Designing PCR Diagnostics that Discriminate HPV Serotypes by DNA Sequence

chebuu

Introduction

The first infectious cause of cancer was identified in 1911 by Peyton Rous who demonstrated the transmissibility of a tumor in fowl through injection of sub 0.2 micron filtrate of the tumor [?].

Installing OligAarrayAux Download OligoArrayAux and see the following vignette for installation instructions.

```
library(devtools)
devtools::install_github('chebuu/Design-Group-Specific-Primers')
library(Design_Group_Specific_Primers)
vignette('Installing-OligoArrayAux', package = 'Design_Group_Specific_Primers')
```

Install Bioconductor packages

```
# Install from Bioconductor
if (!requireNamespace("BiocManager", quietly = T))
   install.packages("BiocManager")
BiocManager::install("Biostrings")
BiocManager::install("DECIPHER")

# Open Biostrings vignettes
library(Biostrings)
browseVignettes("Biostrings")

# Open DECIPHER docs and vignettes
library(DECIPHER)
help("DECIPHER")
browseVignettes("DECIPHER")
```

```
# https://bioconductor.org/packages/release/bioc/html/twoddpcr.html
# https://bioconductor.org/packages/release/bioc/html/ddCt.html
# https://bioconductor.org/packages/3.5/bioc/html/mBPCR.html
```

Data

```
library(dplyr)
library(tidyr)
library(stringr)

library(Biostrings)
library(DECIPHER)
```

I included GenBank queries for all the HPV DNA in this repo. If you want to run them just paste in the search bar at: https://www.ncbi.nlm.nih.gov/nuccore

All HPV

https://www.ncbi.nlm.nih.gov/nuccore

```
"Human papillomavirus" [Primary Organism]
AND viruses [filter]
NOT Polyamides [All Fields]
NOT Method [All Fields]
NOT Patent [All Fields]
```

Complete Genomes

https://www.ncbi.nlm.nih.gov/nuccore

```
"Human papillomavirus" [Primary Organism]
AND "complete genome" [All Fields]
NOT Isolate [Title]
```

Oral Isolates

https://www.ncbi.nlm.nih.gov/nuccore

```
https://www.ncbi.nlm.nih.gov/nuccore

"Human papillomavirus"[Primary Organism]

AND viruses[filter]

NOT Polyamides[All Fields]

NOT Method[All Fields]

NOT Patent[All Fields]

AND Oral[All Fields]
```

L1 gene

A collection of l1 DNA sequences (avg. ~600bp) from various oral isolates of HPV (extracted from results of GenBank query above) are aligned and loaded in SQLite (RAM) along with annotations from GenBank that describe the serotype of each isolate.

```
doAlignment <- function(xset) {
   useqs <- unique(xset)
   uidxs <- match(xset, useqs)
   aseqs <- AlignSeqs(useqs, verbose=F)</pre>
```

```
aseqs[uidxs]
}
dbConn <- dbConnect(SQLite(), ':memory:')</pre>
Oral.L1.seqs <- readDNAStringSet('HPV.oral.L1.fasta') %>% doAlignment
Oral.L1.vars <- read.csv('HPV.oral.L1.csv', stringsAsFactors = F)</pre>
print(Oral.L1.seqs)
##
         A DNAStringSet instance of length 31
##
               width seq
                  607 ----- gi|944543704|gb|K...
## [1]
                  607 ----- gi|944543703|gb|K...
##
      [2]
                  607 ----- gi|944543701|gb|K...
## [3]
                607 ----- gi|944543699|gb|K...
## [4]
## [5]
               607 ----- gi|944543697|gb|K...
                   . . . . . . .
## [27]
                  607 ----- GTTAATAAACTCCATTATCGAA gi|440573440|gb|K...
                   607 -----....GTTAGTTAACAGCACTATTCAG gi|440573438|gb|K...
## [28]
## [29]
                   607 ----- ATTAAAAAATACAGTAATTGAA gi|440573436|gb|K...
## [30]
                   607 ----- gi | 440573434 | gb | K...
## [31]
                   607 ----- gilatoria gilato
Seqs2DB(Oral.L1.seqs, 'XStringSet', dbConn, '')
## Adding 31 sequences to the database.
## 31 total sequences in table Segs.
## Time difference of 0.1 secs
Add2DB(Oral.L1.vars %>% mutate(identifier = SVAR), dbConn)
## Expression:
## alter table Seqs add column GI INTEGER
##
## Expression:
## update Seqs set GI = :GI where row_names = :row_names
## Expression:
## alter table Seqs add column SVAR INTEGER
##
## Expression:
## update Seqs set SVAR = :SVAR where row_names = :row_names
## Expression:
## alter table Seqs add column ISO INTEGER
## Expression:
## update Seqs set ISO = :ISO where row_names = :row_names
##
## Expression:
## alter table Seqs add column GENE INTEGER
## Expression:
```

```
## update Seqs set GENE = :GENE where row_names = :row_names
##
## Expression:
## update Seqs set identifier = :identifier where row_names = :row_names
## Added to table Segs: "GI" and "SVAR" and "ISO" and "GENE" and "identifier".
## Time difference of 0.03 secs
dbGetQuery(dbConn, "select * from Seqs") %>% head(4)
##
    row_names identifier
## 1
            1
                   HPV18
## 2
            2
                   HPV18
## 3
            3
                   HPV16
## 4
            4
                   HPV18
##
                                                                                      description
## 1 gi|944543704|gb|KT365847.1| Human papillomavirus isolate HPV18-14 L1 protein gene, partial cds
## 2 gi|944543703|gb|KT365846.1| Human papillomavirus isolate HPV18-13 L1 protein gene, partial cds
## 3 gi|944543701|gb|KT365845.1| Human papillomavirus isolate HPV16-5 L1 protein gene, partial cds
## 4 gi|944543699|gb|KT365844.1| Human papillomavirus isolate HPV18-12 L1 protein gene, partial cds
##
           GI SVAR ISO GENE
## 1 944543704 HPV18 14
## 2 944543703 HPV18 13
                          T.1
## 3 944543701 HPV16
                      5
                          L1
## 4 944543699 HPV18 12
                          T.1
Design HPV16-specific F/R primers using DECIPHER utilities.
tiles.L1 <- TileSeqs(</pre>
 dbFile = dbConn,
 minLength = 18,
 maxLength = 29,
 minCoverage = 0.8
## -----
## Time difference of 7.48 secs
print(
  tiles.L1[,c(6,11)] %>% sample_n(6)
                               target_site
##
    misprime
## 1
       FALSE GTATTGGGACACAACTAAATTTTGTGATG
## 2
       FALSE TTACCTGATGGCACCCTATACAATCCAGA
## 3
       FALSE ATAAGCAGGATATTCCTAAGGTTTCTGCA
## 4
        TRUE ATGTCCACCTATTCAGTTAATAAATACAG
## 5
       FALSE GCAGATATGTCTGTATACAATCCAGACAA
       FALSE AAACAATCAGATGATAATAGACAGAATGT
oligos.L1 <- DesignPrimers(</pre>
 tiles = tiles.L1,
  identifier = 'HPV16',
 worstScore = -1E3,
```

maxPermutations = 5,

```
minGroupCoverage = 0.85,
  minCoverage = 0.85,
  minLength = 20,
  maxLength = 28
)
##
## HPV16 (7 candidate primers):
  _____
## Time difference of 7.4 secs
head(oligos.L1)
##
       identifier start_forward start_reverse start_aligned_forward
## 201
           HPV16
                            249
                                          275
                                                                248
## 231
           HPV16
                            284
                                          302
                                                                278
## 232
                            287
                                                                279
           HPV16
                                          304
  236
           HPV16
                            288
                                          306
                                                                283
##
## 237
           HPV16
                            288
                                          306
                                                                284
## 238
           HPV16
                            288
                                          307
                                                                285
##
       start_aligned_reverse permutations_forward permutations_reverse
## 201
                         276
                                                5
                                                                     5
## 231
                         306
                                                5
                                                                     5
## 232
                         307
                                                5
                                                                     5
## 236
                         311
                                                5
                                                                     5
                                                5
## 237
                         312
                                                                     5
                                                5
## 238
                         313
                                                                     5
       score_forward score_reverse
##
                                            forward_primer.1
## 201
       -6.27037.... -0.00038.... TTGGTTTTCCTGACACCTCATTTTA
  231
       -0.00333.... -0.00082....
                                       ACACAGCGGCTGGTTTGGGC
  232
       -0.00932.... -0.00024....
                                        CACAGCGGCTGGTTTGGGCC
  236
       -0.20587.... -0.00023....
##
                                        GCGGCTGGTTTGGGCCTGTG
  237
        -0.01501.... -0.00047....
                                        CGGCTGGTTTGGGCCTGTGT
##
  238
       -6.07531.... -0.00115....
                                        GGCTGGTTTGGGCCTGTGTA
##
                  forward_primer.2
                                           forward_primer.3
## 201 AAAGTGAAGTTCCACTGGATATTTGTA TGCCTTAGTGGACCCTACAGTATA
  231
          GAAAAGGAAAGACTAGTGTGGGC
                                       CGCGAGCGATTAGTGTGGAA
## 232
             AAGGAAAGACTAGTGTGGGCC
                                      CGCGAGCGATTAGTGTGGAAA
## 236
              AAGACTAGTGTGGGCCTGTG GCGAGCGATTAGTGTGGAAATTTA
##
  237
              AGACTAGTGTGGGCCTGTGC
                                       AGACTGGTTTGGGCCTGTAG
##
  238
              GACTAGTGTGGGCCTGTGCA
                                       GACTGGTTTGGGCCTGTAGA
##
                   forward_primer.4
                                              forward_primer.5
## 201 AATTTGCTTTAGCAGATATGTCAGTCTA
                                     TCGCCTTGGTAGATATGAATGTCTA
## 231
               CATGAGCGTTTAGTGTGGCG
                                          AAGGAAAGACTGGTTTGGGC
## 232
               ATGAGCGTTTAGTGTGGCGT
                                          AGGAAAGACTGGTTTGGGCC
## 236
               AAGACTGGTTTGGGCCTGTA
                                         AGCGTTTAGTGTGGCGTTTAC
## 237
              GCGTTTAGTGTGGCGTTTACG
                                     GCGAGCGATTAGTGTGGAAATTTAC
##
  238
            GCGTTTAGTGTGGCGTTTACGT GCGAGCGATTAGTGTGGAAATTTACA
##
              reverse_primer.1
                                           reverse_primer.2
## 201 GAGGTGTCAGGAAAACCAAACTT TACAAATATCCAGTGGAACTTCACTTTT
## 231
          AGCCGCTGTGTATCTGGATT
                                  ACACTAGTCTTTCCTTTTCTGGGTT
## 232
          CAGCCGCTGTGTATCTGGAT
                                  CACACTAGTCTTTCCTTTTCTGGGT
## 236
          AAACCAGCCGCTGTGTATCT
                                   GCCCACACTAGTCTTTCCT
## 237
         CAAACCAGCCGCTGTGTATC
                                    GCCCACACTAGTCTTTCCTTTTC
```

```
## 238
          CCAAACCAGCCGCTGTGTAT
                                     GGCCCACACTAGTCTTTCCTTTT
##
               reverse_primer.3
                                              reverse_primer.4
## 201 TGTAGGGTCCACTAAGGCAAATTT AGACTGACATATCTGCTAAAGCAAATTT
## 231
           AATCGCTCGCGGTCTGGGTT
                                          AAACGCTCATGGTCAGAGTT
## 232
           TAATCGCTCGCGGTCTGGGT
                                      CACTAAACGCTCATGGTCAGAGT
## 236
           ACACTAATCGCTCGCGGTCT
                                     GCCCAAACCAGTCTTTCCA
## 237
        GCCCAAACCAGTCTTTCCTTTTC
                                        CCACACTAAACGCTCATGGTC
## 238
         GCCCAAACCAGTCTTTCCTTTT
                                        GCCACACTAAACGCTCATGGT
##
                  reverse_primer.5 forward_efficiency.1 forward_efficiency.2
## 201 GACATTCATATCTACCAAGGCGAATCT
                                                0.8339538
                                                                      0.8284785
         AAACCAGTCTTTCCTTTTCAGGATT
                                                0.9976087
                                                                      0.8209337
## 232
        CCAAACCAGTCTTTCCTTTTCAGGAT
                                                0.9987960
                                                                      0.8996088
## 236
            CCACACTAAACGCTCATGGTCA
                                                0.9987474
                                                                      0.9127847
## 237
              CACACTAATCGCTCGCGGTC
                                                0.9957214
                                                                      0.9361697
## 238
              CCACACTAATCGCTCGCGGT
                                                                      0.9767059
                                                0.9859330
##
       forward_efficiency.3 forward_efficiency.4 forward_efficiency.5
## 201
                  0.8905282
                                        0.8600553
                                                               0.8531185
## 231
                  0.8767872
                                        0.8416041
                                                               0.8159230
## 232
                  0.9008893
                                        0.8601513
                                                               0.8485258
## 236
                  0.9127556
                                        0.9438210
                                                               0.8215438
## 237
                  0.8015350
                                        0.8500537
                                                               0.9127556
## 238
                  0.9105089
                                        0.9458488
                                                               0.9484353
##
       reverse_efficiency.1 reverse_efficiency.2 reverse_efficiency.3
## 201
                  0.9283584
                                        0.8692461
                                                               0.9066815
## 231
                  0.8941688
                                        0.8974904
                                                               0.9989823
## 232
                  0.8768771
                                        0.8541983
                                                               0.9957801
## 236
                  0.9203204
                                                               0.9243034
                                        0.8333086
## 237
                  0.9137364
                                        0.8209337
                                                               0.9233699
## 238
                  0.9500386
                                        0.9443670
                                                               0.8935778
##
       reverse_efficiency.4 reverse_efficiency.5 forward_coverage.1
## 201
                  0.8127476
                                        0.9368589
                                                             0.444444
## 231
                  0.8755932
                                        0.8085530
                                                             0.444444
## 232
                  0.8794141
                                        0.8211595
                                                             0.444444
## 236
                                                             0.444444
                  0.9405149
                                        0.8775017
## 237
                  0.8451844
                                        0.9707554
                                                             0.444444
## 238
                  0.9113278
                                                             0.444444
                                        0.9687265
##
       forward coverage.2 forward coverage.3 forward coverage.4 forward coverage.5
## 201
                0.1111111
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
## 231
                0.1111111
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
## 232
                0.1111111
                                                        0.1111111
                                    0.1111111
                                                                            0.1111111
## 236
                0.1111111
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
## 237
                0.1111111
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
   238
                0.1111111
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
##
       reverse_coverage.1 reverse_coverage.2 reverse_coverage.3 reverse_coverage.4
## 201
                0.444444
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
## 231
                0.444444
                                                        0.1111111
                                    0.1111111
                                                                            0.1111111
## 232
                0.444444
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
## 236
                0.444444
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
## 237
                0.444444
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
## 238
                0.444444
                                    0.1111111
                                                        0.1111111
                                                                            0.1111111
##
                                                         mismatches_forward
       reverse_coverage.5
## 201
                0.1111111
## 231
                0.1111111 HPV18 (0.0986%) HPV11 (0.0393%) HPV17 (0.192%)
## 232
                0.1111111
                                             HPV18 (0.437%) HPV17 (0.495%)
```

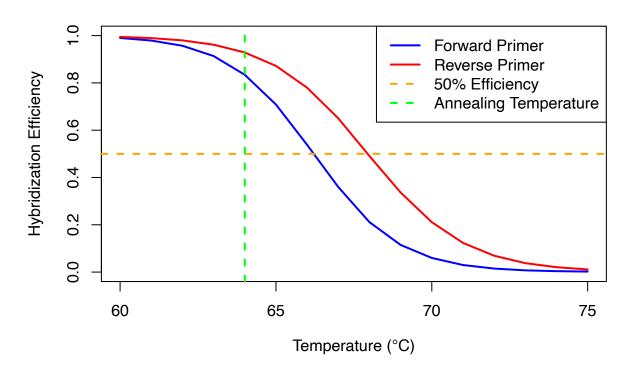
```
## 236
                0.1111111
                                             HPV18 (20.5%) HPV17 (0.114%)
## 237
                0.1111111
                                             HPV18 (1.26%) HPV17 (0.238%)
## 238
                0.1111111
##
                    mismatches_reverse
## 201
                      HPV17 (0.0296%)
## 231 HPV4 (0.0656%) HPV17 (0.0125%)
                       HPV4 (0.0189%)
## 232
                      HPV17 (0.0207%)
## 236
## 237
                      HPV17 (0.0426%)
## 238
                        HPV17 (0.11%)
```

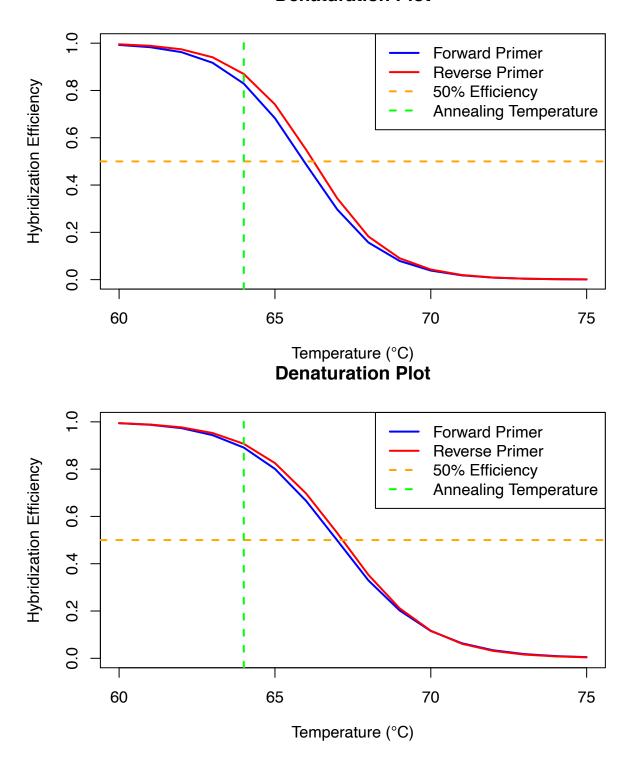
Honestly, I don't really understand the dimensions of the dataframe output by DECIPHER::DesignPimers. If I remember correctly, it's a 7x17 matrix where each cell holds a list of 5 oligos. Unfortunately, I can't print the matrix to stdout, which makes debugging slow, so I'll just deal with this issue later I guess...

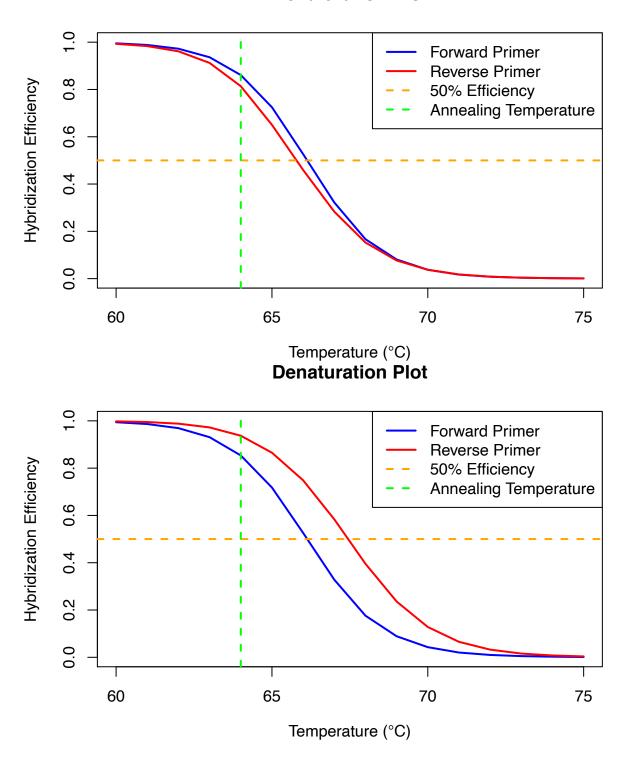
Plot hybridization curves for the reverse compliment of each primer pair (5) in each primer set (7).

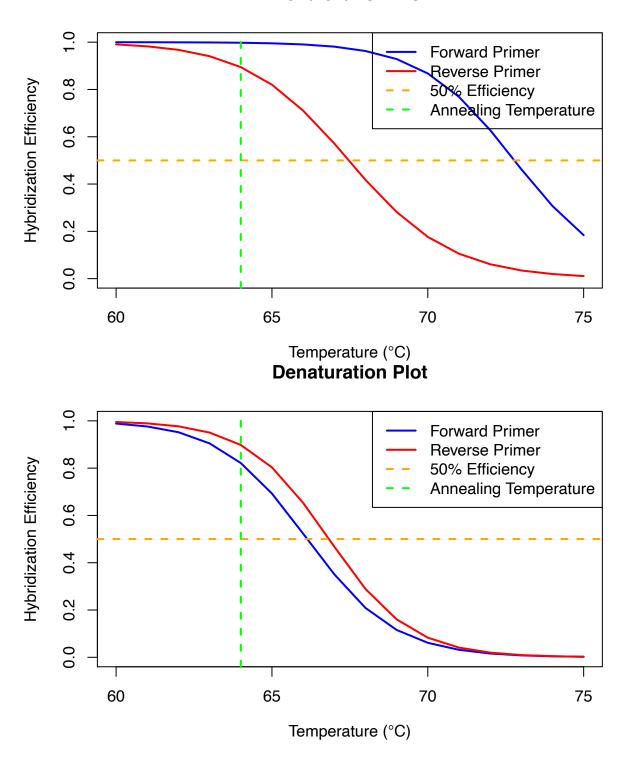
```
plotMeltCurves <- function(temps, effs) {</pre>
  plot(
    temps, effs[,1], ylim=c(0,1),
    ylab="Hybridization Efficiency",
    xlab=expression(paste("Temperature (", degree, "C)", sep="")),
    type="1", 1wd=2, col="Blue", main="Denaturation Plot"
  lines(temps, effs[,2], col="Red", lwd=2)
  abline(h=0.5, lty=2, lwd=2, col="Orange")
  abline(v=64, lty=2, lwd=2, col="Green")
  legend(
    "topright",
    legend = c(
      "Forward Primer",
      "Reverse Primer",
      "50% Efficiency",
      "Annealing Temperature"
    ),
    col = c("Blue", "Red", "Orange", "Green"),
    lwd = c(2, 2, 2, 2), lty = c(1, 1, 2, 2)
}
meltCurves <-
  function(primers, target=reverseComplement(DNAStringSet(primers)), temps=60:75, P=4e-7, ions=.225, do
    fxn <- function(temp) CalculateEfficiencyPCR(primers, target, temp, P=P, ions=ions, ...)</pre>
    effs <- matrix(unlist(lapply(temps, fxn)), ncol=2, byrow=TRUE)
    if (doPlot) plotMeltCurves(temps, effs)
    list(temps = temps, effs = effs)
  }
nsets <- nrow(oligos.L1)</pre>
npair <- ncol(oligos.L1)</pre>
for (i in 1:nsets)
  for (j in 1:npair)
    tryCatch(
```

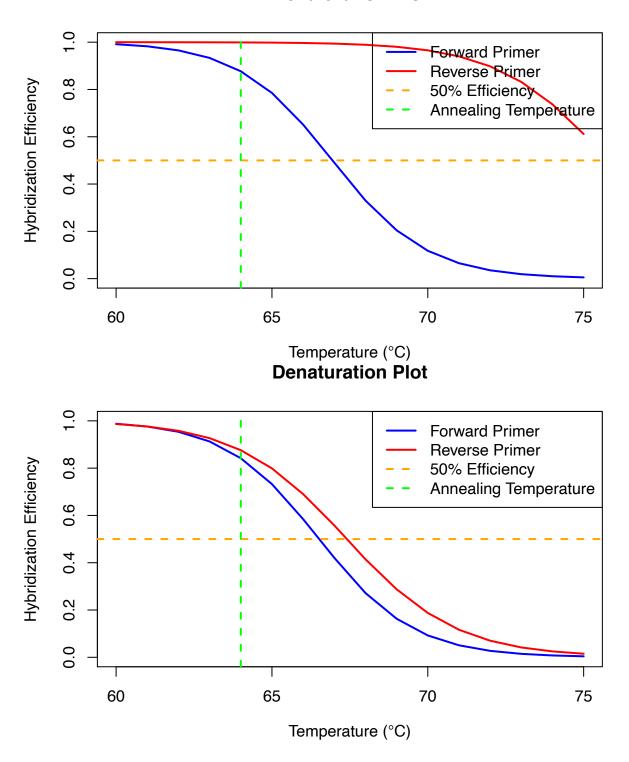
```
c(
    oligos.L1$forward_primer[i,j],
    oligos.L1$reverse_primer[i,j]
    ) %>% meltCurves
},
error = function(e) NULL
    # # ¿ --- It's supposed to be 70 x 17p --- ?
    # warning(sprintf('%s [iteration i=%s j=%s]', e, i, j))
)
```

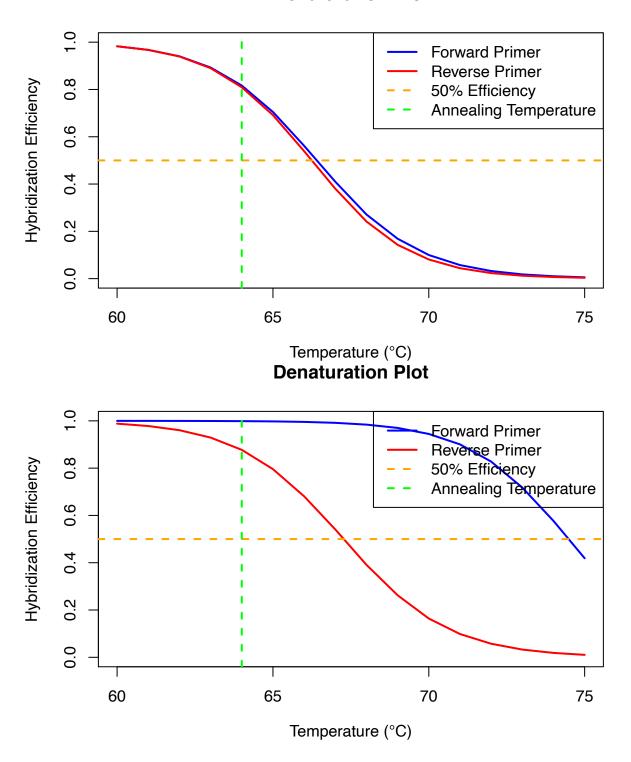


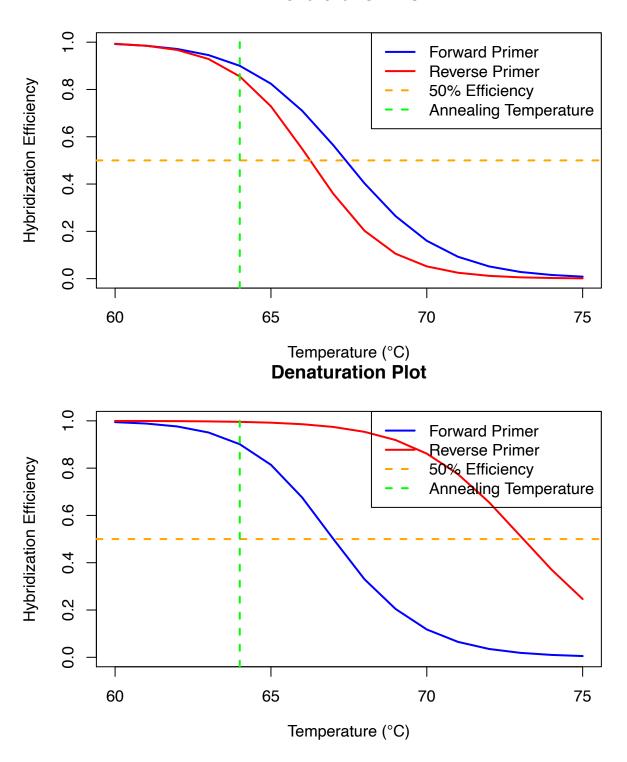


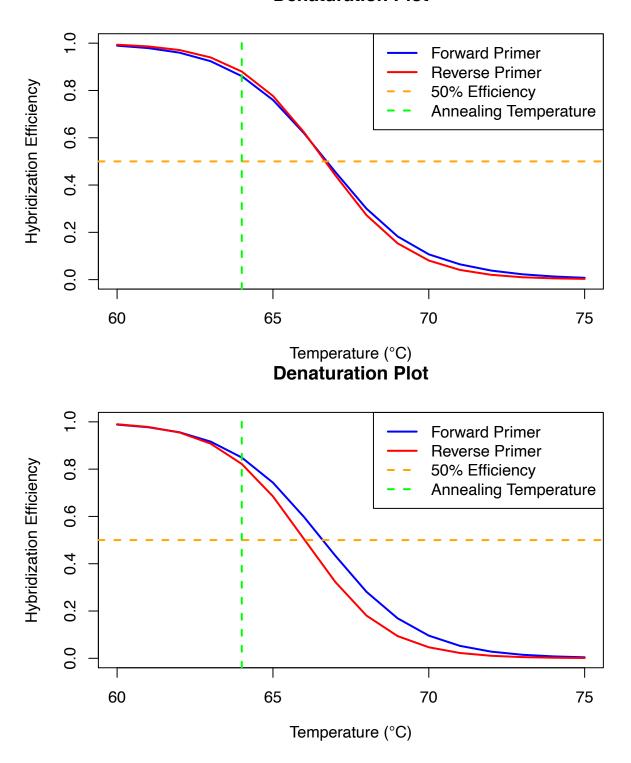


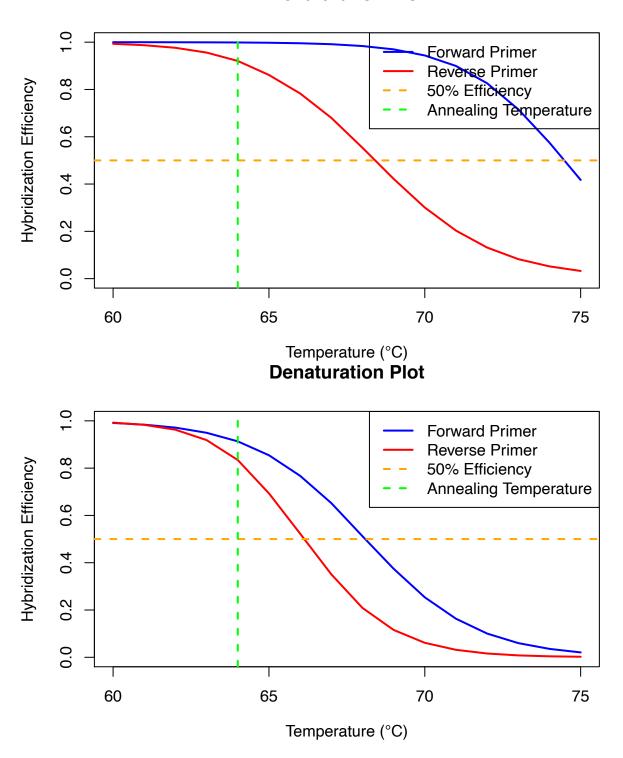


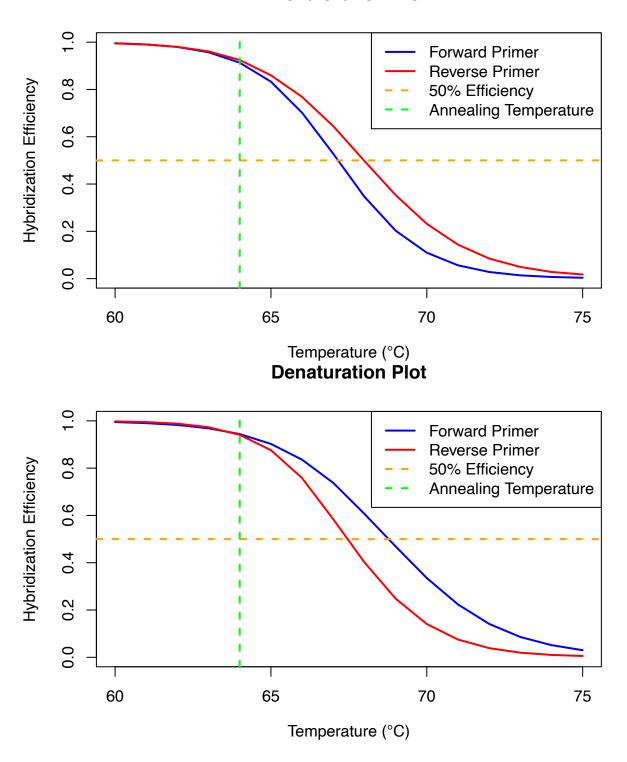


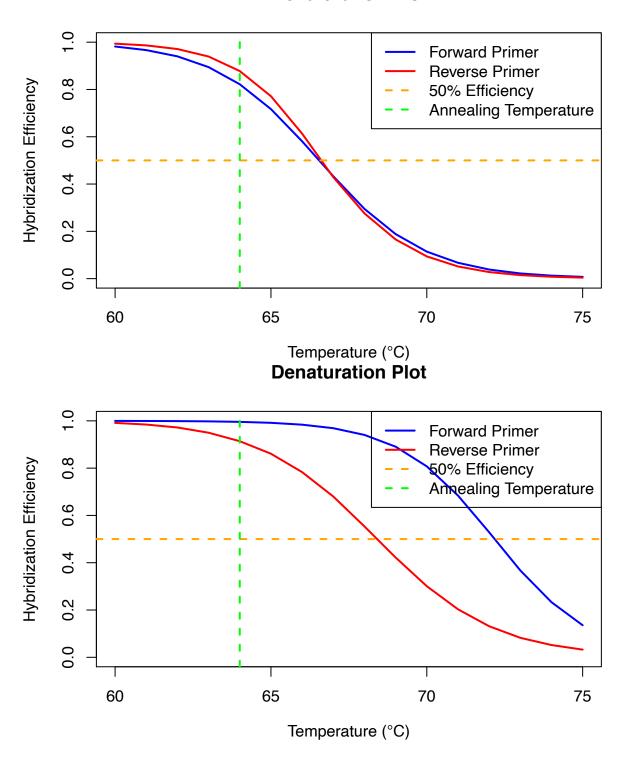


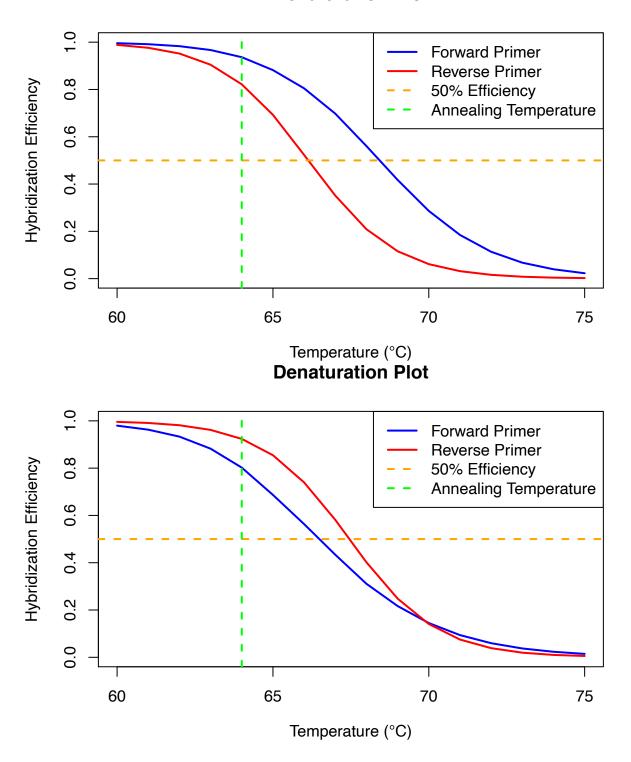


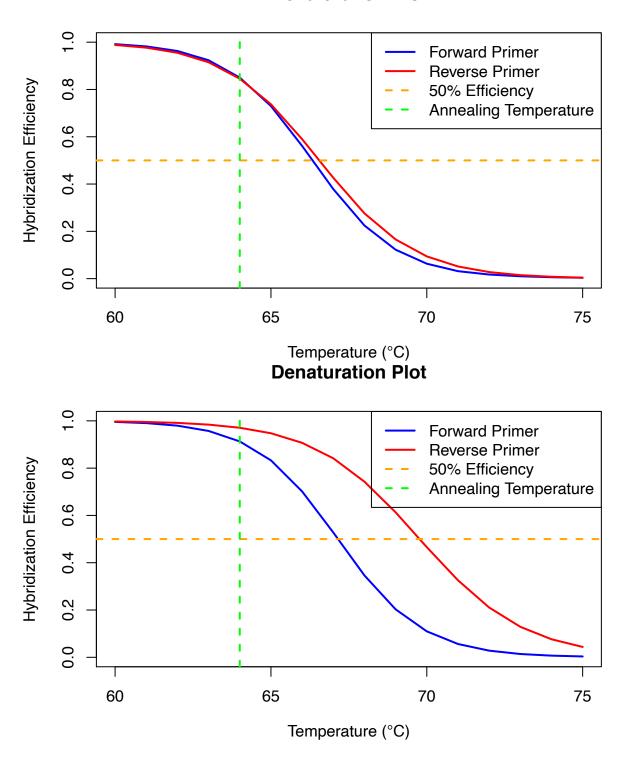


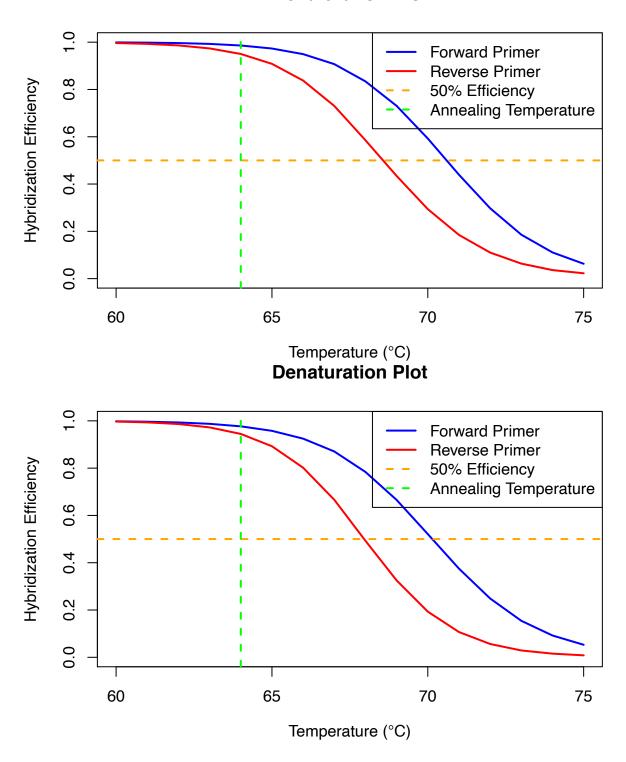


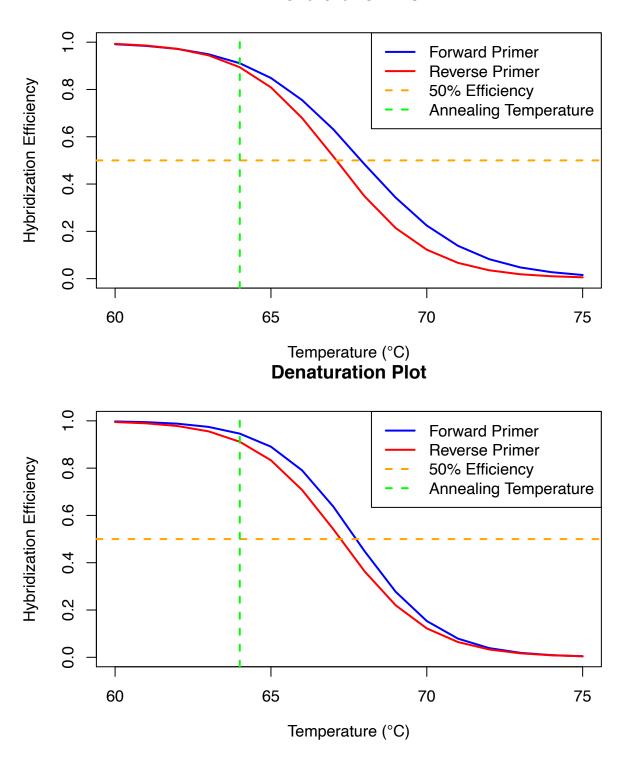


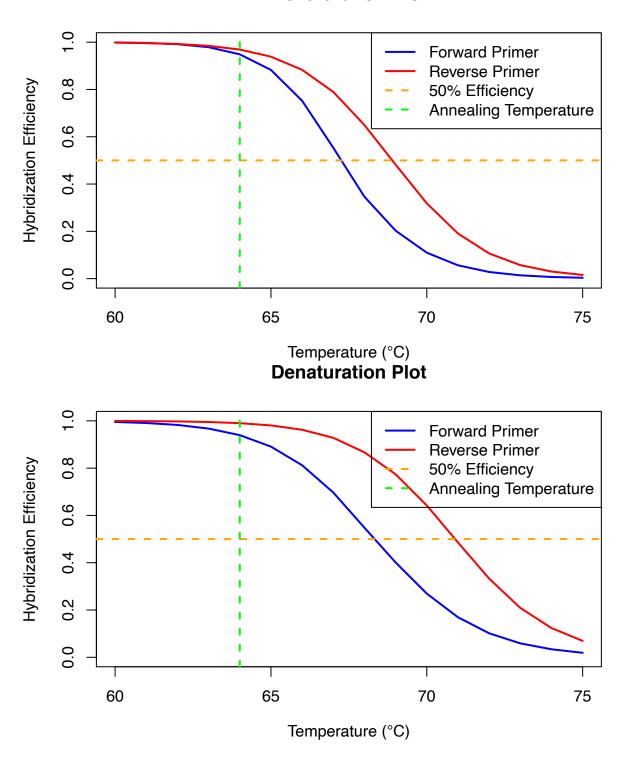


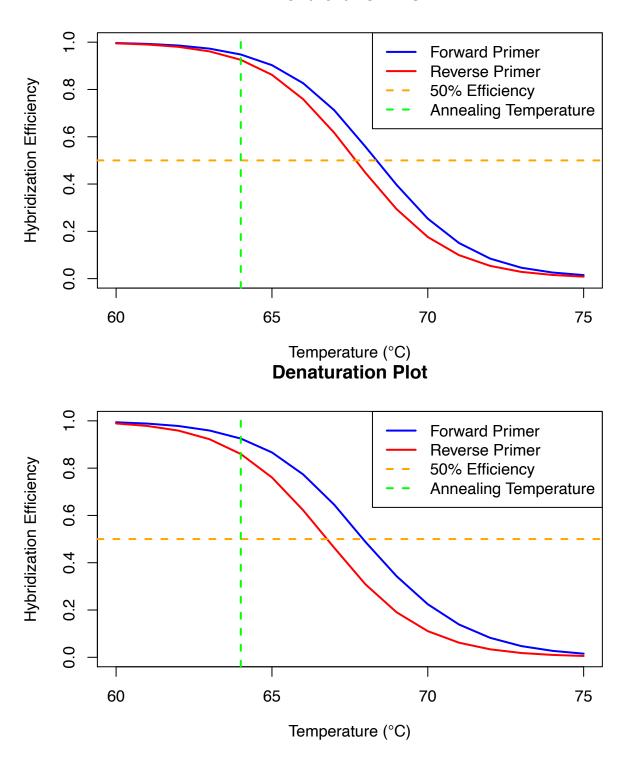


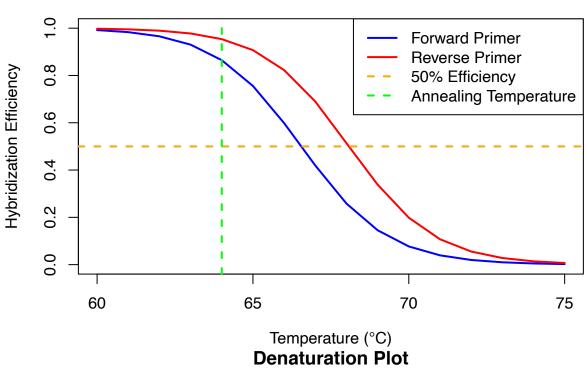


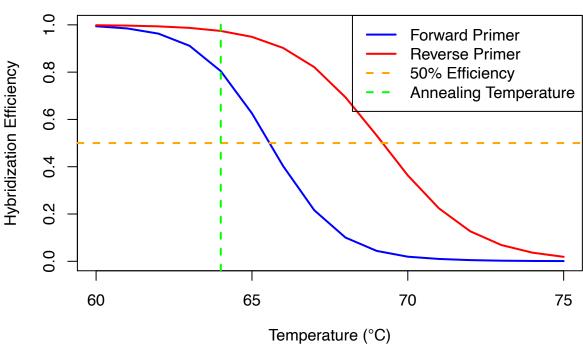












More primer designs (RFLP, sequencing, etc.):

```
TYPE <- 'sequence'
MIN_LENGTH <- 15
MAX_LENGTH <- 25
MIN_SIZE <- 60
```

```
MAX_SIZE <- 100
LEVELS <- 2
RESOLUTION <- 3
ENZYMES <- NULL
DesignSignatures(
 dbConn,
 type=TYPE,
 minLength=MIN_LENGTH,
 maxLength=MAX_LENGTH,
 minProductSize=MIN_SIZE,
 maxProductSize=MAX_SIZE,
 resolution=RESOLUTION,
 levels=LEVELS,
 enzymes=ENZYMES
)
## Tallying 8-mers for 5 groups:
## =----
##
## Time difference of 1.65 secs
##
## Designing primer sequences based on the group 'HPV18':
##
## Time difference of 82.94 secs
## Selecting the most common primer sequences:
## -----
##
## Time difference of 21.82 secs
##
## Determining PCR products from each group:
##
## Time difference of 8.55 secs
##
## Scoring primer pair combinations:
##
## Time difference of 0.01 secs
## Choosing optimal forward and reverse pairs:
## -----
##
## Time difference of 4.03 secs
##
             forward_primer
                                 reverse_primer score coverage products
## 1
       CCAACGACGCAGAGAAACACAA ATGTCTTGCAATGTTGCCTTAGGT
                                               0
                                                     0.2
## 2
      CCAACGACGCAGAGAAACACAAG
                         ATGTCTTGCAATGTTGCCTTAGGT
                                               0
                                                     0.2
                                                             0
## 3
        GCTTTGAGGATCCAACACGGC
                                               0
                                                    0.2
                                                             0
                           GCAGTGAAGTGTTCAGTTCCGT
## 4
        GCTTTGAGGATCCAACACGGC
                           GTGTTCAGTTCCGTGCACAGAT
                                                   0.2
                                                             0
        GCTTTGAGGATCCAACACGGC
                                                     0.2
                                                             0
## 5
                         GCAGTGAAGTGTTCAGTTCCGTG
                                               0
## 6
        GCTTTGAGGATCCAACACGGC
                            AGTGTTCAGTTCCGTGCACAG
                                                     0.2
```

##	7	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCAGTTCCGTGC	0	0.2	0
##	8	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGA	0	0.2	0
##	9	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTCAGTTCCGTGCA	0	0.2	0
##	10	GCTTTGAGGATCCAACACGGC	GAAGTGTTCAGTTCCGTGCACA	0	0.2	0
	11	TCGTGCTGCAACCGAGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2	0
	12		GTTGCCTTAGGTCCATGCATACTTA	0	0.2	0
##		CAGGAAMGACTCCAACGACGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2	0
	14		GTTGCCTTAGGTCCATGCATACTTA	0	0.2	0
	15	GGAAMGACTCCAACGACGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2	0
	16		GTTGCCTTAGGTCCATGCATACTTA	0	0.2	0
	17	CCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2	0
	18	CCCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2	0
	19	CCCCCCGCCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2	0
	20		GTGCAGCATCCTTTTGACAGGTAAT	0	0.2	0
	21		CCTTATTTTCAGCYGGTGCAGCATC	0	0.2	0
	22	CCCCCCGCCAACTACTA	TCCTTATTTTCAGCTGGTGCAGCATC	0	0.2	0
##		CCCCCCGCCAACTACTA				
	23 24	***************************************	CCTTATTTTCAGCYGGTGCAGC	0	0.2	0
		CCCCCCGCCAACTACTA CCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTA CCTTATTTTCAGCYGGTGCAGCA	0	0.2	0
	25			0	0.2	0
	26	CCCCCCGCCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2	0
	27	CCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2	0
	28		TCYTCAACATGTCTGCTATACTGCT	0	0.2	0
	29	TCTCCTGTACCTGGGCAATATGAT	CCTCAACATGTCTGCTATACTGCC	0	0.2	0
##		GCATGCTGCATGCCATAAATGTATA		0	0.2	0
##			GGCACAGCCCAAAATACATAACTGT	0	0.2	0
##		TGCCGCCACGTCTAATGTTTC	GGGCACAGCCCAAAATACATAACT	0	0.2	0
##			GGGCACAGCCCAAAATACATAACTG	0	0.2	0
##		TGCCGCCACGTCTAATGTTTC	CAATAGCAGGGGCACAGCC	0	0.2	0
##		TGCCGCCACGTCTAATGTTTC	GGGGCACAGCCCAAAATACATAAC	0	0.2	0
	36	TGCCGCCACGTCTAATGTTTC	GCAGGGKYACAGCCCA	0	0.2	0
	37	CAACGACGCAGAGAAACACAAGTAT	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2	0
	38	GATGTGAGAAACRCACCACAATACT	GCTTGTAGGGTCGCCGTGTT	0	0.2	0
	39	GATGTGAGAAACRCACCACAATACT	GCTTGTAGGGTCGCCGTGT	0	0.2	0
##		GATGTGAGAAACRCACCACAATACT	CACAGATCAGGTAGCTTGTAGGGT	0	0.2	0
##		GATGTGAGAAACRCACCACAATACT	AGTTCCGTGCACAGATCAGGT	0	0.2	0
##	42	GATGTGAGAAACRCACCACAATACT	GTGTTCAGTTCCGTGCACAGAT	0	0.2	0
	43	GATGTGAGAAACRCACCACAATACT	CTTGTAGGGTCGCCGTGTTG	0	0.2	0
##	44	GATGTGAGAAACRCACCACAATACT	GCTTGTAGGGTCGCCGTG	0	0.2	0
##	45	GATGTGAGAAACRCACCACAATACT	GTAGGGTCGCCGTGTTGG	0	0.2	0
##	46	GATGTGAGAAACRCACCACAATACT	GCACAGATCAGGTAGCTTGTAGGG	0	0.2	0
##	47	GATGTGAGAAACRCACCACAATACT	CAGTTCCGTGCACAGATCAGG	0	0.2	0
##	48	GATGTGAGAAACRCACCACAATACT	AGATCAGGTAGCTTGTAGGGTCG	0	0.2	0
##	49	GATGTGAGAAACRCACCACAATACT	GTAGCTTGTAGGGTCGCCG	0	0.2	0
##	50	GATGTGAGAAACRCACCACAATACT	GTTCCGTGCACAGATCAGGTAG	0	0.2	0
##	51	GATGTGAGAAACRCACCACAATACT	GTTCAGTTCCGTGCACAGATCAG	0	0.2	0
##	52	GATGTGAGAAACRCACCACAATACT	ACAGATCAGGTAGCTTGTAGGGTC	0	0.2	0
##	53	GATGTGAGAAACRCACCACAATACT	TGTTCAGTTCCGTGCACAGATC	0	0.2	0
##	54	GATGTGAGAAACRCACCACAATACT	TCAGGTAGCTTGTAGGGTCGC	0	0.2	0
##	55	GATGTGAGAAACRCACCACAATACT	AGGTAGCTTGTAGGGTCGCC	0	0.2	0
##	56	GATGTGAGAAACRCACCACAATACT	AGTTCCGTGCACAGATCAGGTA	0	0.2	0
##	57	GATGTGAGAAACRCACCACAATACT	GTGTTCAGTTCCGTGCACAGA	0	0.2	0
##	58	GATGTGAGAAACRCACCACAATACT	GTTCAGTTCCGTGCACAGATCA	0	0.2	0
##	59	TCTGAGGACGTTAGGGACAATGTG	GGCACAGCCCAAAATACATAACTGT	0	0.2	0
##	60	TCTGAGGACGTTAGGGACAATGTG	GGGCACAGCCCAAAATACATAACT	0	0.2	0

```
## 61
        TCTGAGGACGTTAGGGACAATGTG GGGCACAGCCCAAAATACATAACTG
                                                                   0
                                                                           0.2
                                                                                       0
##
  62
        TCTGAGGACGTTAGGGACAATGTG
                                         CAATAGCAGGGCACAGCC
                                                                   0
                                                                           0.2
                                                                                       0
                                    GGGGCACAGCCCAAAATACATAAC
##
   63
        TCTGAGGACGTTAGGGACAATGTG
                                                                    0
                                                                           0.2
                                                                                       0
        TCTGAGGACGTTAGGGACAATGTG
                                             GCAGGGKYACAGCCCA
                                                                   0
                                                                           0.2
                                                                                       0
##
   64
##
   65
         CAACGACGCAGAGAAACACAAGT
                                    ATGTCTTGCAATGTTGCCTTAGGT
                                                                   0
                                                                           0.2
                                                                                       0
##
   66
        GCAGGTACTATGGGTGACACTGTG GCACGCATACCTGTGCCTTTAATAT
                                                                   0
                                                                           0.2
                                                                                       0
##
   67
        GCAGGTACTATGGGTGACACTGTG
                                     GCACGCATACCTGTGCCTTTAAT
                                                                   0
                                                                           0.2
                                                                                       0
## 68
        GCAGGTACTATGGGTGACACTGTG
                                      GCACGCATACCTGTGCCTTTAA
                                                                   0
                                                                           0.2
                                                                                       0
##
   69
         CGGCTGGTTTTATGTACAGGCTA
                                     CCATATCCGACCCTGTGTCTGTT
                                                                   0
                                                                           0.2
                                                                                       0
##
  70
         CGGCTGGTTTTATGTACAGGCTA
                                      CCATATCCGACCCTGTGTCTGT
                                                                   0
                                                                           0.2
                                                                                       0
##
   71
         CGGCTGGTTTTATGTACAGGCTA
                                      ACCATATCCGACCCTGTGTCTG
                                                                   0
                                                                           0.2
                                                                                       0
                                                                                       0
##
   72
         CGGCTGGTTTTATGTACAGGCTA
                                    CGACCCTGTGTCTGTTGCATTTTC
                                                                   0
                                                                           0.2
##
   73
       ACTCTGTGTATGGAGACACATTGGA
                                      GCACCGCAGGCACCTTATTAAT
                                                                   0
                                                                           0.2
                                                                                       0
       ACTCTGTGTATGGAGACACATTGGA
##
   74
                                       GCACCGCAGGCACCTTATTAA
                                                                    0
                                                                           0.2
                                                                                       0
  75
       ACTCTGTGTATGGAGACACATTGGA GCACCGCAGGCACCTTATTAATAAA
                                                                   0
                                                                           0.2
                                                                                       0
##
##
  76
         AGATGTGAGAAACRCACCACAAT
                                        GCTTGTAGGGTCGCCGTGTT
                                                                    0
                                                                           0.2
                                                                                       0
##
  77
         AGATGTGAGAAACRCACCACAAT
                                         GCTTGTAGGGTCGCCGTGT
                                                                   0
                                                                           0.2
                                                                                       0
##
   78
         AGATGTGAGAAACRCACCACAAT
                                    CACAGATCAGGTAGCTTGTAGGGT
                                                                    0
                                                                           0.2
                                                                                       0
##
  79
         AGATGTGAGAAACRCACCACAAT
                                       AGTTCCGTGCACAGATCAGGT
                                                                   0
                                                                           0.2
                                                                                       0
##
   80
         AGATGTGAGAAACRCACCACAAT
                                      GTGTTCAGTTCCGTGCACAGAT
                                                                   0
                                                                           0.2
                                                                                       0
##
  81
         AGATGTGAGAAACRCACCACAAT
                                        CTTGTAGGGTCGCCGTGTTG
                                                                   0
                                                                           0.2
                                                                                       Λ
  82
##
         AGATGTGAGAAACRCACCACAAT
                                           GCTTGTAGGGTCGCCGTG
                                                                    0
                                                                           0.2
                                                                                       0
## 83
         AGATGTGAGAAACRCACCACAAT
                                           GTAGGGTCGCCGTGTTGG
                                                                   0
                                                                           0.2
                                                                                       0
##
   84
         AGATGTGAGAAACRCACCACAAT
                                    GCACAGATCAGGTAGCTTGTAGGG
                                                                   0
                                                                           0.2
                                                                                       0
## 85
         AGATGTGAGAAACRCACCACAAT
                                       CAGTTCCGTGCACAGATCAGG
                                                                   0
                                                                           0.2
                                                                                       0
##
   86
         AGATGTGAGAAACRCACCACAAT
                                     AGATCAGGTAGCTTGTAGGGTCG
                                                                   0
                                                                           0.2
                                                                                       0
  87
                                         GTAGCTTGTAGGGTCGCCG
                                                                   0
                                                                           0.2
                                                                                       0
##
         AGATGTGAGAAACRCACCACAAT
##
   88
         AGATGTGAGAAACRCACCACAAT
                                      GTTCCGTGCACAGATCAGGTAG
                                                                   0
                                                                           0.2
                                                                                       0
  89
                                                                                       0
##
         AGATGTGAGAAACRCACCACAAT
                                     GTTCAGTTCCGTGCACAGATCAG
                                                                    0
                                                                           0.2
##
  90
         AGATGTGAGAAACRCACCACAAT
                                       AGTGTTCAGTTCCGTGCACAG
                                                                    0
                                                                           0.2
                                                                                       0
## 91
         AGATGTGAGAAACRCACCACAAT
                                    ACAGATCAGGTAGCTTGTAGGGTC
                                                                   0
                                                                           0.2
                                                                                       0
##
  92
         AGATGTGAGAAACRCACCACAAT
                                      TGTTCAGTTCCGTGCACAGATC
                                                                   0
                                                                           0.2
                                                                                       0
##
   93
         AGATGTGAGAAACRCACCACAAT
                                      AGTGAAGTGTTCAGTTCCGTGC
                                                                    0
                                                                           0.2
                                                                                       0
                                       TCAGGTAGCTTGTAGGGTCGC
                                                                                       0
##
  94
         AGATGTGAGAAACRCACCACAAT
                                                                   0
                                                                           0.2
##
   95
         AGATGTGAGAAACRCACCACAAT
                                         AGGTAGCTTGTAGGGTCGCC
                                                                   0
                                                                                       0
                                                                           0.2
##
  96
         AGATGTGAGAAACRCACCACAAT
                                      TGAAGTGTTCAGTTCCGTGCAC
                                                                   0
                                                                           0.2
                                                                                       0
##
  97
         AGATGTGAGAAACRCACCACAAT
                                      AGTTCCGTGCACAGATCAGGTA
                                                                    0
                                                                           0.2
                                                                                       0
## 98
         AGATGTGAGAAACRCACCACAAT
                                       GTGTTCAGTTCCGTGCACAGA
                                                                   0
                                                                           0.2
                                                                                       0
## 99
         AGATGTGAGAAACRCACCACAAT
                                      GTTCAGTTCCGTGCACAGATCA
                                                                    0
                                                                           0.2
                                                                                       0
  100
##
         AGATGTGAGAAACRCACCACAAT
                                      GTGAAGTGTTCAGTTCCGTGCA
                                                                   \cap
                                                                           0.2
                                                                                       0
##
       similar signatures
                                   missing signatures
                            HPV16, HPV11, HPV4, HPV17
## 1
                            HPV16, HPV11, HPV4, HPV17
##
  2
                            HPV16, HPV11, HPV4, HPV17
## 3
                            HPV16, HPV11, HPV4, HPV17
## 4
                            HPV16, HPV11, HPV4, HPV17
## 5
## 6
                            HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 7
## 8
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 9
                           HPV16, HPV11, HPV4, HPV17
## 10
                           HPV16, HPV11, HPV4, HPV17
## 11
## 12
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 13
```

```
## 14
                           HPV16, HPV11, HPV4, HPV17
## 15
                           HPV16, HPV11, HPV4, HPV17
## 16
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 17
## 18
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 19
## 20
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 21
## 22
                           HPV16, HPV11, HPV4, HPV17
## 23
                           HPV16, HPV11, HPV4, HPV17
## 24
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 25
## 26
                           HPV16, HPV11, HPV4, HPV17
## 27
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 28
## 29
                           HPV16, HPV11, HPV4, HPV17
## 30
                           HPV16, HPV11, HPV4, HPV17
## 31
                           HPV16, HPV11, HPV4, HPV17
## 32
                           HPV16, HPV11, HPV4, HPV17
## 33
                           HPV16, HPV11, HPV4, HPV17
## 34
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 35
                           HPV16, HPV11, HPV4, HPV17
## 36
                           HPV16, HPV11, HPV4, HPV17
## 37
                           HPV16, HPV11, HPV4, HPV17
## 38
## 39
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 40
## 41
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 42
## 43
                           HPV16, HPV11, HPV4, HPV17
## 44
                           HPV16, HPV11, HPV4, HPV17
## 45
                           HPV16, HPV11, HPV4, HPV17
## 46
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 47
                           HPV16, HPV11, HPV4, HPV17
## 48
## 49
                           HPV16, HPV11, HPV4, HPV17
## 50
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 51
                           HPV16, HPV11, HPV4, HPV17
## 52
## 53
                           HPV16, HPV11, HPV4, HPV17
## 54
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 55
## 56
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 57
## 58
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 59
## 60
                           HPV16, HPV11, HPV4, HPV17
## 61
                           HPV16, HPV11, HPV4, HPV17
## 62
                           HPV16, HPV11, HPV4, HPV17
## 63
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 64
## 65
                           HPV16, HPV11, HPV4, HPV17
## 66
                           HPV16, HPV11, HPV4, HPV17
## 67
                           HPV16, HPV11, HPV4, HPV17
```

```
## 68
                           HPV16, HPV11, HPV4, HPV17
## 69
                           HPV16, HPV11, HPV4, HPV17
## 70
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 71
## 72
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 73
                           HPV16, HPV11, HPV4, HPV17
## 74
                           HPV16, HPV11, HPV4, HPV17
## 75
## 76
                           HPV16, HPV11, HPV4, HPV17
## 77
                           HPV16, HPV11, HPV4, HPV17
## 78
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 79
## 80
                           HPV16, HPV11, HPV4, HPV17
## 81
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 82
## 83
                           HPV16, HPV11, HPV4, HPV17
## 84
                           HPV16, HPV11, HPV4, HPV17
## 85
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 86
## 87
                           HPV16, HPV11, HPV4, HPV17
## 88
                           HPV16, HPV11, HPV4, HPV17
## 89
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 90
                           HPV16, HPV11, HPV4, HPV17
## 91
## 92
                           HPV16, HPV11, HPV4, HPV17
## 93
                           HPV16, HPV11, HPV4, HPV17
                           HPV16, HPV11, HPV4, HPV17
## 94
                           HPV16, HPV11, HPV4, HPV17
## 95
                           HPV16, HPV11, HPV4, HPV17
## 96
## 97
                           HPV16, HPV11, HPV4, HPV17
## 98
                           HPV16, HPV11, HPV4, HPV17
## 99
                           HPV16, HPV11, HPV4, HPV17
## 100
                           HPV16, HPV11, HPV4, HPV17
data(RESTRICTION_ENZYMES)
TYPE <- 'melt'
LEVELS <- 4
MIN_LENGTH <- 15
MAX_LENGTH <- 25
MIN_SIZE <- 60
MAX_SIZE <- 200
RESOLUTION \leftarrow seq(75, 300, 15)
lapply(
  rep(sample(1:3, 3), 3), # Random RE combinations
  function(i)
    DesignSignatures(
      dbConn,
      type=TYPE,
      enzymes=RESTRICTION_ENZYMES[i],
      minProductSize=MIN_SIZE,
      maxProductSize=MAX_SIZE,
      resolution=RESOLUTION,
```

```
levels=LEVELS
  )
## Tallying 8-mers for 5 groups:
##
## Time difference of 0.42 secs
##
## Designing primer sequences based on the group 'HPV18':
## Time difference of 91.52 secs
## Selecting the most common primer sequences:
 _____
##
## Time difference of 18.76 secs
##
## Determining PCR products from each group:
##
## Time difference of 11.26 secs
##
## Scoring primer pair combinations:
 ______
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
##
## Time difference of 2.01 secs
##
## Finding the best restriction enzyme:
##
## Time difference of 2.21 secs
## Tallying 8-mers for 5 groups:
##
## Time difference of 0.4 secs
##
## Designing primer sequences based on the group 'HPV18':
##
## Time difference of 80.57 secs
## Selecting the most common primer sequences:
 ______
##
## Time difference of 14.78 secs
##
## Determining PCR products from each group:
```

```
##
## Time difference of 6.46 secs
##
## Scoring primer pair combinations:
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
 ______
## Time difference of 1.7 secs
##
## Finding the best restriction enzyme:
## Time difference of 2.23 secs
## Tallying 8-mers for 5 groups:
## Time difference of 0.36 secs
##
## Designing primer sequences based on the group 'HPV18':
## Time difference of 83.57 secs
## Selecting the most common primer sequences:
 ______
## Time difference of 17.61 secs
## Determining PCR products from each group:
## Time difference of 6.69 secs
##
## Scoring primer pair combinations:
 _____
##
## Time difference of 0.01 secs
## Choosing optimal forward and reverse pairs:
##
## Time difference of 1.88 secs
## Finding the best restriction enzyme:
##
## Time difference of 2.34 secs
## Tallying 8-mers for 5 groups:
```

```
##
## Time difference of 0.45 secs
##
## Designing primer sequences based on the group 'HPV18':
## -----
##
## Time difference of 77.69 secs
##
## Selecting the most common primer sequences:
 ______
## Time difference of 16.28 secs
## Determining PCR products from each group:
## Time difference of 7.4 secs
## Scoring primer pair combinations:
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
## Time difference of 1.84 secs
## Finding the best restriction enzyme:
## Time difference of 2.06 secs
## Tallying 8-mers for 5 groups:
## Time difference of 0.39 secs
## Designing primer sequences based on the group 'HPV18':
##
## Time difference of 84.91 secs
## Selecting the most common primer sequences:
## Time difference of 19.37 secs
## Determining PCR products from each group:
 ## Time difference of 7.17 secs
## Scoring primer pair combinations:
```

```
##
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
##
## Time difference of 1.75 secs
##
## Finding the best restriction enzyme:
##
## Time difference of 2.65 secs
## Tallying 8-mers for 5 groups:
## Time difference of 0.37 secs
##
## Designing primer sequences based on the group 'HPV18':
 ______
## Time difference of 72.6 secs
## Selecting the most common primer sequences:
## -----
##
## Time difference of 16.82 secs
##
## Determining PCR products from each group:
## Time difference of 6.9 secs
## Scoring primer pair combinations:
## Time difference of 0.01 secs
## Choosing optimal forward and reverse pairs:
##
## Time difference of 1.74 secs
## Finding the best restriction enzyme:
## Time difference of 2.06 secs
## Tallying 8-mers for 5 groups:
## Time difference of 0.39 secs
## Designing primer sequences based on the group 'HPV18':
##
```

```
## Time difference of 72.24 secs
##
## Selecting the most common primer sequences:
## Time difference of 14.17 secs
## Determining PCR products from each group:
 ______
##
## Time difference of 6 secs
##
## Scoring primer pair combinations:
 ______
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
 _____
## Time difference of 1.49 secs
##
## Finding the best restriction enzyme:
## -----
##
## Time difference of 2.16 secs
## Tallying 8-mers for 5 groups:
##
## Time difference of 0.36 secs
## Designing primer sequences based on the group 'HPV18':
 ______
##
## Time difference of 61.99 secs
## Selecting the most common primer sequences:
## Time difference of 14.1 secs
## Determining PCR products from each group:
##
## Time difference of 5.61 secs
##
## Scoring primer pair combinations:
 ______
##
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
```

##

```
## Time difference of 1.49 secs
##
## Finding the best restriction enzyme:
## Time difference of 2.08 secs
## Tallying 8-mers for 5 groups:
## Time difference of 0.34 secs
## Designing primer sequences based on the group 'HPV18':
##
## Time difference of 60.85 secs
##
## Selecting the most common primer sequences:
 ______
##
## Time difference of 14.29 secs
##
## Determining PCR products from each group:
## Time difference of 5.65 secs
## Scoring primer pair combinations:
 ______
##
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
  ______
##
## Time difference of 1.48 secs
## Finding the best restriction enzyme:
##
## Time difference of 1.86 secs
## [[1]]
##
            forward primer
                               reverse primer score coverage
## 1
    GCCCCCTTTAGAACTTAAAAACACA CCCCATAAGGATCTGCAGACATTTGT
                                           0
                                               0.2
## 2
    GCCCCCTTTAGAACTTAAAAACACA CCCCATAAGGATCTGCAGACATTTG
                                                0.2
## 3
    GCCCCCTTTAGAACTTAAAAACACA
                        TGGAATCCCCATAAGGATCTGCAG
                                            0
                                                0.2
## 4
       CCAACGACGCAGAGAAACACAA
                          GCTCGTCGGGCTGGTAAATGT
                                            0
                                                0.2
## 5
                                            0
                                                0.2
       CCAACGACGCAGAGAAACACAA
                           GCTCGTCGGGCTGGTAAATG
## 6
       CCAACGACGCAGAGAACACAA CGCTTAATTGCTCGTGACATAGAAGG
                                            0
                                                0.2
## 7
       CCAACGACGCAGAGAAACACAA
                          GGCTCGTCGGGCTGGTAAA
                                            0
                                                0.2
## 8
    GGTGCAGTTACCTGACCCAAATAAAT
                            GTGGCGCATGGGAACTT
                                            0
                                                0.2
## Q
    GGTGCAGTTACCTGACCCAAATAAAT
                                           0
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## 10 GGTGCAGTTACCTGACCCAAATAAAT
                          GCCCACTAAGGCCAACACCT
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## 11 GGTGCAGTTACCTGACCCAAATAAAT
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	14	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
	15	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
	16	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGTC	0	0.2
	17	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCATC	0	0.2
	18	GGTGCAGTTACCTGACCCAAATAAAT	CCTAAWGGCTGACCACGGC	0	0.2
		GGTGCAGTTACCTGACCCAAATAAAT	CCAATTTCCACTCCAACACAGGC	0	0.2
	20	GGTGCAGTTACCTGACCCAAATAAAT	AAWGGCTGACCACGGCC	0	0.2
	21	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACC	0	0.2
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	2 4 25				
		GGTGCAGTTACCTGACCCAAATAAAT	TGCCCACTAAGGCCAACAC	0	0.2
	26	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTA	0	0.2
	27	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCA	0	0.2
	28	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGCCAATTTCCA	0	0.2
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	30	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
	31	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAKGCCMACACCTAA	0	0.2
	32	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
	33	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAAA	0	0.2
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	36	TCCCAGCAGTAAGCAACAATGG	AATCTACCATATCCGACCCTGTGT	0	0.2
	37	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGT	0	0.2
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##	42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
##	43	TCCCAGCAGTAAGCAACAATGG	ACAATAGCCTGTACATAAAACCAGCC	0	0.2
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##	45	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
##	46		CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	47	CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
##	48	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGT	0	0.2
##	49	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGAT	0	0.2
##	50	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGTG	0	0.2
##	51	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
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##	55	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGA	0	0.2
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##	60	TCGTGCTGCAACCGAGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2
##	61	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTA	0	0.2
	62	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTAA	0	0.2
##	63	CAGGAAMGACTCCAACGACGC	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	64	GGAAMGACTCCAACGACGC	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	65	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2

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## 66
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##
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  67
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##
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  69
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##
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##
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## 73
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##
   74
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##
  75
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##
##
   78
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##
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##
  80
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                                                                            0.2
## 81
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                                          GCTCGTCGGGCTGGTAAATG
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        ACCTAAGGCAACATTGCAAGACATT CGCTTAATTGCTCGTGACATAGAAGG
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##
   82
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                                        CATTTATGGCATGCAGCATGCG
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##
   84
##
   85
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##
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  88
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## 96
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##
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##
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                                            missing signatures enzyme digest score
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## 12
## 13
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##		0	-	HPV11,			0
##		0		HPV11,			0
##		0	•	HPV11,			0
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## 73
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## 23
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## 25
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##	77	0
##	78	0
##	79	0
##	13	J

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## 80
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   84
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##
##
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##
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##
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##
   92
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##
##
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##
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##
##
   97
                0
##
   98
                0
##
   99
                0
##
   100
                0
##
##
   [[2]]
##
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                                                  reverse_primer score coverage
                                                                              0.2
##
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   2
             GCTTTGAGGATCCAACACGGC
                                         ACATTTATGGCATGCAGCATGC
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##
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##
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##
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##
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##
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##
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##
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##
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##
   25
       GGTGCAGTTACCTGACCCAAATAAAT
                                           CACCTAAWGGCTGACCACGG
                                                                      0
                                                                              0.2
                                                                      0
                                                                              0.2
##
   26
       GGTGCAGTTACCTGACCCAAATAAAT
                                         CMACACCTAAWGGCTGACCACG
##
   27
       GGTGCAGTTACCTGACCCAAATAAAT
                                        CCCACTAAGGCCAACACCTAAAG
                                                                      0
                                                                              0.2
##
   28
       GGTGCAGTTACCTGACCCAAATAAAT
                                         CGGCATGGGAACTTTCAGTGTC
                                                                      0
                                                                              0.2
##
  29
       GGTGCAGTTACCTGACCCAAATAAAT
                                       GGCATGGGAACTTTCAGTGTCATC
                                                                      0
                                                                              0.2
## 30
       GGTGCAGTTACCTGACCCAAATAAAT
                                            CCTAAWGGCTGACCACGGC
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                                                                              0.2
```

##	31	GGTGCAGTTACCTGACCCAAATAAAT	CCAATTTCCACTCCAACACAGGC	0	0.2
##		GGTGCAGTTACCTGACCCAAATAAAT	AAWGGCTGACCACGGCC	0	0.2
##	33	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACC	0	0.2
##	34	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACC	0	0.2
##	35	GGTGCAGTTACCTGACCCAAATAAAT	TGACCACGGCCAATTTCCAC	0	0.2
##	36	GGTGCAGTTACCTGACCCAAATAAAT	CCMACACCTAAWGGCTGACCAC	0	0.2
##	37	GGTGCAGTTACCTGACCCAAATAAAT	TGCCCACTAAGGCCAACAC	0	0.2
##	38	GGTGCAGTTACCTGACCCAAATAAAT	GCCACTAAGGCCAACAC	0	0.2
##	39	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCA	0	0.2
	40	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
##	41	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
##	42	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
		GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAKGCCMACACCTAA		0.2
	43			0	
	44	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
	45	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAAA	0	0.2
##	46	GCATGCTGCATGCCATAAATGTAT	GCACCGCAGGCACCTTATTAA	0	0.2
##			ACAATAGCCTGTACATAAAACCAGCC	0	0.2
	48	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
##		CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
##			CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##		CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
##		GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGT	0	0.2
##		GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGAT	0	0.2
##		GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGTG	0	0.2
##		GCTTTGAGGATCCAACACGGC	AGTGTTCAGTTCCGTGCACAG	0	0.2
##		GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCAGTTCCGTGC	0	0.2
##	57	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGA	0	0.2
##	58	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTCAGTTCCGTGCA	0	0.2
##	59	GCTTTGAGGATCCAACACGGC	GAAGTGTTCAGTTCCGTGCACA	0	0.2
##	60	TGTGCACGGAACTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
##	61	TGTGCACGGAACTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
##	62	TCGTGCTGCAACCGAGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2
##	63	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTA	0	0.2
##	64	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTAA	0	0.2
##	65	CAGGAAMGACTCCAACGACGC	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	66	GGAAMGACTCCAACGACGC	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	67	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
##	68	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
##	69	CCCCCCCCCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
##	70	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
##	71	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
##	72	CCCCCCCCCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
##	73	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
##	74	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
##	75	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
##	76	CCCCCCCCCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
##	77	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
##	78	CCCCCCCCCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
##	79	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
##	80	TGATCTGTGCACGGAACTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
##		TGATCTGTGCACGGAACTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
##		ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
	83	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	0.2
	84	ACCTAAGGCAACATTGCAAGACATT	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2

```
## 85
        ACCTAAGGCAACATTGCAAGACATT
                                            GGCTCGTCGGGCTGGTAAA
                                                                             0.2
                                                                             0.2
## 86
         TCTCCTGTACCTGGGCAATATGAT
                                          GGGGGGGAACACCAAAGTT
                                                                     0
##
  87
         TCTCCTGTACCTGGGCAATATGAT
                                            GGGGGGGAACACCAAAGT
                                                                     0
                                                                             0.2
         TCTCCTGTACCTGGGCAATATGAT
                                              AGTAGTTGGCGGGGGG
                                                                     0
                                                                             0.2
##
  88
##
  89
         TCTCCTGTACCTGGGCAATATGAT
                                         CAAACTAGTAGTTGGCGGGG
                                                                     0
                                                                             0.2
                                                                     0
##
  90
         TCTCCTGTACCTGGGCAATATGAT
                                         CCAAACTAGTAGTTGGCGGGG
                                                                             0.2
## 91
         TCTCCTGTACCTGGGCAATATGAT
                                             GGGGGGGAACACCAAAG
                                                                     0
                                                                             0.2
                                                                             0.2
## 92
         TCTCCTGTACCTGGGCAATATGAT
                                           GGGGGGAACACCAAAGTTC
                                                                     0
## 93
         TCTCCTGTACCTGGGCAATATGAT
                                              CGGGGGGGAACACCAA
                                                                     0
                                                                             0.2
## 94
         TCTCCTGTACCTGGGCAATATGAT
                                             CGGGGGGGAACACCAAA
                                                                     0
                                                                             0.2
## 95
        GCATGCTGCATGCCATAAATGTATA
                                         GCACCGCAGGCACCTTATTAA
                                                                     0
                                                                             0.2
## 96
            TGCCGCCACGTCTAATGTTTC GCACAGCCCAAAATACATAACTGTGT
                                                                     0
                                                                             0.2
##
  97
            TGCCGCCACGTCTAATGTTTC
                                     GGCACAGCCCAAAATACATAACTGT
                                                                     0
                                                                             0.2
## 98
            TGCCGCCACGTCTAATGTTTC GCCCAAAATACATAACTGTGTCTGCT
                                                                     0
                                                                             0.2
            TGCCGCCACGTCTAATGTTTC
                                      GGGCACAGCCCAAAATACATAACT
                                                                     0
                                                                             0.2
## 99
## 100
            TGCCGCCACGTCTAATGTTTC GGCACAGCCCAAAATACATAACTGTG
                                                                     0
                                                                             0.2
##
       products similar_signatures
                                             missing_signatures enzyme digest_score
## 1
                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
## 2
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
                                                                   AccI
## 3
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
## 4
               0
                                                                   AccI
                                                                                    0
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 5
                                                                   AccI
                                     HPV16, HPV11, HPV4, HPV17
               0
## 6
                                                                                    0
                                                                   AccI
               0
                                     HPV16, HPV11, HPV4, HPV17
## 7
                                                                   AccI
                                                                                    0
## 8
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
                                                                                    0
## 9
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccT
                                                                                    0
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 10
                                                                   AccI
                                     HPV16, HPV11, HPV4, HPV17
## 11
               0
                                                                   AccI
                                                                                    0
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 12
                                                                   AccI
## 13
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 14
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 15
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 16
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                                     HPV16, HPV11, HPV4, HPV17
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               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 17
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                                     HPV16, HPV11, HPV4, HPV17
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##
  18
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 19
## 20
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 21
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 22
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 23
                                     HPV16, HPV11, HPV4, HPV17
               0
## 24
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               0
                                     HPV16, HPV11, HPV4, HPV17
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## 25
                                     HPV16, HPV11, HPV4, HPV17
## 26
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               0
                                     HPV16, HPV11, HPV4, HPV17
## 27
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## 28
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                                     HPV16, HPV11, HPV4, HPV17
## 29
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## 30
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               0
                                                                                    0
## 31
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## 32
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
## 33
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## 34
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 35
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 36
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 37
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
```

##	38	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	39	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	40	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	41	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	42	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	43	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	44	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	45	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	46	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	47	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	48	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	49	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	50	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	51	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	52	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	53	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	54	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	55	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	56	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	57	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	58	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	59	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	60	0		HPV11,			0
##	61	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	62	0		HPV11,			0
##	63	0		HPV11,			0
##	64	0		HPV11,			0
##	65	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	66	0		HPV11,			0
##	67	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	68	0		HPV11,			0
##	69	0		HPV11,			0
##	70	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	71	0		HPV11,			0
##	72	0		HPV11,			0
##	73	0		HPV11,			0
##	74	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	75	0	HPV16,	HPV11,	HPV4,	HPV17	0
##		0		HPV11,			0
##	77	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	78	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	79	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	80	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	81	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	82	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	83	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	84	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	85	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	86	0		HPV11,			0
##	87	0	•	HPV11,			0
##		0	-	HPV11,			0
##		0	-	HPV11,			0
	90	0		HPV11,			0
##		0		HPV11,			0
			. ,	,	,		-

##	92	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	93	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	94	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	95	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	96	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	97	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	98	0		HPV11,			0
##	99	0		HPV11,			0
	100	0		HPV11,			0
##	fragme	ents		-			
##	_	4					
##	2	4					
##	3	4					
##	4	4					
##	5	2					
##	6	2					
##		2					
##	8	2					
##		2					
##		2					
##	11	2					
##		2					
##		0					
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##		0					
##		0					
##	39	0					
##	40	0					
##		0					
##		0					
##		0					
##	44	0					

##	45	0
##	46	0
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##	89	0
##	90	0
##	91	0
##	92	0
##	93	0
##	94	0
##	95	0
##	96	0
##	97	0
##	98	0
		_

##	aa	0			
	100	0			
##	100	O .			
##	[[3]	1			
##		forward_primer	reverse_primer	score	coverage
##	1	GCCCCCTTTAGAACTTAAAAACACA	— -	0	0.2
##	2	GCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
##	3	GCCCCCTTTAGAACTTAAAAACACA	TGGAATCCCCATAAGGATCTGCAG	0	0.2
##	4	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATGT	0	0.2
##	5	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATG	0	0.2
##	6	CCAACGACGCAGAGAAACACAA	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	7	CCAACGACGCAGAGAAACACAA	GGCTCGTCGGGCTGGTAAA	0	0.2
##	8	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACTT	0	0.2
##	9	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT	0	0.2
##	10	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCT	0	0.2
##	11	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACT	0	0.2
##	12	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCAT	0	0.2
##	13	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
##	14	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
##	15	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
##	16	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGTC	0	0.2
##	17	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCATC	0	0.2
##	18	GGTGCAGTTACCTGACCCAAATAAAT	CCTAAWGGCTGACCACGGC	0	0.2
##	19	GGTGCAGTTACCTGACCCAAATAAAT	CCAATTTCCACTCCAACACAGGC	0	0.2
##	20	GGTGCAGTTACCTGACCCAAATAAAT	AAWGGCTGACCACGGCC	0	0.2
##	21	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACC	0	0.2
##	22	${\tt GGTGCAGTTACCTGACCCAAATAAAT}$	GCCCACTAAGGCCAACACC	0	0.2
##	23	$\tt GGTGCAGTTACCTGACCCAAATAAAT$	TGACCACGGCCAATTTCCAC	0	0.2
##	24	$\tt GGTGCAGTTACCTGACCCAAATAAAT$	CCMACACCTAAWGGCTGACCAC	0	0.2
##	25	$\tt GGTGCAGTTACCTGACCCAAATAAAT$	TGCCCACTAAGGCCAACAC	0	0.2
##	26	$\tt GGTGCAGTTACCTGACCCAAATAAAT$	GCCCACTAAGGCCAACACCTA	0	0.2
##	27	$\tt GGTGCAGTTACCTGACCCAAATAAAT$	GGCATGGGAACTTTCAGTGTCA	0	0.2
##	28	$\tt GGTGCAGTTACCTGACCCAAATAAAT$	CTGACCACGGCCAATTTCCA	0	0.2
##	29	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
##	30	$\tt GGTGCAGTTACCTGACCCAAATAAAT$	GCCMACACCTAAWGGCTGACCA	0	0.2
##	31	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAKGCCMACACCTAA	0	0.2
	32	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
	33	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAAA	0	0.2
	34	GCATGCTGCATGCCATAAATGTAT	GCACCGCAGGCACCTTATTAA	0	0.2
	35	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGTT	0	0.2
	36	TCCCAGCAGTAAGCAACAATGG	AATCTACCATATCCGACCCTGTGT	0	0.2
	37	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGT	0	0.2
	38	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGT	0	0.2
##		TCCCAGCAGTAAGCAACAATGG	CTACCATATCCGACCCTGTGTCT	0	0.2
##			TGAAATCTACCATATCCGACCCTGTG	0	0.2
##		TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
	42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
	43		ACAATAGCCTGTACATAAAACCAGCC	0	0.2
	44	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
##		CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
##			CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	47	CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
##		GCTTTGAGGATCCAACACGC	GCAGTGAAGTGTTCAGTTCCGT	0	0.2
##	49	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGAT	0	0.2

```
## 50
            GCTTTGAGGATCCAACACGGC
                                       GCAGTGAAGTGTTCAGTTCCGTG
                                                                     0
                                                                             0.2
##
   51
            GCTTTGAGGATCCAACACGGC
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                                                                             0.2
##
   52
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                                         AGTGTTCAGTTCCGTGCACAG
                                                                     0
                                                                             0.2
                                                                     0
                                                                             0.2
##
   53
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##
       products similar_signatures
                                            missing_signatures enzyme digest_score
##
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
  1
                                     HPV16, HPV11, HPV4, HPV17
## 2
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##		0	-	HPV11,			0
	14	0	-	HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
	17	0		HPV11,			0
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	24			HPV11,			
		0	-	HPV11,			0
##		0		HPV11,			0
##		0	-	HPV11,			0
	27	0		HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
##		0	-	HPV11,	-		0
##		0	-	HPV11,	-		0
##		0	-	HPV11,	-		0
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##	9	0		

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##	61	0
##	62	0
##	63	0

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## 64
                0
##
  65
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##
  66
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## 67
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   68
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## 83
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## 88
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## 90
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##
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## 92
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##
## 94
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##
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##
  96
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## 97
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##
  98
##
  99
                0
##
  100
                0
##
##
   [[4]]
##
                    forward_primer
                                                 reverse_primer score coverage
##
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##
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## 6
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##
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##
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## 12
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## 13
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##		GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACC	0	0.2
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	23	GGTGCAGTTACCTGACCCAAATAAAT	TGACCACGGCCAATTTCCAC	0	0.2
	23 24	GGTGCAGTTACCTGACCCAAATAAAT	CCMACACCTAAWGGCTGACCAC	0	0.2
##		GGTGCAGTTACCTGACCCAAATAAAT	TGCCCACTAAGGCCAACAC	0	0.2
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		GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCA	0	0.2
##		GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
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	30	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
	31	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAKGCCMACACCTAA	0	0.2
	32	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
##		GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAAA	0	0.2
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##		TCCCAGCAGTAAGCAACAATGG	AATCTACCATATCCGACCCTGTGT	0	0.2
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##		TCCCAGCAGTAAGCAACAATGG	CTACCATATCCGACCCTGTGTCT	0	0.2
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##	45	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
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##	49	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGAT	0	0.2
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##	62	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTAA	0	0.2
##	63	CAGGAAMGACTCCAACGACGC	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
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##	67	CCCCCCCCCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
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##
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##
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##
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##
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##
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##
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  82
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                                                                     0
                                                                            0.2
##
  83
        ACCTAAGGCAACATTGCAAGACATT
                                           GGCTCGTCGGGCTGGTAAA
                                                                     0
                                                                            0.2
##
  84
             CGGCGACCCTACAAGCTACC
                                        CATTTATGGCATGCAGCATGCG
                                                                     0
                                                                            0.2
                                                                     0
##
   85
             CGGCGACCCTACAAGCTACC
                                        ACATTTATGGCATGCAGCATGC
                                                                            0.2
##
   86
         TCTCCTGTACCTGGGCAATATGAT
                                          GGGGGGGAACACCAAAGTT
                                                                     0
                                                                            0.2
         TCTCCTGTACCTGGGCAATATGAT
                                           GGGGGGGAACACCAAAGT
                                                                     0
                                                                            0.2
##
   87
##
   88
         TCTCCTGTACCTGGGCAATATGAT
                                             AGTAGTTGGCGGGGGG
                                                                     0
                                                                            0.2
##
   29
         TCTCCTGTACCTGGGCAATATGAT
                                         CAAACTAGTAGTTGGCGGGG
                                                                     0
                                                                            0.2
   90
         TCTCCTGTACCTGGGCAATATGAT
                                                                     0
                                                                            0.2
##
                                         CCAAACTAGTAGTTGGCGGGG
## 91
         TCTCCTGTACCTGGGCAATATGAT
                                                                     0
                                                                            0.2
                                            GGGGGGGAACACCAAAG
##
   92
         TCTCCTGTACCTGGGCAATATGAT
                                          GGGGGGAACACCAAAGTTC
                                                                     0
                                                                            0.2
##
  93
         TCTCCTGTACCTGGGCAATATGAT
                                             CGGGGGGGAACACCAA
                                                                     0
                                                                            0.2
##
   94
         TCTCCTGTACCTGGGCAATATGAT
                                            CGGGGGGGAACACCAAA
                                                                     0
                                                                            0.2
  95
        GCATGCTGCATGCCATAAATGTATA
                                         GCACCGCAGGCACCTTATTAA
                                                                     0
                                                                            0.2
##
##
   96
            TGCCGCCACGTCTAATGTTTC GCACAGCCCAAAATACATAACTGTGT
                                                                     0
                                                                            0.2
  97
            TGCCGCCACGTCTAATGTTTC
                                     GGCACAGCCCAAAATACATAACTGT
                                                                     0
##
                                                                            0.2
## 98
            TGCCGCCACGTCTAATGTTTC GCCCAAAATACATAACTGTGTCTGCT
                                                                     0
                                                                            0.2
## 99
            TGCCGCCACGTCTAATGTTTC
                                      GGGCACAGCCCAAAATACATAACT
                                                                     0
                                                                            0.2
##
   100
            TGCCGCCACGTCTAATGTTTC GGCACAGCCCAAAATACATAACTGTG
                                                                     0
                                                                            0.2
##
       products similar_signatures
                                            missing_signatures enzyme digest_score
                                     HPV16, HPV11, HPV4, HPV17
##
              0
   1
##
   2
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
##
  3
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 4
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 5
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 6
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 7
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
              0
                                     HPV16, HPV11, HPV4, HPV17
## 8
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
## 9
              0
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
## 10
              0
                                                                                    0
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 11
              0
                                     HPV16, HPV11, HPV4, HPV17
## 12
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
## 13
              0
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
##
  14
              0
                                                                                    0
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 15
## 16
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
##
  17
              0
                                                                                    0
## 18
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
## 19
              0
                                                                                    0
## 20
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
## 21
              0
                                                                                    0
```

## 2	:2 0) H	PV16,	HPV11,	HPV4,	HPV17	0
## 2	:3 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 2	:4 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 2	.5 C			HPV11,			0
## 2				HPV11,			0
## 2				HPV11,			0
	_						
## 2				HPV11,	•		0
## 2	:9 0			HPV11,	•		0
## 3	60 C) H	PV16,	HPV11,	HPV4,	HPV17	0
## 3	i1 C	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 3	2 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 3	3 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 3	4 0) Н	PV16.	HPV11,	HPV4.	HPV17	0
## 3				HPV11,			0
## 3				HPV11,			0
## 3				HPV11,			0
## 3				HPV11,	•		0
## 3	9 0		•	HPV11,			0
## 4	:0 C) H	PV16,	HPV11,	HPV4,	HPV17	0
## 4	:1 0	H C	PV16,	HPV11,	HPV4,	HPV17	0
## 4	.2 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 4	.3 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 4	.4 0			HPV11,			0
## 4				HPV11,			0
## 4				HPV11,	-		0
## 4				HPV11,			0
							0
## 4				HPV11,			
## 4			-	HPV11,			0
## 5			-	HPV11,			0
## 5	51 C		-	HPV11,	-		0
## 5	2 0) H	PV16,	HPV11,	HPV4,	HPV17	0
## 5	3 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 5	4 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 5	5 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 5	6 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 5	7 0			HPV11,			0
## 5	8 0			HPV11,	-		0
## 5				HPV11,			0
## 6				HPV11,			0
			•	•			_
## 6			,	HPV11,	•		0
## 6			,	HPV11,	•		0
## 6				HPV11,	•		0
## 6			•	HPV11,			0
## 6	55 C) H	PV16,	HPV11,	HPV4,	HPV17	0
## 6	6 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 6	57 C	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 6	8 0	Н	PV16,	HPV11,	HPV4,	HPV17	0
## 6	9 0			HPV11,			0
## 7	0 0			HPV11,	•		0
## 7			•	HPV11,			0
## 7				HPV11,	-		0
## 7			•	HPV11,			0
## 7				HPV11,			0
## 7	5 C) H	rvib,	HPV11,	пРV4,	nrv1/	0

```
HPV16, HPV11, HPV4, HPV17
## 76
               0
                                                                                     0
## 77
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                     HPV16, HPV11, HPV4, HPV17
## 78
               0
                                                                                     0
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 79
                                     HPV16, HPV11, HPV4, HPV17
## 80
               0
                                                                                     0
## 81
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 82
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                     HPV16, HPV11, HPV4, HPV17
## 83
               0
                                                                                     0
## 84
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 85
## 86
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
               0
                                     HPV16, HPV11, HPV4, HPV17
## 87
                                                                                     0
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 88
## 89
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 90
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 91
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 92
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 93
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 94
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                     HPV16, HPV11, HPV4, HPV17
## 95
               0
                                                                                     0
## 96
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 97
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                     HPV16, HPV11, HPV4, HPV17
## 98
               0
                                                                                     0
## 99
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                                                                     0
## 100
               0
                                     HPV16, HPV11, HPV4, HPV17
##
       fragments
## 1
                0
## 2
                0
                0
## 3
                0
## 4
## 5
                0
## 6
                0
                0
## 7
## 8
                0
## 9
                0
## 10
                0
## 11
                0
## 12
                0
## 13
                0
                0
## 14
## 15
                0
## 16
                0
                0
## 17
                0
## 18
## 19
                0
## 20
                0
                0
## 21
## 22
                0
## 23
                0
                0
## 24
## 25
                0
                0
## 26
## 27
                0
                0
## 28
```

## 29			
## 31	##	29	0
## 32	##	30	0
## 33	##	31	0
## 34	##	32	0
## 35	##	33	0
## 36	##	34	0
## 37	##	35	0
## 38	##	36	0
## 39	##	37	0
## 40	##	38	0
## 41 0 0 ## 42 0 0 ## 43 0 0 ## 44 0 0 ## 45 0 0 ## 46 0 0 ## 47 0 0 ## 50 0 0 ## 51 0 0 ## 52 0 0 ## 53 0 0 ## 55 0 0 ## 55 0 0 ## 56 0 0 ## 57 0 0 ## 58 0 0 ## 60 0 0 ## 61 0 0 ## 62 0 0 ## 63 0 0 ## 64 0 0 ## 65 0 0 ## 66 0 0 ## 67 0 0 ## 68 0 0 ## 69 0 0 ## 70 0 0 ## 71 0 0 ## 72 0 0 ## 73 0 0 ## 74 0 0 ## 75 0 0 ## 75 0 0 ## 76 0 0 ## 77 0 0 ## 77 0 0 ## 78 0 0 ## 79 0 ## 7	##	39	0
## 42	##	40	0
## 43	##	41	0
## 44 0 0 ## 45 0 ## 46 0 ## 47 0 ## 48 0 ## 49 0 ## 50 0 ## 51 0 ## 52 0 ## 53 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 78 0 ## 79 0 ## 7	##	42	0
## 45	##	43	0
## 46	##	44	0
## 47	##	45	0
## 48 0 0 ## 49 0 ## 50 0 ## 51 0 ## 52 0 ## 53 0 ## 55 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0	##	46	0
## 48 0 0 ## 49 0 ## 50 0 ## 51 0 ## 52 0 ## 53 0 ## 55 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0	##		0
## 49	##		0
## 50 0 0 ## 51 0 ## 52 0 ## 53 0 ## 54 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 67 0 ## 70 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0	##		
## 51 0 ## 52 0 ## 53 0 ## 54 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 70 0 ## 71 0 ## 72 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 79 0 ## 79 0 ## 79 0 ## 80 0 ## 81 0	##		
## 52	##	51	
## 53	##	52	
## 54 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 79 0 ## 80 0 ## 81 0			
## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 79 0 ## 80 0 ## 81 0			
## 56 0 ## 57 0 ## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 65 0 ## 66 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 79 0 ## 80 0 ## 81 0			
## 57			
## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 65 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0			
## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 66 0 ## 67 0 ## 68 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 63			
## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0			
## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0			
## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0			
## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0			
## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0			
## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0			
## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81			
## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0			
## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0			
## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0			
## 78 0 ## 79 0 ## 80 0 ## 81 0			
## 79 0 ## 80 0 ## 81 0			
## 80 0 ## 81 0			
## 81 0			
## 82 0			
	##	82	U

```
## 83
                0
##
   84
                0
##
   85
                0
##
                0
   86
##
   87
                0
   88
                0
##
   89
                0
  90
                0
##
##
   91
                0
                0
##
   92
   93
                0
                0
   94
##
##
   95
                0
                0
##
   96
##
   97
                0
##
   98
                0
   99
                0
##
##
   100
                0
##
##
   [[5]]
##
                    forward_primer
                                                 reverse_primer score coverage
##
             GCTTTGAGGATCCAACACGGC
                                         CATTTATGGCATGCAGCATGCG
                                                                      0
  2
                                                                      0
                                                                              0.2
##
             GCTTTGAGGATCCAACACGGC
                                         ACATTTATGGCATGCAGCATGC
##
              CGGCGACCCTACAAGCTACC
                                         CATTTATGGCATGCAGCATGCG
                                                                      0
                                                                              0.2
                                                                      0
                                                                              0.2
##
              CGGCGACCCTACAAGCTACC
                                         ACATTTATGGCATGCAGCATGC
   5
           TCCCAGCAGTAAGCAACAATGG
                                        CCATATCCGACCCTGTGTCTGTT
                                                                      0
                                                                              0.2
##
   6
           TCCCAGCAGTAAGCAACAATGG
                                       AATCTACCATATCCGACCCTGTGT
                                                                      0
                                                                              0.2
                                         CCATATCCGACCCTGTGTCTGT
                                                                      0
                                                                              0.2
##
           TCCCAGCAGTAAGCAACAATGG
                                                                      0
##
   8
           TCCCAGCAGTAAGCAACAATGG
                                      TGAAATCTACCATATCCGACCCTGT
                                                                              0.2
##
   9
           TCCCAGCAGTAAGCAACAATGG
                                        CTACCATATCCGACCCTGTGTCT
                                                                      0
                                                                              0.2
##
  10
           TCCCAGCAGTAAGCAACAATGG TGAAATCTACCATATCCGACCCTGTG
                                                                      0
                                                                              0.2
##
   11
           TCCCAGCAGTAAGCAACAATGG
                                         ACCATATCCGACCCTGTGTCTG
                                                                      0
                                                                              0.2
                                                                              0.2
##
   12
           TCCCAGCAGTAAGCAACAATGG
                                       CGACCCTGTGTCTGTTGCATTTTC
                                                                      0
                                    CCCCATAAGGATCTGCAGACATTTGT
                                                                      0
                                                                              0.2
##
   13
       GCCCCCTTTAGAACTTAAAAACACA
##
   14
       GCCCCCTTTAGAACTTAAAAACACA
                                      CCCCATAAGGATCTGCAGACATTTG
                                                                      0
                                                                              0.2
##
   15
       GCCCCCTTTAGAACTTAAAAACACA
                                       TGGAATCCCCATAAGGATCTGCAG
                                                                      0
                                                                              0.2
##
   16
           CCAACGACGCAGAGAAACACAA
                                          GCTCGTCGGGCTGGTAAATGT
                                                                      0
                                                                              0.2
##
   17
           CCAACGACGCAGAGAAACACAA
                                           GCTCGTCGGGCTGGTAAATG
                                                                      0
                                                                              0.2
##
   18
           CCAACGACGCAGAGAAACACAA CGCTTAATTGCTCGTGACATAGAAGG
                                                                      0
                                                                              0.2
                                                                              0.2
##
   19
           CCAACGACGCAGAGAAACACAA
                                                                      0
                                            GGCTCGTCGGGCTGGTAAA
       GGTGCAGTTACCTGACCCAAATAAAT
                                             GTGGCGCATGGGAACTT
                                                                      0
                                                                              0.2
   20
##
   21
       GGTGCAGTTACCTGACCCAAATAAAT
                                          CGGCATGGGAACTTTCAGTGT
                                                                      0
                                                                              0.2
   22
       GGTGCAGTTACCTGACCCAAATAAAT
                                           GCCCACTAAGGCCAACACCT
                                                                      0
                                                                              0.2
                                                                      0
                                                                              0.2
##
   23
       GGTGCAGTTACCTGACCCAAATAAAT
                                              GTGGCGCATGGGAACT
       GGTGCAGTTACCTGACCCAAATAAAT
                                                                      0
                                                                              0.2
##
   24
                                        GGCATGGGAACTTTCAGTGTCAT
   25
       GGTGCAGTTACCTGACCCAAATAAAT
                                                                              0.2
##
                                           CACCTAAWGGCTGACCACGG
                                                                      0
##
   26
       GGTGCAGTTACCTGACCCAAATAAAT
                                         CMACACCTAAWGGCTGACCACG
                                                                      0
                                                                              0.2
##
                                                                              0.2
   27
       GGTGCAGTTACCTGACCCAAATAAAT
                                        CCCACTAAGGCCAACACCTAAAG
                                                                      0
##
   28
       GGTGCAGTTACCTGACCCAAATAAAT
                                         CGGCATGGGAACTTTCAGTGTC
                                                                      0
                                                                              0.2
                                                                              0.2
##
   29
       GGTGCAGTTACCTGACCCAAATAAAT
                                       GGCATGGGAACTTTCAGTGTCATC
                                                                      0
##
   30
       GGTGCAGTTACCTGACCCAAATAAAT
                                            CCTAAWGGCTGACCACGGC
                                                                      0
                                                                              0.2
##
   31
       GGTGCAGTTACCTGACCCAAATAAAT
                                        CCAATTTCCACTCCAACACAGGC
                                                                      0
                                                                              0.2
##
  32
       GGTGCAGTTACCTGACCCAAATAAAT
                                              AAWGGCTGACCACGGCC
                                                                      0
                                                                              0.2
## 33
       GGTGCAGTTACCTGACCCAAATAAAT
                                          GCCMACACCTAAWGGCTGACC
                                                                      0
                                                                              0.2
```

##	34	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACC	0	0.2
	35	GGTGCAGTTACCTGACCCAAATAAAT	TGACCACGGCCAATTTCCAC	0	0.2
##	36	GGTGCAGTTACCTGACCCAAATAAAT	CCMACACCTAAWGGCTGACCAC	0	0.2
##	37	GGTGCAGTTACCTGACCCAAATAAAT	TGCCCACTAAGGCCAACAC	0	0.2
##	38	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTA	0	0.2
##	39	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCA	0	0.2
##	40	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
##	41	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
##	42	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
##	43	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAKGCCMACACCTAA	0	0.2
##	44	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
##	45	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAAA	0	0.2
##	46	GCATGCTGCATGCCATAAATGTAT	GCACCGCAGGCACCTTATTAA	0	0.2
##	47	TCCCAGCAGTAAGCAACAATGG	ACAATAGCCTGTACATAAAACCAGCC	0	0.2
##	48	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
##	49	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
##	50	CCAACGACGCAGAGAAACACAAG	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	51	CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
##	52	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGT	0	0.2
##	53	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGAT	0	0.2
##	54	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGTG	0	0.2
##	55	GCTTTGAGGATCCAACACGGC	AGTGTTCAGTTCCGTGCACAG	0	0.2
##	56	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCAGTTCCGTGC	0	0.2
##	57	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGA	0	0.2
##	58	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTCAGTTCCGTGCA	0	0.2
##	59	GCTTTGAGGATCCAACACGGC	GAAGTGTTCAGTTCCGTGCACA	0	0.2
##	60	TGTGCACGGAACTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
##	61	TGTGCACGGAACTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
##	62	TCGTGCTGCAACCGAGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2
	63	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTA	0	0.2
	64	TCGTGCTGCAACCGAGC		0	0.2
	65		CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	66		CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	67	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
	68	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
	69	CCCCCCCCCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
##		CCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
	71	CCCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
	72	CCCCCCGCCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
	73	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
	74 75	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
	75 76		GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
##	76 77	CCCCCCGCCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA CCTTATTTTCAGCYGGTGCAGCA	0 0	0.2
	78	CCCCCCGCCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
	79	CCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
	80	TGATCTGTGCACGGAACTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
##		TGATCTGTGCACGGAACTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
	82		CATACACAACATTGTGTGACGTTGTG	0	0.2
	83	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	0.2
	84		CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	85	ACCTAAGGCAACATTGCAAGACATT	GGCTCGTCGGGCTGGTAAA	0	0.2
	86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGAACACCAAAGTT	0	0.2
	87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGAACACCAAAGT	0	0.2

```
## 88
         TCTCCTGTACCTGGGCAATATGAT
                                              AGTAGTTGGCGGGGGG
                                                                     0
                                                                             0.2
## 89
         TCTCCTGTACCTGGGCAATATGAT
                                         CAAACTAGTAGTTGGCGGGG
                                                                     0
                                                                             0.2
## 90
         TCTCCTGTACCTGGGCAATATGAT
                                         CCAAACTAGTAGTTGGCGGGG
                                                                     0
                                                                             0.2
         TCTCCTGTACCTGGGCAATATGAT
                                                                     0
                                                                             0.2
## 91
                                             GGGGGGGAACACCAAAG
## 92
         TCTCCTGTACCTGGGCAATATGAT
                                           GGGGGGAACACCAAAGTTC
                                                                     0
                                                                             0.2
                                                                     0
## 93
         TCTCCTGTACCTGGGCAATATGAT
                                              CGGGGGGGAACACCAA
                                                                             0.2
## 94
         TCTCCTGTACCTGGGCAATATGAT
                                             CGGGGGGGAACACCAAA
                                                                     0
                                                                             0.2
## 95
        GCATGCTGCATGCCATAAATGTATA
                                         GCACCGCAGGCACCTTATTAA
                                                                     0
                                                                             0.2
## 96
            TGCCGCCACGTCTAATGTTTC GCACAGCCCAAAATACATAACTGTGT
                                                                     0
                                                                             0.2
## 97
            TGCCGCCACGTCTAATGTTTC
                                     GGCACAGCCCAAAATACATAACTGT
                                                                     0
                                                                             0.2
## 98
            TGCCGCCACGTCTAATGTTTC GCCCAAAATACATAACTGTGTCTGCT
                                                                     0
                                                                             0.2
            TGCCGCCACGTCTAATGTTTC
                                                                     0
                                                                             0.2
## 99
                                      GGGCACAGCCCAAAATACATAACT
## 100
            TGCCGCCACGTCTAATGTTTC GGCACAGCCCAAAATACATAACTGTG
                                                                     0
                                                                             0.2
       products similar_signatures
                                             missing_signatures enzyme digest_score
##
               0
                                     HPV16, HPV11, HPV4, HPV17
## 1
                                                                   AccI
## 2
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                                                   AccI
               0
                                                                                     0
## 3
                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
## 4
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                                                   AccI
               0
                                     HPV16, HPV11, HPV4, HPV17
## 5
                                                                                    0
                                                                   AccI
## 6
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
                                                                                     0
## 7
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                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
                                                                                    0
## 8
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                                                   AccI
                                     HPV16, HPV11, HPV4, HPV17
               0
## 9
                                                                                     0
                                                                   AccI
                                     HPV16, HPV11, HPV4, HPV17
## 10
               0
                                                                   AccI
                                                                                     0
               0
## 11
                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
                                                                                     0
## 12
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccT
                                                                                    0
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 13
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## 14
               0
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               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 15
## 16
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                                     HPV16, HPV11, HPV4, HPV17
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## 17
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                                     HPV16, HPV11, HPV4, HPV17
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## 18
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                                     HPV16, HPV11, HPV4, HPV17
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                                     HPV16, HPV11, HPV4, HPV17
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## 20
## 21
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                                     HPV16, HPV11, HPV4, HPV17
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## 22
## 23
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## 30
## 31
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                                     HPV16, HPV11, HPV4, HPV17
               0
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## 32
## 33
               0
                                     HPV16, HPV11, HPV4, HPV17
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## 34
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## 35
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                                     HPV16, HPV11, HPV4, HPV17
## 36
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               0
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## 37
## 38
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                                     HPV16, HPV11, HPV4, HPV17
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## 39
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 40
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
```

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##		0		HPV11,			0
##	42	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	43	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	44	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	45	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	46	0		HPV11,			0
##		0		HPV11,			0
##		0	•	HPV11,			0
			•				_
##		0	-	HPV11,			0
##		0		HPV11,			0
##	51	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	52	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	53	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	54	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	55	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	56	0		HPV11,			0
##		0		HPV11,			0
##		0	•	HPV11,	,		0
##		0	•	HPV11,	,		0
##		0		HPV11,			0
##		0	-	HPV11,			0
##		0	-	HPV11,			0
##	63	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	64	0	HPV16,	HPV11,	HPV4,	HPV17	0
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##	66	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	67	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	68	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	69	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	70	0		HPV11,	-		0
##		0	-	HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
##							
		0	-	HPV11,			0
##		0		HPV11,			0
##		0	-	HPV11,			0
##	77	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	78	0		HPV11,			0
##	79	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	80	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	81	0	HPV16,	HPV11,	HPV4,	HPV17	0
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##	83	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	84	0	-	HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
			-				_
##		0		HPV11,			0
##		0	•	HPV11,			0
##		0	•	HPV11,			0
##		0	-	HPV11,			0
##	92	0	HPV16,	HPV11,	HPV4,	HPV17	0
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##	94	0	HPV16,	HPV11,	HPV4,	HPV17	0

##	95	0	HPV16, HPV11, HPV4, HPV17	0
##	96	0	HPV16, HPV11, HPV4, HPV17	0
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	99	0	HPV16, HPV11, HPV4, HPV17	0
	100	0	HPV16, HPV11, HPV4, HPV17	0
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##		4		
##		4		
##		4		
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##		2		
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	17	0		
	18	0		
##		0		
##		0		
##		0		
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##		0		
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## ##		0		
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##		0		
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##		0		
	34	0		
##		0		
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	46	0		
	47	0		
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## 50 0 0 ## 51 0 ## 52 0 ## 53 0 ## 55 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 66 0 ## 67 0 ## 68 0 ## 68 0 ## 70 0 ## 71 0 ## 72 0 ## 72 0 ## 73 0 ## 74 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 78 0 ## 79 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 89 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 9			
## 51 0 ## 52 0 ## 53 0 ## 54 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 66 0 ## 66 0 ## 66 0 ## 66 0 ## 67 0 ## 68 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 78 0 ## 79 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 89 0 ## 89 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99			
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## 54 0 ## 55 0 ## 56 0 ## 57 0 ## 58 0 ## 59 0 ## 60 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 78 0 ## 78 0 ## 79 0 ## 78 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 88 0 ## 88 0 ## 88 0 ## 88 0 ## 89 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99			
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## 60 0 0 ## 61 0 ## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 89 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 90 0 ## 9			
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## 62 0 ## 63 0 ## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 85 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 90 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 99 0 ## 99 0 ## 99 0			
## 63			
## 64 0 ## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 90			
## 65 0 ## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 91 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 99 0 ## 99 0 ## 99 0			
## 66 0 ## 67 0 ## 68 0 ## 69 0 ## 70 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 90 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 99 0 ## 99 0 ## 99 0 ## 99 0 ## 99 0			
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## 70 0 0 ## 71 0 ## 72 0 ## 73 0 ## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 90 0 ## 91 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 99 0			
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## 74 0 ## 75 0 ## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 90 0 ## 91 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 99 0			
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## 76 0 ## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 90 0 ## 91 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 99 0			
## 77 0 ## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 90 0 ## 91 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 99 0			
## 78 0 ## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 90 0 ## 91 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 95 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 100 0			
## 79 0 ## 80 0 ## 81 0 ## 82 0 ## 83 0 ## 84 0 ## 85 0 ## 86 0 ## 87 0 ## 88 0 ## 89 0 ## 91 0 ## 91 0 ## 92 0 ## 91 0 ## 92 0 ## 91 0 ## 95 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0			
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## 87 0 ## 88 0 ## 89 0 ## 90 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0			
## 88 0 ## 89 0 ## 90 0 ## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 95 0 ## 97 0 ## 98 0 ## 99 0			
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## 90 0 0			
## 91 0 ## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0			
## 92 0 ## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0 ## 100 0			
## 93 0 ## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0			
## 94 0 ## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0			
## 95 0 ## 96 0 ## 97 0 ## 98 0 ## 99 0			
## 96 0 ## 97 0 ## 98 0 ## 99 0			
## 97 0 ## 98 0 ## 99 0			
## 98 0 ## 99 0 ## 100 0			
## 99 0 ## 100 0			
## 100 0			
##		100	0
	##		

##	[[6]	11			
##		forward_primer	reverse_primer	score	coverage
##	1	GCCCCCTTTAGAACTTAAAAACACA	$\tt CCCCATAAGGATCTGCAGACATTTGT$	0	0.2
##	2	GCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
##	3	GCCCCCTTTAGAACTTAAAAACACA	TGGAATCCCCATAAGGATCTGCAG	0	0.2
##	4	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATGT	0	0.2
##	5	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATG	0	0.2
##	6	CCAACGACGCAGAGAAACACAA	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	7	CCAACGACGCAGAGAAACACAA	GGCTCGTCGGGCTGGTAAA	0	0.2
##	8	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACTT	0	0.2
##	9	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT	0	0.2
##	10	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCT	0	0.2
##	11	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACT	0	0.2
##	12	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCAT	0	0.2
##	13	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
##	14	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
##	15	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
##	16	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGTC	0	0.2
##	17	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCATC	0	0.2
##	18	GGTGCAGTTACCTGACCCAAATAAAT	CCTAAWGGCTGACCACGGC	0	0.2
##	19	GGTGCAGTTACCTGACCCAAATAAAT	CCAATTTCCACTCCAACACAGGC	0	0.2
##	20	GGTGCAGTTACCTGACCCAAATAAAT	AAWGGCTGACCACGGCC	0	0.2
##	21	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACC	0	0.2
##	22	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACC	0	0.2
	23	GGTGCAGTTACCTGACCCAAATAAAT	TGACCACGGCCAATTTCCAC	0	0.2
##	24	GGTGCAGTTACCTGACCCAAATAAAT	CCMACACCTAAWGGCTGACCAC	0	0.2
##	25	GGTGCAGTTACCTGACCCAAATAAAT	TGCCCACTAAGGCCAACAC	0	0.2
##	26	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTA	0	0.2
##	27	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCA	0	0.2
##	28	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
##	29	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
##	30	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
##	31 32	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAKGCCMACACCTAA	0	0.2
##	32 33	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
##	34	GGTGCAGTTACCTGACCCAAATAAAT GCATGCTGCATGCCATAAATGTAT	GCCCACTAAGGCCAACACCTAAA GCACCGCAGGCACCTTATTAA	0	0.2
##	35	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGTT	0	0.2
##		TCCCAGCAGTAAGCAACAATGG	AATCTACCATATCCGACCCTGTGT	0	0.2
	37	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGT	0	0.2
	38	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGT	0	0.2
	39	TCCCAGCAGTAAGCAACAATGG	CTACCATATCCGACCCTGTGTCT	0	0.2
	40		TGAAATCTACCATATCCGACCCTGTG	0	0.2
	41	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
	42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
	43		ACAATAGCCTGTACATAAAACCAGCC	0	0.2
	44	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
	45	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
	46		CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	47	CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
	48	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGT	0	0.2
	49	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGAT	0	0.2
	50	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGTG	0	0.2
##		GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
	52	GCTTTGAGGATCCAACACGGC	AGTGTTCAGTTCCGTGCACAG	0	0.2

```
## 53
            GCTTTGAGGATCCAACACGGC
                                        AGTGAAGTGTTCAGTTCCGTGC
                                                                     0
                                                                             0.2
##
   54
                                                                     0
                                                                             0.2
            GCTTTGAGGATCCAACACGGC
                                        ACATTTATGGCATGCAGCATGC
            GCTTTGAGGATCCAACACGGC
##
   55
                                         GTGTTCAGTTCCGTGCACAGA
                                                                     0
                                                                             0.2
   56
            GCTTTGAGGATCCAACACGGC
                                        GTGAAGTGTTCAGTTCCGTGCA
                                                                     0
                                                                             0.2
##
##
   57
            GCTTTGAGGATCCAACACGGC
                                        GAAGTGTTCAGTTCCGTGCACA
                                                                     0
                                                                             0.2
                                                                     0
                                                                            0.2
##
   58
           TGTGCACGGAACTGAACACTTC
                                        CATTTATGGCATGCAGCATGCG
                                                                     0
##
   59
           TGTGCACGGAACTGAACACTTC
                                        ACATTTATGGCATGCAGCATGC
                                                                             0.2
##
  60
                 TCGTGCTGCAACCGAGC
                                      ATGTCTTGCAATGTTGCCTTAGGT
                                                                     0
                                                                            0.2
##
   61
                 TCGTGCTGCAACCGAGC
                                     GTTGCCTTAGGTCCATGCATACTTA
                                                                     0
                                                                             0.2
                                                                     0
##
   62
                 TCGTGCTGCAACCGAGC GTTGCCTTAGGTCCATGCATACTTAA
                                                                             0.2
##
   63
            CAGGAAMGACTCCAACGACGC
                                    CGCTTAATTGCTCGTGACATAGAAGG
                                                                     0
                                                                             0.2
   64
               GGAAMGACTCCAACGACGC
                                    CGCTTAATTGCTCGTGACATAGAAGG
                                                                     0
                                                                             0.2
##
##
   65
                CCCCCCCCCAACTACTA
                                        GTGCAGCATCCTTTTGACAGGT
                                                                     0
                                                                             0.2
                                                                     0
##
   66
                CCCCCCCCCAACTACTA
                                      CCTTATTTTCAGCYGGTGCAGCAT
                                                                            0.2
   67
                CCCCCCGCCAACTACTA
                                            TTTCAGCYGGTGCAGCAT
                                                                     0
                                                                             0.2
##
##
   68
                CCCCCCCCCAACTACTA
                                     GTGCAGCATCCTTTTGACAGGTAAT
                                                                     0
                                                                             0.2
                                                                     0
                                                                             0.2
##
   69
                CCCCCCCCCAACTACTA
                                     CCTTATTTTCAGCYGGTGCAGCATC
##
   70
                CCCCCCCCCAACTACTA
                                       TCCTTATTTTCAGCYGGTGCAGC
                                                                     0
                                                                             0.2
                CCCCCCCCCAACTACTA
                                        CCTTATTTTCAGCYGGTGCAGC
                                                                     0
                                                                             0.2
##
   71
##
   72
                CCCCCCCCCAACTACTA
                                       GTGCAGCATCCTTTTGACAGGTA
                                                                     0
                                                                            0.2
##
   73
                CCCCCCCCCAACTACTA GTGCAGCATCCTTTTGACAGGTAATA
                                                                     0
                                                                            0 2
   74
                CCCCCCCCCAACTACTA CAGCATCCTTTTGACAGGTAATAGCA
                                                                     0
                                                                            0.2
##
  75
                CCCCCCGCCAACTACTA
                                       CCTTATTTTCAGCYGGTGCAGCA
                                                                     0
                                                                            0.2
##
                                                                     0
##
   76
                CCCCCCCCCAACTACTA
                                             TTTCAGCYGGTGCAGCA
                                                                             0.2
##
   77
                CCCCCCGCCAACTACTA
                                      GTGCAGCATCCTTTTGACAGGTAA
                                                                     0
                                                                             0.2
##
   78
           TGATCTGTGCACGGAACTGAAC
                                        CATTTATGGCATGCAGCATGCG
                                                                     0
                                                                             0.2
   79
           TGATCTGTGCACGGAACTGAAC
                                        ACATTTATGGCATGCAGCATGC
                                                                     0
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##
                                                                     0
##
   80
        ACCTAAGGCAACATTGCAAGACATT
                                    CATACACAACATTGTGTGACGTTGTG
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                                                                     0
##
   81
        ACCTAAGGCAACATTGCAAGACATT
                                          GCTCGTCGGGCTGGTAAATG
                                                                             0.2
##
   82
        ACCTAAGGCAACATTGCAAGACATT CGCTTAATTGCTCGTGACATAGAAGG
                                                                     0
                                                                             0.2
##
   83
        ACCTAAGGCAACATTGCAAGACATT
                                           GGCTCGTCGGGCTGGTAAA
                                                                     0
                                                                             0.2
##
   84
             CGGCGACCCTACAAGCTACC
                                        CATTTATGGCATGCAGCATGCG
                                                                     0
                                                                             0.2
##
   85
              CGGCGACCCTACAAGCTACC
                                        ACATTTATGGCATGCAGCATGC
                                                                     0
                                                                             0.2
         TCTCCTGTACCTGGGCAATATGAT
                                                                     0
                                                                             0.2
##
   86
                                          GGGGGGGAACACCAAAGTT
##
   87
         TCTCCTGTACCTGGGCAATATGAT
                                           GGGGGGGAACACCAAAGT
                                                                     0
                                                                             0.2
##
   88
                                             AGTAGTTGGCGGGGGG
                                                                     0
                                                                             0.2
         TCTCCTGTACCTGGGCAATATGAT
##
   89
         TCTCCTGTACCTGGGCAATATGAT
                                         CAAACTAGTAGTTGGCGGGG
                                                                     0
                                                                             0.2
##
  90
         TCTCCTGTACCTGGGCAATATGAT
                                         CCAAACTAGTAGTTGGCGGGG
                                                                     0
                                                                            0 2
   91
         TCTCCTGTACCTGGGCAATATGAT
                                             GGGGGGGAACACCAAAG
                                                                     0
                                                                             0.2
##
         TCTCCTGTACCTGGGCAATATGAT
   92
                                                                     0
                                                                            0 2
##
                                          GGGGGGAACACCAAAGTTC
   93
         TCTCCTGTACCTGGGCAATATGAT
                                             CGGGGGGGAACACCAA
                                                                     0
                                                                             0.2
   94
         TCTCCTGTACCTGGGCAATATGAT
                                             CGGGGGGGAACACCAAA
                                                                     0
                                                                            0.2
##
##
   95
        GCATGCTGCATGCCATAAATGTATA
                                         GCACCGCAGGCACCTTATTAA
                                                                     0
                                                                             0.2
                                                                     0
##
   96
            TGCCGCCACGTCTAATGTTTC
                                    GCACAGCCCAAAATACATAACTGTGT
                                                                            0.2
                                                                     0
##
   97
            TGCCGCCACGTCTAATGTTTC
                                     GGCACAGCCCAAAATACATAACTGT
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                                                                             0.2
  98
            TGCCGCCACGTCTAATGTTTC GCCCAAAATACATAACTGTGTCTGCT
                                                                     0
##
##
   99
            TGCCGCCACGTCTAATGTTTC
                                      GGGCACAGCCCAAAATACATAACT
                                                                     0
                                                                             0.2
##
   100
            TGCCGCCACGTCTAATGTTTC GGCACAGCCCAAAATACATAACTGTG
                                                                     0
                                                                             0.2
##
       products
                similar_signatures
                                            missing_signatures enzyme digest_score
##
               0
                                     HPV16, HPV11, HPV4, HPV17
##
   2
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
               0
                                     HPV16, HPV11, HPV4, HPV17
## 3
                                                                                    0
## 4
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
                                     HPV16, HPV11, HPV4, HPV17
## 5
               0
                                                                                    0
```

##	6	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	7	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	8	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	9	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	10	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	11	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	12	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	13	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	14	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	15	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	16	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	17	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	18	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	19	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	20	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	21	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	22	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	23	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	24	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	25	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	26	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	27	0	HPV16,	HPV11,	HPV4,	HPV17	0
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##	29	0		HPV11,			0
##	30	0		HPV11,			0
##	31	0		HPV11,			0
##		0		HPV11,			0
##	33	0		HPV11,			0
##	34	0		HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
##	37	0		HPV11,			0
##		0	-	HPV11,	-		0
##	39	0		HPV11,			0
##		0		HPV11,			0
##	41	0		HPV11,			0
##		0		HPV11,			0
	43	0		HPV11,			0
	44	0		HPV11,			0
##	45	0	HPV16,	HPV11,	HPV4,	HPV17	0
##		0	•	HPV11,			0
##		0	•	HPV11,	,		0
##		0	•	HPV11,			0
##	49	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	50	0		HPV11,			0
##	51	0		HPV11,			0
##	52	0	•	HPV11,			0
##		0	•	HPV11,	,		0
##		0		HPV11,			0
##		0	•	HPV11,			0
##		0	-	HPV11,			0
##		0	-	HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
		•	• • ,	,	v - ,	•	•

##	60	0	HPV16, HPV11, HPV4, HPV17	0
##	61	0	HPV16, HPV11, HPV4, HPV17	0
##	62	0	HPV16, HPV11, HPV4, HPV17	0
##	63	0	HPV16, HPV11, HPV4, HPV17	0
##	64	0	HPV16, HPV11, HPV4, HPV17	0
##	65	0	HPV16, HPV11, HPV4, HPV17	0
##	66	0	HPV16, HPV11, HPV4, HPV17	0
##	67	0	HPV16, HPV11, HPV4, HPV17	0
##	68	0	HPV16, HPV11, HPV4, HPV17	0
##	69	0	HPV16, HPV11, HPV4, HPV17	0
##	70	0	HPV16, HPV11, HPV4, HPV17	0
##	71	0	HPV16, HPV11, HPV4, HPV17	0
##	72	0	HPV16, HPV11, HPV4, HPV17	0
##	73	0	HPV16, HPV11, HPV4, HPV17	0
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	76	0	HPV16, HPV11, HPV4, HPV17	0
	77	0	HPV16, HPV11, HPV4, HPV17	0
	78	0	HPV16, HPV11, HPV4, HPV17	0
	79	0	HPV16, HPV11, HPV4, HPV17	0
	80	0	HPV16, HPV11, HPV4, HPV17	0
	81	0	HPV16, HPV11, HPV4, HPV17	0
	82	0	HPV16, HPV11, HPV4, HPV17	0
	83	0	HPV16, HPV11, HPV4, HPV17	0
	84	0	HPV16, HPV11, HPV4, HPV17	0
	85	0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
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##		0	HPV16, HPV11, HPV4, HPV17	0
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##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
	95	0	HPV16, HPV11, HPV4, HPV17	0
	96	0	HPV16, HPV11, HPV4, HPV17	0
	97	0	HPV16, HPV11, HPV4, HPV17	0
	98	0	HPV16, HPV11, HPV4, HPV17	0
	99	0	HPV16, HPV11, HPV4, HPV17	0
	100	0	HPV16, HPV11, HPV4, HPV17	0
##	100	fragments	m vio, m vii, m v i , m vi	U
##	1	0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
		0		
	10 11	0		
##	12	0		

##	13	0
##	14	0
##	15	0
##	16	0
##	17	0
##	18	0
##	19	0
##	20	0
##	21	0
##	22	0
##	23	0
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##	26	0
##	27	0
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##	57	0
##	58	0
##	59	0
##	60	0
##	61	0
##	62	0
##	63	0
##	64	0
##	65	0
##	66	0

```
## 67
                0
##
  68
                0
##
  69
                0
                0
##
  70
##
  71
                0
##
  72
                0
  73
                0
## 74
                0
##
  75
                0
  76
                0
##
   77
                0
                0
##
  78
                0
##
   79
## 80
                0
##
  81
                0
## 82
                0
##
  83
                0
##
   84
                0
##
  85
                0
                0
##
  86
##
  87
                0
##
  88
                0
                0
## 89
##
  90
                0
## 91
                0
  92
                0
## 93
                0
   94
                0
##
                0
## 95
                0
##
  96
## 97
                0
##
  98
                0
                0
##
  99
##
   100
                0
##
##
   [[7]]
##
                    forward primer
                                                 reverse_primer score
                                                                       coverage
## 1
       GCCCCCTTTAGAACTTAAAAACACA CCCCATAAGGATCTGCAGACATTTGT
                                                                      0
                                                                             0.2
##
   2
       GCCCCCTTTAGAACTTAAAAACACA
                                     CCCCATAAGGATCTGCAGACATTTG
                                                                      0
                                                                             0.2
                                                                             0.2
##
  3
       GCCCCCTTTAGAACTTAAAAACACA
                                      TGGAATCCCCATAAGGATCTGCAG
                                                                      0
##
           CCAACGACGCAGAGAAACACAA
                                          GCTCGTCGGGCTGGTAAATGT
                                                                      0
                                                                             0.2
## 5
           CCAACGACGCAGAGAAACACAA
                                          GCTCGTCGGGCTGGTAAATG
                                                                      0
                                                                             0.2
##
           CCAACGACGCAGAGAACACAA CGCTTAATTGCTCGTGACATAGAAGG
                                                                             0.2
   6
                                                                      0
##
           CCAACGACGCAGAGAAACACAA
                                            GGCTCGTCGGGCTGGTAAA
                                                                      0
                                                                             0.2
##
       GGTGCAGTTACCTGACCCAAATAAAT
                                             GTGGCGCATGGGAACTT
                                                                      0
                                                                             0.2
## 9
       GGTGCAGTTACCTGACCCAAATAAAT
                                          CGGCATGGGAACTTTCAGTGT
                                                                             0.2
                                                                      0
                                           GCCCACTAAGGCCAACACCT
       GGTGCAGTTACCTGACCCAAATAAAT
                                                                             0.2
##
   10
                                                                      0
##
       GGTGCAGTTACCTGACCCAAATAAAT
                                              GTGGCGGCATGGGAACT
                                                                      0
                                                                             0.2
   11
##
   12
       GGTGCAGTTACCTGACCCAAATAAAT
                                       GGCATGGGAACTTTCAGTGTCAT
                                                                      0
                                                                             0.2
                                                                             0.2
##
   13
       GGTGCAGTTACCTGACCCAAATAAAT
                                           CACCTAAWGGCTGACCACGG
                                                                      0
##
   14
       GGTGCAGTTACCTGACCCAAATAAAT
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                                                                      0
                                                                             0.2
       GGTGCAGTTACCTGACCCAAATAAAT
                                                                             0.2
## 15
                                       CCCACTAAGGCCAACACCTAAAG
                                                                      0
## 16
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## 17
       GGTGCAGTTACCTGACCCAAATAAAT
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```

##	18	GGTGCAGTTACCTGACCCAAATAAAT	CCTAAWGGCTGACCACGGC	0	0.2
	19	GGTGCAGTTACCTGACCCAAATAAAT	CCAATTTCCACTCCAACACAGGC	0	0.2
##	20	GGTGCAGTTACCTGACCCAAATAAAT	AAWGGCTGACCACGGCC	0	0.2
##	21	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACC	0	0.2
##	22	GGTGCAGTTACCTGACCCAAATAAAT	GCCACTAAGGCCAACACC	0	0.2
##	23	GGTGCAGTTACCTGACCCAAATAAAT	TGACCACGGCCAATTTCCAC	0	0.2
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##	32	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
##	33	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAAA	0	0.2
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	55 E6		GTGTTCAGTTCCGTGCACAGA	0	0.2
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##	05	0

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   100
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                                                  reverse_primer score
                                                                         coverage
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                                                                              0.2
## 36
       GGTGCAGTTACCTGACCCAAATAAAT
                                         CCMACACCTAAWGGCTGACCAC
                                                                       0
                                                                              0.2
```

##	37	GGTGCAGTTACCTGACCCAAATAAAT	TGCCCACTAAGGCCAACAC	0	0.2
##	38	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTA	0	0.2
##	39	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCA	0	0.2
##	40	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
##	41	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
##	42	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
##	43	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAKGCCMACACCTAA	0	0.2
##	44	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
##	45	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAAA	0	0.2
##	46	GCATGCTGCATGCCATAAATGTAT	GCACCGCAGGCACCTTATTAA	0	0.2
##	47	TCCCAGCAGTAAGCAACAATGG	ACAATAGCCTGTACATAAAACCAGCC	0	0.2
##	48	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
##	49	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
##	50	CCAACGACGCAGAGAAACACAAG	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	51	CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
##	52	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGT	0	0.2
##	53	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGAT	0	0.2
##	54	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGTG	0	0.2
##	55	GCTTTGAGGATCCAACACGGC	AGTGTTCAGTTCCGTGCACAG	0	0.2
##	56	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCAGTTCCGTGC	0	0.2
##	57	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGA	0	0.2
##	58	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTCAGTTCCGTGCA	0	0.2
##	59	GCTTTGAGGATCCAACACGGC	GAAGTGTTCAGTTCCGTGCACA	0	0.2
##	60	TGTGCACGGAACTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
##	61	TGTGCACGGAACTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
##	62	TCGTGCTGCAACCGAGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2
##	63	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTA	0	0.2
##	64	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTAA	0	0.2
##	65	CAGGAAMGACTCCAACGACGC	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	66		CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	67	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
	68	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
	69	CCCCCCCCCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
	70	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
##	. –	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
	72	CCCCCCGCCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
	73	CCCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
	74	CCCCCCCCCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
	75 76		GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
	76		CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
	77	CCCCCCCCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
	78 70	CCCCCCCCCAACTACTA	TTTCAGCYGGTGCAGCA GTGCAGCATCCTTTTGACAGGTAA	0	0.2
	79 80	CCCCCCCCCCAACTACTA TGATCTGTGCACGGAACTGAAC	CATTTATGGCATGCAGCATGCG	0 0	0.2
##		TGATCTGTGCACGGAACTGAAC	ACATTTATGGCATGCAGCATGCG ACATTTATGGCATGCAGCATGC	0	0.2
	82		CATACACAACATTGTGTGACGTTGTG	0	0.2
	83	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	0.2
	84		CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	85	ACCTAAGGCAACATTGCAAGACATT	GGCTCGTCGGGCTGGTAAA	0	0.2
	86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGAACACCAAAGTT	0	0.2
	87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGAACACCAAAGT	0	0.2
	88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGG	0	0.2
	89	TCTCCTGTACCTGGGCAATATGAT	CAAACTAGTAGTTGGCGGGGG	0	0.2
	90	TCTCCTGTACCTGGGCAATATGAT	CCAAACTAGTAGTTGGCGGGG	0	0.2
	-			-	

```
## 91
         TCTCCTGTACCTGGGCAATATGAT
                                             GGGGGGGAACACCAAAG
                                                                     0
                                                                             0.2
## 92
         TCTCCTGTACCTGGGCAATATGAT
                                          GGGGGGAACACCAAAGTTC
                                                                     0
                                                                             0.2
## 93
         TCTCCTGTACCTGGGCAATATGAT
                                              CGGGGGGGAACACCAA
                                                                     0
                                                                             0.2
         TCTCCTGTACCTGGGCAATATGAT
                                             CGGGGGGGAACACCAAA
                                                                     0
                                                                             0.2
## 94
## 95
        GCATGCTGCATGCCATAAATGTATA
                                         GCACCGCAGGCACCTTATTAA
                                                                     0
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                                                                     0
## 96
            TGCCGCCACGTCTAATGTTTC GCACAGCCCAAAATACATAACTGTGT
                                                                             0.2
## 97
            TGCCGCCACGTCTAATGTTTC
                                     GGCACAGCCCAAAATACATAACTGT
                                                                     0
                                                                             0.2
## 98
            TGCCGCCACGTCTAATGTTTC GCCCAAAATACATAACTGTGTCTGCT
                                                                     0
                                                                             0.2
## 99
            TGCCGCCACGTCTAATGTTTC
                                      GGGCACAGCCCAAAATACATAACT
                                                                     0
                                                                             0.2
## 100
            TGCCGCCACGTCTAATGTTTC GGCACAGCCCAAAATACATAACTGTG
                                                                     0
                                                                             0.2
##
       products similar_signatures
                                            missing_signatures enzyme digest_score
                                     HPV16, HPV11, HPV4, HPV17
## 1
              0
                                                                   AccI
## 2
               0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
                                                                   AccI
                                     HPV16, HPV11, HPV4, HPV17
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## 3
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                                     HPV16, HPV11, HPV4, HPV17
                                                                                     0
## 4
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## 5
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                                     HPV16, HPV11, HPV4, HPV17
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                                     HPV16, HPV11, HPV4, HPV17
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## 6
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## 7
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                                     HPV16, HPV11, HPV4, HPV17
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                                     HPV16, HPV11, HPV4, HPV17
## 8
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## 9
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                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
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## 10
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                                     HPV16, HPV11, HPV4, HPV17
                                                                   AccI
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                                     HPV16, HPV11, HPV4, HPV17
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## 11
                                                                   AccI
                                     HPV16, HPV11, HPV4, HPV17
               0
## 12
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                                                                   AccI
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                                     HPV16, HPV11, HPV4, HPV17
## 13
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## 14
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## 15
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                                     HPV16, HPV11, HPV4, HPV17
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## 16
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## 18
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## 31
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## 32
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## 33
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                                     HPV16, HPV11, HPV4, HPV17
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## 35
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## 38
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                                     HPV16, HPV11, HPV4, HPV17
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                                     HPV16, HPV11, HPV4, HPV17
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## 40
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                                     HPV16, HPV11, HPV4, HPV17
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## 42
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## 43
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                                     HPV16, HPV11, HPV4, HPV17
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```

##	44	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	45	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	46	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	47	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	48	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	49	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	50	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	51	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	52	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	53	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	54	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	55	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	56	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	57	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	58	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	59	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	60	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	61	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	62	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	63	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	64	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	65	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	66	0		HPV11,			0
##	67	0		HPV11,			0
##	68	0		HPV11,			0
##	69	0		HPV11,			0
##		0		HPV11,			0
##	71	0		HPV11,			0
##	72	0		HPV11,			0
##	73	0		HPV11,			0
##		0		HPV11,			0
##	75	0		HPV11,			0
##	76	0	-	HPV11,	-		0
##	77	0		HPV11,			0
##	78	0		HPV11,			0
##	79	0		HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
##		0		HPV11,			0
##		0	HPV16,	HPV11,	HPV4,	HPV17	0
##		0	•	HPV11,			0
##		0	HPV16.	HPV11,	HPV4.	HPV17	0
##		0	•	HPV11,	,		0
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##	89	0		HPV11,			0
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##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
	100	0	HPV16, HPV11, HPV4, HPV17	0
##	,	fragments		
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## 97
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## 98
## 99
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## 100
               0
##
## [[9]]
##
                   forward_primer
                                      reverse_primer score coverage
## 1 GCCCCCTTTAGAACTTAAAAACACA CCCCATAAGGATCTGCAGACATTTGT
                                                                   0
                                                                          0.2
```

##	2	GCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
##	3	GCCCCCTTTAGAACTTAAAAACACA	TGGAATCCCCATAAGGATCTGCAG	0	0.2
##	4	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATGT	0	0.2
##	5	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATG	0	0.2
##	6	CCAACGACGCAGAGAAACACAA	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
##	7	CCAACGACGCAGAGAAACACAA	GGCTCGTCGGGCTGGTAAA	0	0.2
##	8	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACTT	0	0.2
##	9	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT	0	0.2
##	10	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCT	0	0.2
##	11	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACT	0	0.2
##	12	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCAT	0	0.2
##	13	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
##	14	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
##	15	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
##	16	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGTC	0	0.2
##	17	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCATC	0	0.2
##	18	GGTGCAGTTACCTGACCCAAATAAAT	CCTAAWGGCTGACCACGGC	0	0.2
##	19	GGTGCAGTTACCTGACCCAAATAAAT	CCAATTTCCACTCCAACACAGGC	0	0.2
##	20	GGTGCAGTTACCTGACCCAAATAAAT	AAWGGCTGACCACGGCC	0	0.2
##	21	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACC	0	0.2
##	22	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACC	0	0.2
##	23	GGTGCAGTTACCTGACCCAAATAAAT	TGACCACGGCCAATTTCCAC	0	0.2
##	24	GGTGCAGTTACCTGACCCAAATAAAT	CCMACACCTAAWGGCTGACCAC	0	0.2
##	25	GGTGCAGTTACCTGACCCAAATAAAT	TGCCCACTAAGGCCAACAC	0	0.2
##	26	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTA	0	0.2
##	27	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTCA	0	0.2
##	28	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
##	29	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
	30	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
##	31	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAKGCCMACACCTAA	0	0.2
##	32	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
	33	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAAA	0	0.2
	34	GCATGCTGCATGCCATAAATGTAT	GCACCGCAGGCACCTTATTAA	0	0.2
	35	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGTT	0	0.2
	36	TCCCAGCAGTAAGCAACAATGG	AATCTACCATATCCGACCCTGTGT	0	0.2
##	37	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGT	0	0.2
	38	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGT	0	0.2
	39	TCCCAGCAGTAAGCAACAATGG	CTACCATATCCGACCCTGTGTCT	0	0.2
	40		TGAAATCTACCATATCCGACCCTGTG	0	0.2
	41	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
	42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
	43		ACAATAGCCTGTACATAAAACCAGCC	0	0.2
	44	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
	45	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
	46		CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
	47	CCAACGACGCAGAGAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
	48	GCTTTGAGGATCCAACACGGC GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGT	0	0.2
	49		GTGTTCAGTTCCGTGCACAGAT	0	0.2
##	50 51	GCTTTGAGGATCCAACACGGC GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAGTTCCGTG CATTTATGGCATGCAGCATGCG	0	0.2
	51	GCTTTGAGGATCCAACACGGC	AGTGTTCAGTTCCGTGCACAG	0	0.2
	52 53	GCTTTGAGGATCCAACACGGC	AGTGTTCAGTTCCGTGCACAG AGTGAAGTGTTCAGTTCCGTGC	0	0.2
	53 54	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
	54 55	GCTTTGAGGATCCAACACGGC	GTGTTCAGTTCCGTGCACAGA	0	0.2
π#	JJ	ODDOROBREOLINDBRETTION	GIGIIONGIIOOGIGONONGA	U	0.2

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## 56
            GCTTTGAGGATCCAACACGGC
                                        GTGAAGTGTTCAGTTCCGTGCA
                                                                     0
                                                                            0.2
##
  57
                                                                     0
                                                                            0.2
            GCTTTGAGGATCCAACACGGC
                                        GAAGTGTTCAGTTCCGTGCACA
           TGTGCACGGAACTGAACACTTC
##
   58
                                        CATTTATGGCATGCAGCATGCG
                                                                     0
                                                                            0.2
           TGTGCACGGAACTGAACACTTC
                                        ACATTTATGGCATGCAGCATGC
                                                                     0
                                                                            0.2
##
  59
##
   60
                 TCGTGCTGCAACCGAGC
                                      ATGTCTTGCAATGTTGCCTTAGGT
                                                                     0
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   61
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##
                 TCGTGCTGCAACCGAGC
                                     GTTGCCTTAGGTCCATGCATACTTA
                                                                     0
##
   62
                 TCGTGCTGCAACCGAGC GTTGCCTTAGGTCCATGCATACTTAA
                                                                            0.2
## 63
            CAGGAAMGACTCCAACGACGC CGCTTAATTGCTCGTGACATAGAAGG
                                                                     0
                                                                            0.2
##
   64
              GGAAMGACTCCAACGACGC CGCTTAATTGCTCGTGACATAGAAGG
                                                                     0
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##
   65
                CCCCCCGCCAACTACTA
                                        GTGCAGCATCCTTTTGACAGGT
                                                                            0.2
##
   66
                CCCCCCCCCAACTACTA
                                      CCTTATTTTCAGCYGGTGCAGCAT
                                                                     0
                                                                            0.2
   67
                CCCCCCGCCAACTACTA
                                            TTTCAGCYGGTGCAGCAT
                                                                     0
                                                                            0.2
##
##
   68
                CCCCCCCCCAACTACTA
                                     GTGCAGCATCCTTTTGACAGGTAAT
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                                                                            0.2
                                                                     0
##
   69
                CCCCCCCCCAACTACTA
                                     CCTTATTTTCAGCYGGTGCAGCATC
                                                                            0.2
##
  70
                CCCCCCGCCAACTACTA
                                       TCCTTATTTTCAGCYGGTGCAGC
                                                                     0
                                                                            0.2
##
  71
                CCCCCCGCCAACTACTA
                                        CCTTATTTTCAGCYGGTGCAGC
                                                                     0
                                                                            0.2
   72
                                                                     0
                                                                            0.2
##
                CCCCCCCCCAACTACTA
                                       GTGCAGCATCCTTTTGACAGGTA
##
   73
                CCCCCCCCCAACTACTA GTGCAGCATCCTTTTGACAGGTAATA
                                                                     0
                                                                            0.2
   74
                CCCCCCCCCAACTACTA CAGCATCCTTTTGACAGGTAATAGCA
                                                                     0
                                                                            0.2
##
##
   75
                CCCCCCCCCAACTACTA
                                       CCTTATTTTCAGCYGGTGCAGCA
                                                                     0
                                                                            0.2
##
  76
                CCCCCCGCCAACTACTA
                                             TTTCAGCYGGTGCAGCA
                                                                     0
                                                                            0 2
   77
                CCCCCCGCCAACTACTA
                                                                     0
                                                                            0.2
##
                                      GTGCAGCATCCTTTTGACAGGTAA
  78
           TGATCTGTGCACGGAACTGAAC
                                                                     0
                                                                            0.2
##
                                        CATTTATGGCATGCAGCATGCG
           TGATCTGTGCACGGAACTGAAC
                                                                     0
##
   79
                                        ACATTTATGGCATGCAGCATGC
                                                                            0.2
                                                                     0
##
   80
        ACCTAAGGCAACATTGCAAGACATT CATACACAACATTGTGTGACGTTGTG
                                                                            0.2
##
   81
        ACCTAAGGCAACATTGCAAGACATT
                                          GCTCGTCGGGCTGGTAAATG
                                                                     0
                                                                            0.2
##
   82
        ACCTAAGGCAACATTGCAAGACATT
                                    CGCTTAATTGCTCGTGACATAGAAGG
                                                                     0
                                                                            0.2
                                                                     0
##
   83
        ACCTAAGGCAACATTGCAAGACATT
                                           GGCTCGTCGGGCTGGTAAA
                                                                            0.2
##
                                                                     0
   84
             CGGCGACCCTACAAGCTACC
                                        CATTTATGGCATGCAGCATGCG
                                                                            0.2
##
   85
             CGGCGACCCTACAAGCTACC
                                        ACATTTATGGCATGCAGCATGC
                                                                     0
                                                                            0.2
##
   86
         TCTCCTGTACCTGGGCAATATGAT
                                          GGGGGGGAACACCAAAGTT
                                                                     0
                                                                            0.2
##
   87
         TCTCCTGTACCTGGGCAATATGAT
                                           GGGGGGGAACACCAAAGT
                                                                     0
                                                                            0.2
##
   88
         TCTCCTGTACCTGGGCAATATGAT
                                             AGTAGTTGGCGGGGGG
                                                                     0
                                                                            0.2
         TCTCCTGTACCTGGGCAATATGAT
                                                                     0
                                                                            0.2
##
   89
                                         CAAACTAGTAGTTGGCGGGG
##
   90
         TCTCCTGTACCTGGGCAATATGAT
                                         CCAAACTAGTAGTTGGCGGGG
                                                                     0
                                                                            0.2
##
  91
                                                                     0
                                                                            0.2
         TCTCCTGTACCTGGGCAATATGAT
                                            GGGGGGGAACACCAAAG
##
  92
         TCTCCTGTACCTGGGCAATATGAT
                                          GGGGGGAACACCAAAGTTC
                                                                     0
                                                                            0.2
##
  93
         TCTCCTGTACCTGGGCAATATGAT
                                             CGGGGGGGAACACCAA
                                                                     0
                                                                            0 2
##
  94
         TCTCCTGTACCTGGGCAATATGAT
                                            CGGGGGGGAACACCAAA
                                                                     0
                                                                            0.2
   95
                                                                     0
                                                                            0 2
##
        GCATGCTGCATGCCATAAATGTATA
                                         GCACCGCAGGCACCTTATTAA
                                                                     0
   96
            TGCCGCCACGTCTAATGTTTC GCACAGCCCAAAATACATAACTGTGT
                                                                            0.2
  97
            TGCCGCCACGTCTAATGTTTC
                                     GGCACAGCCCAAAATACATAACTGT
                                                                     0
                                                                            0.2
##
##
   98
            TGCCGCCACGTCTAATGTTTC GCCCAAAATACATAACTGTGTCTGCT
                                                                     0
                                                                            0.2
                                                                     0
##
  99
            TGCCGCCACGTCTAATGTTTC
                                      GGGCACAGCCCAAAATACATAACT
                                                                            0.2
                                                                     0
##
   100
            TGCCGCCACGTCTAATGTTTC GGCACAGCCCAAAATACATAACTGTG
                                                                            0.2
##
       products similar_signatures
                                            missing_signatures enzyme digest_score
## 1
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
## 2
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                    0
##
  3
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                   0
                                     HPV16, HPV11, HPV4, HPV17
## 4
              0
                                                                                    0
## 5
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                   0
                                     HPV16, HPV11, HPV4, HPV17
## 6
              0
                                                                                   0
## 7
              0
                                     HPV16, HPV11, HPV4, HPV17
                                                                                   0
                                     HPV16, HPV11, HPV4, HPV17
## 8
              0
                                                                                    0
```

##	9	0	HPV16	HPV11,	HPV4	HPV17	0
	10	0		HPV11,			0
	11	0		HPV11,			0
	12	0		HPV11,			0
	13	0		HPV11,			0
	14	0		HPV11,			0
	15	0		HPV11,			0
	16	0		HPV11,			0
	17	0	•	HPV11,			0
	18	0	•	HPV11,			0
	19	0		HPV11,			0
	20	0		HPV11,			0
	21	0		HPV11,			0
	22	0		HPV11,			0
	23	0		HPV11,			0
	24	0		HPV11,			0
	25	0		HPV11,			0
			•				_
	26 27	0	•	HPV11,			0
	28	0		HPV11,			
		0		HPV11,			0
	29	0		HPV11,			0
	30	0		HPV11,			0
	31	0		HPV11,			0
	32	0		HPV11,			0
	33	0		HPV11,			0
	34	0		HPV11,			0
	35	0		HPV11,			0
	36	0		HPV11,	-		0
	37	0		HPV11,	-		0
	38	0		HPV11,			0
	39	0		HPV11,			0
	40	0		HPV11,			0
	41	0		HPV11,			0
	42	0		HPV11,			0
	43	0		HPV11,			0
	44	0		HPV11,			0
	45	0		HPV11,			0
	46	0		HPV11,			0
	47	0		HPV11,			0
	48	0	•	HPV11,	,		0
	49	0	•	HPV11,	,		0
##	50	0	•	HPV11,			0
	51	0	•	HPV11,			0
##	52	0		HPV11,			0
##	53	0	HPV16,	HPV11,	HPV4,	HPV17	0
	54	0		HPV11,			0
	55	0		HPV11,			0
##	56	0	•	HPV11,			0
##	57	0	•	HPV11,			0
##	58	0	HPV16,	HPV11,	HPV4,	HPV17	0
	59	0	•	HPV11,			0
##	60	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	61	0	HPV16,	HPV11,	HPV4,	HPV17	0
##	62	0	HPV16,	HPV11,	HPV4,	HPV17	0

##	63	0	HPV16, HPV11, HPV4, HPV17	0
##	64	0	HPV16, HPV11, HPV4, HPV17	0
##	65	0	HPV16, HPV11, HPV4, HPV17	0
##	66	0	HPV16, HPV11, HPV4, HPV17	0
##	67	0	HPV16, HPV11, HPV4, HPV17	0
##	68	0	HPV16, HPV11, HPV4, HPV17	0
##	69	0	HPV16, HPV11, HPV4, HPV17	0
##	70	0	HPV16, HPV11, HPV4, HPV17	0
##	71	0	HPV16, HPV11, HPV4, HPV17	0
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##	74	0	HPV16, HPV11, HPV4, HPV17	0
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##	76	0	HPV16, HPV11, HPV4, HPV17	0
##	77	0	HPV16, HPV11, HPV4, HPV17	0
##	78	0	HPV16, HPV11, HPV4, HPV17	0
##	79	0	HPV16, HPV11, HPV4, HPV17	0
##	80	0	HPV16, HPV11, HPV4, HPV17	0
##	81	0	HPV16, HPV11, HPV4, HPV17	0
##	82	0	HPV16, HPV11, HPV4, HPV17	0
##	83	0	HPV16, HPV11, HPV4, HPV17	0
##	84	0	HPV16, HPV11, HPV4, HPV17	0
##	85	0	HPV16, HPV11, HPV4, HPV17	0
##	86	0	HPV16, HPV11, HPV4, HPV17	0
##	87	0	HPV16, HPV11, HPV4, HPV17	0
##	88	0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##	90	0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
##		0	HPV16, HPV11, HPV4, HPV17	0
	99	0	HPV16, HPV11, HPV4, HPV17	0
	100	0	HPV16, HPV11, HPV4, HPV17	0
##		fragments		
## ##		0 0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
##		0		
	15	0		
		•		

##	16	0
##	17	0
##	18	0
##	19	0
##	20	0
##	21	0
##	22	0
##	23	0
##	24	0
##	25	0
##	26	0
##	27	0
##	28	0
##	29	0
##	30	0
##	31	0
##	32	0
##	33	0
##	34	0
##	35	0
##	36	0
##	37	0
##	38	0
##	39	0
##	40	0
##	41	0
##	42	0
##	43	0
##	44	0
##	45	0
##	46	0
##	47	0
##	48	0
##	49	0
##	50	0
##	51	0
##	52	0
##	53	0
##	54	0
##	55	0
##	56	0
##	57	0
##	58	0
##	59	0
##	60	0
##	61	0
##	62	0
##	63	0
##	64	0
##	65	0
##	66	0
##	67	0
##	68	0
##	69	0

```
## 70
               0
## 71
               0
## 72
               0
## 73
               0
## 74
               0
## 75
               0
## 76
               0
## 77
               0
## 78
               0
## 79
               0
## 80
               0
               0
## 81
## 82
               0
## 83
               0
## 84
               0
## 85
               0
## 86
               0
## 87
               0
               0
## 88
## 89
               0
## 90
               0
## 91
               0
## 92
               0
## 93
               0
## 94
               0
## 95
               0
## 96
               0
## 97
               0
               0
## 98
## 99
               0
## 100
               0
# TYPE <- 'length'
# LEVELS <- 2
# MIN_SIZE <- 200
# MAX_SIZE <- 1400
# RESOLUTION <- c(
# seq(200, 700, 3),
  seq(705, 1000, 5),
#
   seq(1010, 1400, 10)
# )
#
# TYPE <- 'melt'
# MIN_SIZE <- 55
# MAX_SIZE <- 400
```

Anal Isolates

https://www.ncbi.nlm.nih.gov/nuccore

```
"Human papillomavirus"[Primary Organism]
AND viruses[filter]
NOT Polyamides[All Fields]
NOT Method[All Fields]
```

```
NOT Patent[All Fields]
AND Anal[All Fields]
```

Cutaneous Isolates

https://www.ncbi.nlm.nih.gov/nuccore

```
"Human papillomavirus"[Primary Organism]
NOT Polyamides[All Fields]
NOT Method[All Fields]
NOT Patent[All Fields]
AND Anal[All Fields]
AND "Complete Genome"[All Fields]

tryCatch({dbDisconnect(dbconn)}, error=warning)
tryCatch({dbDisconnect(dbConn)}, error=warning)
```