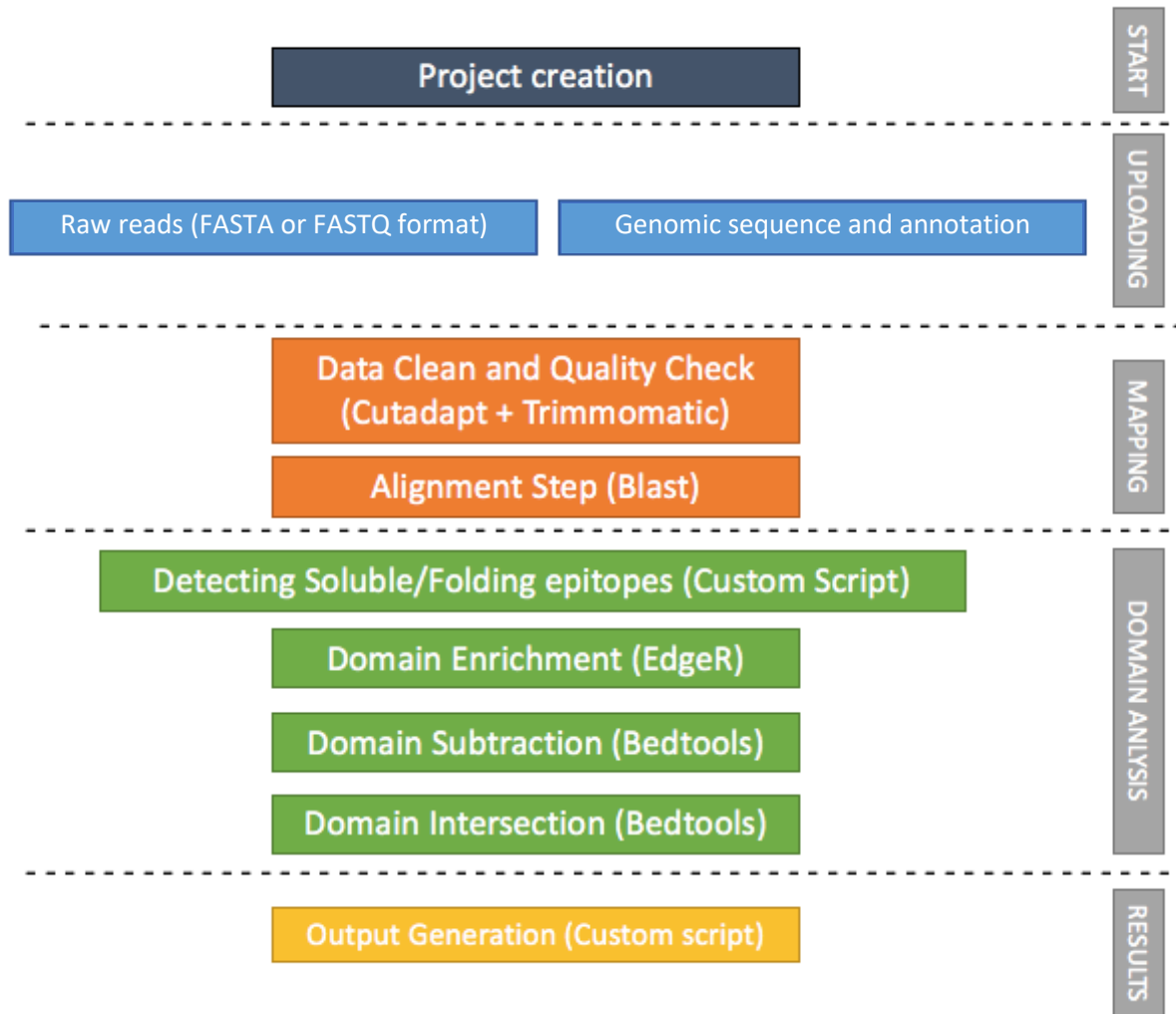


Prokaryote - Tutorial Hp 26695

This introductory section provides an overview of **Prokaryote** pipeline drafting and design. The vertical gray rectangles correspond to the website sections.



This document shows how to perform all the steps of an example analysis with the data provided for Prokaryote pipeline. For further information about the forms and the interpretation of the results, refer to the User Guide.

Input Files: dataset Prokaryote_Hp26695.zip

[Download a zip folder containing the raw datasets from this link \(1.1 GB\).](#)

Mandatory inputs for **InteractomeSeq - Prokaryote Hp 26695** execution are:

- genome reference file in FASTA format (either a custom annotation file or one selected from the drop-down menu) (Organism).
 - GCF_000008525.1_ASM852v1_genomic.fna (1.6 MB)
- a genome annotation (either a custom annotation file or one selected from the drop-down menu) (Organism).
 - GCF_000008525.1_ASM852v1_genomic.gff (620 KB)
- Raw Data files, FASTA or FASTQ format for query reads are allowed in the input, therefore the web interface additionally allows the submission of compressed files (gz format) to reduce the time of data upload (DataSets).
 - HP_genomic_26695_R1.fastq.gz (97 MB)
 - HP_genomic_26695_R2.fastq.gz (133 MB)
 - Sel_AG_R1.fastq.gz (243 MB)
 - Sel_AG_R2.fastq.gz (335 MB)
 - Sel_HPneg_R1.fastq.gz (66 MB)
 - Sel_HPneg_R2.fastq.gz (91 MB)
 - Sel_HPpos_R1.fastq.gz (74 MB)
 - Sel_HPpos_R2.fastq.gz (104 MB)

InteractomeSeq requires the user to upload at least two datasets. The input datasets must be generated with the same sequencing platform.

Time and memory usage for this tutorial

Analysis Step	File	Excution time	Output size
Mapping	26695_S5	~ 9m	46 MB
Mapping	HpNegativeControl	~ 6m	8 MB
Mapping	HpPositiveControl	~ 12m	13 MB
Mapping	AtrophicGastritis	~ 28m	28 MB
Domain Definition	26695_S5	~ 2m	357 KB
Domain Definition	HpNegativeControl	~ 35s	84 KB
Domain Definition	HpPositiveControl	~ 50s	126 KB
Domain Definition	AtrophicGastritis	~ 1m	222 KB
Domain Enrichment	26695_S5 - HpNegativeControl	~ 20s	30 KB
Domain Enrichment	26695_S5 - HpPositiveControl	~ 25s	39 KB
Domain Enrichment	26695_S5 - AtrophicGastritis	~ 30s	82 KB
Domain Subtraction	HpPositiveControl - AtrophicGastritis	< 5s	52 KB
Domain Subtraction	HpNegativeControl - HpPositiveControl	< 5s	27 KB
Domain Subtraction	HpNegativeControl - AtrophicGastritis	< 5s	67 KB
Domain Intersection	HpPositiveControl - AtrophicGastritis	< 5s	97 KB
Domain Intersection	HpNegativeControl - HpPositiveControl - AtrophicGastritis	< 5s	122 KB

Create a project

Click the button **START** to create a new project. Give the project a name (mandatory), a description (optional) and an email address (to receive messages during the execution. Select **PROKARYOTE** as project type and **SAVE**.

Create a Project

Project Name ⓘ

Project Description ⓘ

Email Address ⓘ

Project Type ⓘ EUKARYOTE PROKARYOTE

The project now has an ID that is a link, active for 15 days. Save this link if you didn't provide an email address (the link will be sent via email).

☰ Information Summary

↻

Project Name	Hp 26695
Project ID	yb3qjka08p40f6rftb0mywsg5p7w %
Project Description	Helicobacter pylori 26695 Project

Project Type	Prokaryote
Project Status	

Creation Date	Monday March 9, 2020 - 19:03:09	Expiration Date	Tuesday March 24, 2020 - 19:03:09
---------------	---------------------------------	-----------------	-----------------------------------

Uploading

Click on **UPLOADING** to upload the FASTQ files.

Select the **Custom Annotation** form to upload the genome files. Upload the reference file (**GCF_000008525.1_ASM852v1_genomic.fna**), and press **VALIDATE**. After the validation, a preview of the genomic sequences will be shown in a table.

Annotation

Annotation Custom Annotation

Reference

Reference File Drop File

File	Size	Date	Progress	Status	Actions
GCF_000008525.1_ASM852v1_genomic.fna	1.61 MB	12/20/2019 - 14:36:59	100%	✓	<input type="button" value="REMOVE"/>

Reference File - Valid

REFERENCES: 1

Header	Sequence
NC_000915.1 Helicobacter pylori 26695 chromosome, complete genome	TGATTAGTGATTAGTGATTAGTGATTAGTGATTAGTGATTAGTGATTAGTGATTAGTGATTAGTGA...

5 10 25

Upload the annotation (**GCF_000008525.1_ASM852v1_genomic.gff**), select the annotation format (**GFF**) and press **VALIDATE** (it is not necessary to compile the other fields, since GFF is a standard format).

Annotation

Annotation File Drop File

File	Size	Date	Progress	Status	Actions
GCF_000008525.1_ASM852v1_genomic.gff	0.61 MB	12/20/2019 - 14:39:43	100%	✓	<input type="button" value="REMOVE"/>

Annotation File - Valid

ANNOTATIONS: 1,448

Chromosome	Start	End	Strand	Locus Tag	Gene Name	Description
NC_000915.1	217	633	-	HP0001	nusB	transcription antitermination protein NusB
NC_000915.1	635	1105	-	HP0002	ribH	6%2C7-dimethyl-8-ribityllumazine synthase
NC_000915.1	1115	1945	-	HP0003		2-dehydro-3-deoxyphosphoacetate aldolase
NC_000915.1	1932	2597	-	HP0004		carbonic anhydrase IcfA
NC_000915.1	2719	3402	+	HP0005		orotidine 5'-phosphate decarboxylase

File Format: BED GFF CSV/TSV
 Column Separator: TAB
 Header Line:
 # Header Rows: 1

5 10 25

In the **DataSets** section, click on **SELECT FILE** or drag&drop files to upload FASTQ datasets:

- HP_genomic_26695_R1.fastq.gz
- HP_genomic_26695_R2.fastq.gz
- Sel_HPneg_R1.fastq.gz
- Sel_HPneg_R2.fastq.gz
- Sel_HPpos_R1.fastq.gz
- Sel_HPpos_R2.fastq.gz
- Sel_AG_R1.fastq.gz
- Sel_AG_R2.fastq.gz

DataSets

Raw Data Files

FASTA/FASTQ Format ⓘ SELECT FILE Drop File

Dataset loading visualization:

DataSets

Raw Data Files

FASTA/FASTQ Format ⓘ SELECT FILE Drop File

File		Size	Date	Progress	Status	Actions
HP_genomic_26695_R1.fastq.gz		96.64 MB	12/20/2019 - 17:34:28	<div style="width: 100%; height: 15px; background-color: #28a745;"></div> 100%	✓	REMOVE
HP_genomic_26695_R2.fastq.gz		133.02 MB	12/20/2019 - 17:34:51	<div style="width: 100%; height: 15px; background-color: #28a745;"></div> 100%	✓	REMOVE
Sel_AG_R1.fastq.gz		243.40 MB	12/20/2019 - 17:35:14	<div style="width: 100%; height: 15px; background-color: #28a745;"></div> 100%	✓	REMOVE
Sel_AG_R2.fastq.gz		334.96 MB	12/20/2019 - 17:36:33	<div style="width: 100%; height: 15px; background-color: #28a745;"></div> 100%	✓	REMOVE
Sel_HPneg_R1.fastq.gz		66.21 MB	12/20/2019 - 17:36:39	<div style="width: 100%; height: 15px; background-color: #28a745;"></div> 100%	✓	REMOVE
Sel_HPneg_R2.fastq.gz		90.75 MB	12/20/2019 - 17:36:48	<div style="width: 100%; height: 15px; background-color: #28a745;"></div> 100%	✓	REMOVE
Sel_HPpos_R1.fastq.gz		74.03 MB	12/20/2019 - 17:36:55	<div style="width: 100%; height: 15px; background-color: #28a745;"></div> 100%	✓	REMOVE
Sel_HPpos_R2.fastq.gz		104.08 MB		<div style="width: 42%; height: 15px; background-color: #ffc107;"></div> 42%	⌛	CANCEL

Mapping

In the **MAPPING** section, by clicking on the button **+ MAPPING**, 4 sub-sections will appear on the screen:

1. **Mapping Params.** Select paired-end reads (in this example: HP_genomic_26695_R1.fastq.gz and HP_genomic_26695_R2.fastq.gz)

Mapping List

+ MAPPING TOTAL: 0 COLUMNS ▾

Info	Label	Status	Date	Log	Output	Edit	Delete

Mapping :: Insert

Mapping Params

Sequencing Type SINGLE-READ PAIRED-ENDS

Read Forward File HP_genomic_26695_R1.fastq.gz Read Reverse File HP_genomic_26695_R2.fastq.gz

Mapping Label 26695_S5

2. **Organism.** Preloaded FASTA file that will be used as reference to align the sequences.

Organism

Reference GCF_000008525.1_ASM852v1_genomic.fna

Annotation GCF_000008525.1_ASM852v1_genomic.gff

3. **Adapters.** Select **Custom Adapters** and insert:
 - a. Forward Read 5' Adapter: GCAGCAAGCGGCGCATGCCACTAGTGGGAT
 - b. Forward Read 3' Adapter: CCCAGAGCAA
 - c. Reverse Read 5' Adapter: GGGATTGGTTTCCGCTAGCGGAGAT
 - d. Reverse Read 3' Adapter: CCCAGAGCAA

Adapters

Adapters Custom Adapters

Forward Read 5' Adapter GCAGCAAGCGGCGCATGCCACTAGTGGGAT

Forward Read 3' Adapter CCCAGAGCAA

Reverse Read 5' Adapter GGGATTGGTTTCCGCTAGCGGAGAT

Reverse Read 3' Adapter CCCAGAGCAA

4. **Trimming Params.** Selection of minimum length of sequence and number of mismatch allows, reads below this threshold will be discarded. Use the default, and click **EXECUTE**

Trimming Params

Min Clone Length 100 Allowed Mismatches 3

EXECUTE **RESET** **CANCEL**

This mapping will appear in the list of running mappings.

Mapping List							
+ MAPPING		RELOAD	TOTAL: 1	COLUMNS			
Info	Label	Status	Date	Log	Output	Edit	Delete
<input checked="" type="checkbox"/>	26695_S5	Running	20/12/2019 - 17:47:09	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Here are the parameters for the other 3 mappings in this example:

1. Sel_HPneg_R1

SequencingType Paired-Ends

Forward Read File Sel_HPneg_R1.fastq.gz

Reverse Read File Sel_HPneg_R2.fastq.gz

Reference GCF_000008525.1_ASM852v1_genomic.fna

Annotation GCF_000008525.1_ASM852v1_genomic.gff

AdapterType Custom

Forward Read 5' Adapter GCAGCAAGCGGCGCGCATGCCACTAGTGGGAT

Forward Read 3' Adapter CCCAGAGCAA

Reverse Read 5' Adapter GGGATTGGTTTCCGCTAGCGGAGAT

Reverse Read 3' Adapter CCCAGAGCAA

Min Clone Length 100

Allowed Mismatches 3

2. Sel_HPpos_R1

SequencingType Paired-Ends

Forward Read File Sel_HPpos_R1.fastq.gz

Reverse Read File Sel_HPpos_R2.fastq.gz

Reference GCF_000008525.1_ASM852v1_genomic.fna

Annotation GCF_000008525.1_ASM852v1_genomic.gff

AdapterType Custom

Forward Read 5' Adapter GCAGCAAGCGGCGCGCATGCCACTAGTGGGAT

Forward Read 3' Adapter CCCAGAGCAA

Reverse Read 5' Adapter GGGATTGGTTTCCGCTAGCGGAGAT

Reverse Read 3' Adapter CCCAGAGCAA

Min Clone Length 100

Allowed Mismatches 3

3. Sel_AG_R1

SequencingType Paired-Ends

Forward Read File Sel_AG_R1.fastq.gz

Reverse Read File Sel_AG_R2.fastq.gz

Reference GCF_000008525.1_ASM852v1_genomic.fna

Annotation GCF_000008525.1_ASM852v1_genomic.gff

AdapterType Custom

Forward Read 5' Adapter GCAGCAAGCGGCGCGCATGCCACTAGTGGGAT

Forward Read 3' Adapter CCCAGAGCAA

Reverse Read 5' Adapter GGGATTGGTTTCCGCTAGCGGAGAT

Reverse Read 3' Adapter CCCAGAGCAA

Min Clone Length 100

Allowed Mismatches 3

This is the list of running mappings:

Mapping List						
TOTAL: 4		COLUMNS				
Info	Label	Status	Date	Log	Output	
	26695_S5	Done	01/10/2019 - 14:00:00			
	HpNegativeControl	Running	01/10/2019 - 14:00:00			
	HpPositiveControl	Running	01/10/2019 - 14:00:00			
	AtrophicGastritis	Running	01/10/2019 - 14:00:00			

5 10 25

Domain Analysis

Domain analysis is composed by four sheets:

1. **Domain Definition**
2. **Domain Enrichment**
3. **Domain Subtraction**
4. **Domain Intersection**

Domain Definition takes as input the mapping file previously generated. Define the domains for each of the 4 datasets uploaded and mapped by choosing them in the **Mapping** menu, then press **Execute**.

Domain Definition :: Insert

Domain Definition Params

Mapping ⓘ 26695_S5

Domain Definition Label ⓘ 26695_S5

Organism

Reference ⓘ GCF_000008525.1_ASM852v1_genomic.fna

Annotation ⓘ GCF_000008525.1_ASM852v1_genomic.gff

EXECUTE ⚡
RESET 🗑️
CANCEL ✕

Domain Definition List shows the running domain definitions

Domain Definition List

+ DOMAIN DEFINITION
↻
TOTAL : 4
COLUMNS ▾

Info	Label	Status	Date	Log	Output	Edit	Delete
▼	26695_S5	Running	23/12/2019 - 9:49:33	👁️	📄	✎	✕
▼	HpNegativeControl	Running	23/12/2019 - 9:49:40	👁️	📄	✎	✕
▼	HpPositiveControl	Running	23/12/2019 - 9:49:46	👁️	📄	✎	✕
▼	AtrophicGastritis	Running	23/12/2019 - 9:49:51	👁️	📄	✎	✕

5
10
25

Info – Drop-down menu with information of Mapping input file.

Label – Sample label.

Status – When the execution ends successfully, the button turns green, otherwise, it turns red.

Date – Day and time of analysis execution

Log – Button that hides/opens a box with execution log file. When the execution is running, the log shows the possibility to stop it:

Domain Definition :: Log :: 26695_S5

STATUS **STOP** Domain Definition Running Processing

Computing the depth-of-coverage complete.

CLOSE

When the process has finished, the log shows summary information:

Domain Definition :: Log :: 26695_S5

STATUS Domain Definition Done Completed Processing

Conversion Tabular ==> FastA complete.
 Representative clones picking complete.
 Blastn analysis complete.
 Output Bed parsed complete.
 Checking clones gene intersection complete.
 Filtering Clones outside CDS.
 Clone cluster count.Complete
 Filtering cluster complete.
 Filtering cluster complete.
 Pybedtools getfasta complete.
 Checking clones gene intersection complete.
 Add gene description complete.
 Conversion FastA ==> Tabular complete.
 Add nucleotide sequence complete.

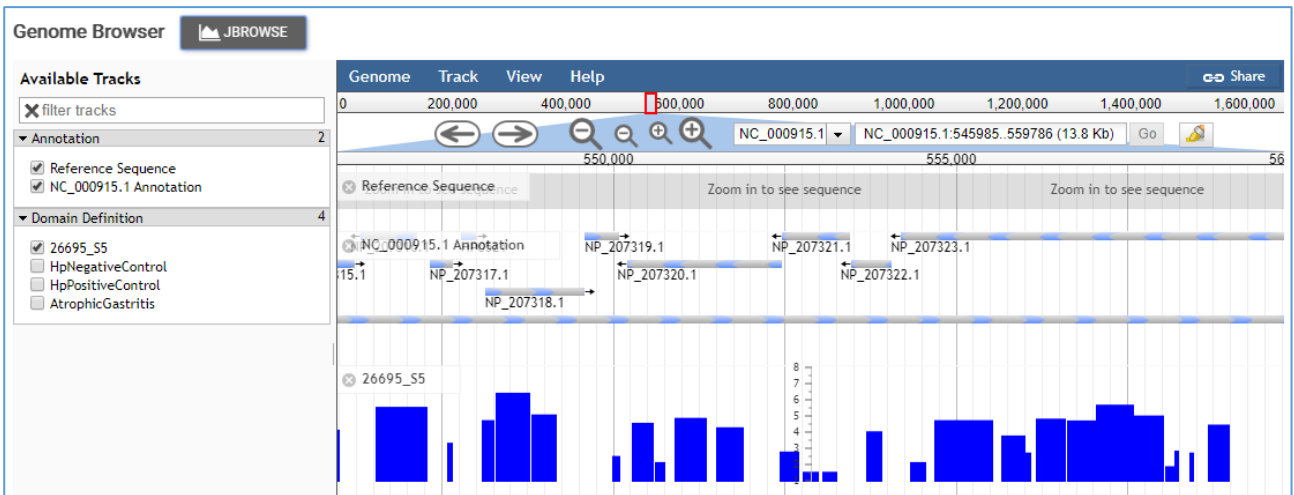
Output – Hides/opens panel with output preview

Domain Definition Output File **DOWNLOAD**

TOTAL: 2,986 RESET FILTERING RESET SORTING COLUMNS

Info	Chromosome	Clone Start	Clone End	Clone Length	Gene Start	Gene End	Gene	Strand
▼	NC_000915.1	346	526	180	217	633	HP0001	-
▼	NC_000915.1	724	1073	349	635	1105	HP0002	-
▼	NC_000915.1	1178	1721	543	1115	1945	HP0003	-
▼	NC_000915.1	1775	1955	170	1115	1945	HP0003	-
▼	NC_000915.1	1983	2463	480	1932	2597	HP0004	-
▼	NC_000915.1	2751	3018	267	2719	3402	HP0005	+
▼	NC_000915.1	3060	3168	108	2719	3402	HP0005	+
▼	NC_000915.1	3789	3897	108	3403	4233	HP0006	+
▼	NC_000915.1	3900	4035	135	3403	4233	HP0006	+
▼	NC_000915.1	5743	5985	242	5241	7145	HP0009	-

1 2 3 ... 299 5 10 25 50



Domain Enrichment takes as input the Genomic and Target output of Domain Definition step. Enrich domains for each defined domain by selecting the Genomic and the target domains. In the current example, select:

- 26695_S5 and NegativeControl
- H26695_S5 and PositiveControl
- 26695_S5 and AtrophicGastritis

Domain Enrichment :: Insert

Genomic Domain Definition: 26695_S5

Target Domain Definition: HealthyControl

Domain Enrichment Label: 26695_S5 + PositiveControl

EXECUTE ⚡ RESET 🗑️ CANCEL ✖️

Domain Enrichment List

Domain Enrichment List

+ DOMAIN ENRICHMENT TOTAL: 3 COLUMNS ▾

Info	Label	Status	Date	Log	Output	Edit	Delete
▾	26695_S5 - HpNegativeControl	Done	23/12/2019 - 10:49:18	👁️	📄	✏️	✖️
▾	26695_S5 - HpPositiveControl	Running	23/12/2019 - 10:49:34	👁️	📄	✏️	✖️
▾	26695_S5 - AtrophicGastritis	Running	23/12/2019 - 10:49:47	👁️	📄	✏️	✖️

5 10 25

Info – Drop-down menu with information of Domain Definition input file.

Label – Sample label.

Status – When the execution ends successfully, the button turns green, otherwise, it turns red.

Date – Day and time of analysis execution

Log – Button that hides/opens a box with execution log file. When the execution is running, the log shows the possibility to stop it, otherwise the log shows summary information:

Domain Enrichment :: Log :: 26695_S5 + HealthyControl

STATUS Domain Enrichment Done Completed Processing

Parsing of mapping output file complete.
 Parsing of mapping output file complete.
 Parsing of domain definition output file complete.
 Bedtools coverage complete.
 Bedtools coverage complete.
 Parsing output bedtools coverage complete.
 Parsing output bedtools coverage complete.
 Differential expression analysis complete.
 Parsing output edgeR complete.

Output – Hides/opens panel with output preview

Domain Enrichment :: Output :: 26695_S5 - HpNegativeControl

Domain Enrichment Output File DOWNLOAD

TOTAL: 275 RESET FILTERING RESET SORTING COLUMNS

Info	Chromosome	Clone Start	Clone End	Clone Length	Gene Start	Gene End	Gene	Strand	Log FC	Adjust PValue
▼	NC_000915.1	238	373	135	217	633	HP0001	-	2.4653	3.0548e-2
▼	NC_000915.1	8395	8569	174	7603	9243	HP0010	-	2.1790	3.4764e-3
▼	NC_000915.1	10861	11046	185	9911	11590	HP0012	+	1.8962	1.3982e-2
▼	NC_000915.1	14979	15288	309	14248	16611	HP0017	+	3.3727	7.6874e-5
▼	NC_000915.1	16787	17147	284	16863	18272	HP0018	+	2.0296	6.5923e-3
▼	NC_000915.1	17966	18052	86	16863	18272	HP0018	+	6.7736	7.9131e-15
▼	NC_000915.1	33910	33988	78	32680	34905	HP0033	+	2.9902	9.8855e-5
▼	NC_000915.1	41903	42052	149	40651	42063	HP0043	+	5.7755	1.4830e-4
▼	NC_000915.1	43269	43360	91	43243	44175	HP0045	+	2.5775	5.2191e-3
▼	NC_000915.1	46430	46492	62	46042	48351	HP0048	-	2.8890	3.6349e-3

Genome Browser JBROWSE

Domain Subtraction takes as input two differentially enriched epitopes/domains lists, one defined as Control Domain Enrichment and one defined as Selection Domain Enrichment. In this example, select the enrichments defined by the couples:

- 26695_S5 - HpPositiveControl
- 26695_S5 - AtrophicGastritis

then

- 26695_S5 – HpNegativeControl
- 26695_S5 – HpPositiveControl

and

- 26695_S5 – HpNegativeControl
- 26695_S5 – AtrophicGastritis

Domain Subtraction :: Insert

Control Domain Enrichment i 26695_S5 + NegativeControl

Selection Domain Enrichment i 26695_S5 + PositiveControl

Domain Subtraction Label i HpNegativeControl - HpPositiveControl

Params

Overlap i 0.5

EXECUTE ⚡
RESET 🗑️
CANCEL ✕

Domain subtraction list:

Domain Subtraction List

+ DOMAIN SUBTRACTION
TOTAL: 3
COLUMNS ▾

Info	Label	Status	Date	Log	Output	Edit	Delete
▼	HpPositiveControl - AtrophicGastritis	Done	06/03/2020 - 17:28:22	👁️	📄	✎	✕
▼	HpNegativeControl - HpPositiveControl	Done	06/03/2020 - 17:57:53	👁️	📄	✎	✕
▼	HpNegativeControl - AtrophicGastritis	Done	06/03/2020 - 17:58:37	👁️	📄	✎	✕

5
10
25

Info – Drop-down menu with information of Domain Enrichment input file.

Label – Sample label.

Status – When the execution ends successfully, the button turns green, otherwise, it turns red.

Date – Day and time of analysis execution

Log – Button that hides/opens a box with execution log file. When the execution is running, the log shows the possibility to stop it, otherwise the log shows summary information:

Domain Subtraction :: Log :: HpNegativeControl - HpPositiveControl

☰ STATUS ✓
Domain Subtraction Done ✓
Completed Processing

Substraction domains complete.

Output – Hides/opens panel with output preview

Domain Subtraction :: Output :: HpNegativeControl - HpPositiveControl

Domain Subtraction Output File [DOWNLOAD](#)

TOTAL: **251** [RESET FILTERING](#) [RESET SORTING](#) [COLUMNS](#)

Info	Chromosome	Clone Start	Clone End	Clone Length	Gene Start	Gene End	Gene	Strand	Log FC	Adjust PValue
<input checked="" type="checkbox"/>	NC_000915.1	5873	6027	154	5241	7145	HP0009	-	2.7581	1.3126e-3
<input checked="" type="checkbox"/>	NC_000915.1	6284	6387	103	5241	7145	HP0009	-	5.1679	3.4435e-3
<input checked="" type="checkbox"/>	NC_000915.1	8695	8837	142	7603	9243	HP0010	-	1.7501	2.7446e-2
<input checked="" type="checkbox"/>	NC_000915.1	11762	12001	239	11587	12639	HP0013	+	1.7709	4.1700e-2
<input checked="" type="checkbox"/>	NC_000915.1	13992	14096	104	13983	14246	HP0016	+	1.8357	4.3285e-2
<input checked="" type="checkbox"/>	NC_000915.1	21880	21964	84	21152	22717	HP0022	-	2.2877	5.3086e-3
<input checked="" type="checkbox"/>	NC_000915.1	26388	26480	92	26078	27358	HP0026	-	2.1189	8.6137e-3
<input checked="" type="checkbox"/>	NC_000915.1	36527	36705	149	36556	37611	HP0037	+	3.0844	2.6988e-3
<input checked="" type="checkbox"/>	NC_000915.1	37340	37464	124	36556	37611	HP0037	+	2.8550	1.2769e-3
<input checked="" type="checkbox"/>	NC_000915.1	60677	60803	126	57741	61298	HP0056	-	2.3361	1.1336e-2

Genome Browser [JBROWSE](#)

Domain Intersection takes as input two differentially enriched epitopes/domains lists output of Domain Definition step. Domain Intersection allows one to screen for overlaps between two sets of epitopes/domains lists. Select both the subtractions previously executed and press **EXECUTE**

Domain Intersection :: Insert

Selections HpPositiveControl - AtrophicGastritis
 HpNegativeControl - HpPositiveControl
 HpNegativeControl - AtrophicGastritis

Domain Intersection Label

[EXECUTE](#) [RESET](#) [CANCEL](#)

Domain intersection list:

Info	Label	Status	Date	Log	Output	Edit	Delete
<input type="checkbox"/>	HpPositiveControl - AtrophicGastritis	Done	09/03/2020 - 11:12:35	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>	<input type="checkbox"/>

Info – Drop-down menu with information of Domain Enrichment input file.

Label – Sample label.

Status – When the execution ends successfully, the button turns green, otherwise, it turns red.

Date – Day and time of analysis execution

Log – Button that hides/opens a box with execution log file. When the execution is running, the log shows the possibility to stop it, otherwise the log shows summary information:

STATUS	Domain Intersection Done	Completed Processing
Intersection domains complete.		

Output – Hides/opens panel with output preview

Domain Intersection :: Output :: HpNegativeControl - HpPositiveControl - AtrophicGastritis

LEGEND

- [A] HpPositiveControl - AtrophicGastritis
- [B] HpNegativeControl - HpPositiveControl
- [C] HpNegativeControl - AtrophicGastritis

Domain Intersection Output Files DOWNLOAD

Domain Intersection Graph File PNG SVG

- A - (B ∪ C) +
- B - (A ∪ C) +
- C - (A ∪ B) +
- A ∩ B +
- A ∩ C +
- B ∩ C +
- A ∩ B ∩ C -

Domain Intersection Output File DOWNLOAD

TOTAL : 26 RESET FILTERING RESET SORTING COLUMNS

Info	Chromosome	Clone Start	Clone End	Clone Length	Gene Start	Gene End	Gene	Strand	Log FC	Adjust PValue
<input checked="" type="checkbox"/>	NC_000915.1	8695	9048	353	7603	9243	HP0010	-	2.4847	1.0268e-3
<input checked="" type="checkbox"/>	NC_000915.1	65698	65905	207	64016	66457	HP0060	+	2.4895	1.8192e-3
<input checked="" type="checkbox"/>	NC_000915.1	120280	120498	218	119980	120675	HP0112	+	5.2941	5.3429e-8
<input checked="" type="checkbox"/>	NC_000915.1	196397	196650	253	195596	197104	HP0190	-	2.9338	1.5543e-4
<input checked="" type="checkbox"/>	NC_000915.1	198654	198889	235	197856	200000	HP0192	-	2.1820	3.9586e-3
<input checked="" type="checkbox"/>	NC_000915.1	206920	207090	170	206915	207910	HP0202	+	2.3630	3.5821e-3

Results

The summary of all the analysis performed is showed in the results page

Results			
TOTAL: 5			
Analysis			
	Label	Date	Download
Mapping			
	HealthyControl	27/02/2020 - 11:46:51	Download
	PositiveControl	27/02/2020 - 11:55:37	Download
	26695_S5	27/02/2020 - 15:45:00	Download
	Atrophic_Gastritis	27/02/2020 - 11:55:40	Download
Domain Definition			
	26695_S5	09/03/2020 - 18:52:32	Download
	HealthyControl	27/02/2020 - 12:30:08	Download
	PositiveControl	27/02/2020 - 12:30:13	Download
	Atrophic_Gastritis	27/02/2020 - 12:30:16	Download
Domain Enrichment			
	26695_S5 + HealthyControl	27/02/2020 - 12:50:59	Download
	26695_S5 + PositiveControl	27/02/2020 - 12:51:01	Download
	26695_S5 + Atrophic_Gastritis	27/02/2020 - 12:51:04	Download
Domain Subtraction			
	HpPositiveControl - AtrophicGastritis	06/03/2020 - 17:28:22	Download
	HpNegativeControl - HpPositiveControl	06/03/2020 - 17:57:53	Download
	HpNegativeControl - AtrophicGastritis	06/03/2020 - 17:58:37	Download
Domain Intersection			
	HpNegativeControl - HpPositiveControl - AtrophicGastritis	09/03/2020 - 13:51:27	Download
	HpPositiveControl - AtrophicGastritis	09/03/2020 - 11:12:35	Download

And a genome browser with the results aligned to the reference genome

