

Generate a complete library range object

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This short script generates a lookup scoring table of the AAV plasmid library so that it follows the same structure as the mRNA samples so that they can be compared for coverages.

```
suppressPackageStartupMessages(library(knitr))
```

Generate library range object

```
load("data/alignedLibraries.rda")
load("data/LUTdna.rda")
load("data/multipleContfragmentsComplete.rda")
setkey(output.Table, LUTnr)
setkey(LUT.dna, LUTnr)
output.Table <- output.Table[LUT.dna, nomatch = 0]
output.Table[, `:=`(c("Names", "i.Structure"), NULL)]
setnames(output.Table, "Sequence", "fragment")
setkey(output.Table, fragment)

range.idx <- data.table(fragment = mcols(allFragments.ranges)$Sequence, idxFrag = 1:length(allFragments.ranges$Sequence),
  key = "fragment")
output.Table <- output.Table[range.idx, nomatch = 0, allow.cartesian = TRUE]

foundFragments.ranges <- allFragments.ranges[output.Table$idxFrag]
output.Table[, `:=`(c("Reads", "fragment", "idxFrag", "Structure", "LUTnr"),
  NULL)]
output.Table[, `:=`(RNAcount, tCount)]

mcols(foundFragments.ranges) <- c(mcols(foundFragments.ranges), output.Table)

saveRDS(foundFragments.ranges, file = "output/completeLibraryRanges.rds")

devtools::session_info()
```

Session info -----

setting	value
version	R version 3.4.2 (2017-09-28)
system	x86_64, linux-gnu
ui	X11
language	(EN)
collate	en_US.UTF-8
tz	UTC
date	2020-11-02

Packages -----

package	* version	date	source
backports	1.1.1	2017-09-25	CRAN (R 3.4.2)
base	* 3.4.2	2017-10-06	local
Biobase	* 2.36.2	2017-11-29	Bioconductor
BiocGenerics	* 0.22.1	2017-11-29	Bioconductor

BiocParallel	* 1.10.1	2017-11-29	Bioconductor
Biostrings	* 2.44.2	2017-11-29	Bioconductor
bitops	1.0-6	2013-08-17	CRAN (R 3.4.2)
codetools	0.2-15	2016-10-05	CRAN (R 3.4.2)
compiler	3.4.2	2017-10-06	local
data.table	* 1.10.4-2	2017-10-12	url
datasets	* 3.4.2	2017-10-06	local
DelayedArray	* 0.2.7	2017-11-29	Bioconductor
devtools	* 1.13.3	2017-08-02	CRAN (R 3.4.2)
digest	0.6.12	2017-01-27	CRAN (R 3.4.2)
doParallel	* 1.0.11	2017-09-28	CRAN (R 3.4.2)
evaluate	0.10.1	2017-06-24	CRAN (R 3.4.2)
foreach	* 1.4.3	2015-10-13	CRAN (R 3.4.2)
formatR	1.5	2017-04-25	CRAN (R 3.4.2)
GenomeInfoDb	* 1.12.3	2017-11-29	Bioconductor
GenomeInfoDbData	0.99.0	2017-11-29	Bioconductor
GenomicAlignments	* 1.12.2	2017-11-29	Bioconductor
GenomicRanges	* 1.28.6	2017-11-29	Bioconductor
graphics	* 3.4.2	2017-10-06	local
grDevices	* 3.4.2	2017-10-06	local
grid	3.4.2	2017-10-06	local
hms	0.3	2016-11-22	CRAN (R 3.4.2)
htmltools	0.3.6	2017-04-28	CRAN (R 3.4.2)
httr	1.3.1	2017-08-20	CRAN (R 3.4.2)
hwriter	1.3.2	2014-09-10	CRAN (R 3.4.2)
IRanges	* 2.10.5	2017-11-29	Bioconductor
iterators	* 1.0.8	2015-10-13	CRAN (R 3.4.2)
kableExtra	* 0.5.2	2017-09-15	url
knitr	* 1.17	2017-08-10	CRAN (R 3.4.2)
lattice	0.20-35	2017-03-25	CRAN (R 3.4.2)
latticeExtra	0.6-28	2016-02-09	CRAN (R 3.4.2)
magrittr	1.5	2014-11-22	CRAN (R 3.4.2)
Matrix	1.2-11	2017-08-21	url
matrixStats	* 0.52.2	2017-04-14	CRAN (R 3.4.2)
memoise	1.1.0	2017-04-21	CRAN (R 3.4.2)
methods	* 3.4.2	2017-10-06	local
parallel	* 3.4.2	2017-10-06	local
R6	2.2.2	2017-06-17	CRAN (R 3.4.2)
RColorBrewer	1.1-2	2014-12-07	CRAN (R 3.4.2)
Rcpp	0.12.13	2017-09-28	url
RCurl	1.95-4.8	2016-03-01	CRAN (R 3.4.2)
readr	1.1.1	2017-05-16	CRAN (R 3.4.2)
rlang	0.1.2	2017-08-09	CRAN (R 3.4.2)
rmarkdown	1.6	2017-06-15	url
rprojroot	1.2	2017-01-16	CRAN (R 3.4.2)
Rsamtools	* 1.28.0	2017-11-29	Bioconductor
rvest	0.3.2	2016-06-17	CRAN (R 3.4.2)
S4Vectors	* 0.14.7	2017-11-29	Bioconductor
ShortRead	* 1.34.2	2017-11-29	Bioconductor
stats	* 3.4.2	2017-10-06	local
stats4	* 3.4.2	2017-10-06	local
stringi	1.1.5	2017-04-07	url
stringr	1.2.0	2017-02-18	CRAN (R 3.4.2)
SummarizedExperiment	* 1.6.5	2017-11-29	Bioconductor
tibble	1.3.4	2017-08-22	CRAN (R 3.4.2)
tools	3.4.2	2017-10-06	local
utils	* 3.4.2	2017-10-06	local

withr	2.0.0	2017-07-28	url
xml2	1.1.1	2017-01-24	CRAN (R 3.4.2)
XVector	* 0.16.0	2017-11-29	Bioconductor
yaml	2.1.14	2016-11-12	CRAN (R 3.4.2)
zlibbioc	1.22.0	2017-11-29	Bioconductor