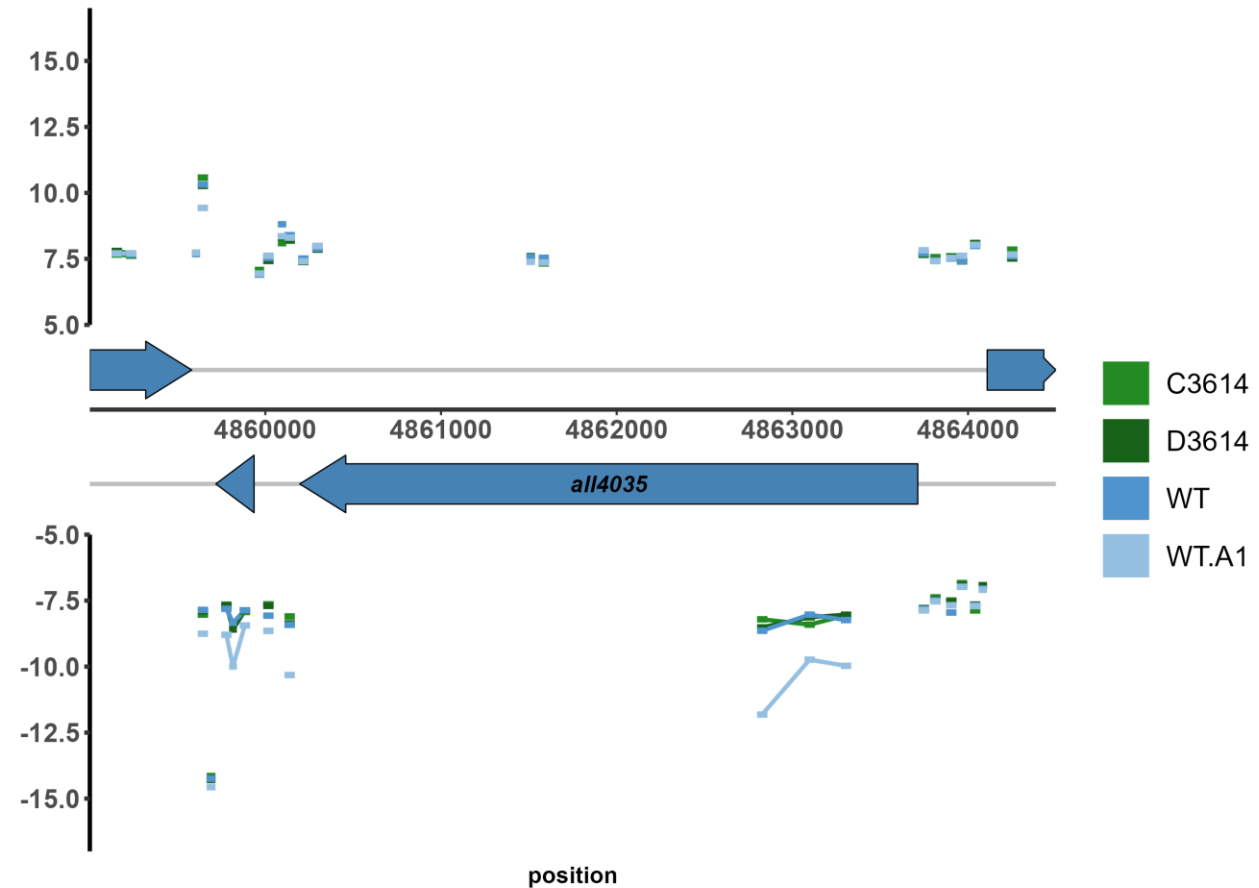


# MicroarrayPlotter

Manual



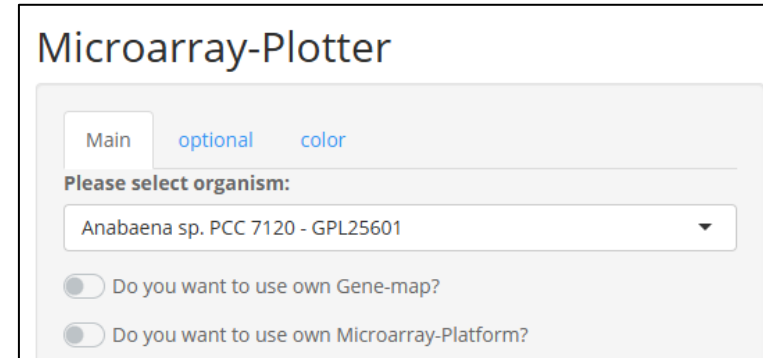
# Upload Data

- The program has two Microarray platforms/organisms you can choose from.  
Anabaena sp. PCC 7120 - GPL25601 / Synechocystis sp. PCC 6803 - GPL23938

- Optionally, you can provide your own Gene-map and/or Microarray-Platform by checking the corresponding switches and uploading the files.

Please make sure that the csv files will contain the following column names:

- Gene-map: Replicon, gene, start, end, orientation, [optional: type, color, from, to, subcolor, label\_type, lane]
- Platform: Replicon, start, end, orientation, Name
- The column items in Replicon also need to be consistent in both Gene-map and Platform-file.



Microarray-Plotter

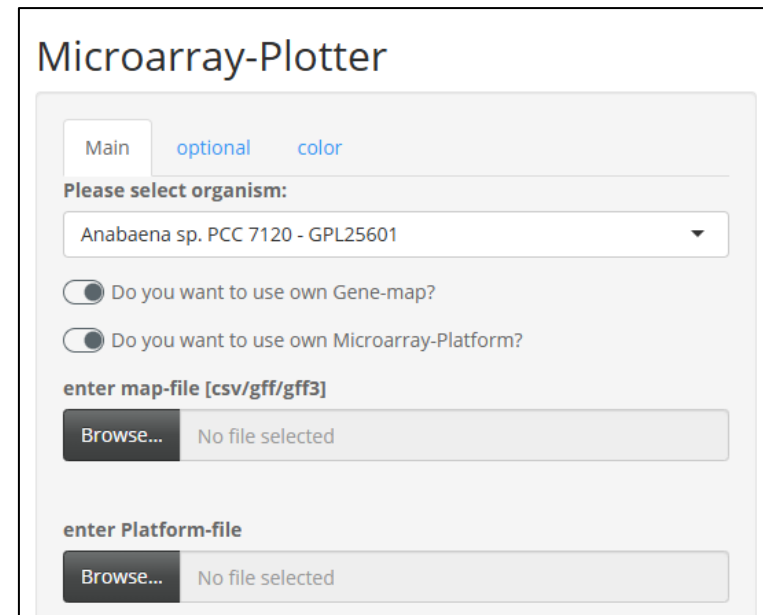
Main optional color

Please select organism:

Anabaena sp. PCC 7120 - GPL25601

☐ Do you want to use own Gene-map?

☐ Do you want to use own Microarray-Platform?



Microarray-Plotter

Main optional color

Please select organism:

Anabaena sp. PCC 7120 - GPL25601

☒ Do you want to use own Gene-map?

☒ Do you want to use own Microarray-Platform?

enter map-file [csv/gff/gff3]

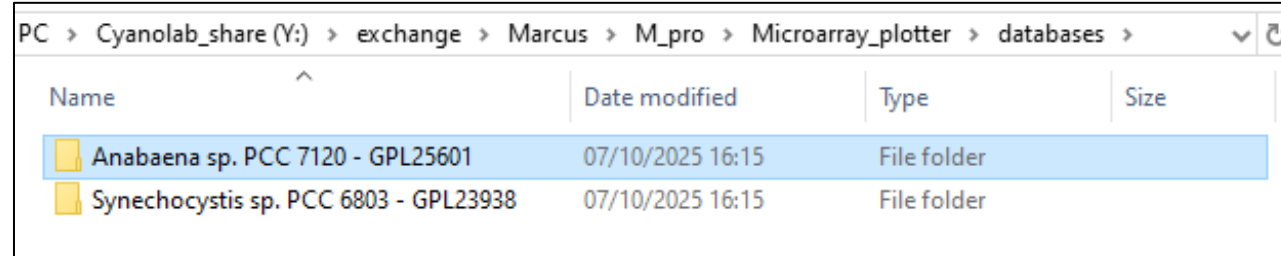
Browse... No file selected



enter Platform-file

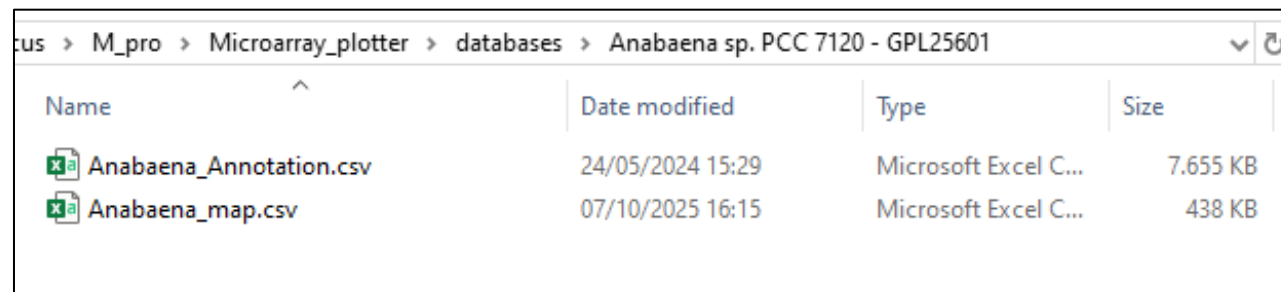
Browse... No file selected



# Upload Data

- Alternatively, you can also run the program locally and create a prepared directory file containing the map and platform-file in it.
- In the directory of the MicroarrayPlotter is a folder called databases. In this folder, you can add additional folders with map and platform-file. The program will automatically detect these folders and can be chosen.



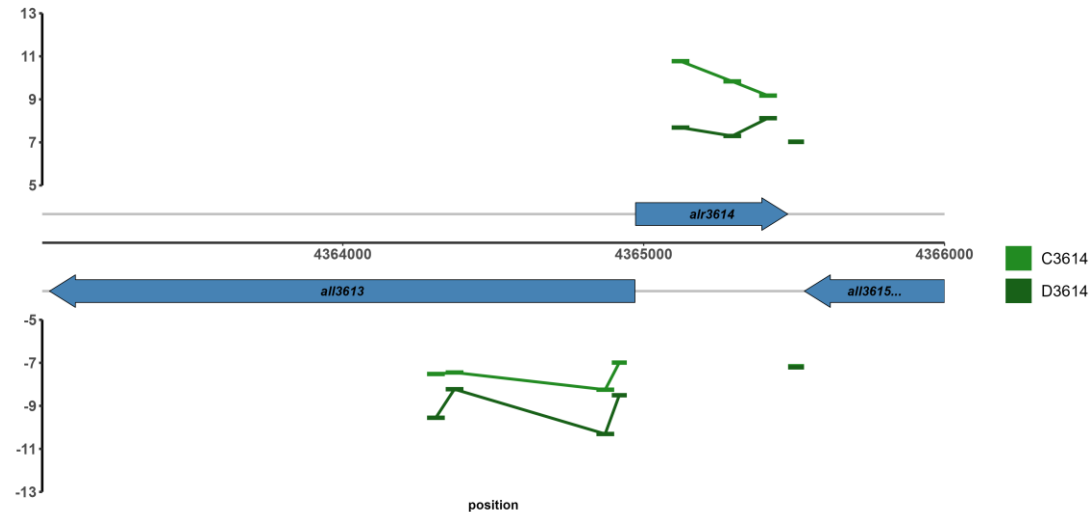
Name	Date modified	Type	Size
 Anabaena sp. PCC 7120 - GPL25601	07/10/2025 16:15	File folder	
 Synechocystis sp. PCC 6803 - GPL23938	07/10/2025 16:15	File folder	



Name	Date modified	Type	Size
 Anabaena_Annotation.csv	24/05/2024 15:29	Microsoft Excel C...	7.655 KB
 Anabaena_map.csv	07/10/2025 16:15	Microsoft Excel C...	438 KB

# Input

- Insert Microarray results by uploading a file or enter GEO-ID (both and multiple IDs are possible, but not recommended).
- Insert Replicon, start and end point that should be plotted.
- Insert Name file for Microarray-condition (optional)
  - If no Name-file is given, the program will use the names given in the Geo-data or the file.



## Microarray-Plotter

Main optional color

Please select organism:

Anabaena sp. PCC 7120 - GPL25601

☐ Do you want to use own Gene-map?

☐ Do you want to use own Microarray-Platform?

Choose Microarray GEO-file

Browse...

No file selected

Do you want to add Geo-data?

GSE183629

enter names of Microarrays

Browse...

No file selected

Please select chromosome or plasmid:

chromosome

Please enter the start-position

1

Please enter the end-position

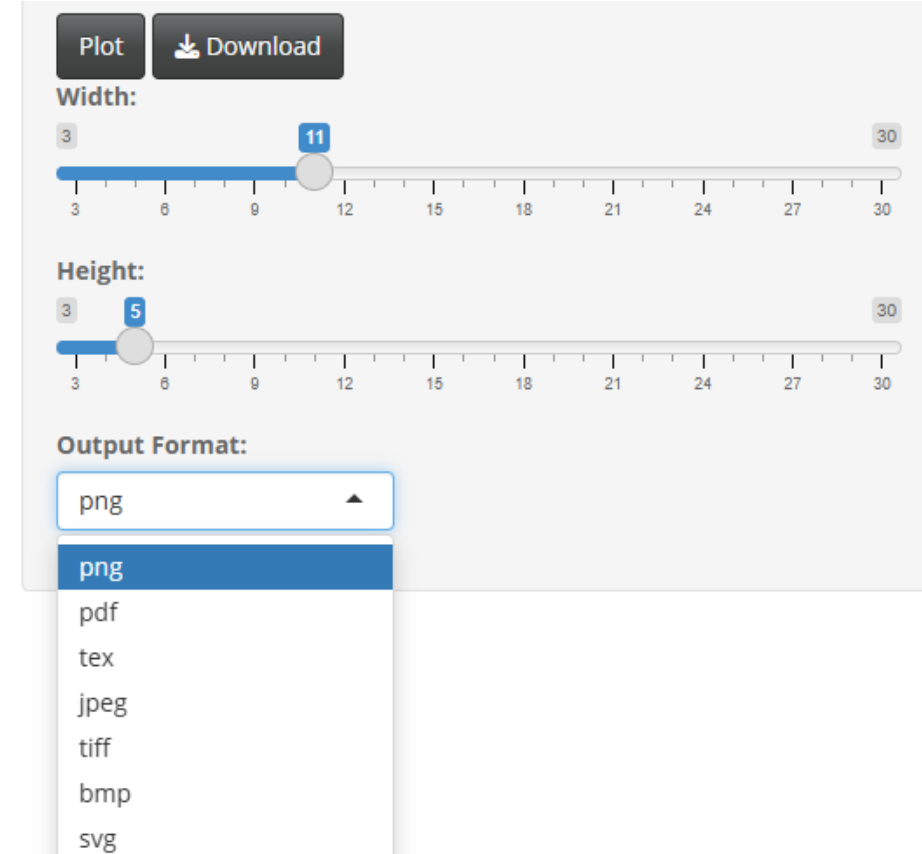
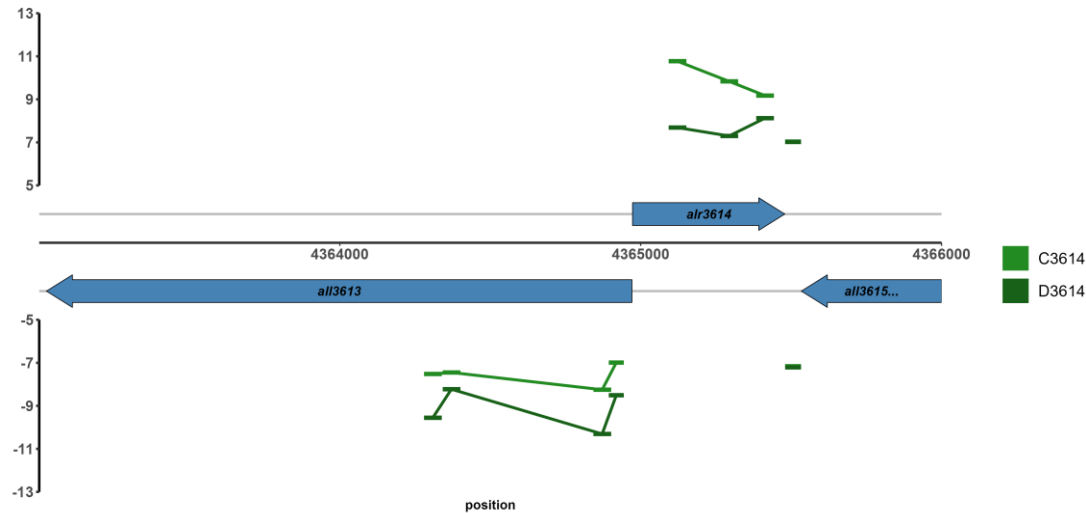
10000

Plot

Download

# Output - plot

The size of the plot can be manipulated and then be downloaded as in different picture formats (by default png):



# Output – map-table

The second main-panel shows the table of map elements. This table is either the uploaded csv-file or a converted table from an uploaded gff-file. The former are easier to change, so the table can be downloaded as a csv-file, using the “Download table” button.

Plot

Gene\_map

Microarray\_table

Show 10 entries

Search:

	Replicon	gene	start	end	orientation
1	chromosome	all0002	981	1718	-1
2	chromosome	asl0003	2617	2805	-1
3	chromosome	ssrA	2858	3247	-1
4	chromosome	atpC	3418	4365	-1
5	chromosome	atpA	4454	5974	-1
6	chromosome	atpD	6138	6689	-1
7	chromosome	atpF	6686	7249	-1
8	chromosome	atpG	7359	7850	-1
9	chromosome	atpH	7996	8241	-1
10	chromosome	atpI	8324	9079	-1

Showing 1 to 10 of 6,153 entries

Previous12345...616Next

Download table

# Output – Platform-table


The third main-panel shows the table of the Microarray Platform. This table can also be downloaded as a csv-file, using the “Download table” button.

Plot Gene\_map Microarray\_table

Show 10 entries Search:

	Row	Col	ControlType	Name	Replicon	start	end	orientation
1	1	1	1	61536				
2	1	2	1	61537				
3	1	3	1	61538				
4	1	4	0	alr4161_5007627	chromosome	5007912	5007971	-
5	1	5	0	alr0558_650328	chromosome	650636	650695	-
6	1	6	0	2419	chromosome	1666036	1666095	-
7	1	7	0	2420	chromosome	4914695	4914754	-
8	1	8	0	2421	chromosome	5495794	5495853	-
9	1	9	0	63	beta	123014	123073	-
10	1	10	0	nTSS_2050703_2050703	chromosome	2050716	2050775	-

Showing 1 to 10 of 62,976 entries Previous 1 2 3 4 5 ... 6,298 Next

 Download table

# Optional Input

The optional menu gives you further choices for your plotting, like changing the linewidth of your graph or deleting individual conditions.

## Microarray-Plotter

Main optional color

**Graphsize:**

**min. y-axis:**

**max. y-axis:**

☒ display subgenes

☐ change labelsiz?

☒ line in maps?

**Which Microarray should be displayed?**  
☒ C3614  
☒ D3614

Choose the order of Microarrays in the plot:

**ending of incomplete genes:**

**map-graph ratio:**



# Optional Input

Min /max. y-axis:

Limits the y-axis on both sequencing plots.

Display subgenes:

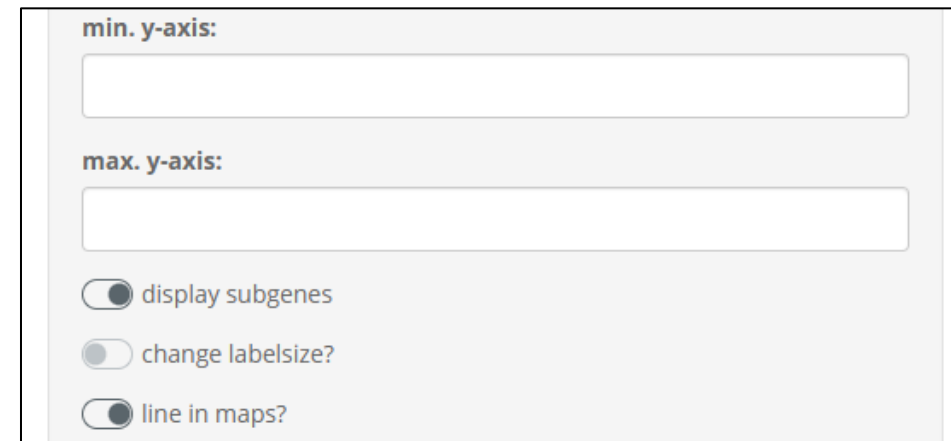
Subgenes can be added to the gene map, by setting values in the column “from”, “to” and “subcolor”. The plot will show a different colored area inside a gene. However, if the program should not depict subgenes, set this switch to FALSE.

Line in maps?

Depict a line in the gene map.

Change label size:

If this switch is TRUE, the program will ask for map-element font size and the maximum size of map-elements that should be labeled. The program can usually detect if a label is too long for a specific map element, however there are too many variables for this automatization with variable font size.



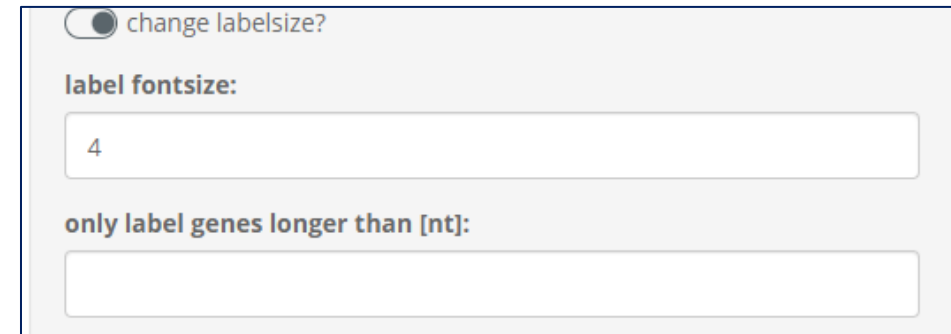
min. y-axis:

max. y-axis:

☒ display subgenes

☐ change labelsize?

☒ line in maps?



☒ change labelsize?

label fontsize:

only label genes longer than [nt]:

# Optional Input

Which graphs should be displayed?:

Individual sequence runs can be chosen to be depicted.

ending of incomplete genes:

If a map-element is depicted in the plot, but lies partially outside the depicted parameter, the program will add text to clarify, that the element is incomplete. This can be avoided by leaving this input empty.

map-graph ratio:

Here, the height-ratio between gene map and the RNA-sequence graph inside the plot, can be changed.

Height/width of arrow / height of arrow body:

These input areas can be used to change the gene map arrows in the plot.

Which Microarray should be displayed?

☒ C3614

☒ D3614

Choose the order of Microarrays in the plot:

C3614

D3614

ending of incomplete genes:

...

map-graph ratio:

3

height of arrowbody:

7

height of arrow:

10

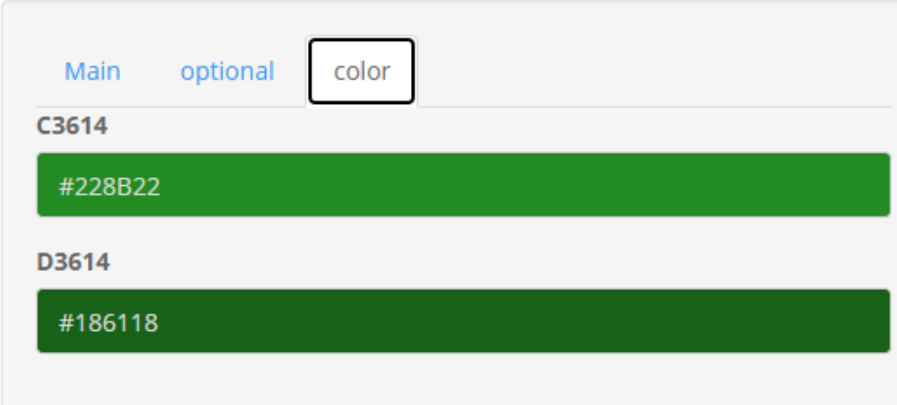
width of arrow:

8

## Optional Input (color)

The individual color of sequencing conditions can be changed in the “color”-panel.

### Microarray-Plotter



The image shows a web interface for a Microarray-Plotter. At the top, there are three tabs: 'Main', 'optional', and 'color'. The 'color' tab is selected and highlighted with a black border. Below the tabs, there are two sections for color selection. The first section is labeled 'C3614' and contains a green color bar with the hex code '#228B22'. The second section is labeled 'D3614' and contains a dark green color bar with the hex code '#186118'.

Condition	Color
C3614	#228B22
D3614	#186118