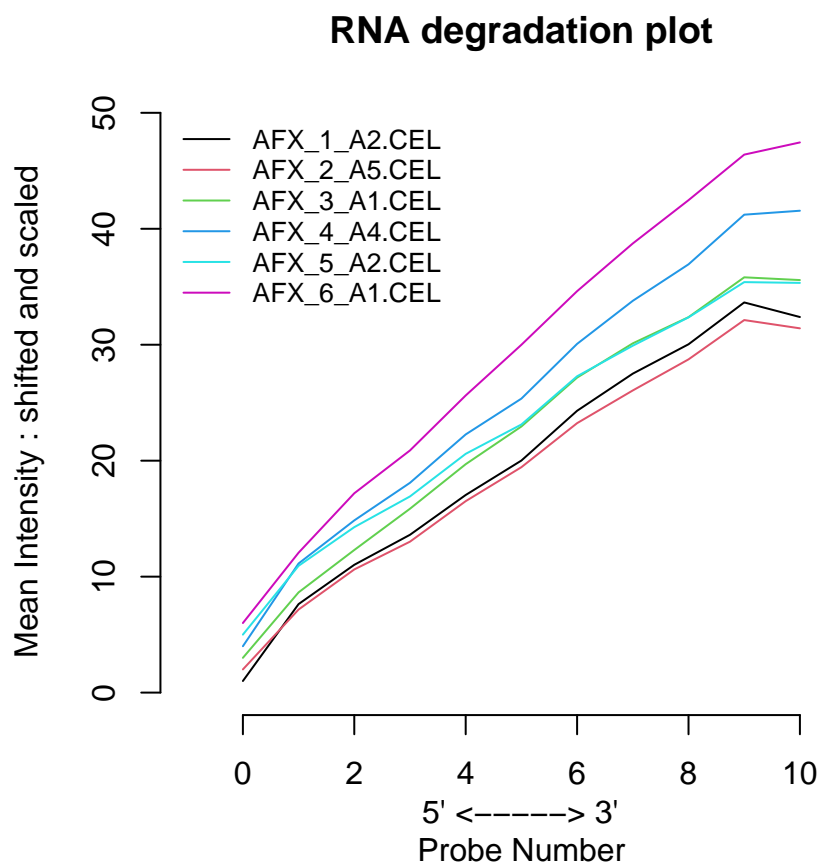# Quality control report generated with `qcmetrics`

lgatto

November 26, 2020
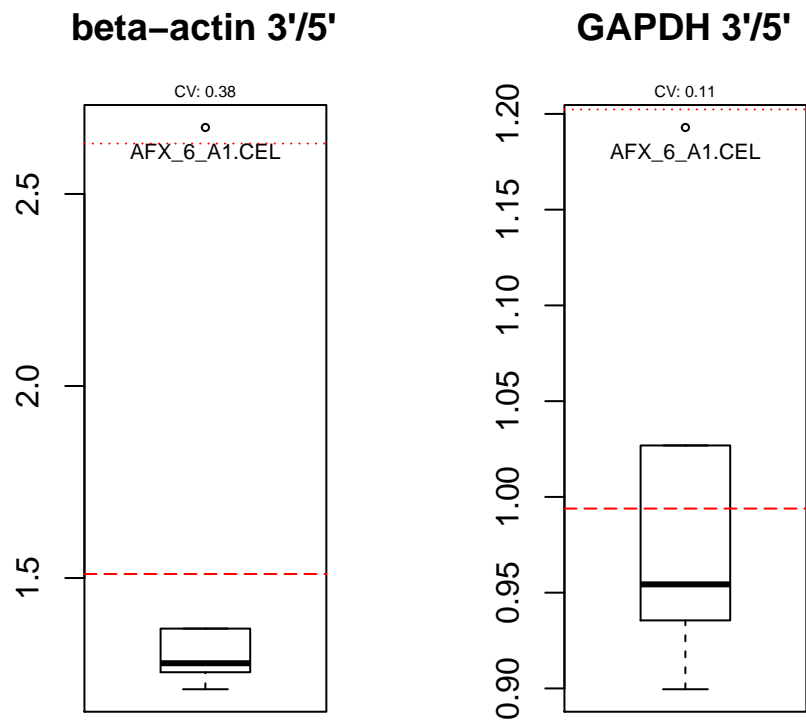
1 Affy RNA degradation slopes

```
## Object of class "QcMetric"
##  Name: Affy RNA degradation slopes
##  Status: TRUE
##  Data: deg
```

2 Affy RNA degradation ratios

```
## Object of class "QcMetric"
##   Name: Affy RNA degradation ratios
##   Status: FALSE
##   Data: yqc
```


beta−actin 3'/5'

CV: 0.38

AFX_6_A1.CEL

GAPDH 3'/5'

CV: 0.11

AFX_6_A1.CEL

3 QC summary

	name	status
1	Affy RNA degradation slopes	TRUE
2	Affy RNA degradation ratios	FALSE

4 Session information

- R version 4.0.0 (2020-04-24), `x86_64-pc-linux-gnu`

- Locale: `LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=fr_FR.UTF-8, LC_COLLATE=en_US.UTF-8,` `LC_MONETARY=fr_FR.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=fr_FR.UTF-8, LC_NAME=C,` `LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=fr_FR.UTF-8, LC_IDENTIFICATION=C`

- Running under: `Ubuntu 18.04.5 LTS`

- Matrix products: default

- BLAS: `/usr/lib/x86_64-linux-gnu/libf77blas.so.3.10.3`

- LAPACK: `/usr/lib/x86_64-linux-gnu/atlas/liblapack.so.3.10.3`

- Base packages: base, datasets, graphics, grDevices, methods, parallel, stats, utils

- Other packages: affy 1.68.0, Biobase 2.50.0, BiocGenerics 0.36.0, gcrma 2.62.0, genefilter 1.72.0, qcmetrics 1.28.0, simpleaffy 2.66.0, xtable 1.8-4, yaqcaffy 1.50.0

- Loaded via a namespace (and not attached): affyio 1.60.0, annotate 1.68.0, AnnotationDbi 1.52.0, BiocManager 1.30.10, Biostrings 2.58.0, bit 4.0.4, bit64 4.0.5, blob 1.2.1, compiler 4.0.0, crayon 1.3.4, DBI 1.1.0, digest 0.6.27, evaluate 0.14, grid 4.0.0, highr 0.8, httr 1.4.2, IRanges 2.24.0, knitr 1.30, lattice 0.20-41, magrittr 2.0.1, Matrix 1.2-18, memoise 1.1.0, Nozzle.R1 1.1-1, pander 0.6.3, preprocessCore 1.52.0, R6 2.5.0, Rcpp 1.0.5, rlang 0.4.8, RSQLite 2.2.1, S4Vectors 0.28.0, splines 4.0.0, stats4 4.0.0, stringi 1.5.3, stringr 1.4.0, survival 3.2-7, tools 4.0.0, vctrs 0.3.5, xfun 0.19, XML 3.99-0.5, XVector 0.30.0, zlibbioc 1.36.0