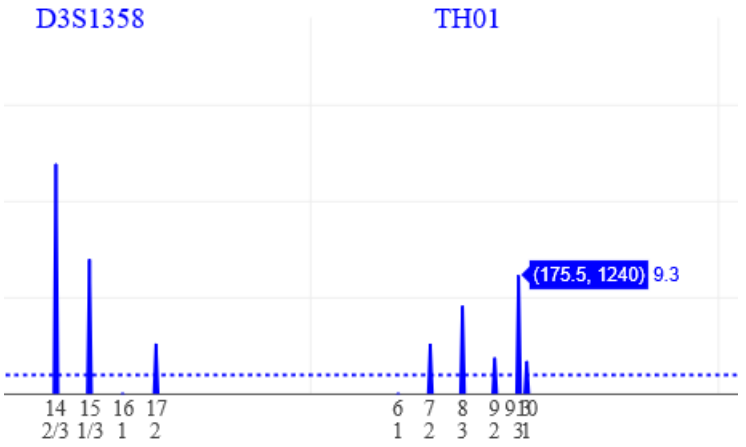
The plot(ly) update in EuroForMix v2.2

What's new?

- From v2.2.x EFM will provide **interactive** plots in browser
  - Supports "mouse-hovering" for detailed data.
  - Supported for both CE and MPS based data (STR/SNP).
- Visualization of MPS based data:
  - Each loci shown separately.
  - Any number of loci possible*.
  - Possible to group different alleles on same allele types (examples next slide)

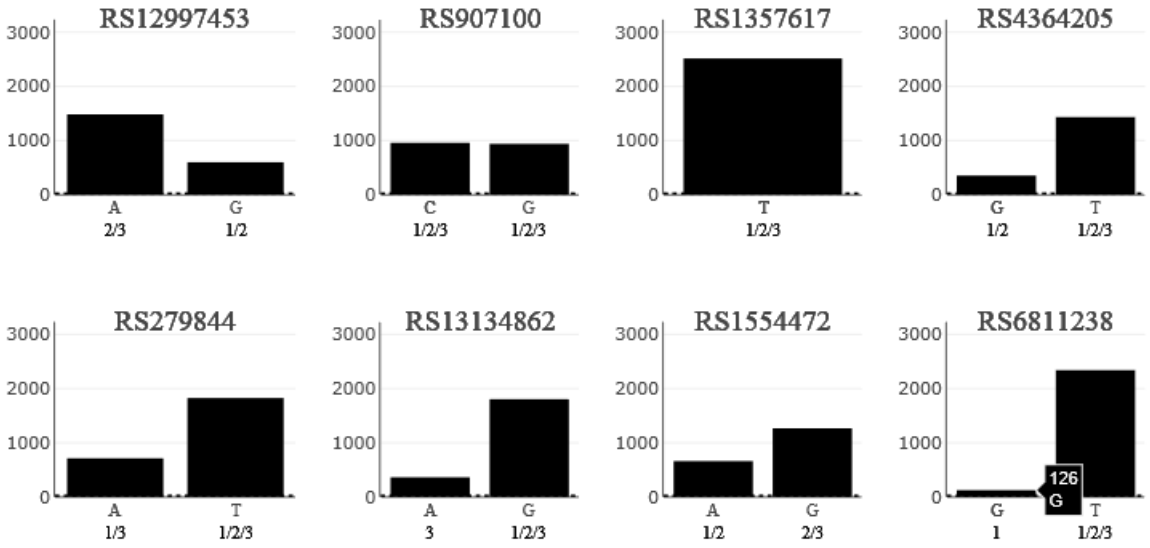
*but 100s of loci will take long time to visualize

CE based STR



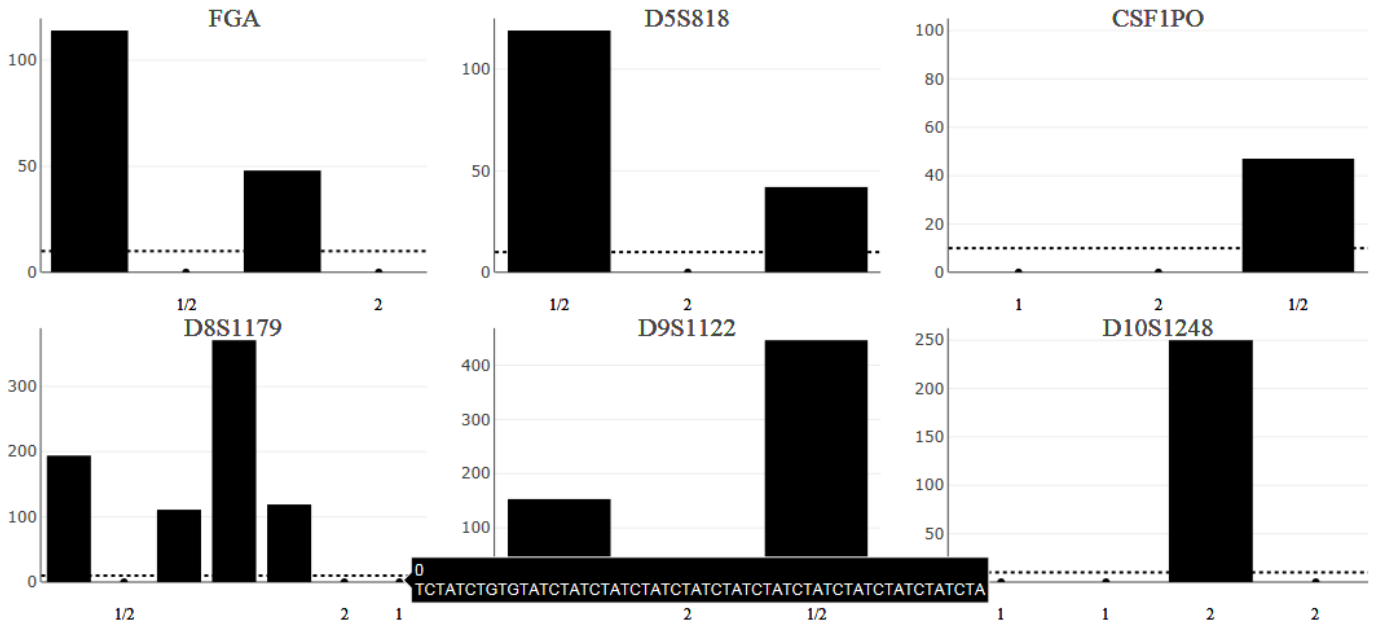
Same allele format as before!

SNPs (MPS based)



Allele is string format:
One of the letters A,C,G,T

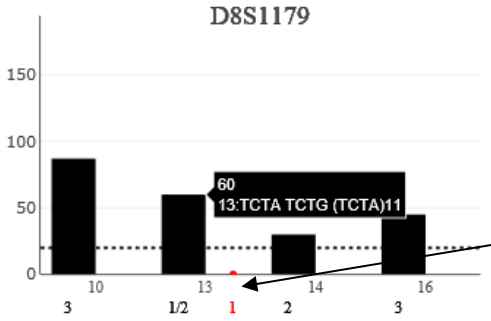
STRs (MPS based)



Allele is string format (any length)

Must not contain “:” or “_” (this leads to grouping)

STRs grouped on RU/CE



Same RU/CE but different sequence variant!
Given by a different color.

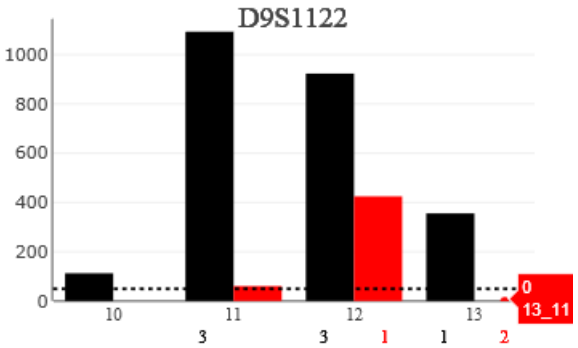
Allele is string format (any length)

The group format is “:”, to seperate RU/CE from sequence.

Must not contain “_”

Example: “13:TCTA TCTG (TCTA)11”

STRs grouped on RU/CE
”The LUS format”



Same as previous but now alleles are given on the “LUS format” **RU_LUS**

Allele is string format (any length)
→ Contains numbers separated with “_”

The group format is “_”, to seperate RU/CE from LUS.

Must not contain “:”

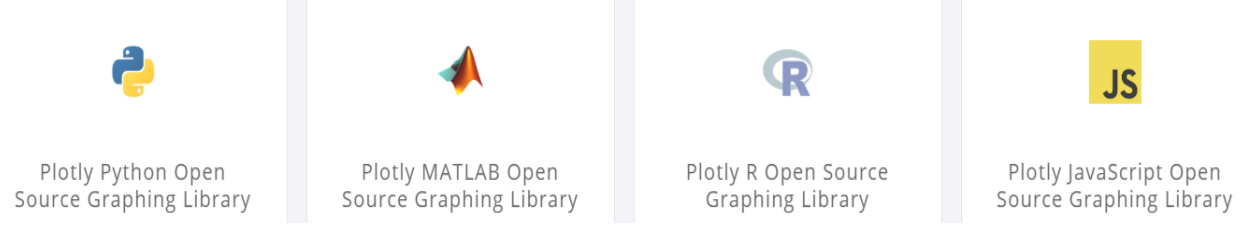
Example: “13_11”

LUS+ format “x_y_z_etc” only group on “x”

Requirement

- Install plotly R-package in R:
  - install.packages("plotly")
- Remove the plotly R-package to avoid showing the interactive visualizations:
  - remove.packages("plotly")

Plotly provides open-source visualization libraries for



New functions added to EFM v2.2.0:

- For visualizing profiles:
  - plotEPG2 (CE based)
  - plotMPS2 (MPS based STR/SNPs)

- For visualizing “Model fitted P.H.”:
  - plotTopEPG2 (CE based)
  - plotTopMPS2 (MPS based STR/SNPs)