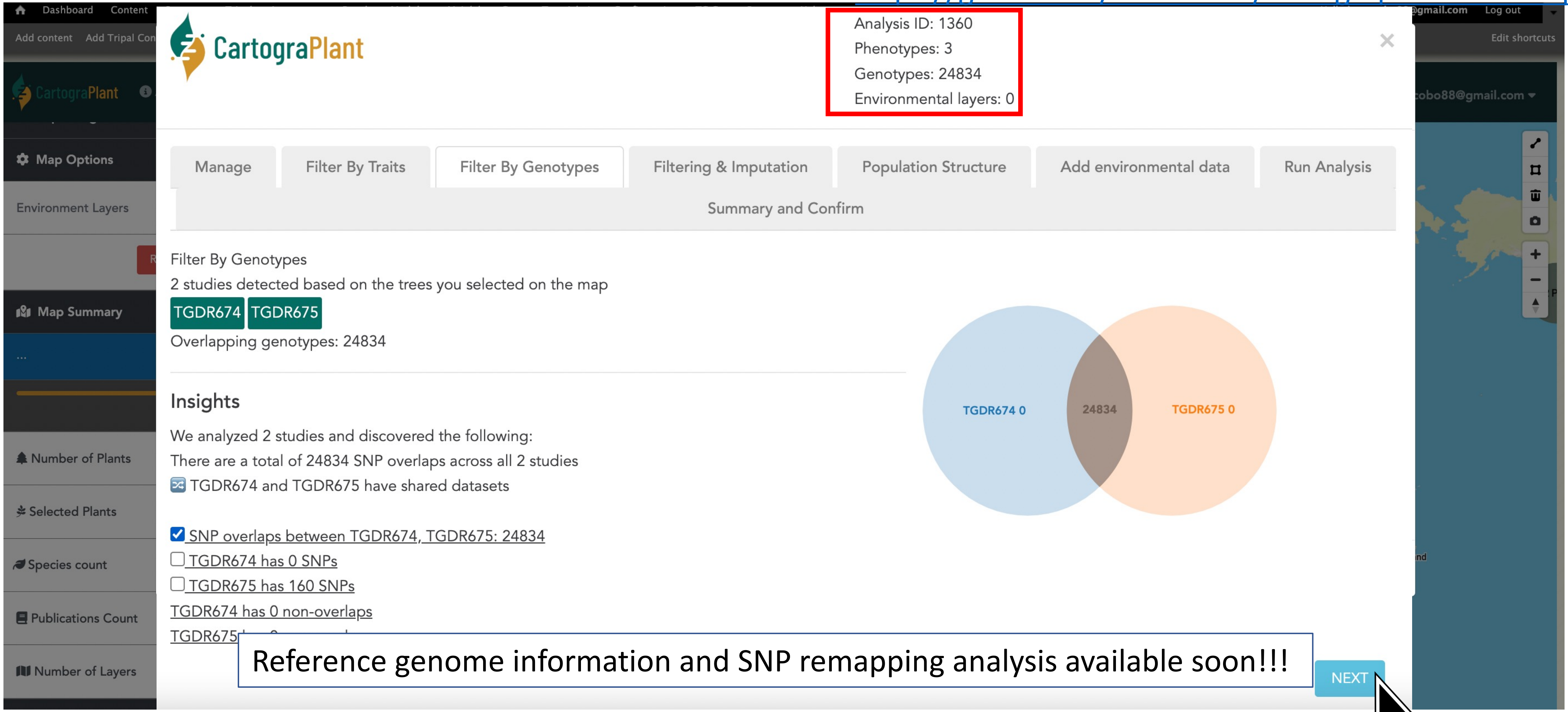
☑ SNP overlaps between TGDR674, TGDR675: 24834
☐ GDR674 has 0 SNPs
☐ R675 has 160 SNPs
TG 674 has 0 non-overlaps
TGDR675 has 0 non-overlaps

DATA ANALYSIS: GENOTYPIC DATA SELECTION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1360
Phenotypes: 3
Genotypes: 24834
Environmental layers: 0

Filter By Genotypes

2 studies detected based on the trees you selected on the map

TGDR674 TGDR675

Overlapping genotypes: 24834

Insights

We analyzed 2 studies and discovered the following:
There are a total of 24834 SNP overlaps across all 2 studies
TGDR674 and TGDR675 have shared datasets

☑ SNP overlaps between TGDR674, TGDR675: 24834
☐ TGDR674 has 0 SNPs
☐ TGDR675 has 160 SNPs
TGDR674 has 0 non-overlaps
TGDR675

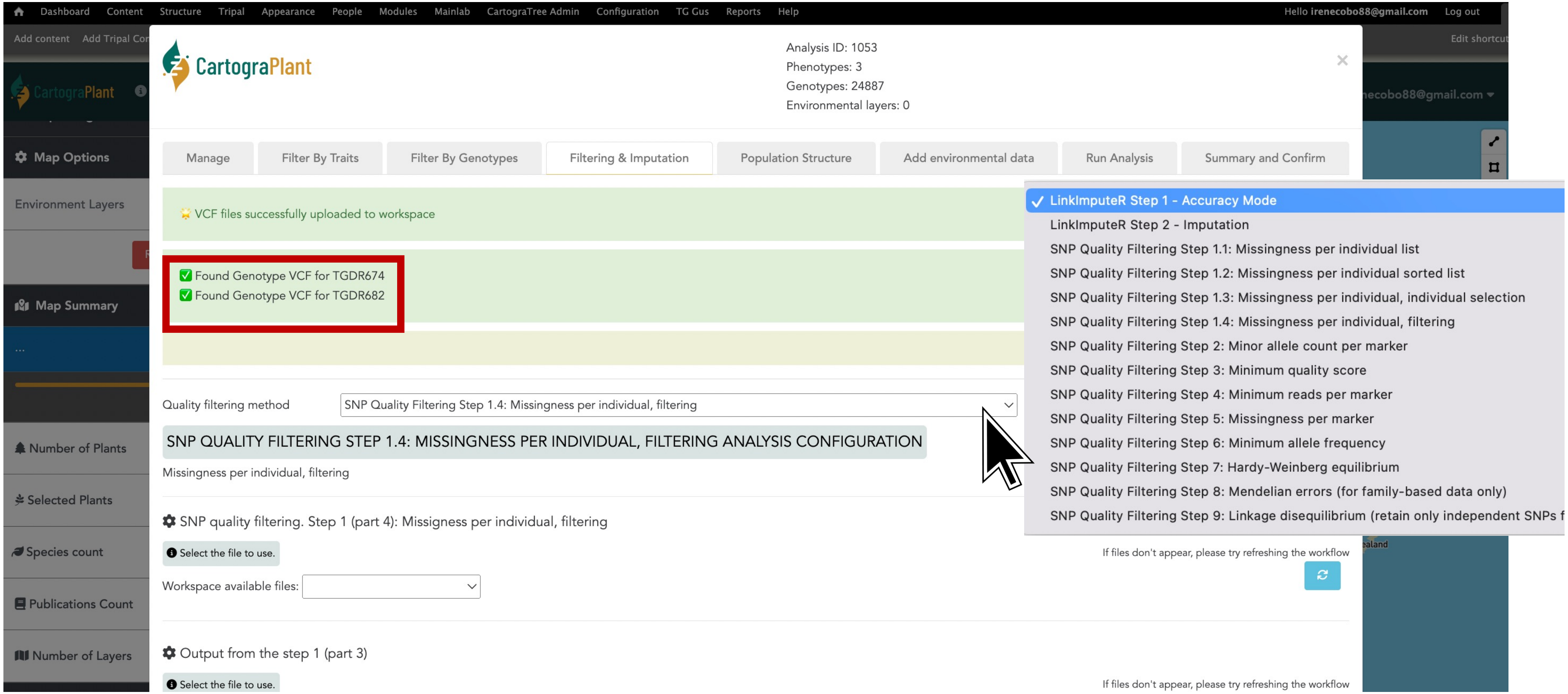
Reference genome information and SNP remapping analysis available soon!!!

DATA ANALYSIS: GENOTYPIC DATA SELECTION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

VCF files successfully uploaded to workspace

☑ Found Genotype VCF for TGDR674
☑ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 1.4: Missingness per individual, filtering

- ✓ LinkImputeR Step 1 - Accuracy Mode
- LinkImputeR Step 2 - Imputation
- SNP Quality Filtering Step 1.1: Missingness per individual list
- SNP Quality Filtering Step 1.2: Missingness per individual sorted list
- SNP Quality Filtering Step 1.3: Missingness per individual, individual selection
- SNP Quality Filtering Step 1.4: Missingness per individual, filtering
- SNP Quality Filtering Step 2: Minor allele count per marker
- SNP Quality Filtering Step 3: Minimum quality score
- SNP Quality Filtering Step 4: Minimum reads per marker
- SNP Quality Filtering Step 5: Missingness per marker
- SNP Quality Filtering Step 6: Minimum allele frequency
- SNP Quality Filtering Step 7: Hardy-Weinberg equilibrium
- SNP Quality Filtering Step 8: Mendelian errors (for family-based data only)
- SNP Quality Filtering Step 9: Linkage disequilibrium (retain only independent SNPs f

SNP QUALITY FILTERING STEP 1.4: MISSINGNESS PER INDIVIDUAL, FILTERING ANALYSIS CONFIGURATION

Missingness per individual, filtering

SNP quality filtering. Step 1 (part 4): Missigness per individual, filtering

Select the file to use.

If files don't appear, please try refreshing the workflow

Workspace available files:

Output from the step 1 (part 3)

Select the file to use.

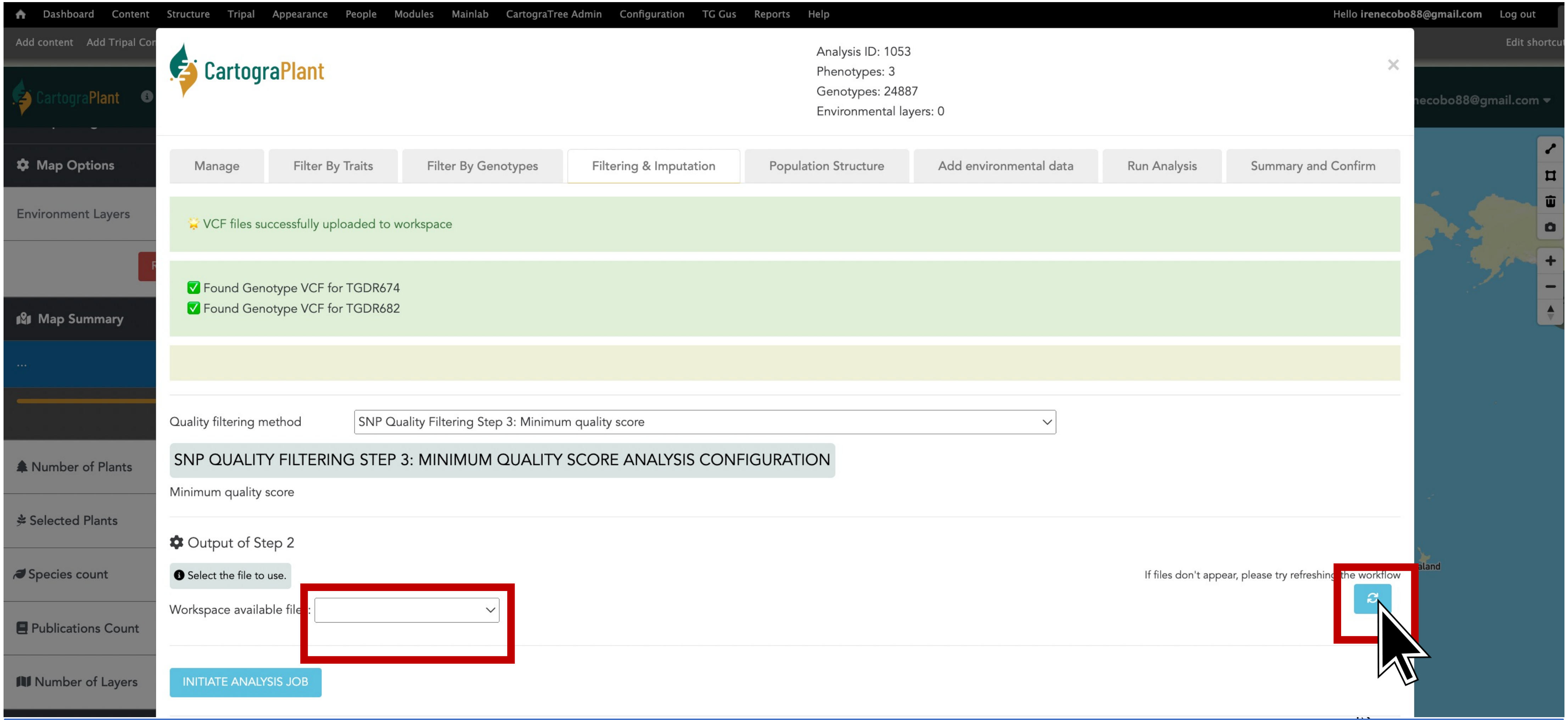
If files don't appear, please try refreshing the workflow

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 3: Minimum quality score

SNP QUALITY FILTERING STEP 3: MINIMUM QUALITY SCORE ANALYSIS CONFIGURATION

Minimum quality score

Output of Step 2

Select the file to use.

Workspace available file:

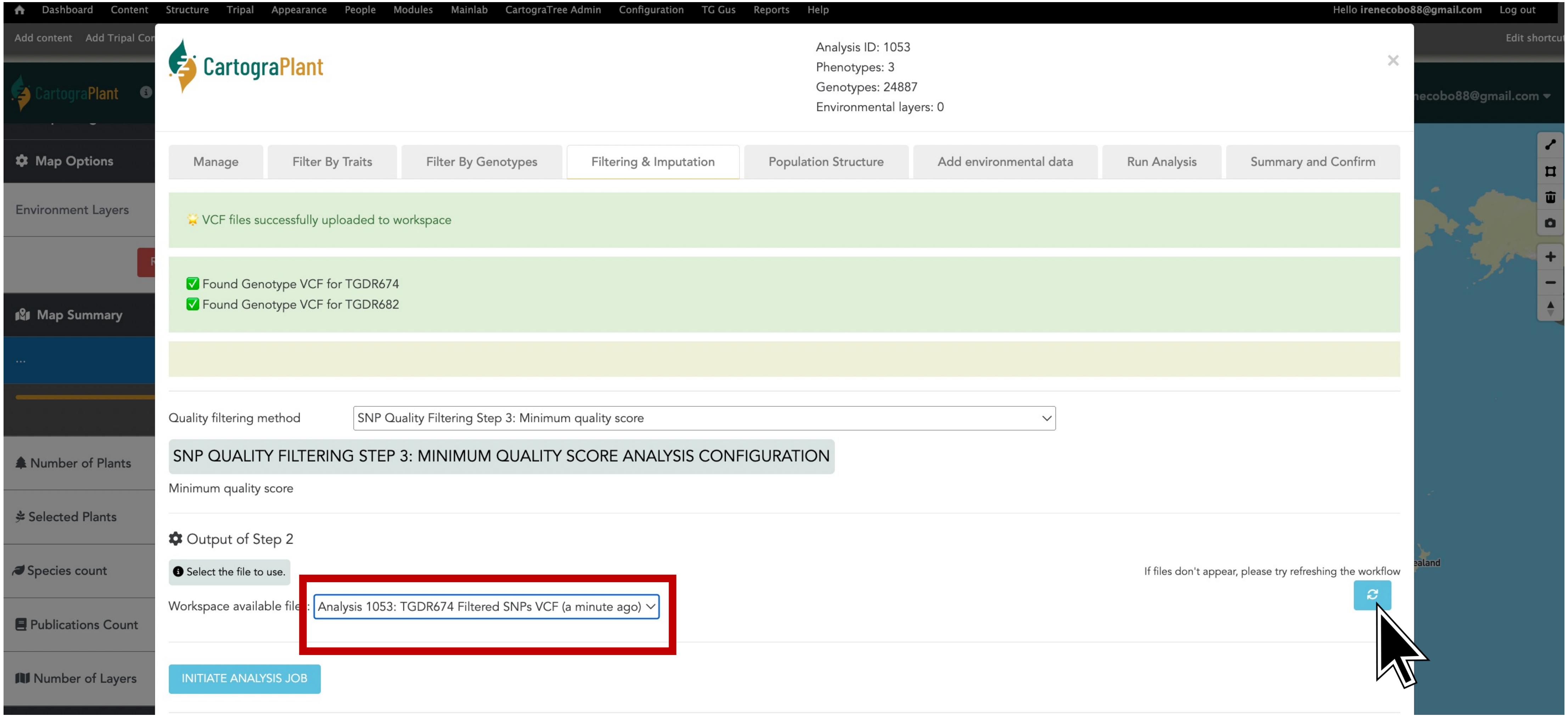
If files don't appear, please try refreshing the workflow

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 3: Minimum quality score

SNP QUALITY FILTERING STEP 3: MINIMUM QUALITY SCORE ANALYSIS CONFIGURATION

Minimum quality score

Output of Step 2

Select the file to use.

If files don't appear, please try refreshing the workflow

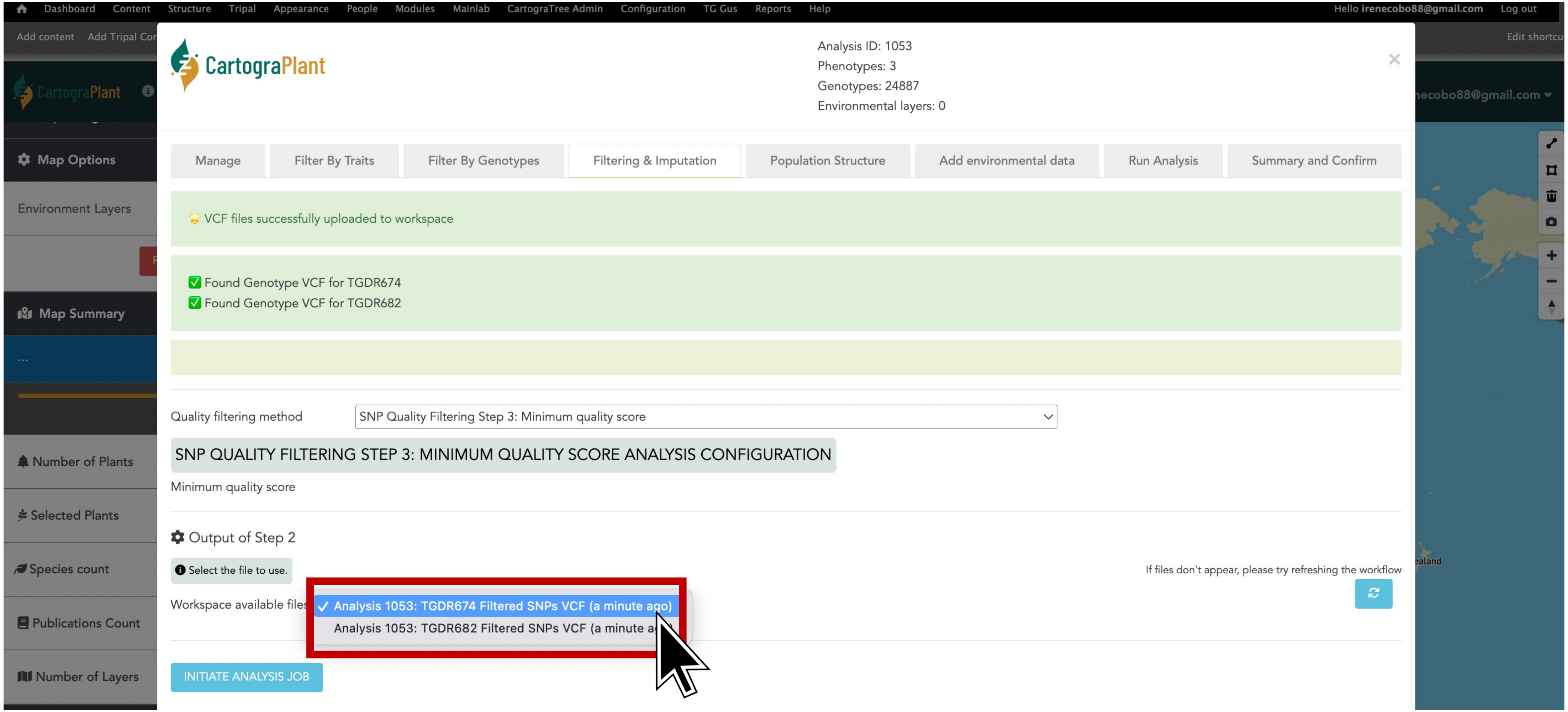
Workspace available files: Analysis 1053: TGDR674 Filtered SNPs VCF (a minute ago)

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 3: Minimum quality score

SNP QUALITY FILTERING STEP 3: MINIMUM QUALITY SCORE ANALYSIS CONFIGURATION

Minimum quality score

Output of Step 2

Select the file to use.

If files don't appear, please try refreshing the workflow

Workspace available files

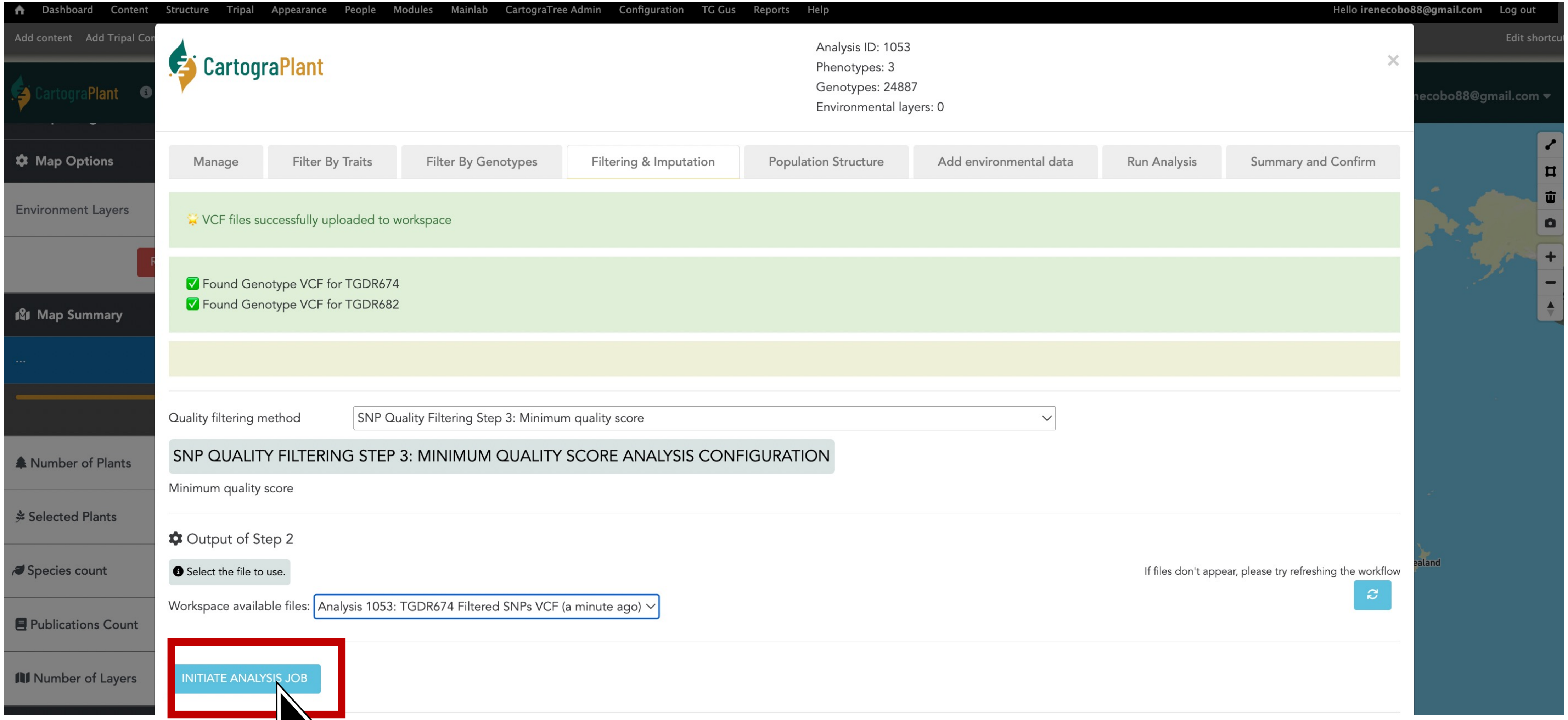
✓ Analysis 1053: TGDR674 Filtered SNPs VCF (a minute ago)
Analysis 1053: TGDR682 Filtered SNPs VCF (a minute a

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 3: Minimum quality score

SNP QUALITY FILTERING STEP 3: MINIMUM QUALITY SCORE ANALYSIS CONFIGURATION

Minimum quality score

Output of Step 2

Select the file to use.

If files don't appear, please try refreshing the workflow

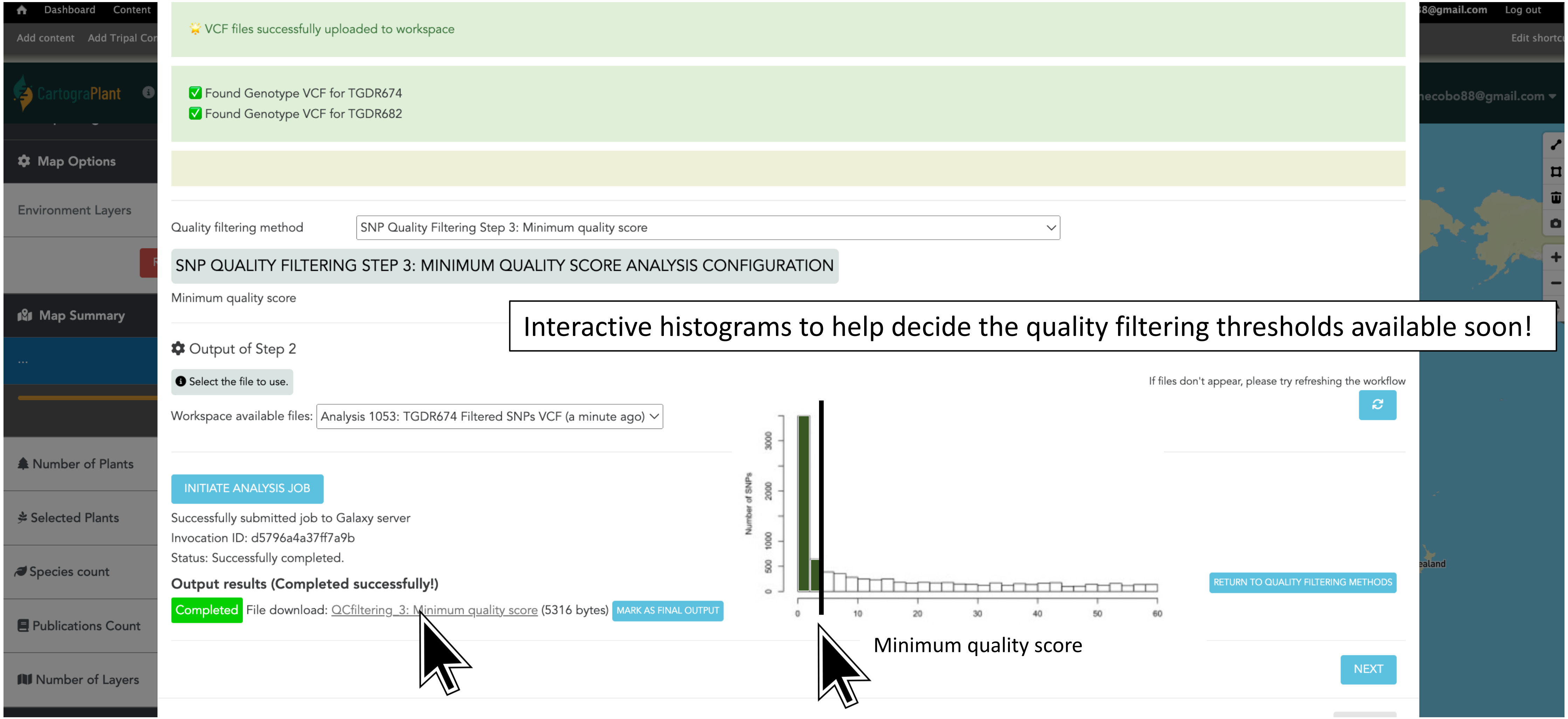
Workspace available files: Analysis 1053: TGDR674 Filtered SNPs VCF (a minute ago)

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



VCF files successfully uploaded to workspace

☑ Found Genotype VCF for TGDR674
☑ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 3: Minimum quality score

SNP QUALITY FILTERING STEP 3: MINIMUM QUALITY SCORE ANALYSIS CONFIGURATION

Minimum quality score

Interactive histograms to help decide the quality filtering thresholds available soon!

Output of Step 2

Select the file to use.

If files don't appear, please try refreshing the workflow

Workspace available files: Analysis 1053: TGDR674 Filtered SNPs VCF (a minute ago)

INITIATE ANALYSIS JOB

Successfully submitted job to Galaxy server
Invocation ID: d5796a4a37ff7a9b
Status: Successfully completed.

Output results (Completed successfully!)

Completed File download: QCfiltering_3: Minimum quality score (5316 bytes) MARK AS FINAL OUTPUT

RETURN TO QUALITY FILTERING METHODS

NEXT

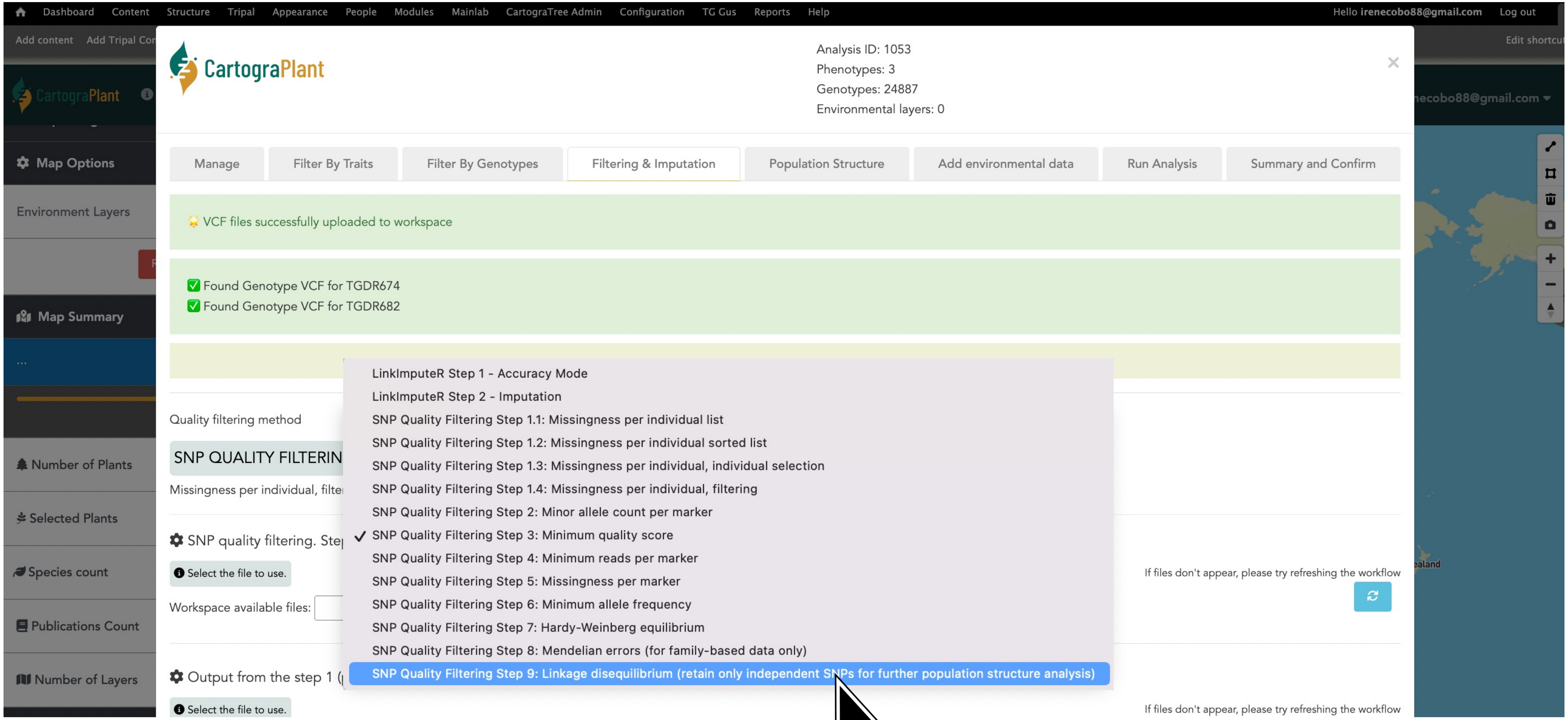
Minimum quality score

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method

SNP QUALITY FILTERIN

Missingness per individual, filte

SNP quality filtering. Ste

Select the file to use.

Workspace available files:

If files don't appear, please try refreshing the workflow

Output from the step 1 (

Select the file to use.

If files don't appear, please try refreshing the workflow

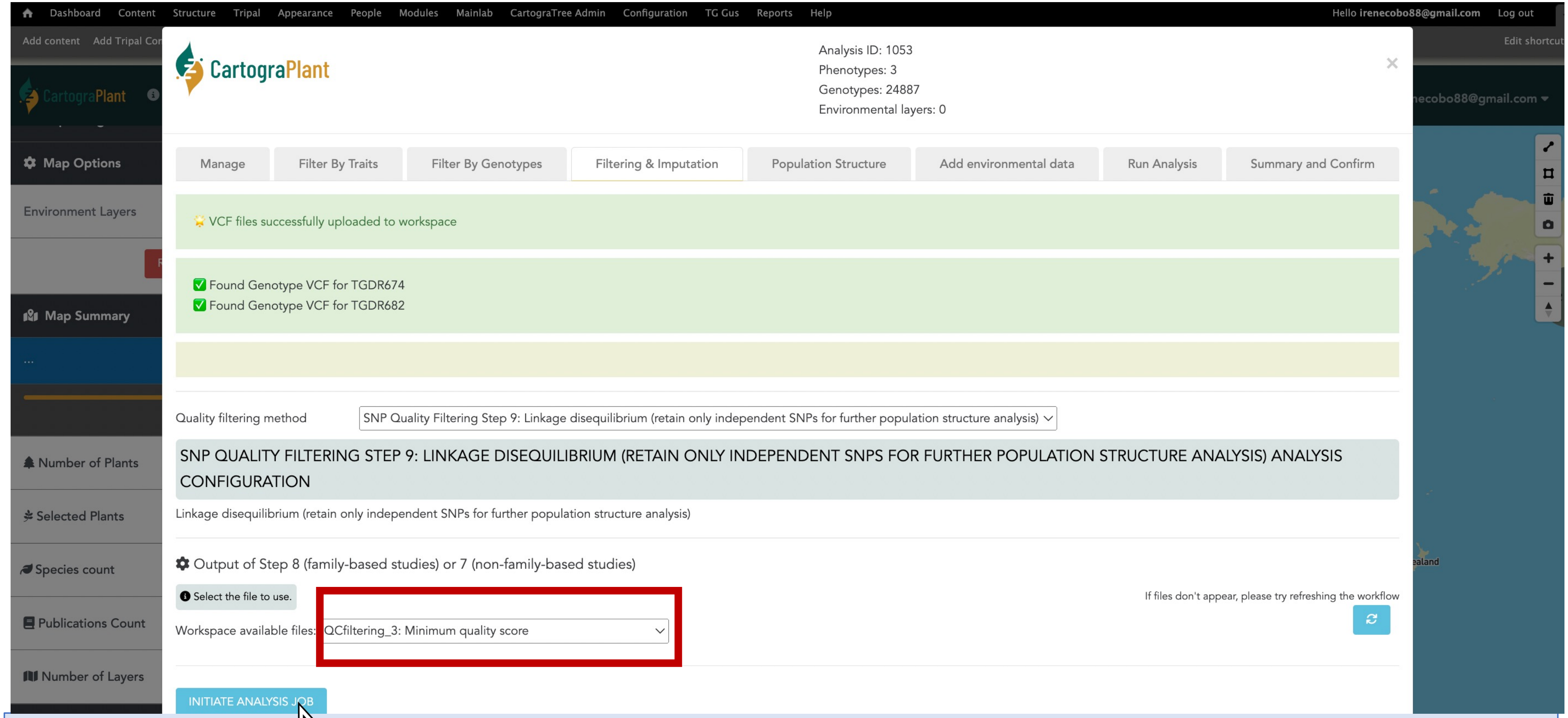
- LinkImputeR Step 1 - Accuracy Mode
- LinkImputeR Step 2 - Imputation
- SNP Quality Filtering Step 1.1: Missingness per individual list
- SNP Quality Filtering Step 1.2: Missingness per individual sorted list
- SNP Quality Filtering Step 1.3: Missingness per individual, individual selection
- SNP Quality Filtering Step 1.4: Missingness per individual, filtering
- SNP Quality Filtering Step 2: Minor allele count per marker
- ✓ SNP Quality Filtering Step 3: Minimum quality score
- SNP Quality Filtering Step 4: Minimum reads per marker
- SNP Quality Filtering Step 5: Missingness per marker
- SNP Quality Filtering Step 6: Minimum allele frequency
- SNP Quality Filtering Step 7: Hardy-Weinberg equilibrium
- SNP Quality Filtering Step 8: Mendelian errors (for family-based data only)
- SNP Quality Filtering Step 9: Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 9: Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

SNP QUALITY FILTERING STEP 9: LINKAGE DISEQUILIBRIUM (RETAIN ONLY INDEPENDENT SNPS FOR FURTHER POPULATION STRUCTURE ANALYSIS) ANALYSIS CONFIGURATION

Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

Output of Step 8 (family-based studies) or 7 (non-family-based studies)

Select the file to use.

If files don't appear, please try refreshing the workflow

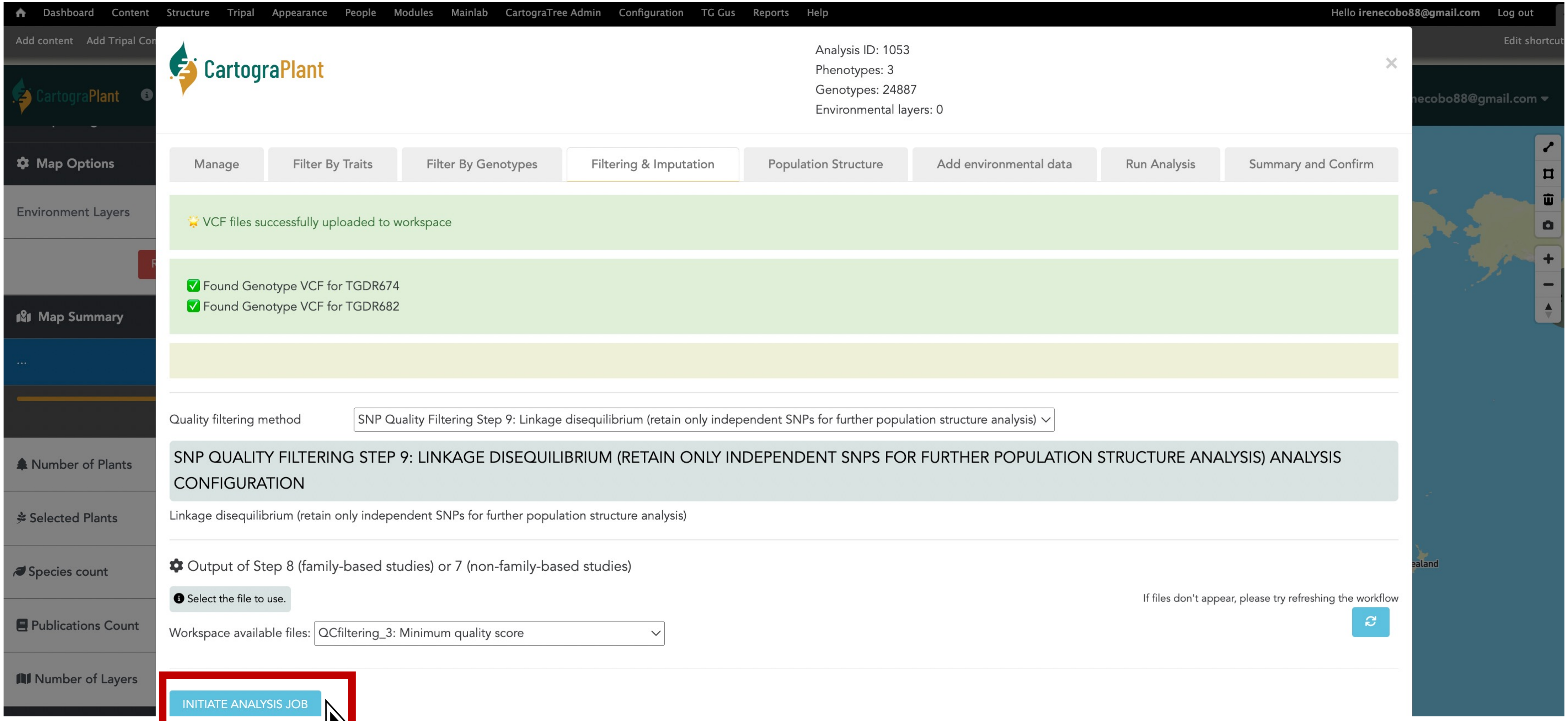
Workspace available files: QCfiltering_3: Minimum quality score

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 9: Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

SNP QUALITY FILTERING STEP 9: LINKAGE DISEQUILIBRIUM (RETAIN ONLY INDEPENDENT SNPS FOR FURTHER POPULATION STRUCTURE ANALYSIS) ANALYSIS CONFIGURATION

Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

Output of Step 8 (family-based studies) or 7 (non-family-based studies)

Select the file to use.

If files don't appear, please try refreshing the workflow

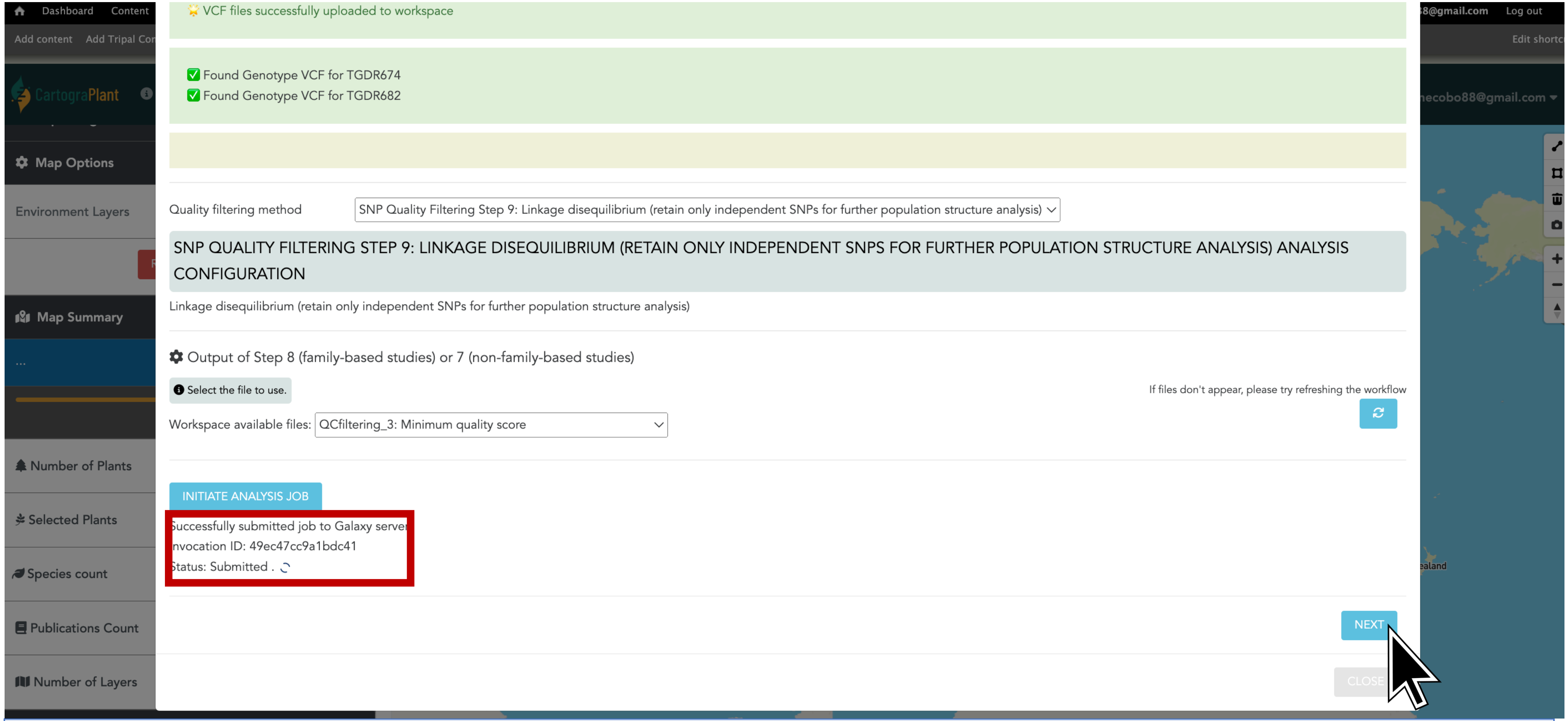
Workspace available files: QCfiltering_3: Minimum quality score

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 9: Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

SNP QUALITY FILTERING STEP 9: LINKAGE DISEQUILIBRIUM (RETAIN ONLY INDEPENDENT SNPS FOR FURTHER POPULATION STRUCTURE ANALYSIS) ANALYSIS CONFIGURATION

Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

Output of Step 8 (family-based studies) or 7 (non-family-based studies)

Select the file to use.

If files don't appear, please try refreshing the workflow

Workspace available files: QCfiltering_3: Minimum quality score

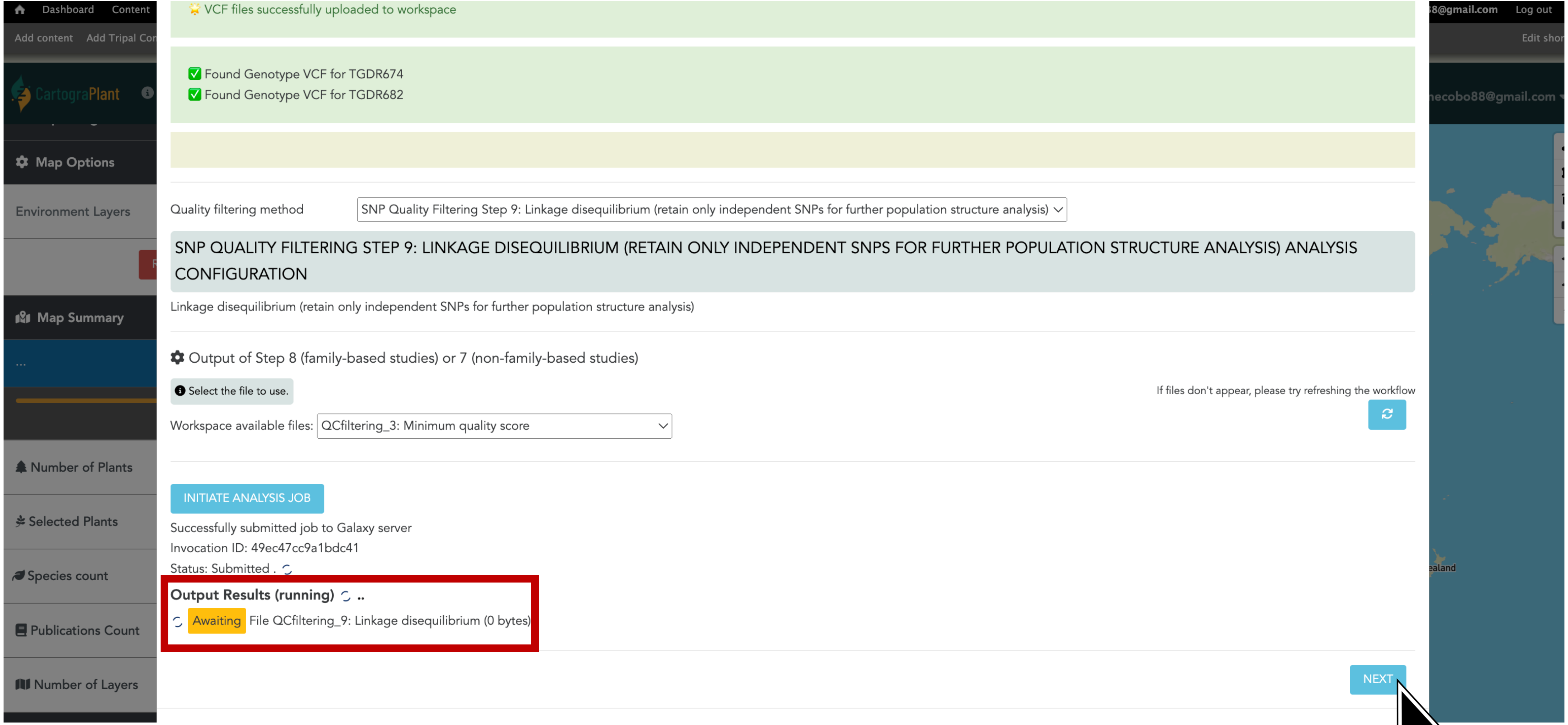
uccessfully submitted job to Galaxy serve
nvocation ID: 49ec47cc9a1bdc41
tatus: Submitted .

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



VCF files successfully uploaded to workspace

✅ Found Genotype VCF for TGDR674
✅ Found Genotype VCF for TGDR682

Quality filtering method: SNP Quality Filtering Step 9: Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

SNP QUALITY FILTERING STEP 9: LINKAGE DISEQUILIBRIUM (RETAIN ONLY INDEPENDENT SNPS FOR FURTHER POPULATION STRUCTURE ANALYSIS) ANALYSIS CONFIGURATION

Linkage disequilibrium (retain only independent SNPs for further population structure analysis)

Output of Step 8 (family-based studies) or 7 (non-family-based studies)

Select the file to use.

If files don't appear, please try refreshing the workflow

Workspace available files: QCfiltering_3: Minimum quality score

Successfully submitted job to Galaxy server
Invocation ID: 49ec47cc9a1bdc41
Status: Submitted .

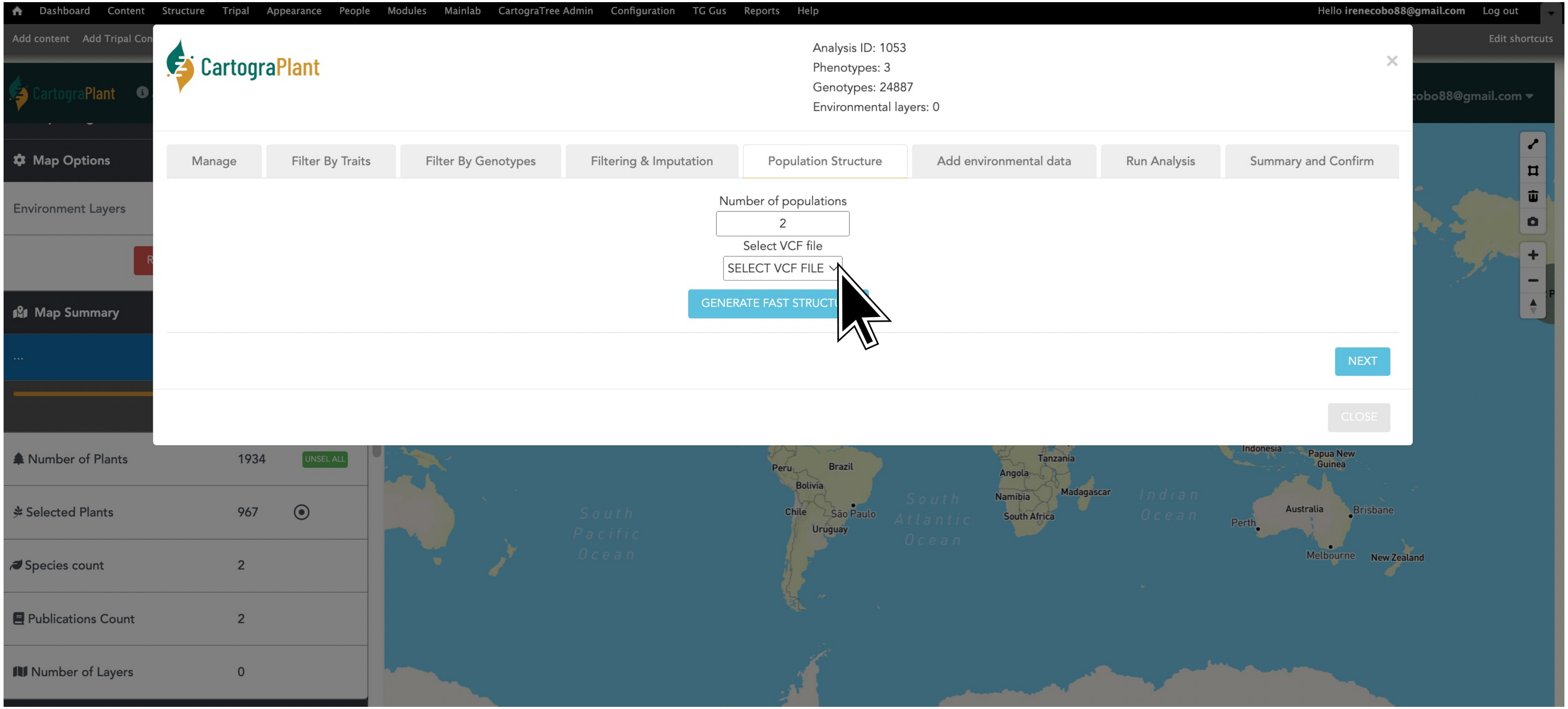
Output Results (running) ..
Awaiting File QCfiltering_9: Linkage disequilibrium (0 bytes)

DATA ANALYSIS: QUALITY FILTERING AND SNP IMPUTATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

Number of populations: 2

Select VCF file: SELECT VCF FILE

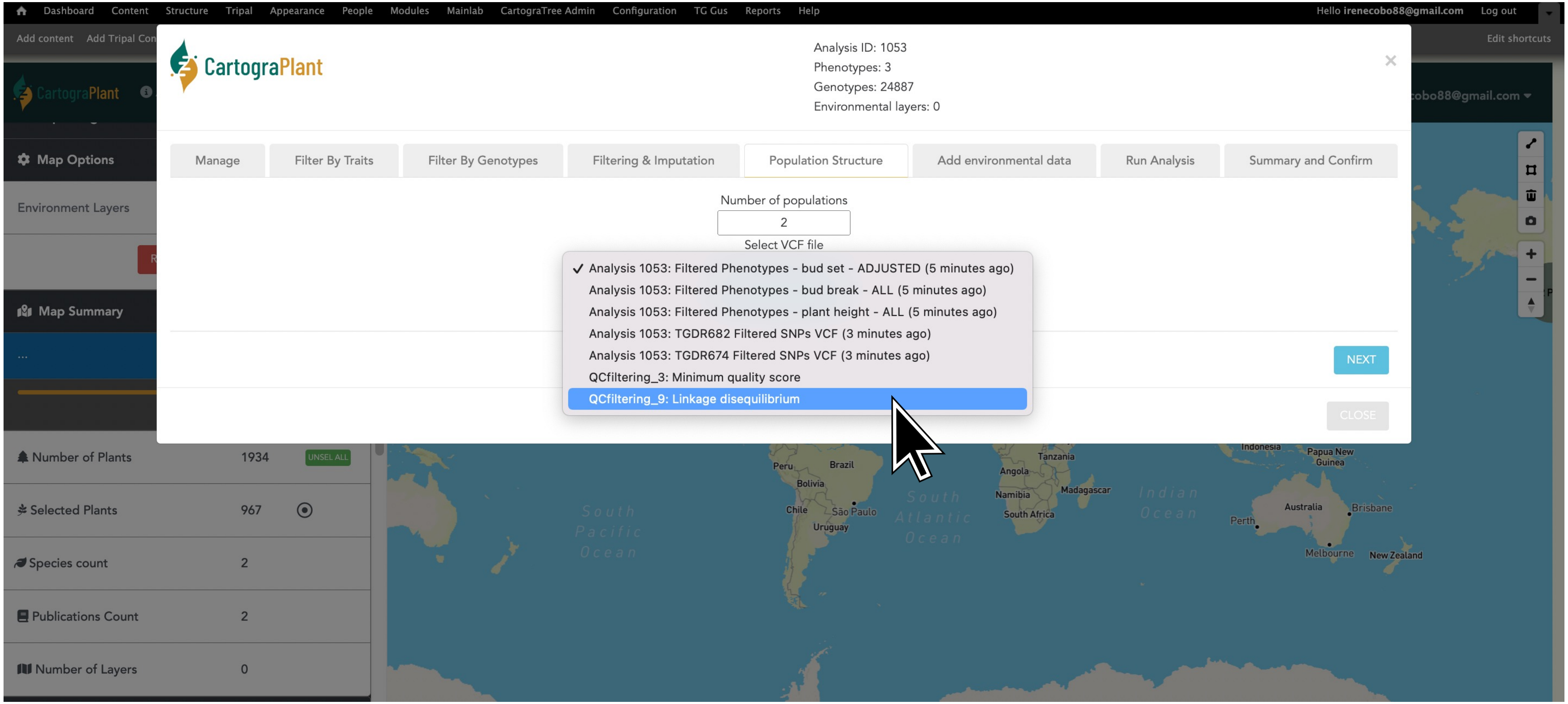
Number of Plants	1934	
Selected Plants	967	
Species count	2	
Publications Count	2	
Number of Layers	0	

DATA ANALYSIS: POPULATION STRUCTURE CALCULATION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

Number of populations: 2

Select VCF file

- ✓ Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (5 minutes ago)
- Analysis 1053: Filtered Phenotypes - bud break - ALL (5 minutes ago)
- Analysis 1053: Filtered Phenotypes - plant height - ALL (5 minutes ago)
- Analysis 1053: TGDR682 Filtered SNPs VCF (3 minutes ago)
- Analysis 1053: TGDR674 Filtered SNPs VCF (3 minutes ago)
- QCfiltering_3: Minimum quality score
- QCfiltering_9: Linkage disequilibrium

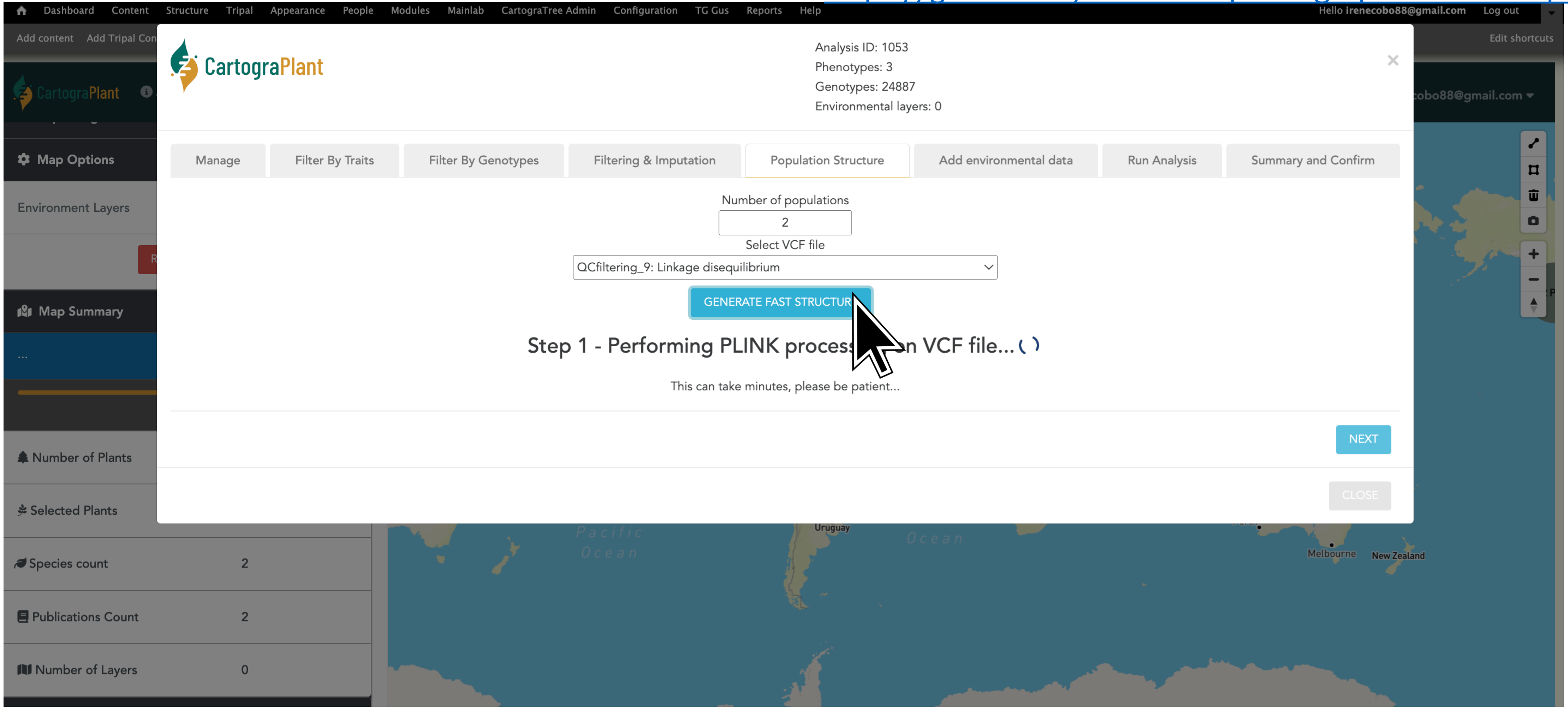
Number of Plants	1934	
Selected Plants	967	
Species count	2	
Publications Count	2	
Number of Layers	0	

DATA ANALYSIS: POPULATION STRUCTURE CALCULATION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

Number of populations: 2

Select VCF file: QCfiltering_9: Linkage disequilibrium

Step 1 - Performing PLINK process n VCF file...

This can take minutes, please be patient...

Number of Plants

Selected Plants

Species count: 2

Publications Count: 2

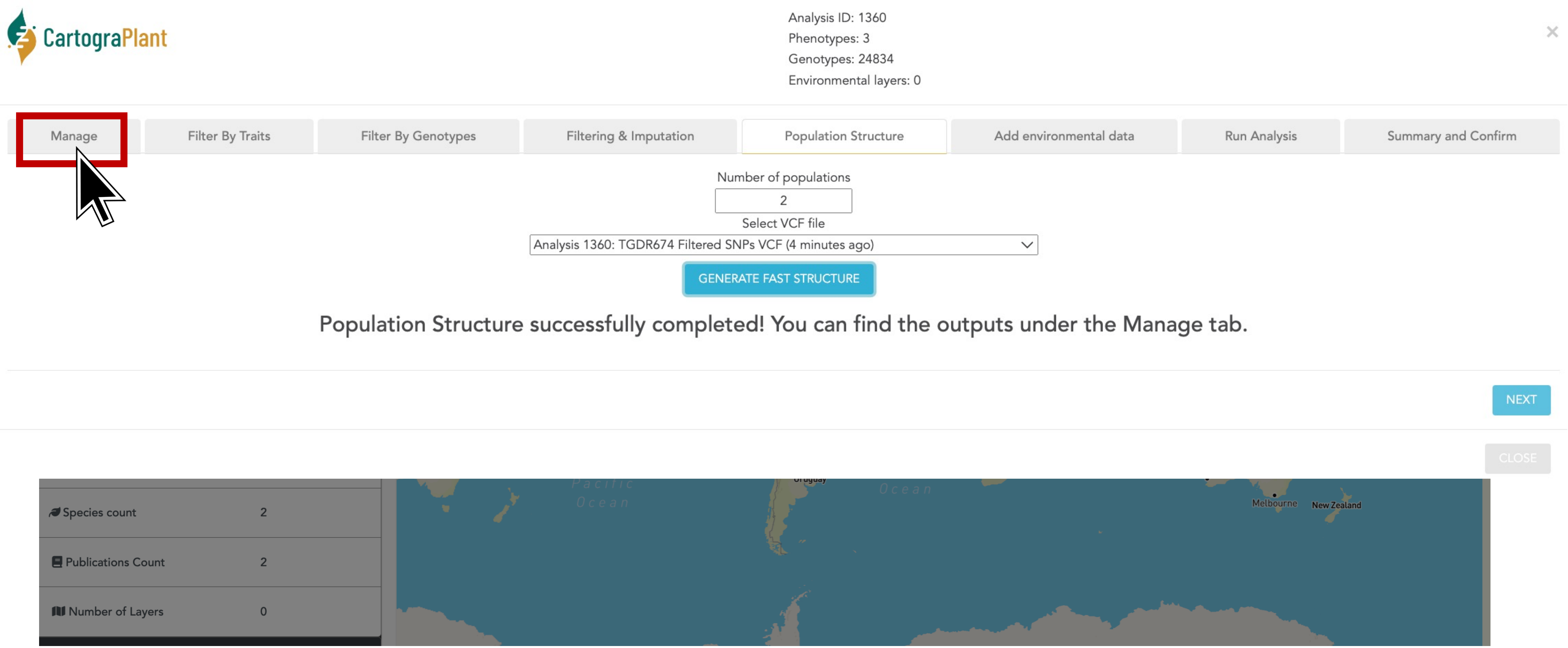
Number of Layers: 0

DATA ANALYSIS: POPULATION STRUCTURE CALCULATION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1360
Phenotypes: 3
Genotypes: 24834
Environmental layers: 0

Number of populations: 2

Select VCF file: Analysis 1360: TGDR674 Filtered SNPs VCF (4 minutes ago)

Population Structure successfully completed! You can find the outputs under the Manage tab.

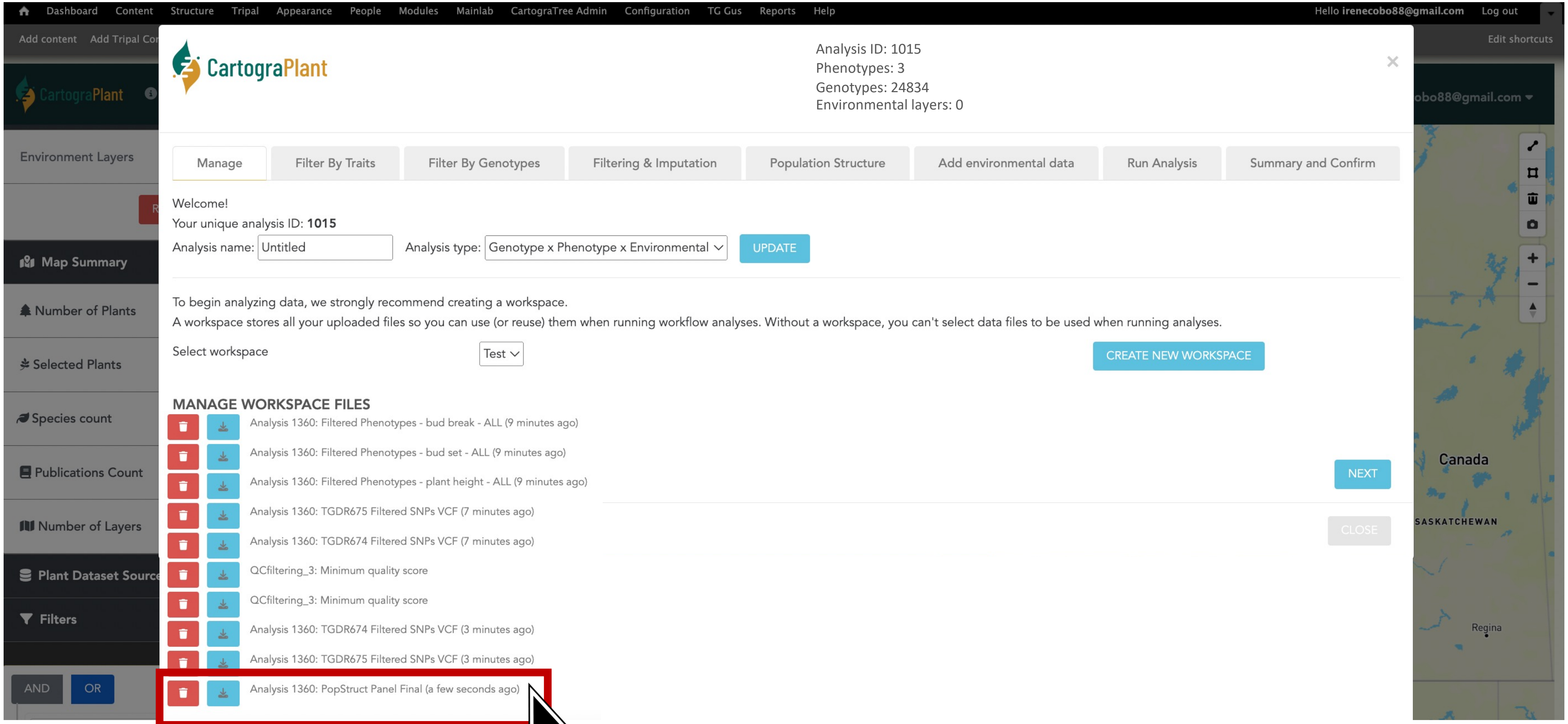
Species count	2
Publications Count	2
Number of Layers	0

DATA ANALYSIS: POPULATION STRUCTURE CALCULATION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1015
Phenotypes: 3
Genotypes: 24834
Environmental layers: 0

Welcome!
Your unique analysis ID: **1015**

Analysis name: Untitled
Analysis type: Genotype x Phenotype x Environmental

To begin analyzing data, we strongly recommend creating a workspace.
A workspace stores all your uploaded files so you can use (or reuse) them when running workflow analyses. Without a workspace, you can't select data files to be used when running analyses.

Select workspace: Test

MANAGE WORKSPACE FILES

- Analysis 1360: Filtered Phenotypes - bud break - ALL (9 minutes ago)
- Analysis 1360: Filtered Phenotypes - bud set - ALL (9 minutes ago)
- Analysis 1360: Filtered Phenotypes - plant height - ALL (9 minutes ago)
- Analysis 1360: TGDR675 Filtered SNPs VCF (7 minutes ago)
- Analysis 1360: TGDR674 Filtered SNPs VCF (7 minutes ago)
- QCfiltering_3: Minimum quality score
- QCfiltering_3: Minimum quality score
- Analysis 1360: TGDR674 Filtered SNPs VCF (3 minutes ago)
- Analysis 1360: TGDR675 Filtered SNPs VCF (3 minutes ago)
- Analysis 1360: PopStruct Panel Final (a few seconds ago)

DATA ANALYSIS: WORKSPACE CREATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/

Analysis ID: 1015
Phenotypes: 3
Genotypes: 24834
Environmental layers: 0

Study Accession
equal
TGDR725

Number of populations
2

Select VCF file
Analysis 1016: TGDR725 Filtered SNPs VCF (14 minutes ago)

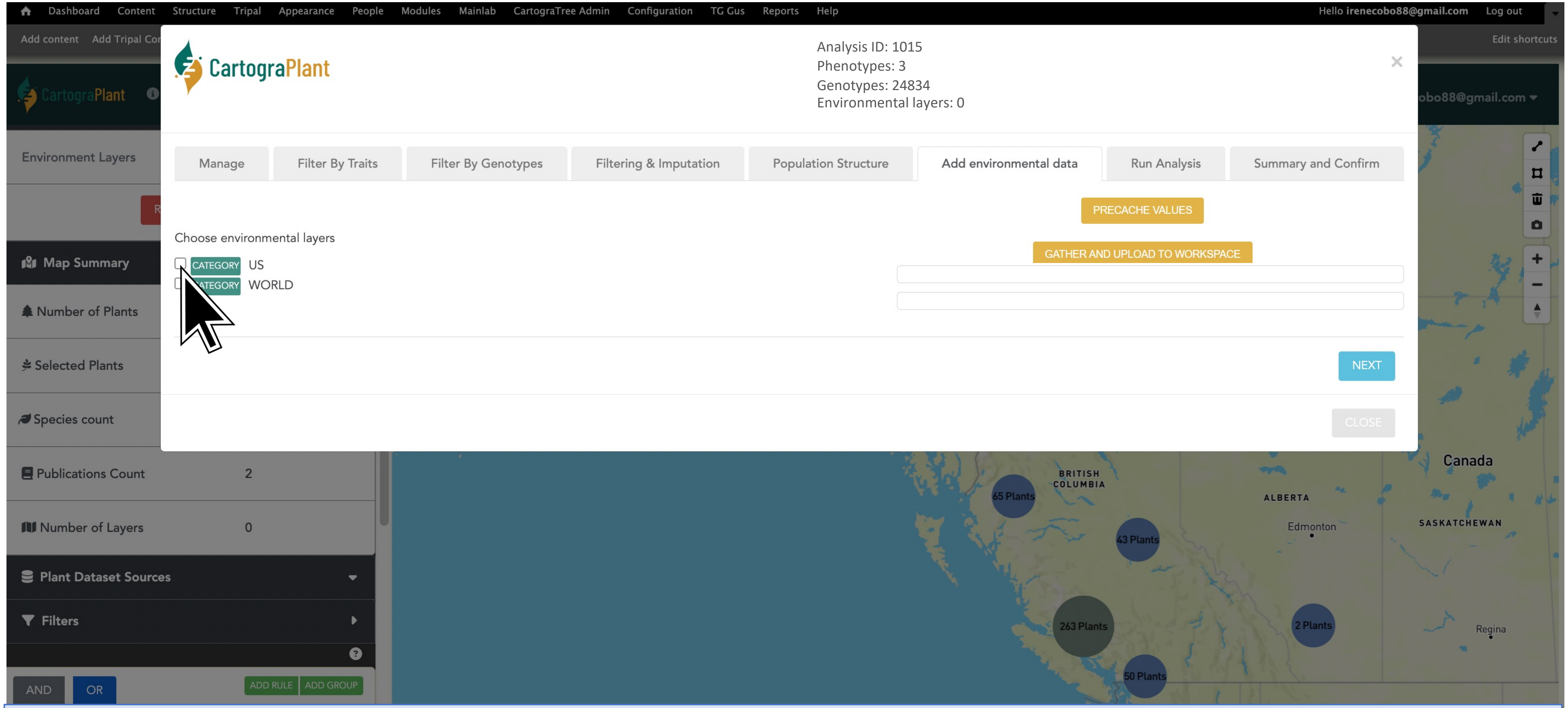
Population structure calculation (PCA) and visualization (fastSTRUCTURE, PCA) available soon!!!

DATA ANALYSIS: POPULATION STRUCTURE CALCULATION/VISUALIZATION

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1015
Phenotypes: 3
Genotypes: 24834
Environmental layers: 0

Choose environmental layers

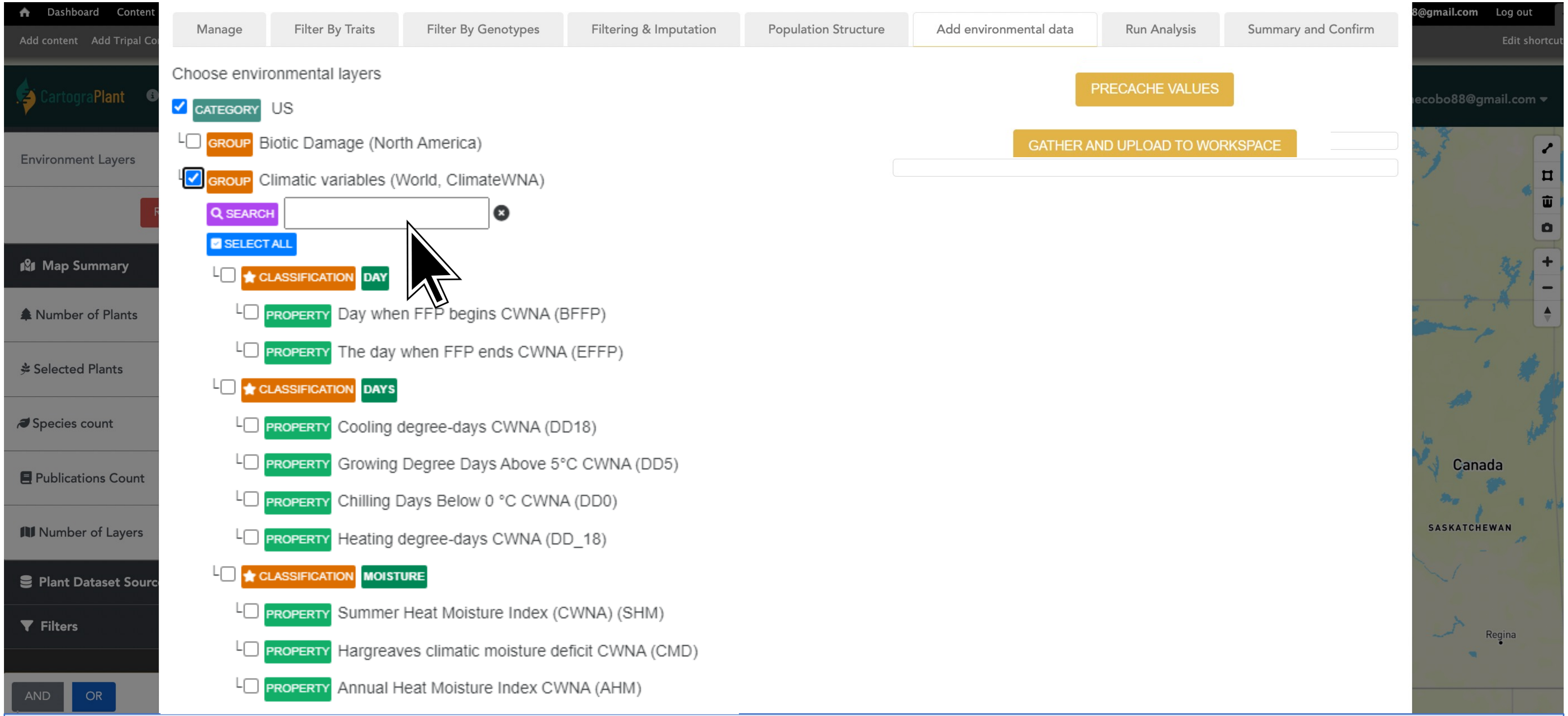
☐ CATEGORY US
☐ CATEGORY WORLD

DATA ANALYSIS: ENVIRONMENTAL DATA SELECTION/ MULTICOLLINEARITY

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Choose environmental layers

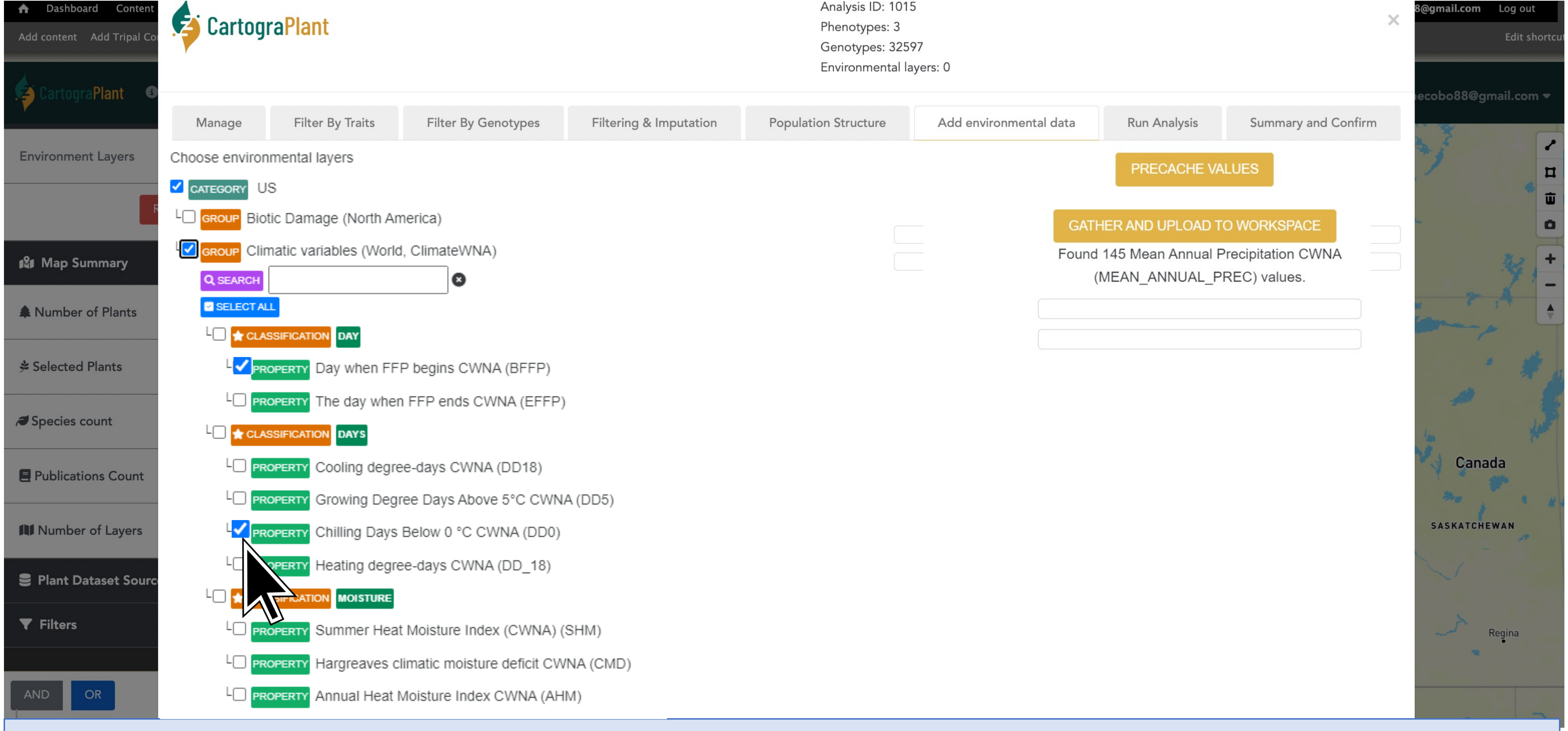
- ☑ CATEGORY US
  - ☐ GROUP Biotic Damage (North America)
  - ☑ GROUP Climatic variables (World, ClimateWNA)
    - ☐ CLASSIFICATION DAY
      - ☐ PROPERTY Day when FFP begins CWNA (BFFP)
      - ☐ PROPERTY The day when FFP ends CWNA (EFFP)
    - ☐ CLASSIFICATION DAYS
      - ☐ PROPERTY Cooling degree-days CWNA (DD18)
      - ☐ PROPERTY Growing Degree Days Above 5°C CWNA (DD5)
      - ☐ PROPERTY Chilling Days Below 0 °C CWNA (DD0)
      - ☐ PROPERTY Heating degree-days CWNA (DD_18)
    - ☐ CLASSIFICATION MOISTURE
      - ☐ PROPERTY Summer Heat Moisture Index (CWNA) (SHM)
      - ☐ PROPERTY Hargreaves climatic moisture deficit CWNA (CMD)
      - ☐ PROPERTY Annual Heat Moisture Index CWNA (AHM)

DATA ANALYSIS: ENVIRONMENTAL DATA SELECTION/ MULTICOLLINEARITY

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1015
Phenotypes: 3
Genotypes: 32597
Environmental layers: 0

Choose environmental layers

☑ CATEGORY US
- ☐ GROUP Biotic Damage (North America)
- ☑ GROUP Climatic variables (World, ClimateWNA)
  - ☐ CLASSIFICATION DAY
    - ☑ PROPERTY Day when FFP begins CWNA (BFFP)
    - ☐ PROPERTY The day when FFP ends CWNA (EFFP)
  - ☐ CLASSIFICATION DAYS
    - ☐ PROPERTY Cooling degree-days CWNA (DD18)
    - ☐ PROPERTY Growing Degree Days Above 5°C CWNA (DD5)
    - ☑ PROPERTY Chilling Days Below 0 °C CWNA (DD0)
    - ☐ PROPERTY Heating degree-days CWNA (DD_18)
  - ☐ CLASSIFICATION MOISTURE
    - ☐ PROPERTY Summer Heat Moisture Index (CWNA) (SHM)
    - ☐ PROPERTY Hargreaves climatic moisture deficit CWNA (CMD)
    - ☐ PROPERTY Annual Heat Moisture Index CWNA (AHM)

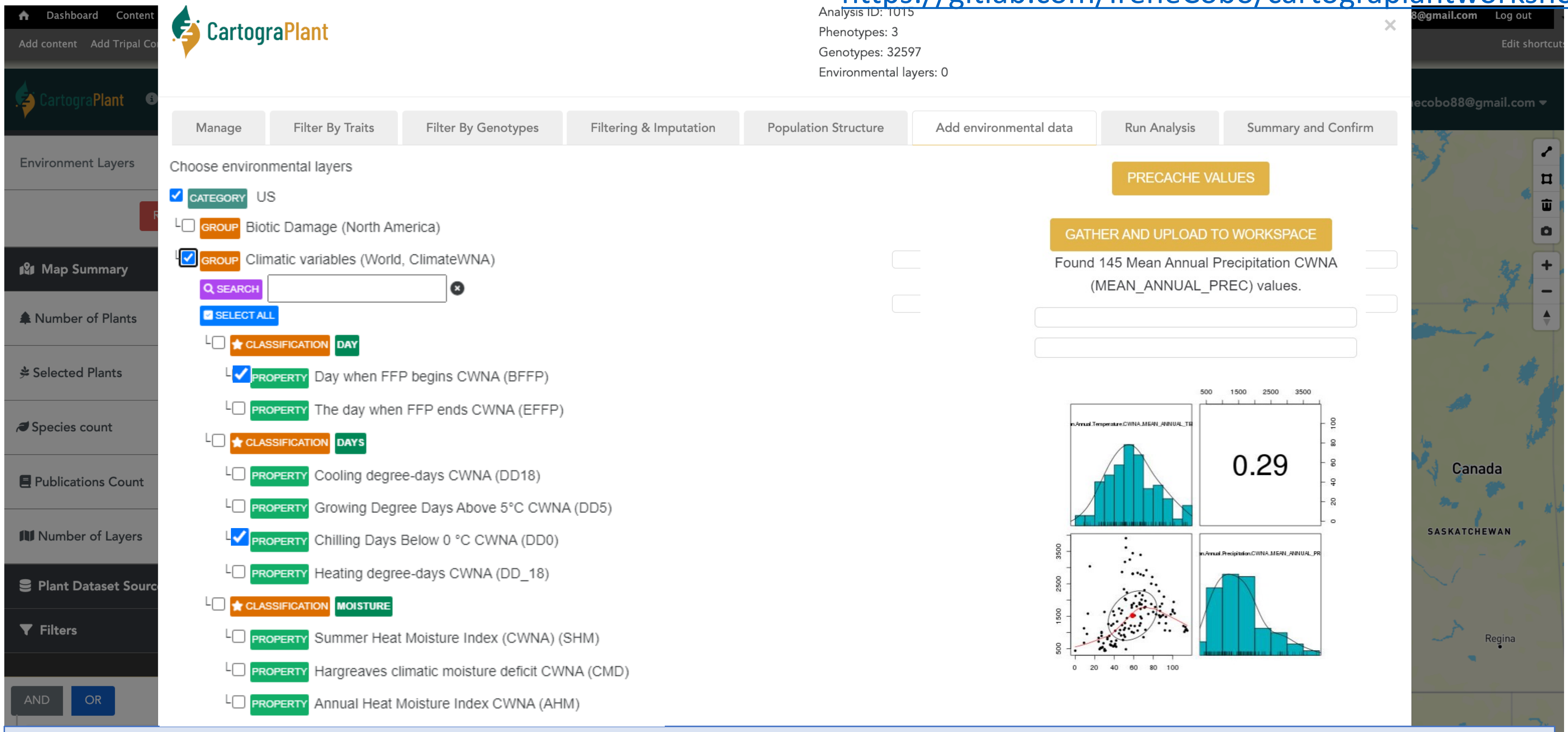
Found 145 Mean Annual Precipitation CWNA (MEAN_ANNUAL_PREC) values.

DATA ANALYSIS: ENVIRONMENTAL DATA SELECTION/ MULTICOLLINEARITY

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1015
Phenotypes: 3
Genotypes: 32597
Environmental layers: 0

Choose environmental layers

- ☑ CATEGORY US
  - ☐ GROUP Biotic Damage (North America)
  - ☑ GROUP Climatic variables (World, ClimateWNA)
    - ☐ CLASSIFICATION DAY
      - ☑ PROPERTY Day when FFP begins CWNA (BFFP)
      - ☐ PROPERTY The day when FFP ends CWNA (EFFP)
    - ☐ CLASSIFICATION DAYS
      - ☐ PROPERTY Cooling degree-days CWNA (DD18)
      - ☐ PROPERTY Growing Degree Days Above 5°C CWNA (DD5)
      - ☑ PROPERTY Chilling Days Below 0 °C CWNA (DD0)
      - ☐ PROPERTY Heating degree-days CWNA (DD_18)
    - ☐ CLASSIFICATION MOISTURE
      - ☐ PROPERTY Summer Heat Moisture Index (CWNA) (SHM)
      - ☐ PROPERTY Hargreaves climatic moisture deficit CWNA (CMD)
      - ☐ PROPERTY Annual Heat Moisture Index CWNA (AHM)

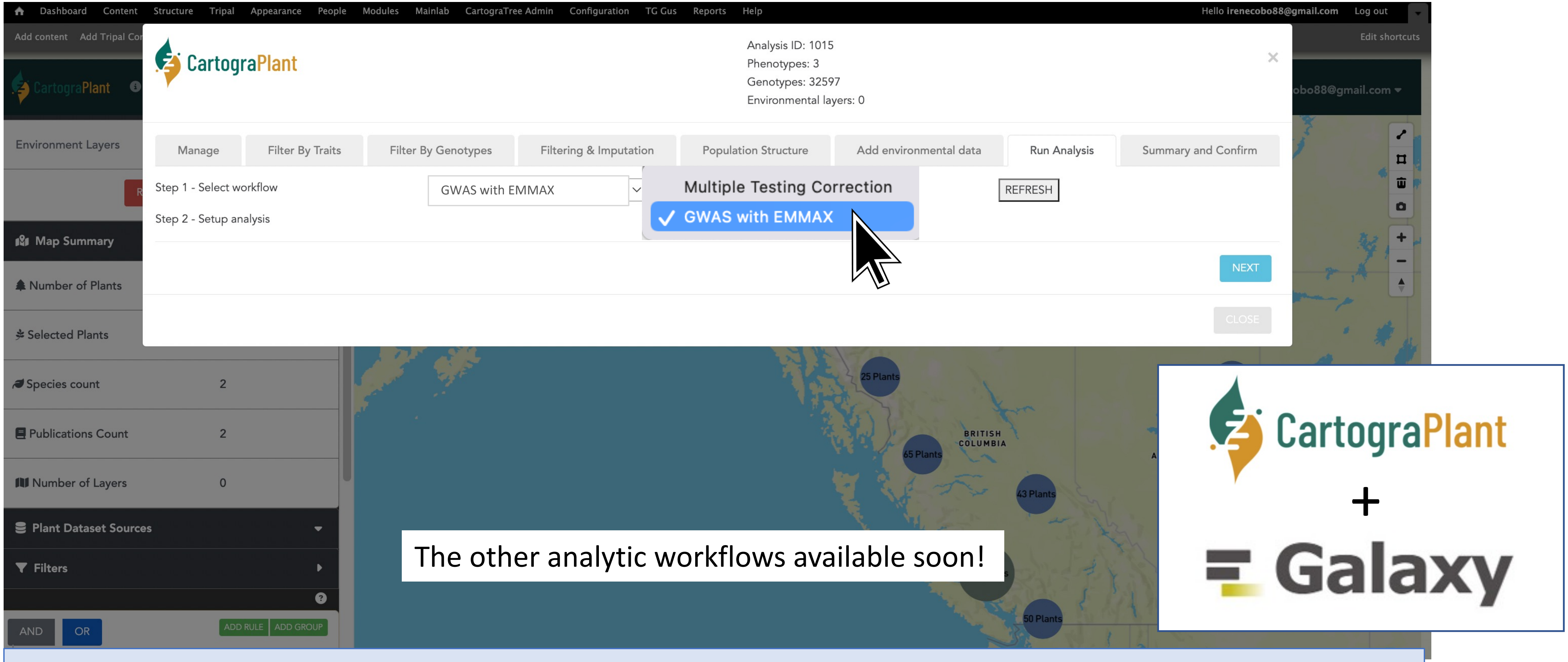
Found 145 Mean Annual Precipitation CWNA (MEAN_ANNUAL_PREC) values.

DATA ANALYSIS: ENVIRONMENTAL DATA SELECTION/ MULTICOLLINEARITY

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1015
Phenotypes: 3
Genotypes: 32597
Environmental layers: 0

Step 1 - Select workflow: GWAS with EMMAX

Step 2 - Setup analysis

Species count: 2
Publications Count: 2
Number of Layers: 0

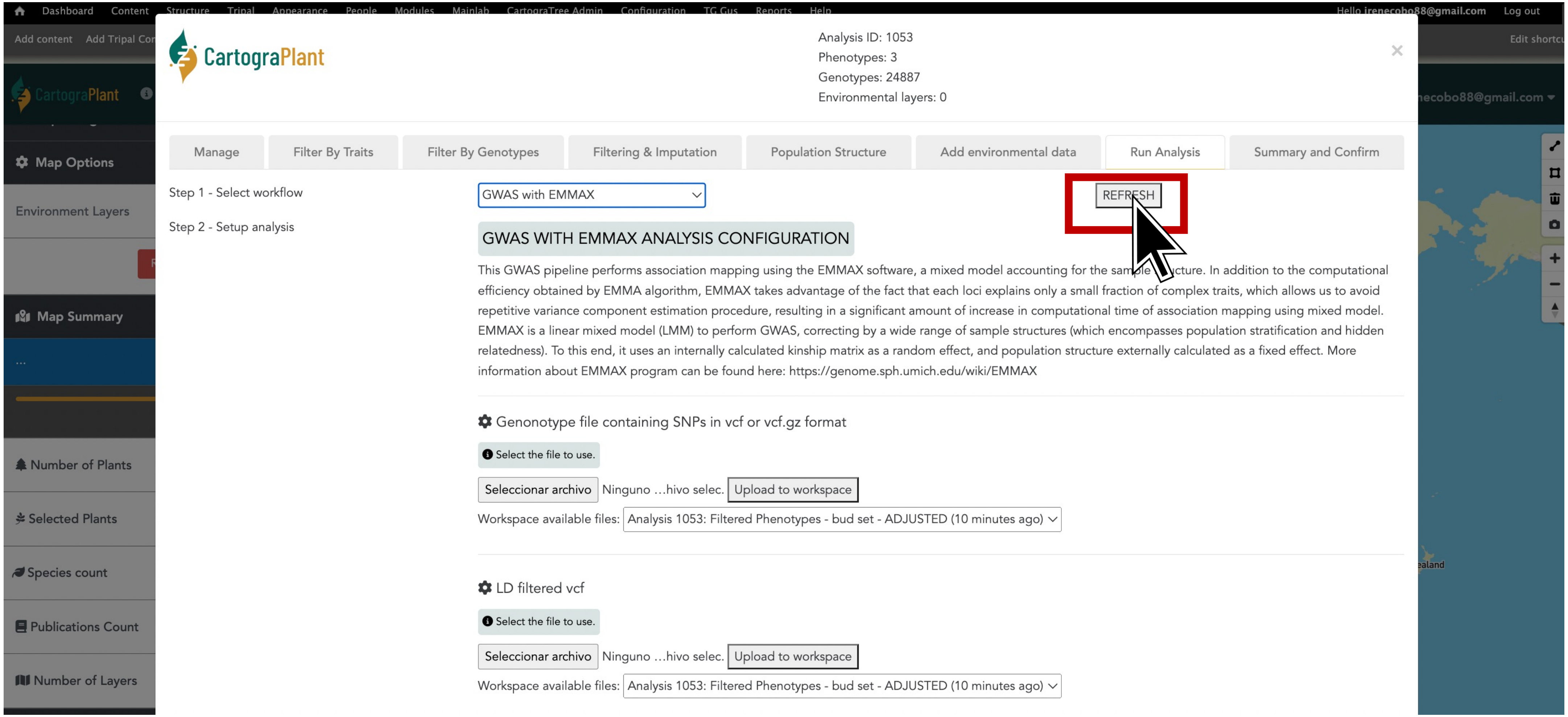
The other analytic workflows available soon!

DATA ANALYSIS: SELECT/RUN ANALYTIC WORKFLOWS

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Analysis ID: 1053
Phenotypes: 3
Genotypes: 24887
Environmental layers: 0

Step 1 - Select workflow: GWAS with EMMAX

Step 2 - Setup analysis

GWAS WITH EMMAX ANALYSIS CONFIGURATION

This GWAS pipeline performs association mapping using the EMMAX software, a mixed model accounting for the sample structure. In addition to the computational efficiency obtained by EMMA algorithm, EMMAX takes advantage of the fact that each loci explains only a small fraction of complex traits, which allows us to avoid repetitive variance component estimation procedure, resulting in a significant amount of increase in computational time of association mapping using mixed model. EMMAX is a linear mixed model (LMM) to perform GWAS, correcting by a wide range of sample structures (which encompasses population stratification and hidden relatedness). To this end, it uses an internally calculated kinship matrix as a random effect, and population structure externally calculated as a fixed effect. More information about EMMAX program can be found here: https://genome.sph.umich.edu/wiki/EMMAX

Genonotype file containing SNPs in vcf or vcf.gz format

Select the file to use.

Ninguno ...hivo selec.

Workspace available files: Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (10 minutes ago)

LD filtered vcf

Select the file to use.

Ninguno ...hivo selec.

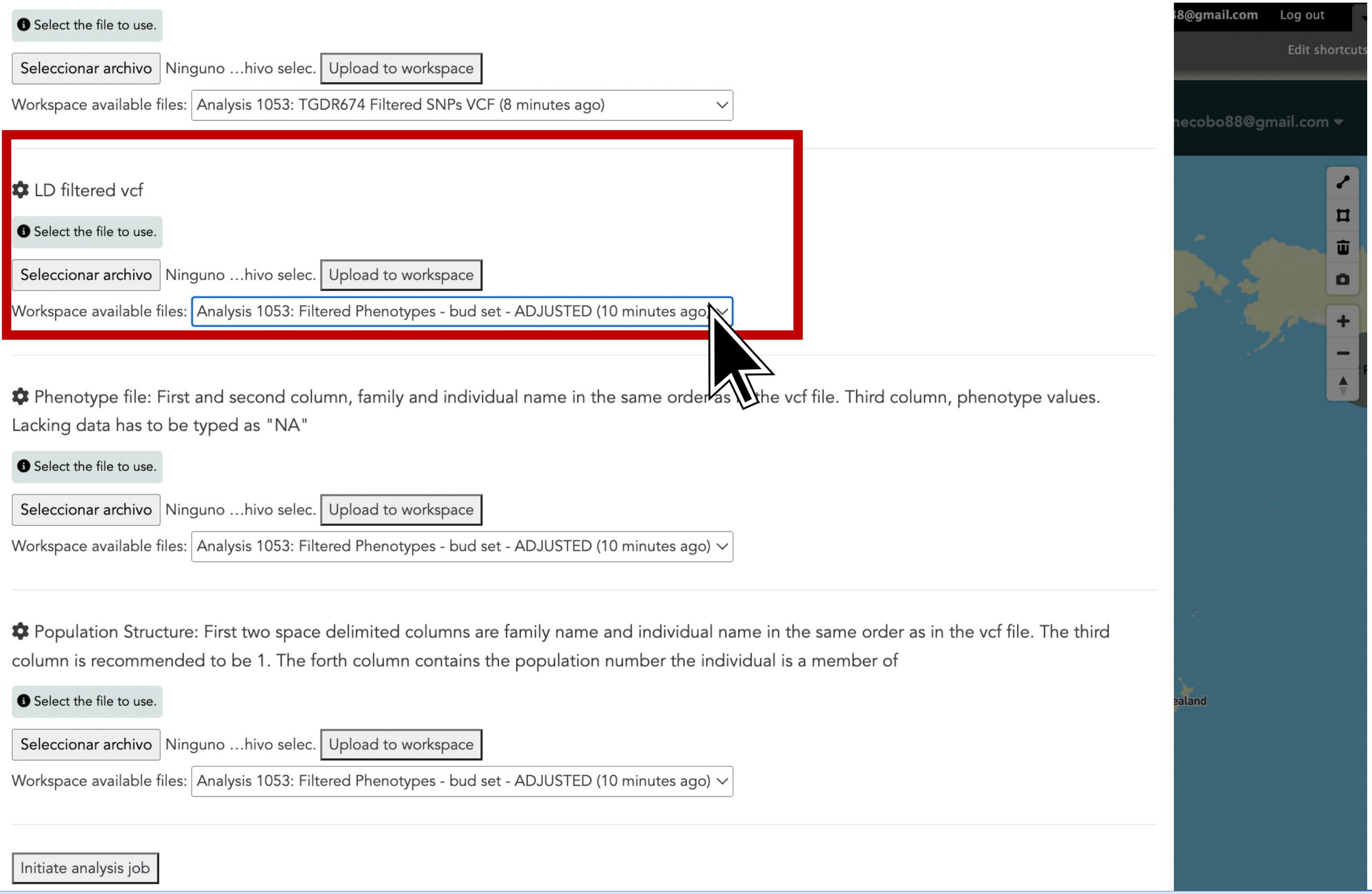
Workspace available files: Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (10 minutes ago)

DATA ANALYSIS: SELECT/RUN ANALYTIC WORKFLOWS

DATA ANALYSIS

https://cartograplant.org/

https://gitlab.com/IreneCobo/cartograplantworkshop2022/



Select the file to use.

Seleccionar archivo Ninguno ...hivo selec. Upload to workspace

Workspace available files: Analysis 1053: TGDR674 Filtered SNPs VCF (8 minutes ago)

LD filtered vcf

Select the file to use.

Seleccionar archivo Ninguno ...hivo selec. Upload to workspace

Workspace available files: Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (10 minutes ago)

Phenotype file: First and second column, family and individual name in the same order as in the vcf file. Third column, phenotype values. Lacking data has to be typed as "NA"

Select the file to use.

Seleccionar archivo Ninguno ...hivo selec. Upload to workspace

Workspace available files: Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (10 minutes ago)

Population Structure: First two space delimited columns are family name and individual name in the same order as in the vcf file. The third column is recommended to be 1. The forth column contains the population number the individual is a member of

Select the file to use.

Seleccionar archivo Ninguno ...hivo selec. Upload to workspace

Workspace available files: Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (10 minutes ago)

Initiate analysis job

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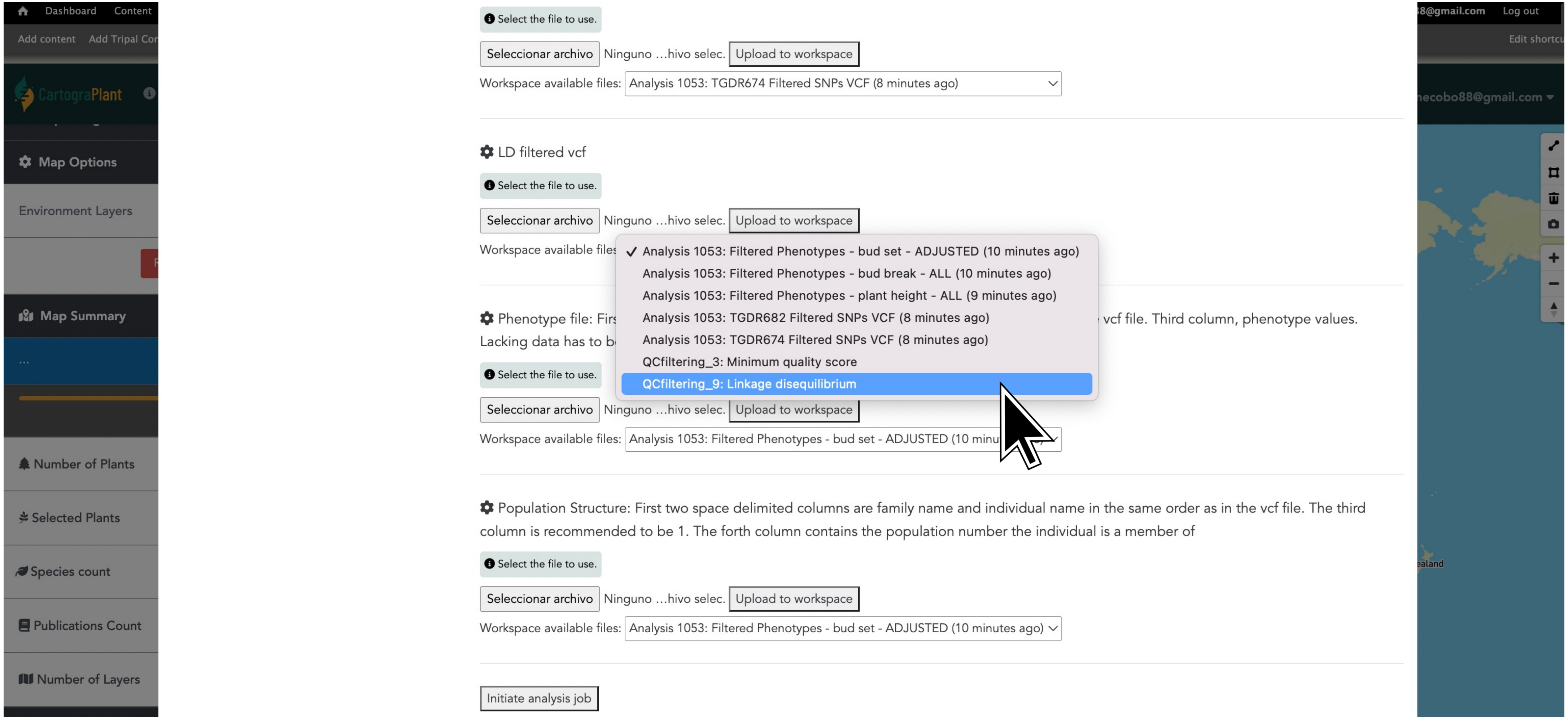

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LD filtered vcf

Select the file to use.

Seleccionar archivo Ninguno …hivo selec. Upload to workspace

Workspace available files

- ✓ Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (10 minutes ago)
- Analysis 1053: Filtered Phenotypes - bud break - ALL (10 minutes ago)
- Analysis 1053: Filtered Phenotypes - plant height - ALL (9 minutes ago)
- Analysis 1053: TGDR682 Filtered SNPs VCF (8 minutes ago)
- Analysis 1053: TGDR674 Filtered SNPs VCF (8 minutes ago)
- QCfiltering_3: Minimum quality score
- QCfiltering_9: Linkage disequilibrium

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Seleccionar archivo Ninguno …hivo selec. Upload to workspace

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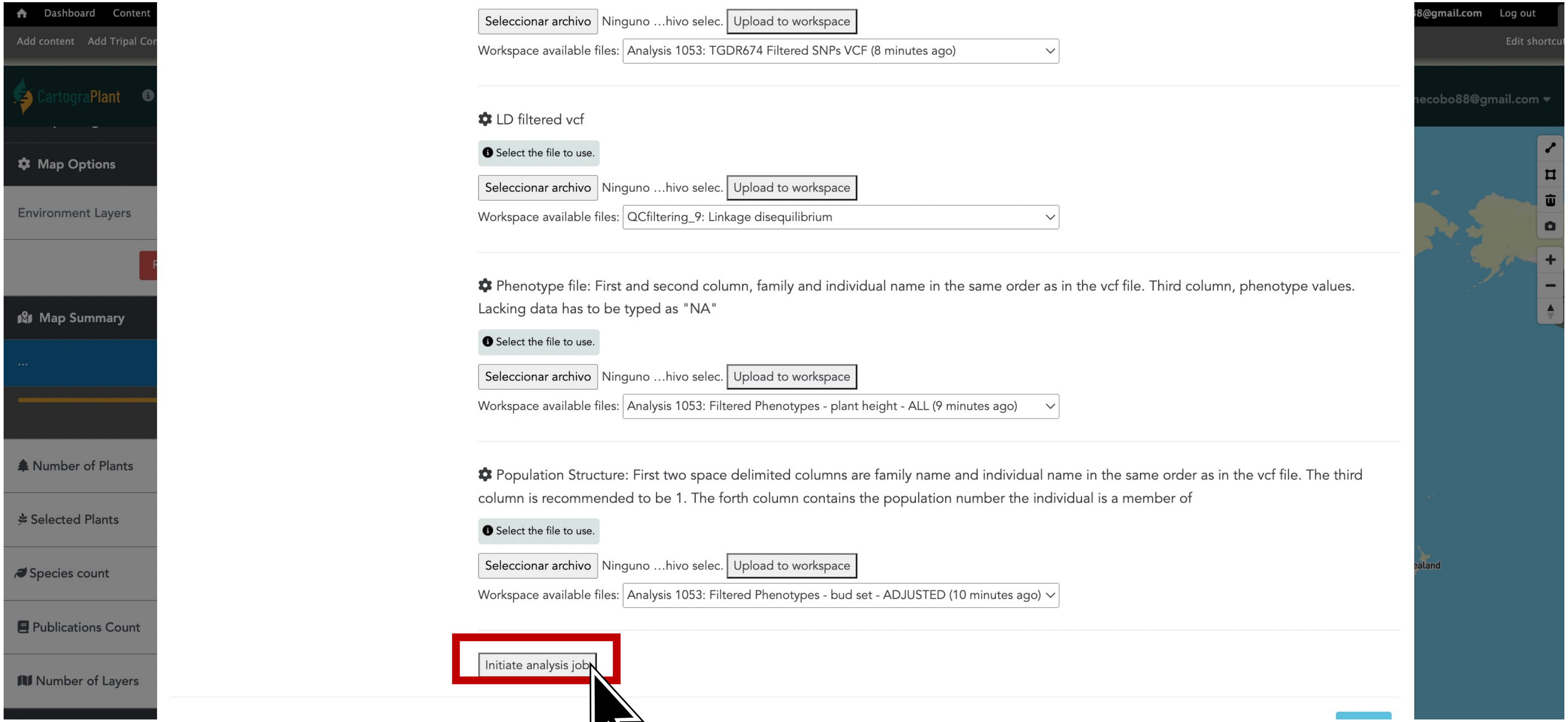

Seleccionar archivo Ninguno ...hivo selec. Upload to workspace

Workspace available files: Analysis 1053: TGDR674 Filtered SNPs VCF (8 minutes ago)

LD filtered vcf

Select the file to use.

Seleccionar archivo Ninguno ...hivo selec. Upload to workspace

Workspace available files: QCfiltering_9: Linkage disequilibrium

Phenotype file: First and second column, family and individual name in the same order as in the vcf file. Third column, phenotype values. Lacking data has to be typed as "NA"

Select the file to use.

Seleccionar archivo Ninguno ...hivo selec. Upload to workspace

Workspace available files: Analysis 1053: Filtered Phenotypes - plant height - ALL (9 minutes ago)

Population Structure: First two space delimited columns are family name and individual name in the same order as in the vcf file. The third column is recommended to be 1. The forth column contains the population number the individual is a member of

Select the file to use.

Seleccionar archivo Ninguno ...hivo selec. Upload to workspace

Workspace available files: Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (10 minutes ago)

Initiate analysis job

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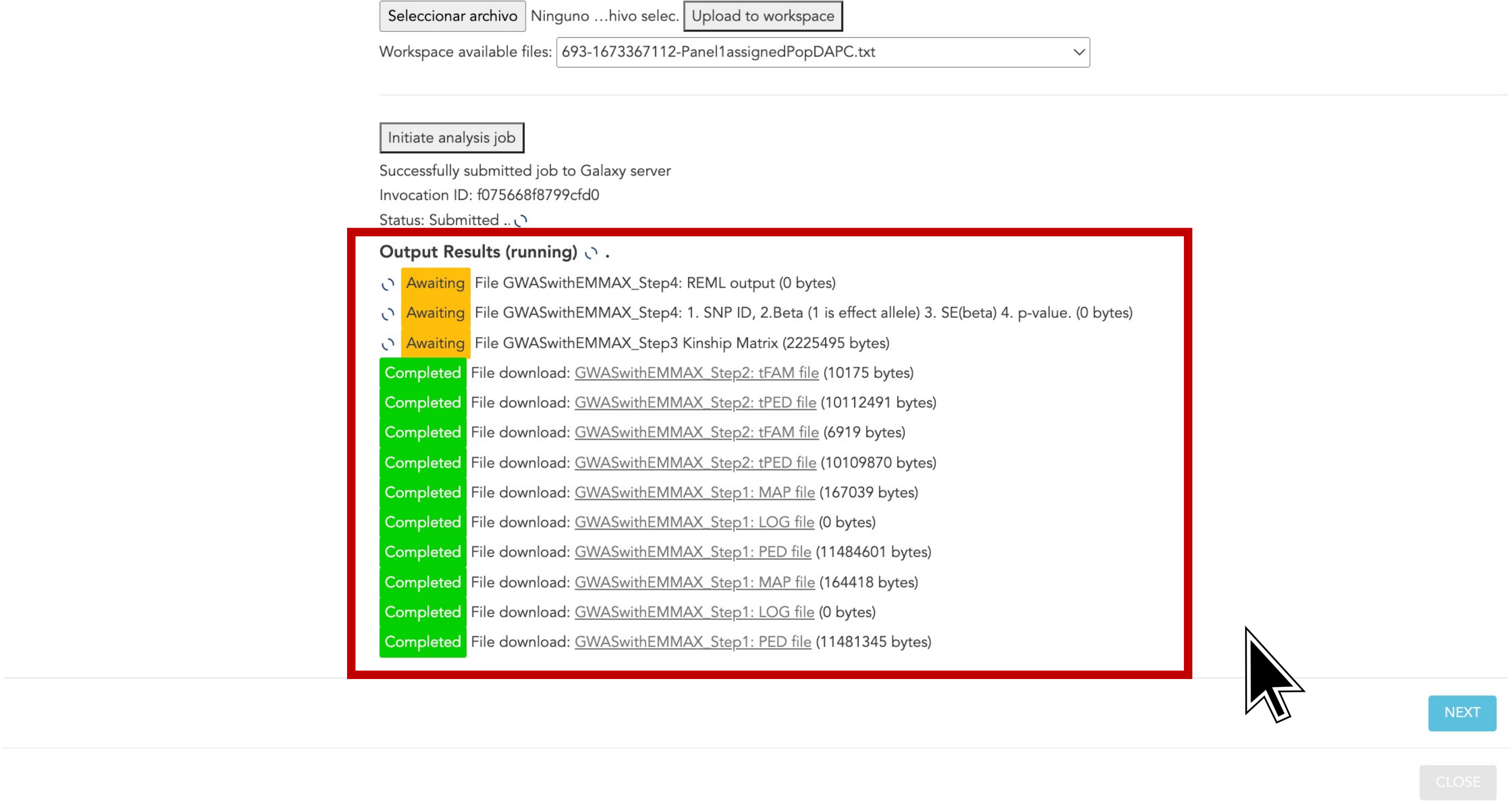

Workspace available files: 693-1673367112-Panel1assignedPopDAPC.txt

Successfully submitted job to Galaxy server
Invocation ID: f075668f8799cfd0
Status: Submitted ..

Output Results (running) .

Awaiting File GWASwithEMMAX_Step4: REML output (0 bytes)
Awaiting File GWASwithEMMAX_Step4: 1. SNP ID, 2.Beta (1 is effect allele) 3. SE(beta) 4. p-value. (0 bytes)
Awaiting File GWASwithEMMAX_Step3 Kinship Matrix (2225495 bytes)
Completed File download: GWASwithEMMAX_Step2: tFAM file (10175 bytes)
Completed File download: GWASwithEMMAX_Step2: tPED file (10112491 bytes)
Completed File download: GWASwithEMMAX_Step2: tFAM file (6919 bytes)
Completed File download: GWASwithEMMAX_Step2: tPED file (10109870 bytes)
Completed File download: GWASwithEMMAX_Step1: MAP file (167039 bytes)
Completed File download: GWASwithEMMAX_Step1: LOG file (0 bytes)
Completed File download: GWASwithEMMAX_Step1: PED file (11484601 bytes)
Completed File download: GWASwithEMMAX_Step1: MAP file (164418 bytes)
Completed File download: GWASwithEMMAX_Step1: LOG file (0 bytes)
Completed File download: GWASwithEMMAX_Step1: PED file (11481345 bytes)

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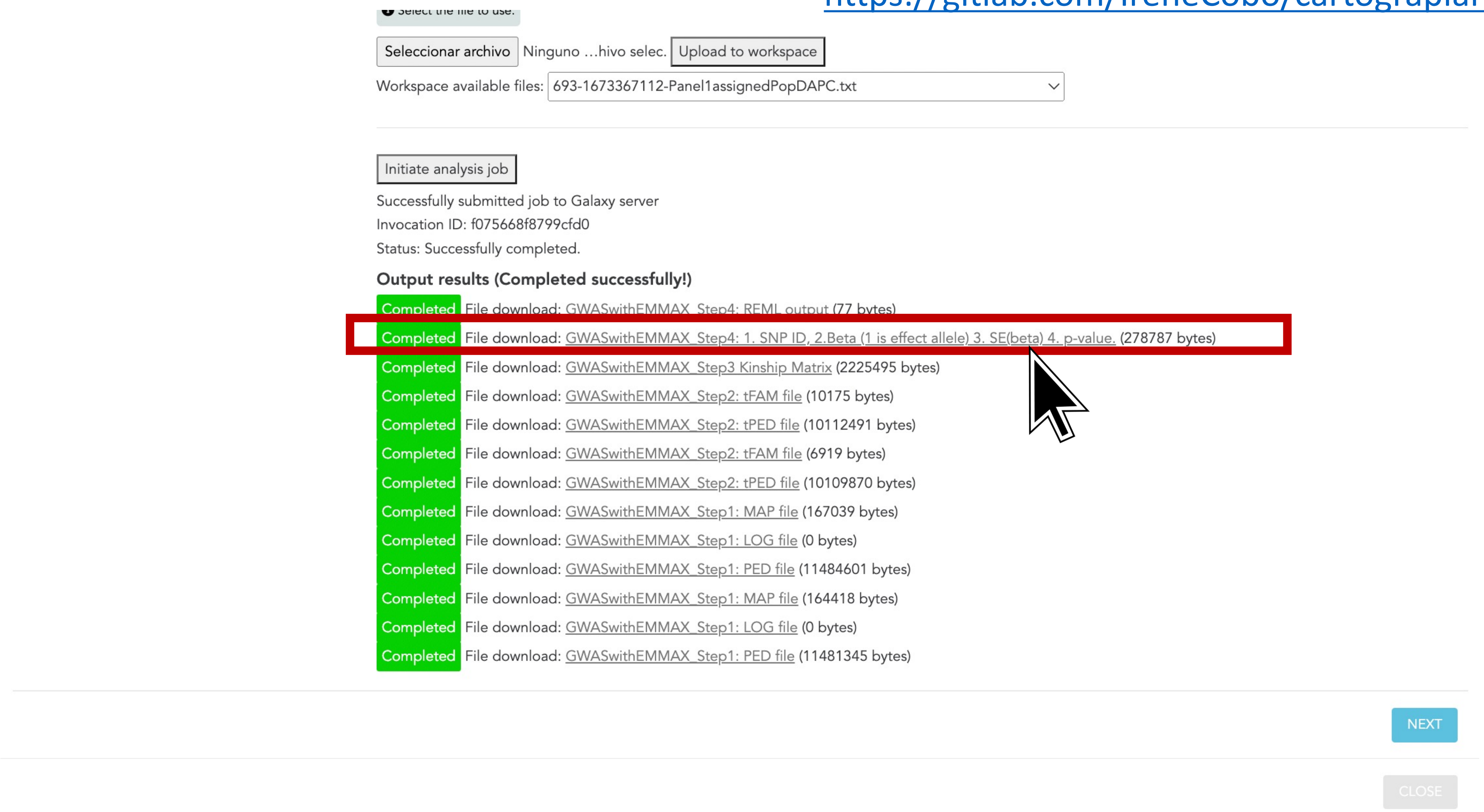

Select the file to use.

Workspace available files: 693-1673367112-Panel1assignedPopDAPC.txt

Successfully submitted job to Galaxy server

Invocation ID: f075668f8799cfd0

Status: Successfully completed.

Output results (Completed successfully!)

Completed File download: GWASwithEMMAX_Step4: REML output (77 bytes)

Completed File download: GWASwithEMMAX_Step4: 1. SNP ID, 2.Beta (1 is effect allele) 3. SE(beta) 4. p-value. (278787 bytes)

Completed File download: GWASwithEMMAX_Step3 Kinship Matrix (2225495 bytes)

Completed File download: GWASwithEMMAX_Step2: tFAM file (10175 bytes)

Completed File download: GWASwithEMMAX_Step2: tPED file (10112491 bytes)

Completed File download: GWASwithEMMAX_Step2: tFAM file (6919 bytes)

Completed File download: GWASwithEMMAX_Step2: tPED file (10109870 bytes)

Completed File download: GWASwithEMMAX_Step1: MAP file (167039 bytes)

Completed File download: GWASwithEMMAX_Step1: LOG file (0 bytes)

Completed File download: GWASwithEMMAX_Step1: PED file (11484601 bytes)

Completed File download: GWASwithEMMAX_Step1: MAP file (164418 bytes)

Completed File download: GWASwithEMMAX_Step1: LOG file (0 bytes)

Completed File download: GWASwithEMMAX_Step1: PED file (11481345 bytes)

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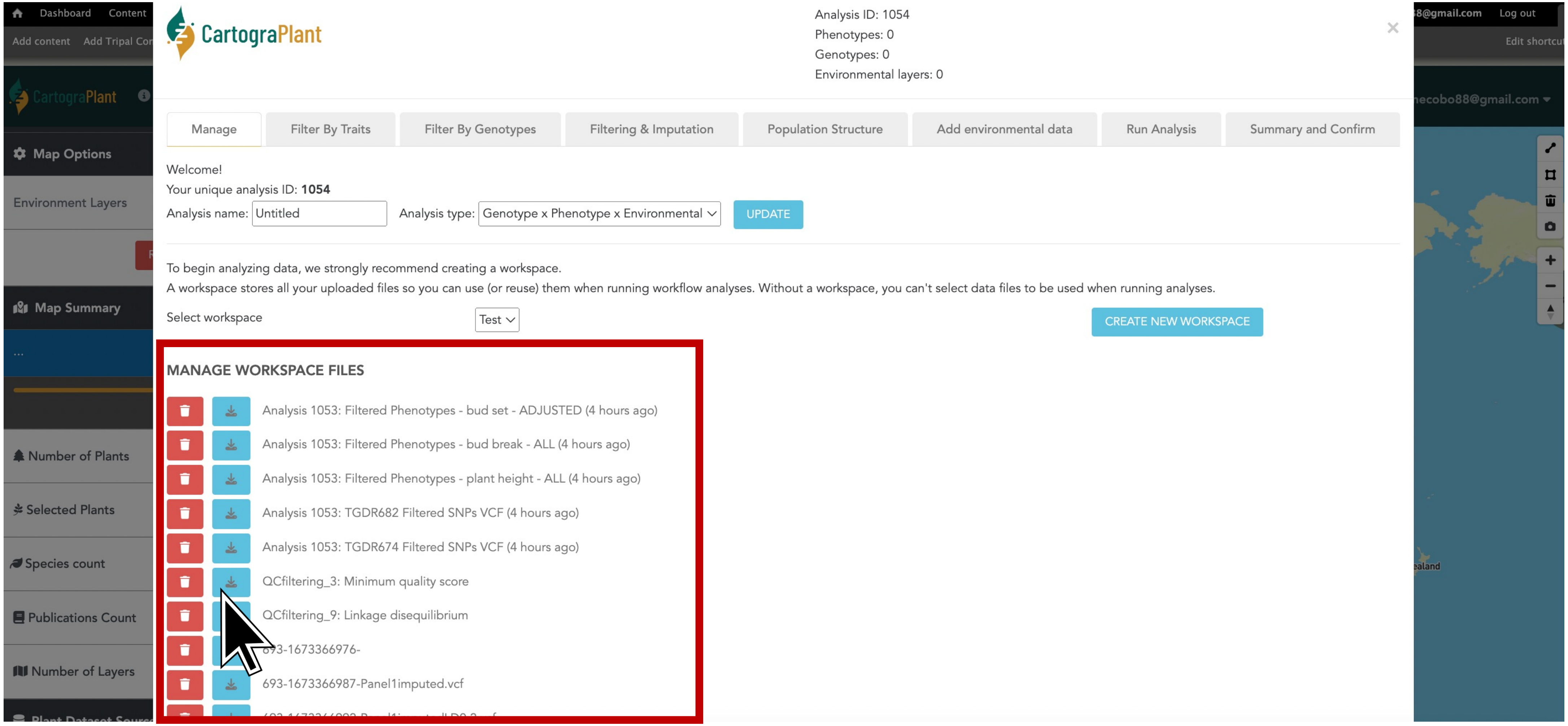

Analysis ID: 1054
Phenotypes: 0
Genotypes: 0
Environmental layers: 0

Welcome!
Your unique analysis ID: **1054**
Analysis name: Untitled
Analysis type: Genotype x Phenotype x Environmental

To begin analyzing data, we strongly recommend creating a workspace.
A workspace stores all your uploaded files so you can use (or reuse) them when running workflow analyses. Without a workspace, you can't select data files to be used when running analyses.

Select workspace: Test

MANAGE WORKSPACE FILES

- Analysis 1053: Filtered Phenotypes - bud set - ADJUSTED (4 hours ago)
- Analysis 1053: Filtered Phenotypes - bud break - ALL (4 hours ago)
- Analysis 1053: Filtered Phenotypes - plant height - ALL (4 hours ago)
- Analysis 1053: TGDR682 Filtered SNPs VCF (4 hours ago)
- Analysis 1053: TGDR674 Filtered SNPs VCF (4 hours ago)
- QCfiltering_3: Minimum quality score
- QCfiltering_9: Linkage disequilibrium
- 693-1673366976-
- 693-1673366987-Panel1imputed.vcf

DATA ANALYSIS: SELECT/RUN ANALYTIC WORKFLOWS

TEAM MEMBERS! QUESTIONS?

Members of the project

WASHINGTON STATE UNIVERSITY

- Stephen P. Ficklin

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- Abdullah Almsaeed

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USDA-NIFA #2018-09223

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TreeGenes Tripal GMOD AgBioData DBTREES GTTN Galaxy USDA CartograPlant