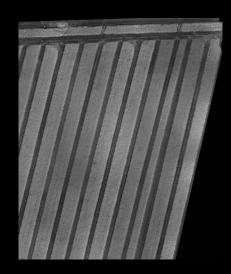
# Science-DB

		•			
marker	mother_penn_nimbus	father_penn	father_nimbus	mother_hattrick	father_hattrick
Bn-A01-p1001022	G	G	G	G	G
Bn-A01-p10026020	G	G	Α	R	Α
Bn-A01-p10027328	Α	Α	G	R	G
Bn-A01-p100441	Т	Т	Т	Т	Т
Bn-A01-p100693	Т	Т	Т	Т	Т
Bn-A01-p10105499	Т	Т	С	Υ	С

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race	cultivar	level	multiplier	batch	batch_status	storage	harvest_year	booking_date	admission_number	laboratory	examination_date	purity
3955 RAW	RAW	BS	7000347	MR 1404	TMTD gebeizt	3	2013	2013-08-01 00:00:00.000	DE013-1472005	NPZ	2013-08-03 00:00:00.000	0
3955 RAW	RAW	BS	7000347	MR 1404	TMTD gebeizt	3	2013	2013-08-01 00:00:00.000	DE013-1472005	NPZ	2013-08-03 00:00:00.000	0
3955 RAW	RAW	BS	7000347	MR 1404	TMTD gebeizt	3	2013	2013-08-01 00:00:00.000	DE013-1472005	NPZ	2013-08-05 00:00:00.000	99.8
3955 RAW	RAW	BS	7000347	MR 1404	TMTD gebeizt	3	2013	2013-08-01 00:00:00.000	DE013-1472005	NPZ	2013-08-06 00:00:00.000	0

Marker chr	position	1	
Bn_A01_p1000115	chrA01	617757	
Bn_A01_p100441	chrA01	2468965	
Bn_A01_p100693	chrA01	2469216	
Bn_A01_p101021	chrA01	2469547	
Bn_A01_p101094	chrA01	2469620	
Bn_A01_p101451	chrA01	2469977	
Bn_A01_p10181972	2	chrA01	8782944
Bn_A01_p101943	chrA01	2470471	
Bn_A01_p10231786	9	chrA01	8828045
Bn_A01_p10249225	5	chrA01	8852208
Bn_A01_p10250255	5	chrA01	8853237
Bn_A01_p10251052	2	chrA01	8854034





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### Science-Db

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### Plant

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- 1. sequelize model:create --name Plant attributes 'title:string, taxon:string,
   gmo:boolean'
- 2. sequelize db:migrate
- 3. express\_route\_gen . --name Plant attributes 'title:string, taxon:string,
   qmo:boolean'

## Plant

• D

```
✓curl -data
  "title=Plant_1&taxon=x&gmo=false"
  http:/
```

### Plant

```
✓ curl -X PUT --data "taxon=y" http://www.science.db/plant/1
```

```
✓curl -X DELETE

http://www.science.db/plant/1
```

### DT

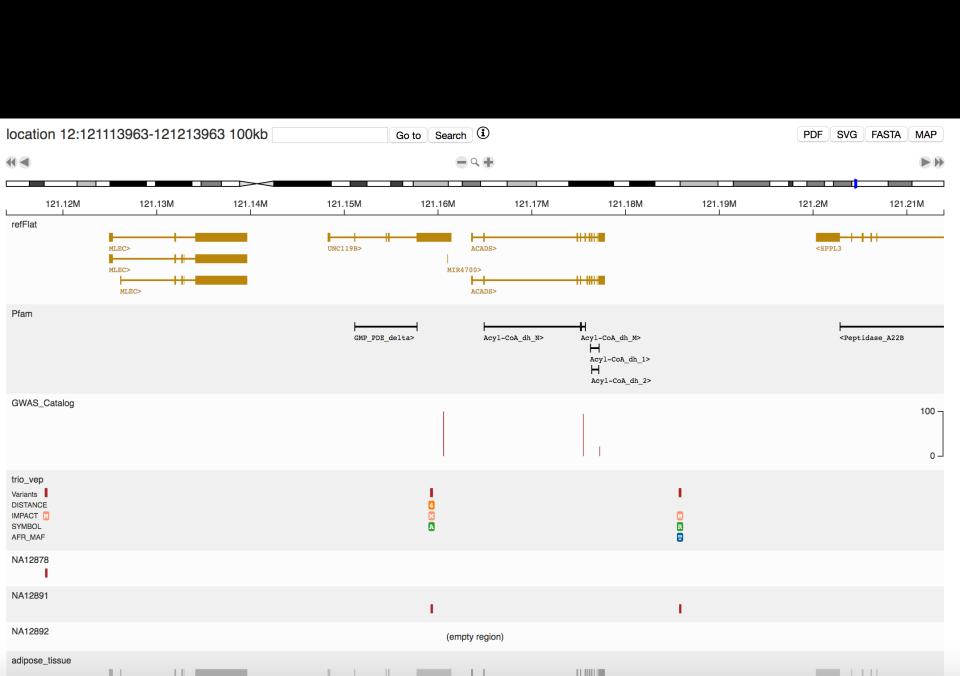
• DT

- curl
 'http://www.science.db/plants/example\_cs
 v'

DT

- curl -F "csv\_file=@plants\_csv.csv"
www.science.db/plants/upload\_csv

#	Name ^	Shits	Fur_color	Actions
1	Alien	false	Transparant	(a) (b) (x)
2	Ghost	false	White	(a) (b) (x)



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```
# Load dependencies
require(httr)
# Login
login.res <- POST('http://213.136.88.239:3030/login',
body=list('email'='m.enders@npz-innovation.de',
'password'='####')
# Load all marker data
markers.res <- GET('http://213.136.88.239:3030/markers')
# To obtain the content of the response as a list of
lists, use:
markers.lst <- content(markers.res)</pre>
```

```
# Convert to data.frame (table)
Reduce(rbind, lapply( content(markers.res)[1:3],
as.data.frame,
stringsAsFactors=FALSE ))[,1:4]

# Gives the following tabular output:
id name chromosome position
1 x chr1 12
```

4 Bn A01 p1000115 chrA01 617757

5 Bn A01 p100441 chrA01 2468965

 $\prod$ 

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minimal coding required

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