

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 OligoArrayAux 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)
```

```

    aseqs[uidxs]
}

dbConn <- dbConnect(SQLite(), ':memory:')

Oral.L1.seqs <- readDNASTringSet('HPV.oral.L1.fasta') %>% doAlignment
Oral.L1.vars <- read.csv('HPV.oral.L1.csv', stringsAsFactors = F)

print(Oral.L1.seqs)

## A DNASTringSet instance of length 31
##      width seq                      names
## [1]  607 ----- gi|944543704|gb|K...
## [2]  607 ----- gi|944543703|gb|K...
## [3]  607 ----- gi|944543701|gb|K...
## [4]  607 ----- gi|944543699|gb|K...
## [5]  607 ----- gi|944543697|gb|K...
## ...    ...
## [27] 607 -----...GTTAATAAACTCCATTATCGAA gi|440573440|gb|K...
## [28] 607 -----...GTTAGTTAACAGCACTATTTCAG gi|440573438|gb|K...
## [29] 607 -----...ATTAAAAAATACAGTAATTGAA gi|440573436|gb|K...
## [30] 607 -----...ATTAGTAAATACTGTAATTGAA gi|440573434|gb|K...
## [31] 607 -----...GTTAATAAATACAGTAATTGAA gi|440573432|gb|K...

Seqs2DB(Oral.L1.seqs, 'XStringSet', dbConn, '')

## Adding 31 sequences to the database.
##
## 31 total sequences in table Seqs.
## 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 Seqs: "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  L1
## 2 944543703 HPV18 13  L1
## 3 944543701 HPV16  5  L1
## 4 944543699 HPV18 12  L1
```

Design HPV16-specific F/R primers using DECIPHER utilities.

```
tiles.L1 <- TileSeqs(
  dbFile = dbConn,
  minLength = 18,
  maxLength = 29,
  minCoverage = 0.8
)

## =====
##
## Time difference of 7.48 secs

print(
  tiles.L1[,c(6,11)] %>% sample_n(6)
)

##   misprime      target_site
## 1   FALSE GTATTGGGACAACTAAATTTGTGATG
## 2   FALSE TTACCTGATGGCACCTATACAATCCAGA
## 3   FALSE ATAAGCAGGATATTCCTAAGGTTTCTGCA
## 4    TRUE ATGTCCACCTATTCAGTTAATAAATACAG
## 5   FALSE GCAGATATGTCTGTATACAATCCAGACAA
## 6   FALSE AAACAATCAGATGATAATAGACAGAATGT

oligos.L1 <- DesignPrimers(
  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      HPV16          287          304          279
## 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
## 237              312              5              5
## 238              313              5              5
##      score_forward score_reverse      forward_primer.1
## 201 -6.27037.... -0.00038.... TTGTTTTCTGACACCTCATTTTA
## 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 AAAGTGAAGTTCCTACTGGATATTTGTA 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 TACAAATATCCAGTGGAACCTCACTTTT
## 231 AGCCGCTGTGTATCTGGATT ACACTAGTCTTTCCTTTTCTGGGTT
## 232 CAGCCGCTGTGTATCTGGAT CACACTAGTCTTTCCTTTTCTGGGT
## 236 AAACCAGCCGCTGTGTATCT GCCCACACTAGTCTTTCCTTTTCT
## 237 CAAACCAGCCGCTGTGTATC GCCCACACTAGTCTTTCCTTTTC

```

```

## 238      CCAAACCAGCCGCTGTGTAT      GGCCCACACTAGTCTTTCCTTTT
##          reverse_primer.3          reverse_primer.4
## 201 TGTAGGGTCCACTAAGGCAAATTT AGACTGACATATCTGCTAAAGCAAATTT
## 231      AATCGCTCGCGGTCTGGGT      AAACGCTCATGGTCAGAGTT
## 232      TAATCGCTCGCGGTCTGGGT      CACTAAACGCTCATGGTCAGAGT
## 236      ACATAATCGCTCGCGGTCT      GCCCAAACCACTCTTTCCTTTTCA
## 237      GCCCAAACCACTCTTTCCTTTT      CCACACTAAACGCTCATGGTC
## 238      GCCCAAACCACTCTTTCCTTTT      GCCACACTAAACGCTCATGGT
##          reverse_primer.5 forward_efficiency.1 forward_efficiency.2
## 201 GACATTCATATCTACCAAGGCGAATCT      0.8339538      0.8284785
## 231      AAACCACTCTTTCCTTTTCAGGATT      0.9976087      0.8209337
## 232      CCAAACCACTCTTTCCTTTTCAGGAT      0.9987960      0.8996088
## 236      CCACACTAAACGCTCATGGTCA      0.9987474      0.9127847
## 237      CACACTAATCGCTCGCGGTC      0.9957214      0.9361697
## 238      CCACACTAATCGCTCGCGGT      0.9859330      0.9767059
##          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      0.8333086      0.9243034
## 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      0.4444444
## 231      0.8755932      0.8085530      0.4444444
## 232      0.8794141      0.8211595      0.4444444
## 236      0.9405149      0.8775017      0.4444444
## 237      0.8451844      0.9707554      0.4444444
## 238      0.9113278      0.9687265      0.4444444
##          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      0.4444444      0.1111111      0.1111111      0.1111111
## 231      0.4444444      0.1111111      0.1111111      0.1111111
## 232      0.4444444      0.1111111      0.1111111      0.1111111
## 236      0.4444444      0.1111111      0.1111111      0.1111111
## 237      0.4444444      0.1111111      0.1111111      0.1111111
## 238      0.4444444      0.1111111      0.1111111      0.1111111
##          reverse_coverage.5      mismatches_forward
## 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%)
## 232          HPV4 (0.0189%)
## 236          HPV17 (0.0207%)
## 237          HPV17 (0.0426%)
## 238          HPV17 (0.11%)
```

Honestly, I don't really understand the dimensions of the dataframe output by `DECIPHER::DesignPrimers`. 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 complement of each primer pair (5) in each primer set (7).

```
plotMeltCurves <- function(temps, effs) {
  plot(
    temps, effs[,1], ylim=c(0,1),
    ylab="Hybridization Efficiency",
    xlab=expression(paste("Temperature (", degree, "C)", sep="")),
    type="l", lwd=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, doPlot=TRUE) {
    fxn <- function(temp) CalculateEfficiencyPCR(primers, target, temp, P=P, ions=ions, ...)
    effs <- matrix(unlist(lapply(temps, fxn)), ncol=2, byrow=TRUE)
    if (doPlot) plotMeltCurves(temps, effs)
    list(temps = temps, effs = effs)
  }

nsets <- nrow(oligos.L1)
npair <- ncol(oligos.L1)

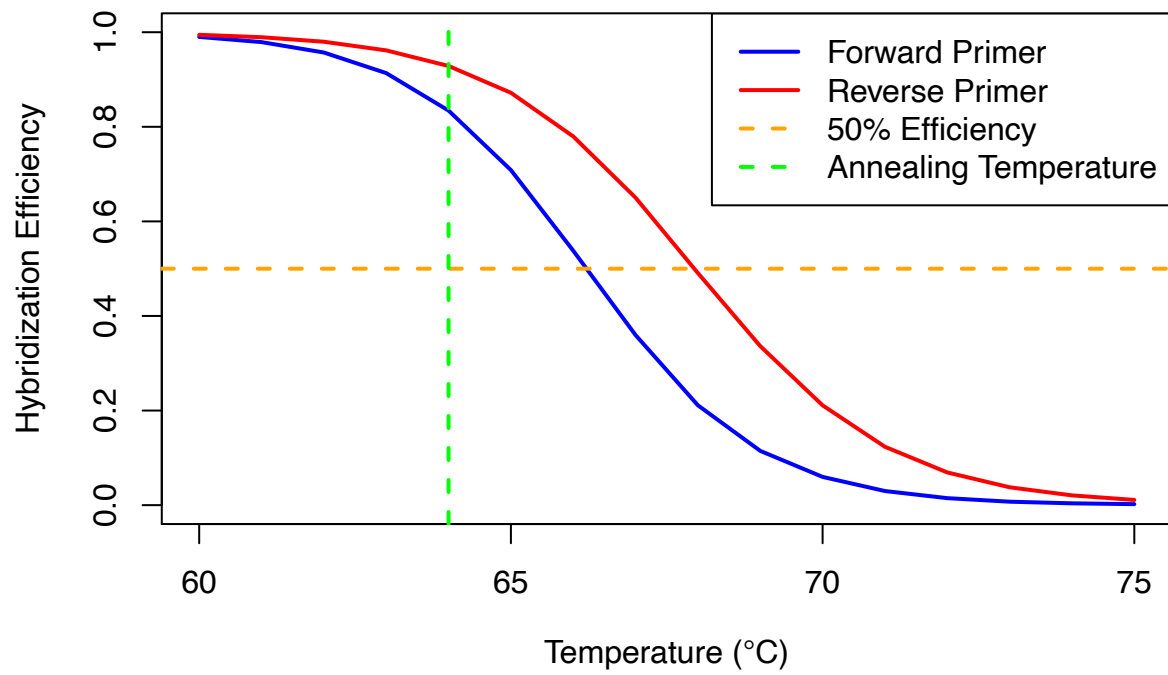
for (i in 1:nsets)
  for (j in 1:npair)
    tryCatch(
      {
```

```

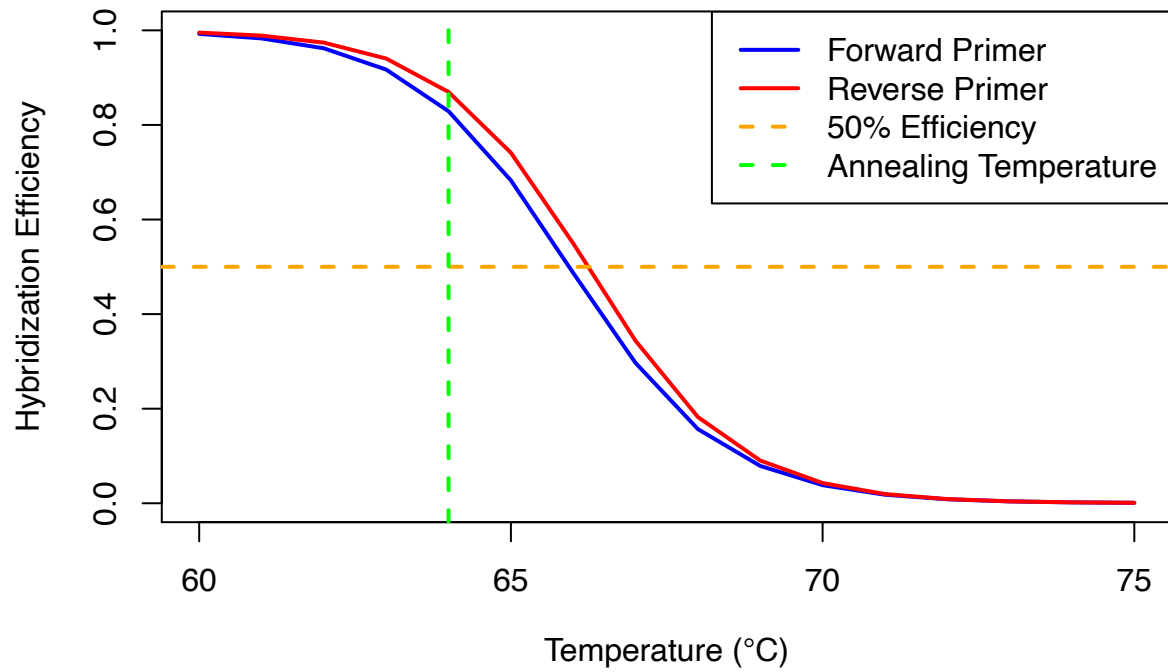
c(
  oligos.L1$forward_primer[i,j],
  oligos.L1$reverse_primer[i,j]
) %>% meltCurves
},
error = function(e) NULL
# # ¿ --- It's supposed to be 70 x 17p --- ?
# warning(sprintf('%s [iteration i=%s j=%s]', e, i, j))
)

```

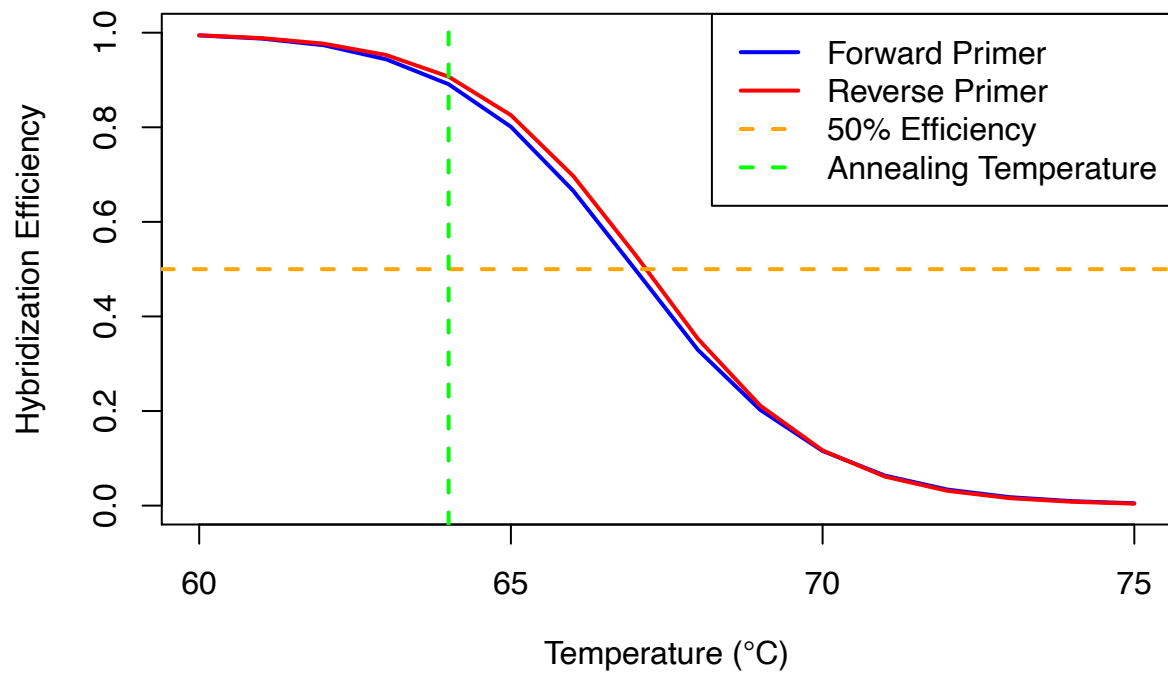
Denaturation Plot



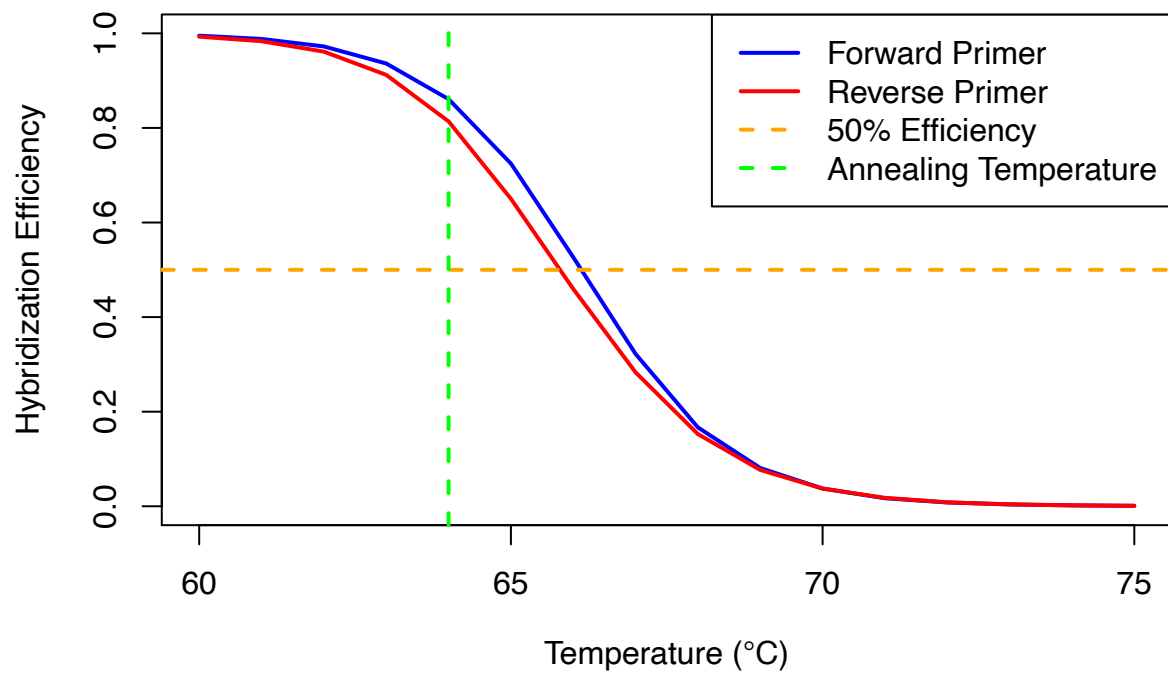
Denaturation Plot



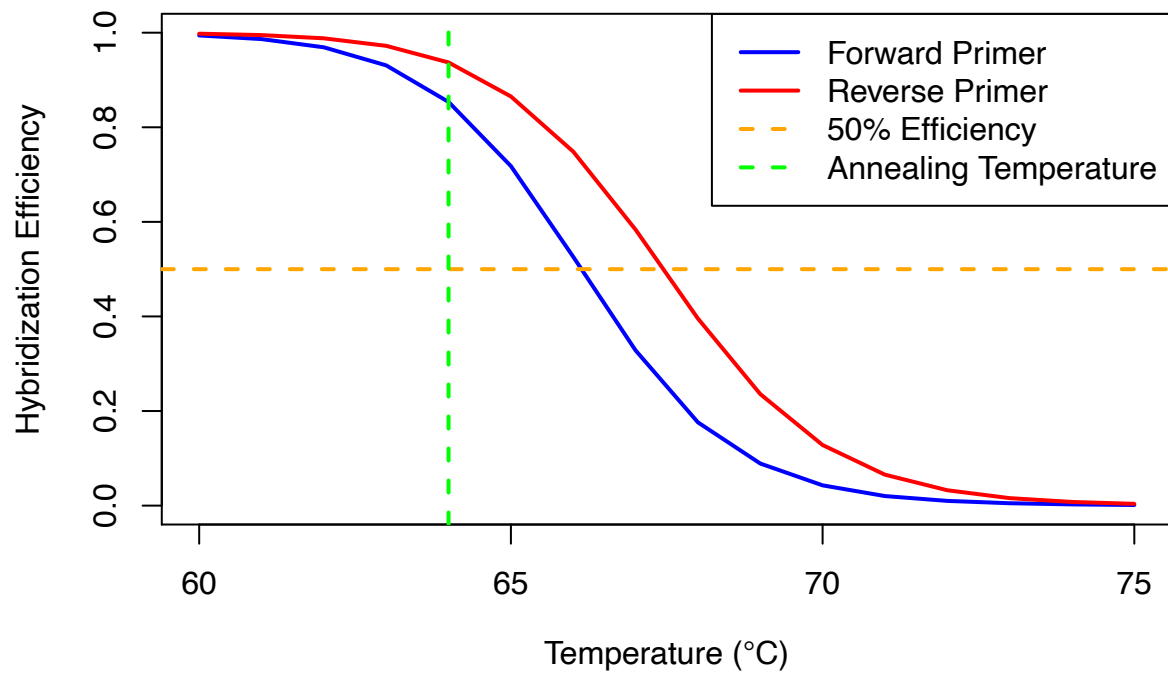
Denaturation Plot



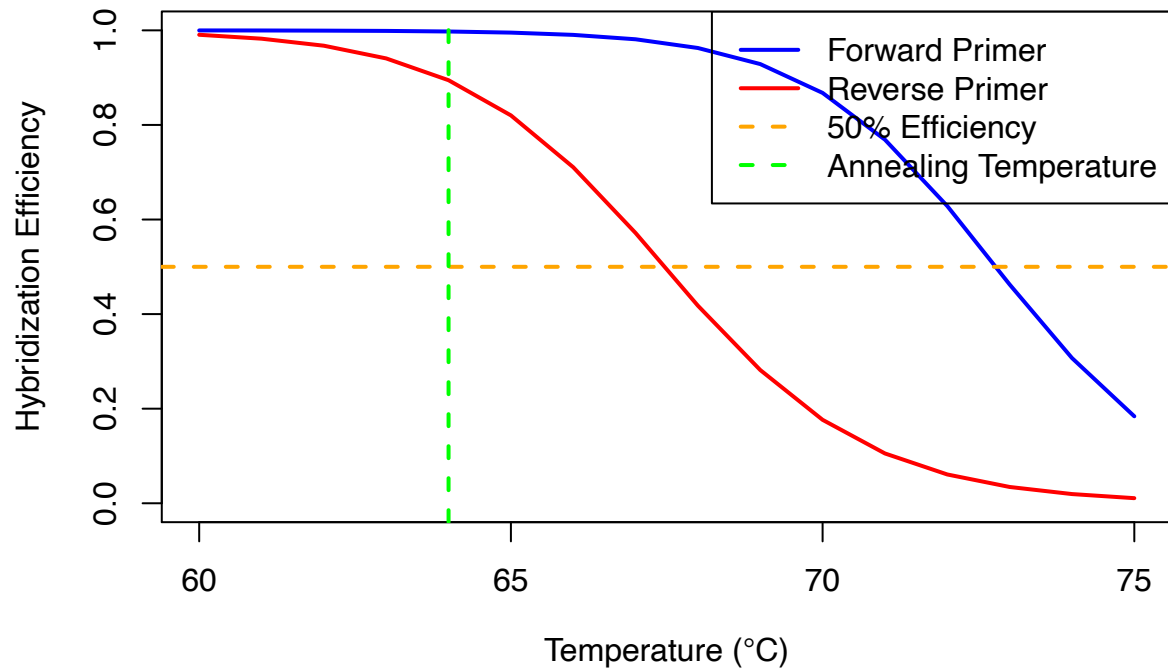
Denaturation Plot



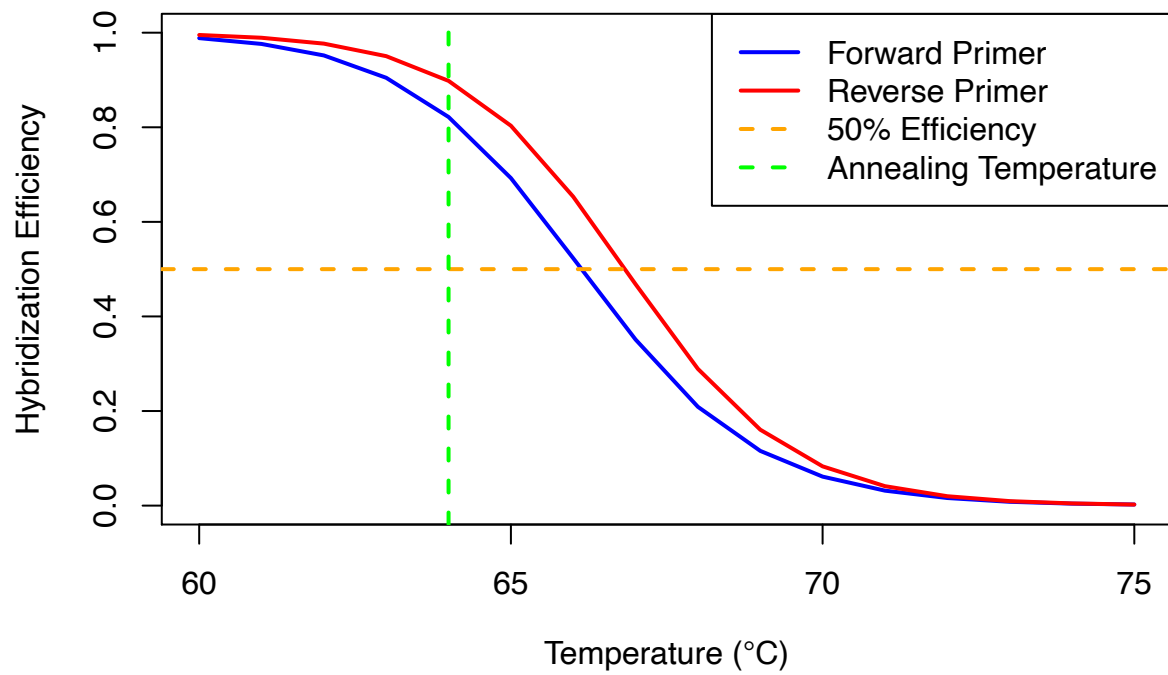
Denaturation Plot



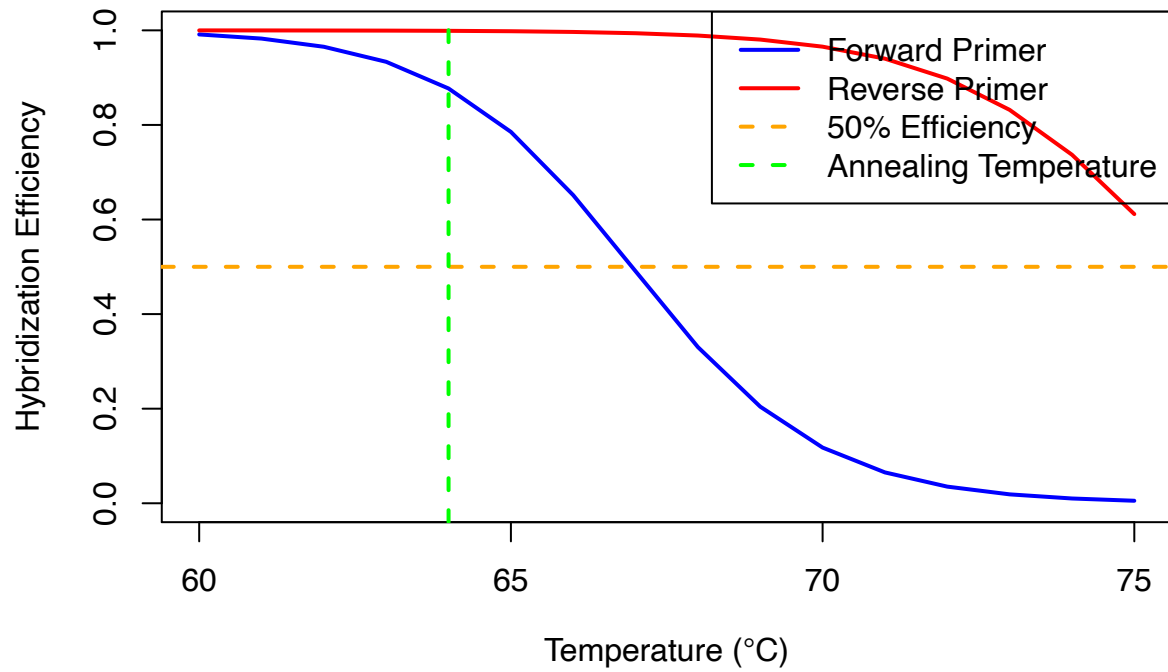
Denaturation Plot



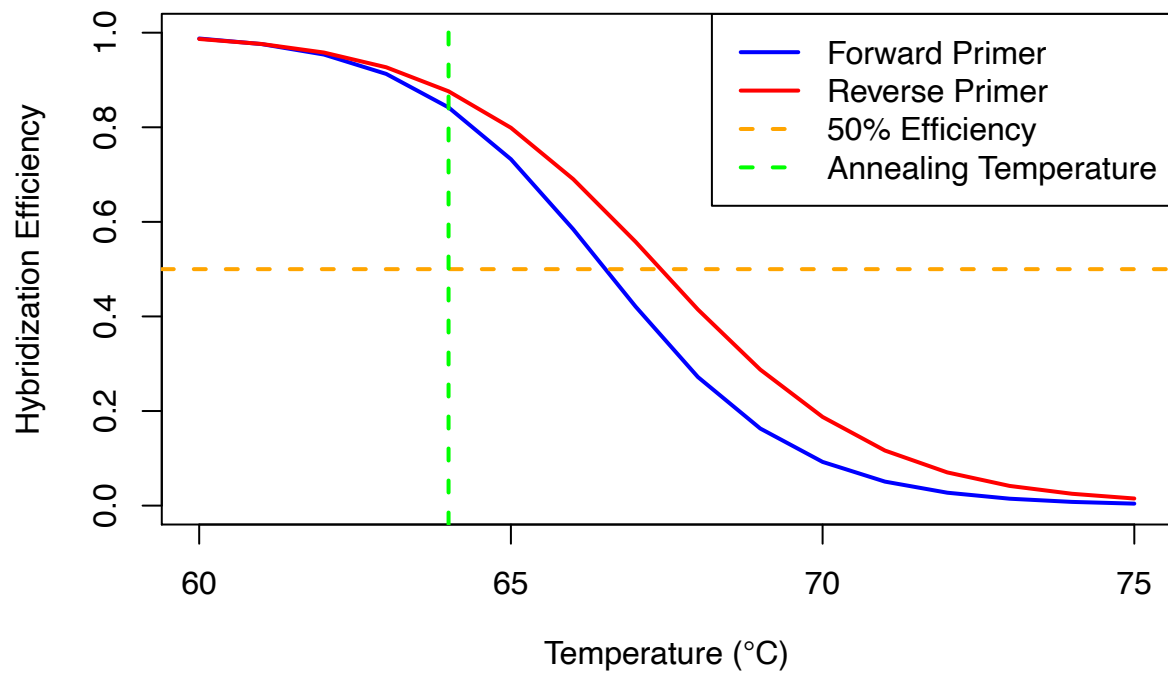
Denaturation Plot



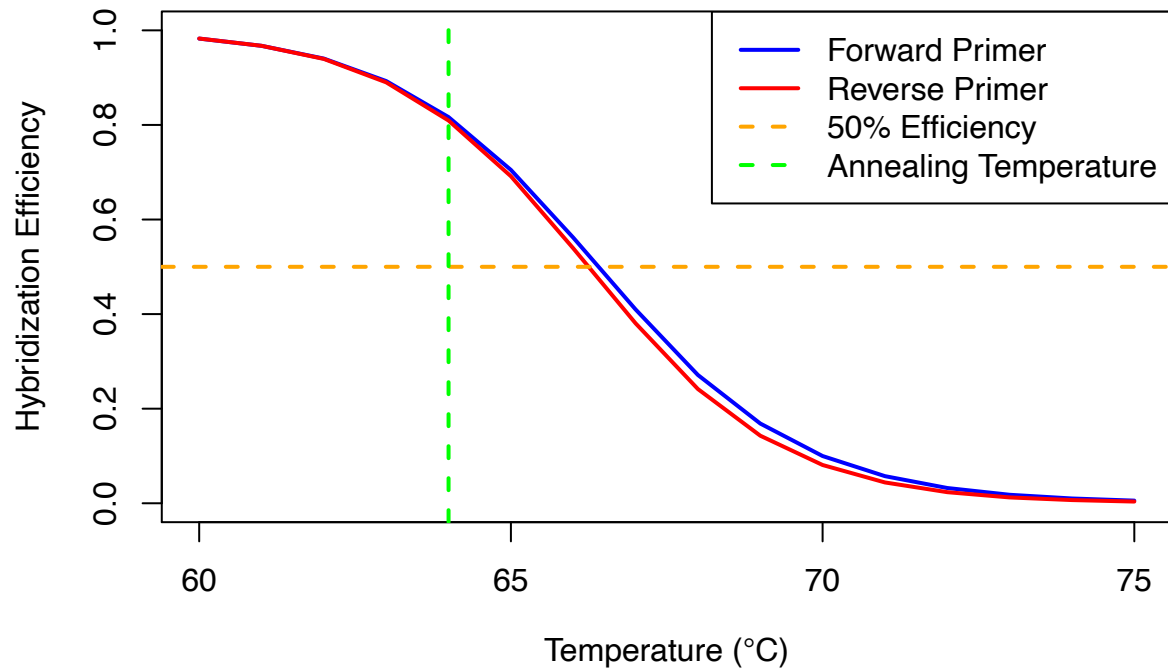
Denaturation Plot



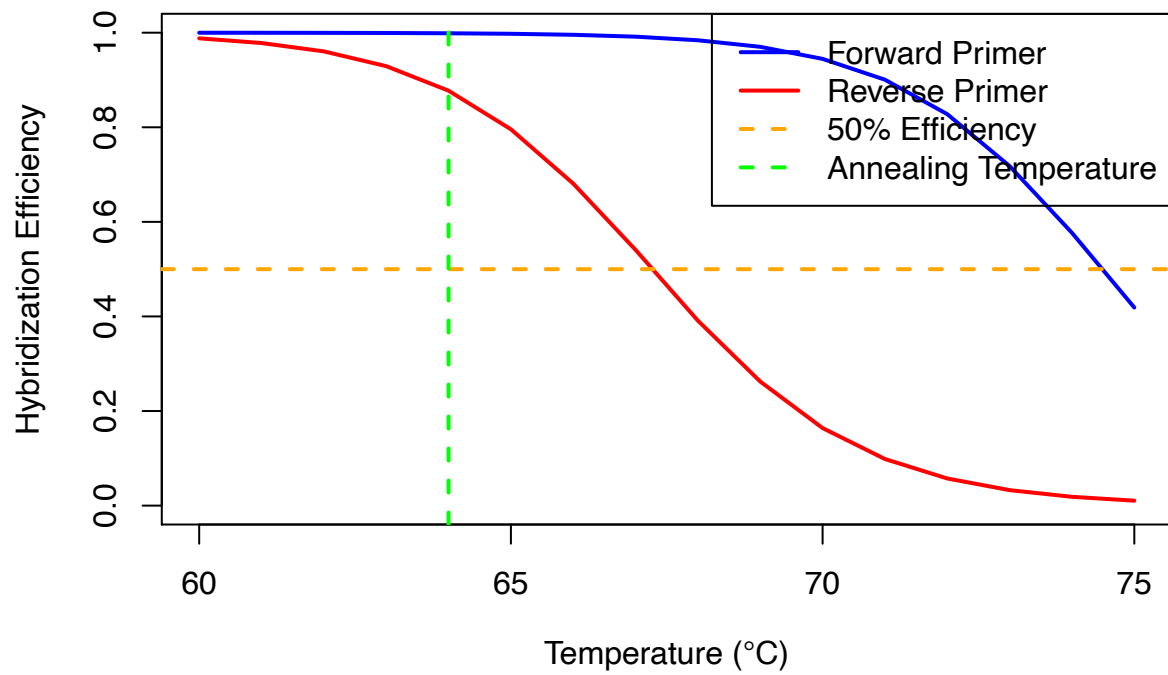
Denaturation Plot



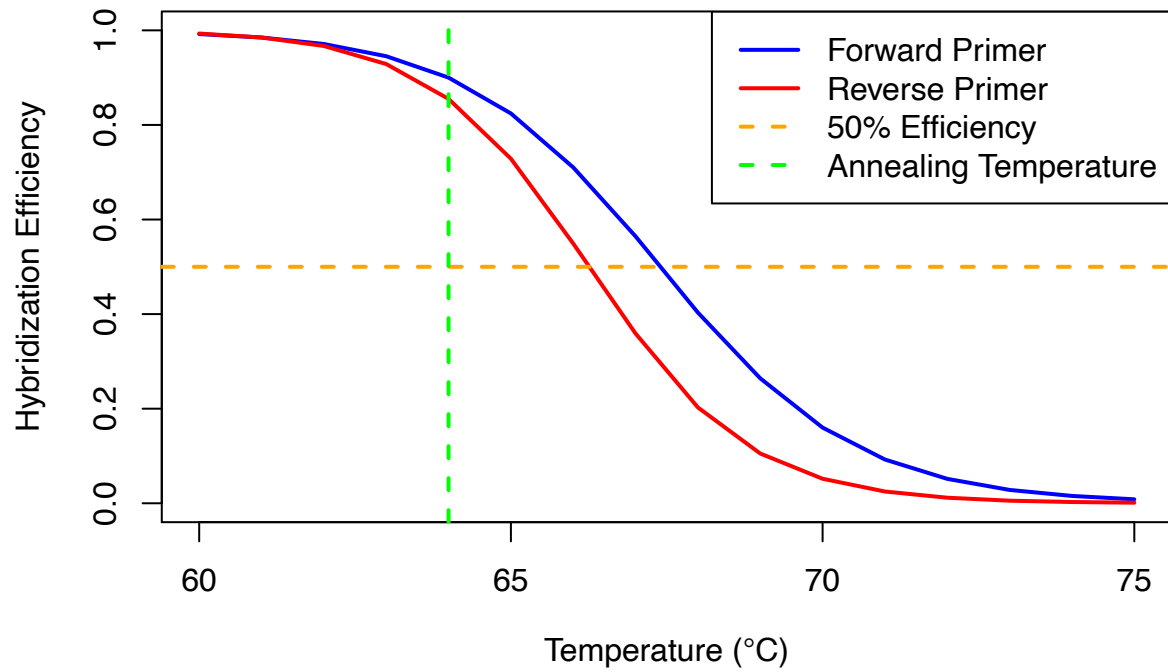
Denaturation Plot



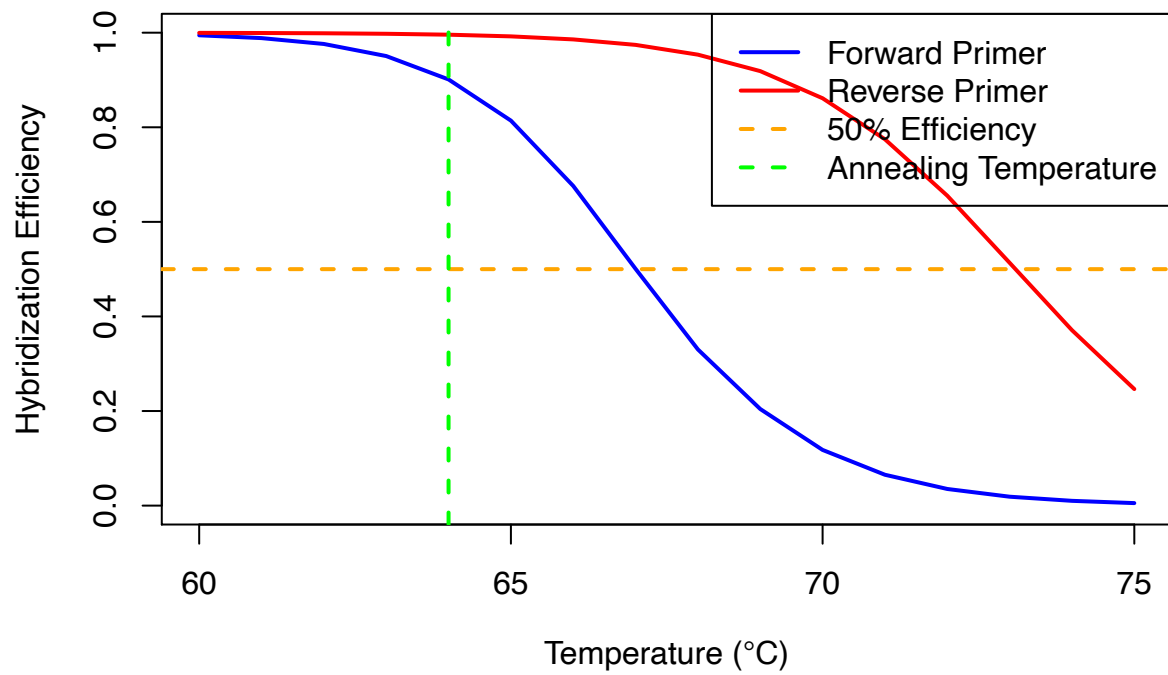
Denaturation Plot



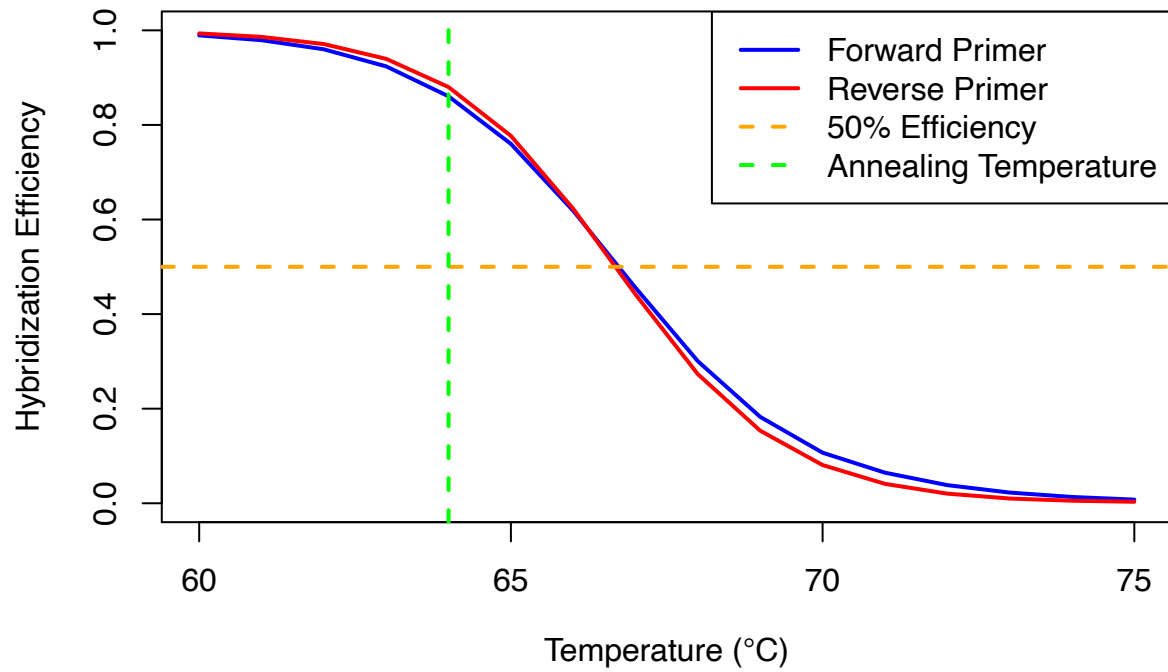
Denaturation Plot



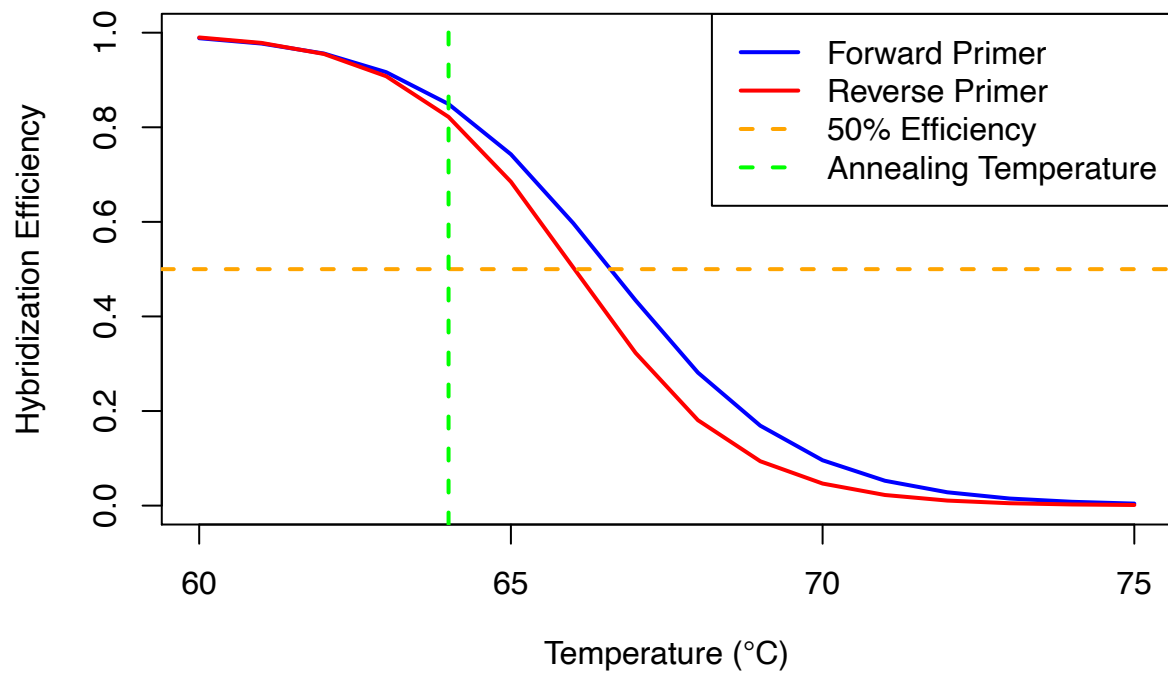
Denaturation Plot



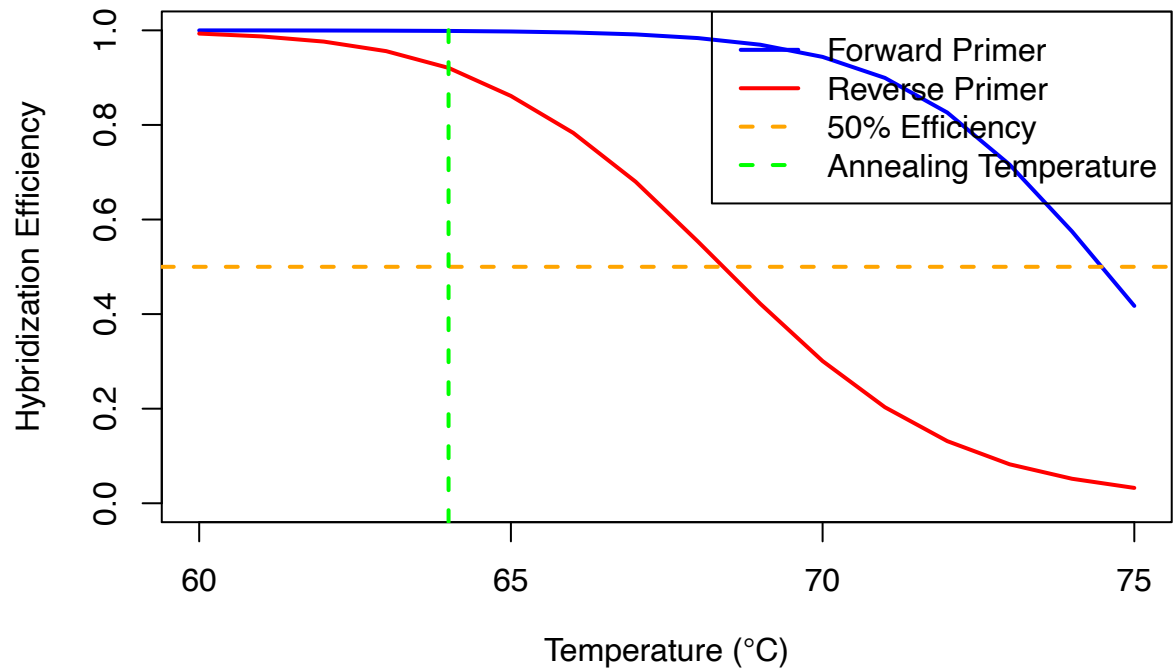
Denaturation Plot



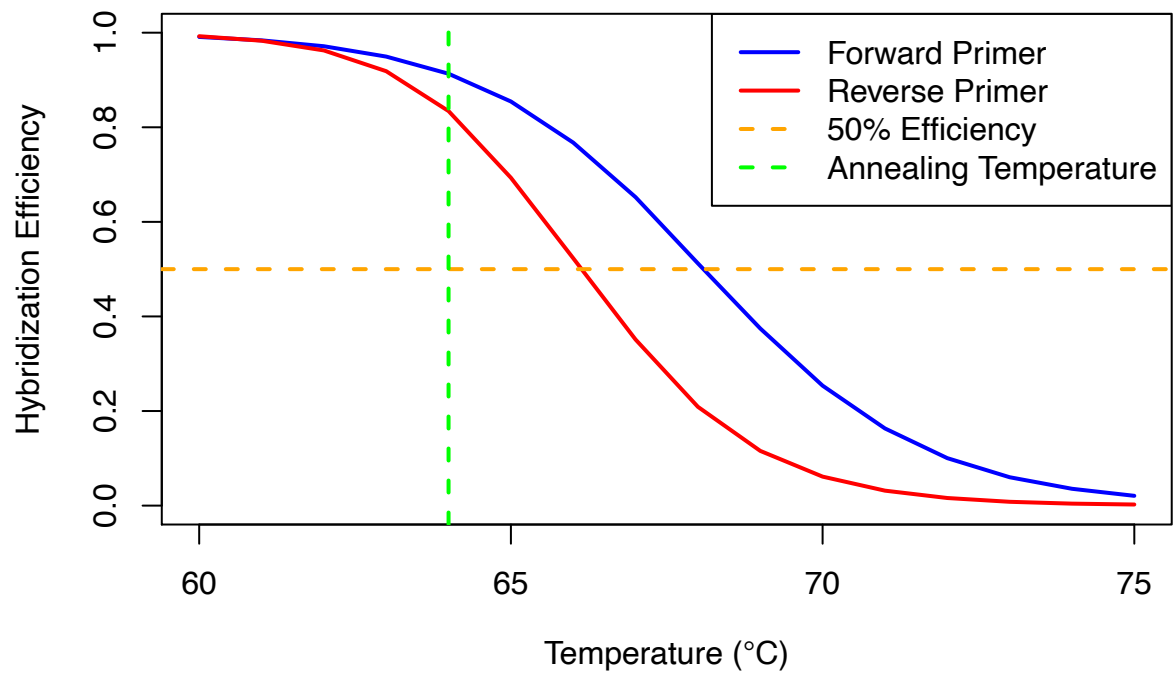
Denaturation Plot



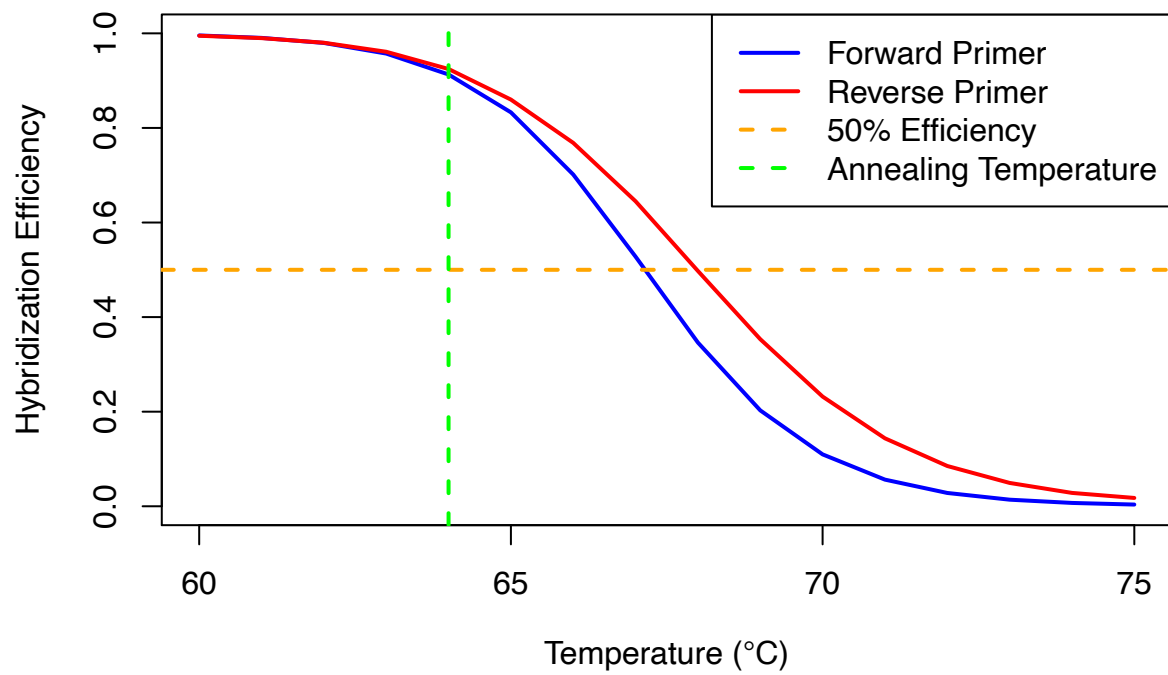
Denaturation Plot



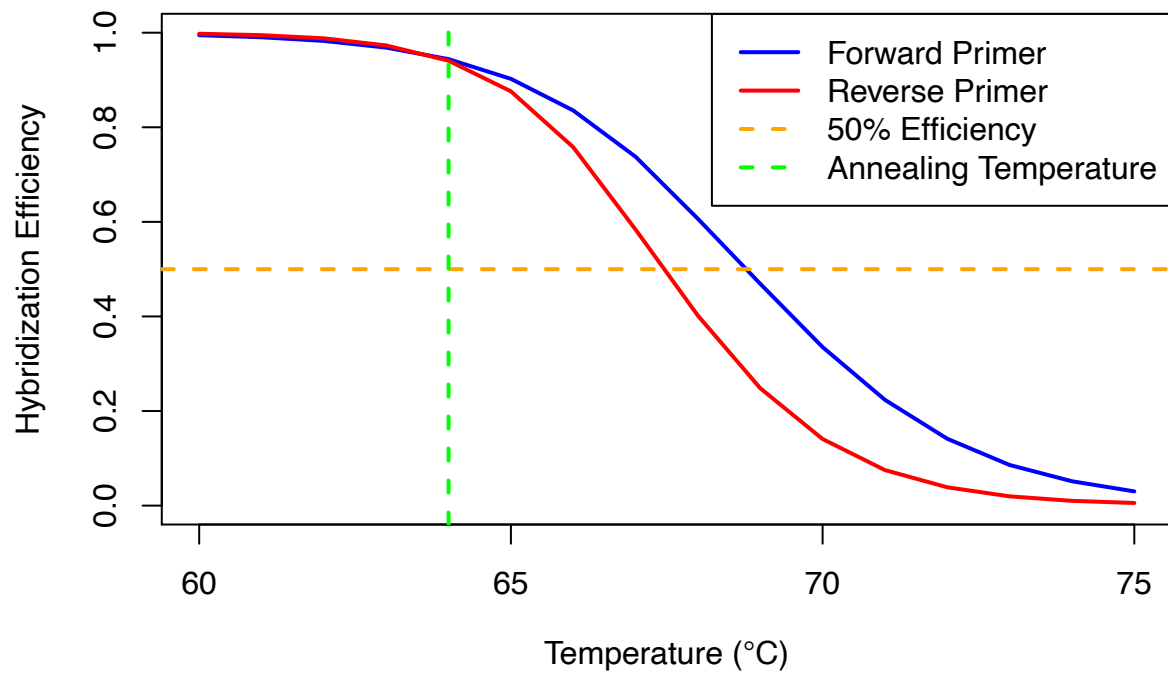
Denaturation Plot



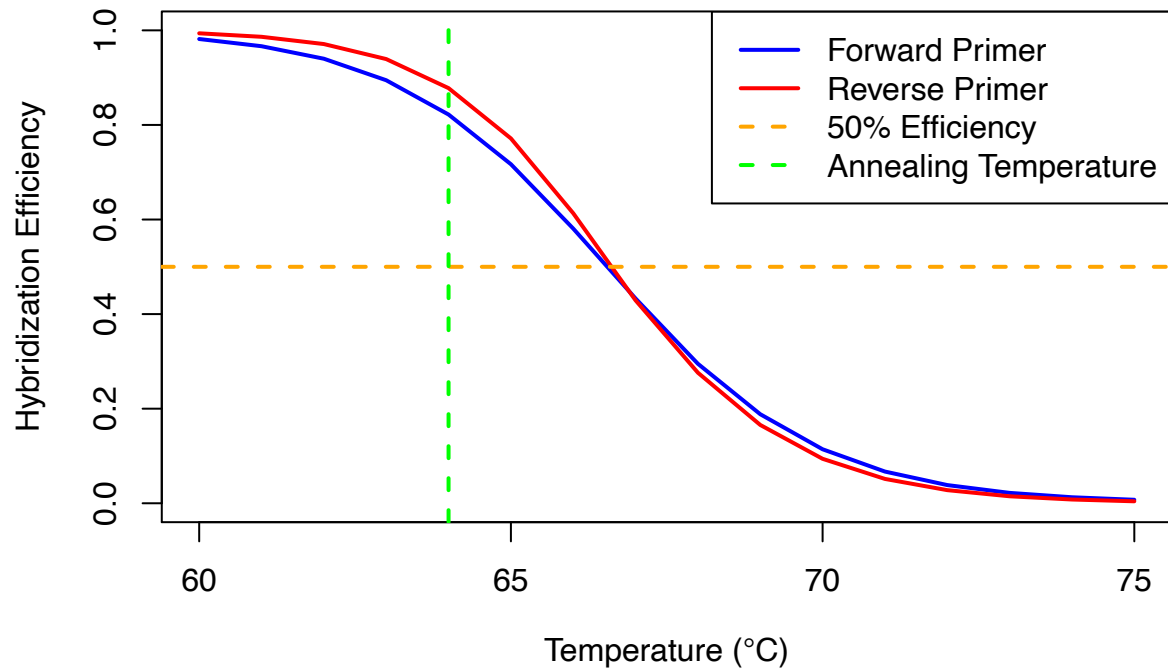
Denaturation Plot



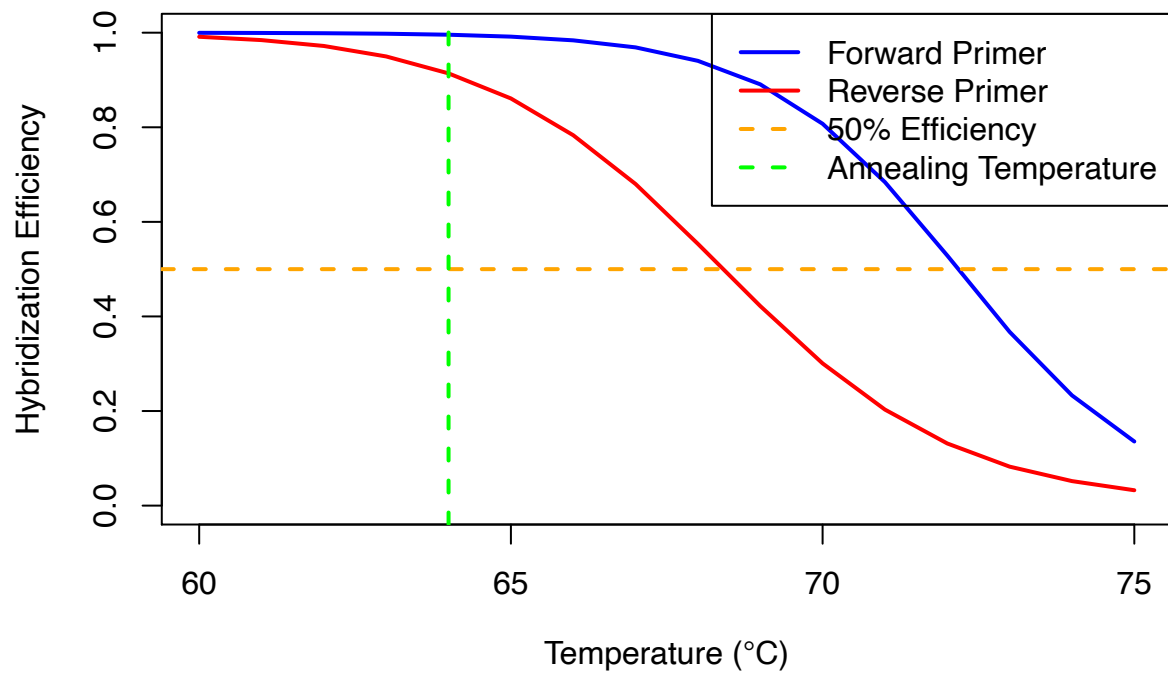
Denaturation Plot



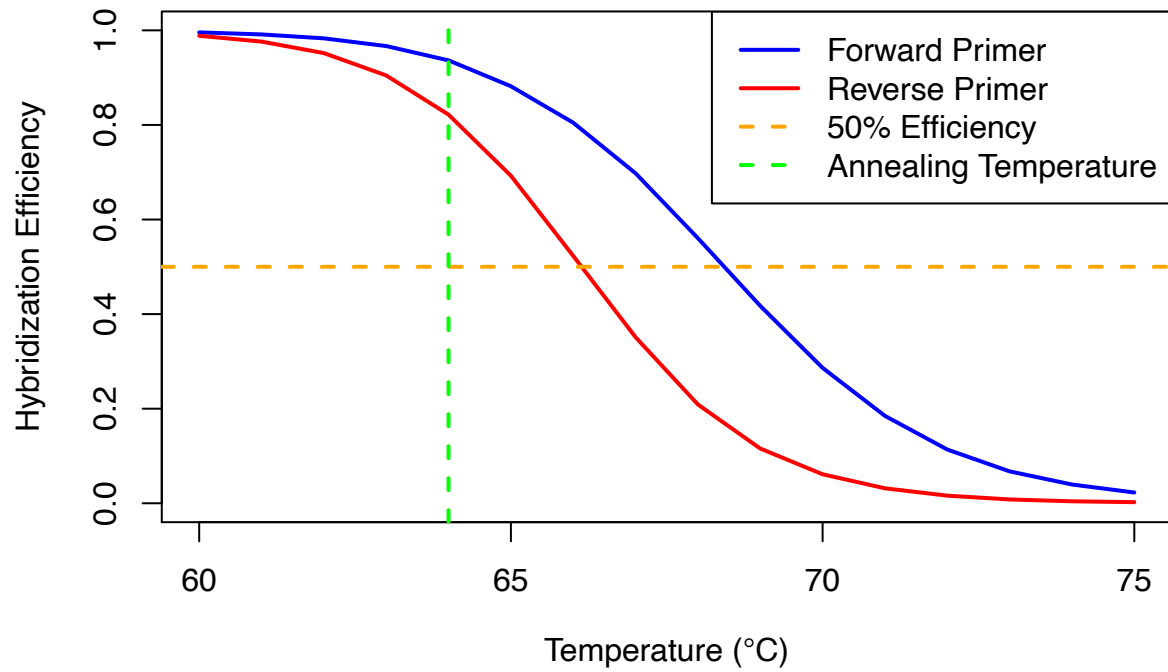
Denaturation Plot



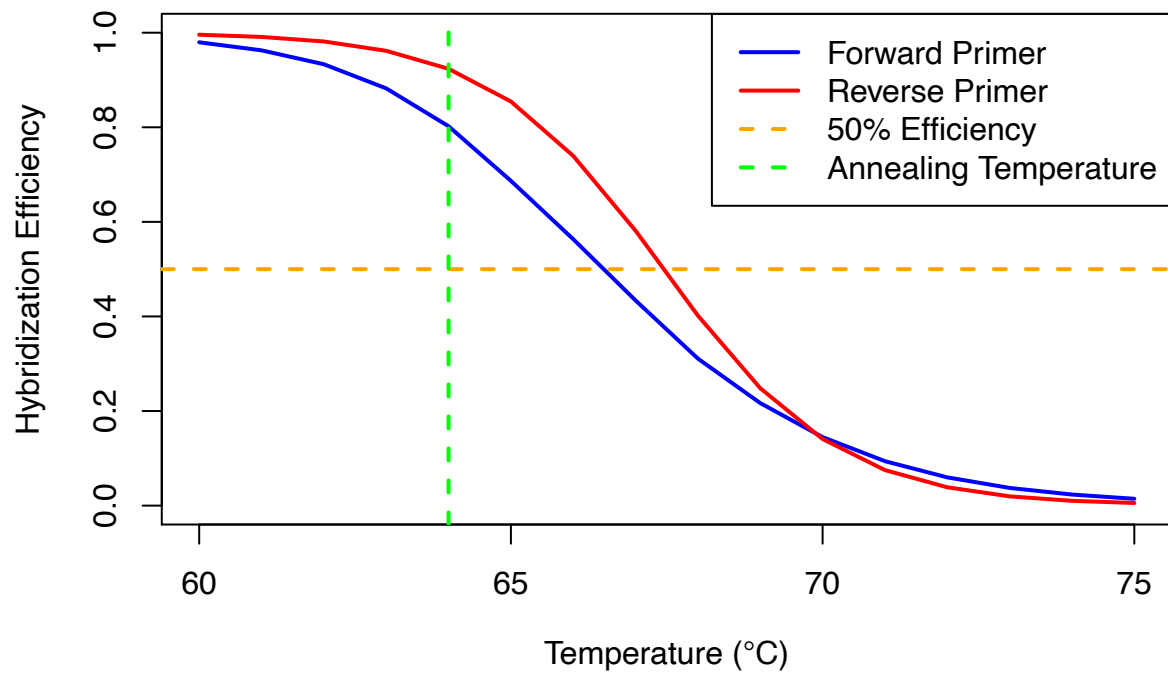
Denaturation Plot



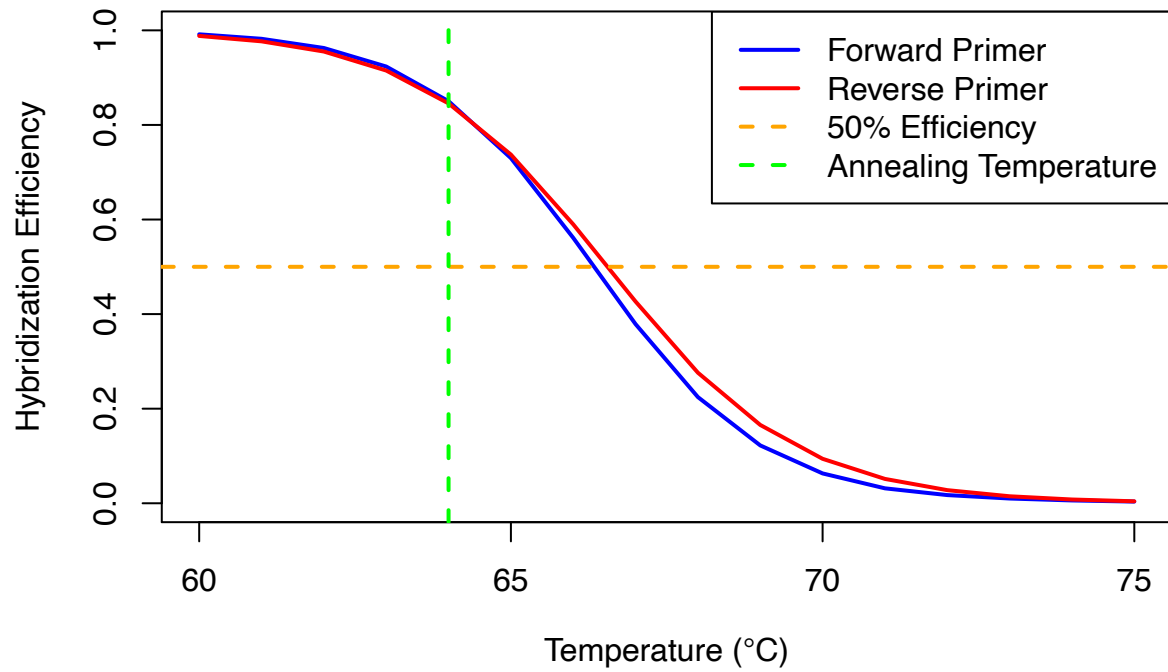
Denaturation Plot



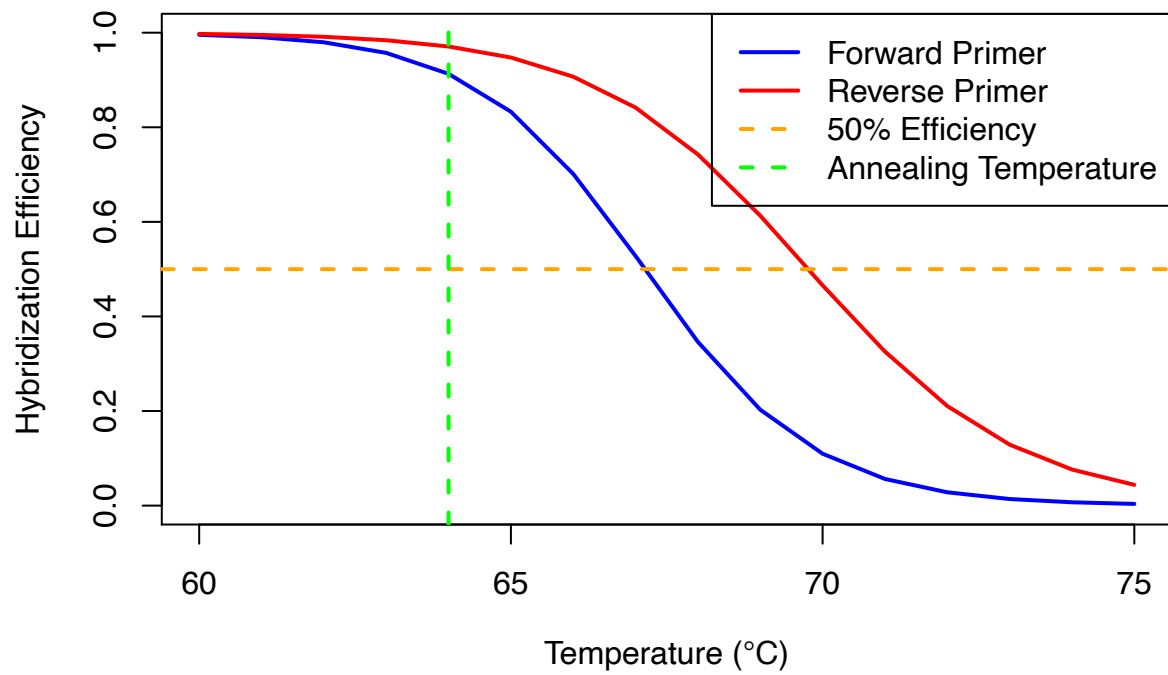
Denaturation Plot



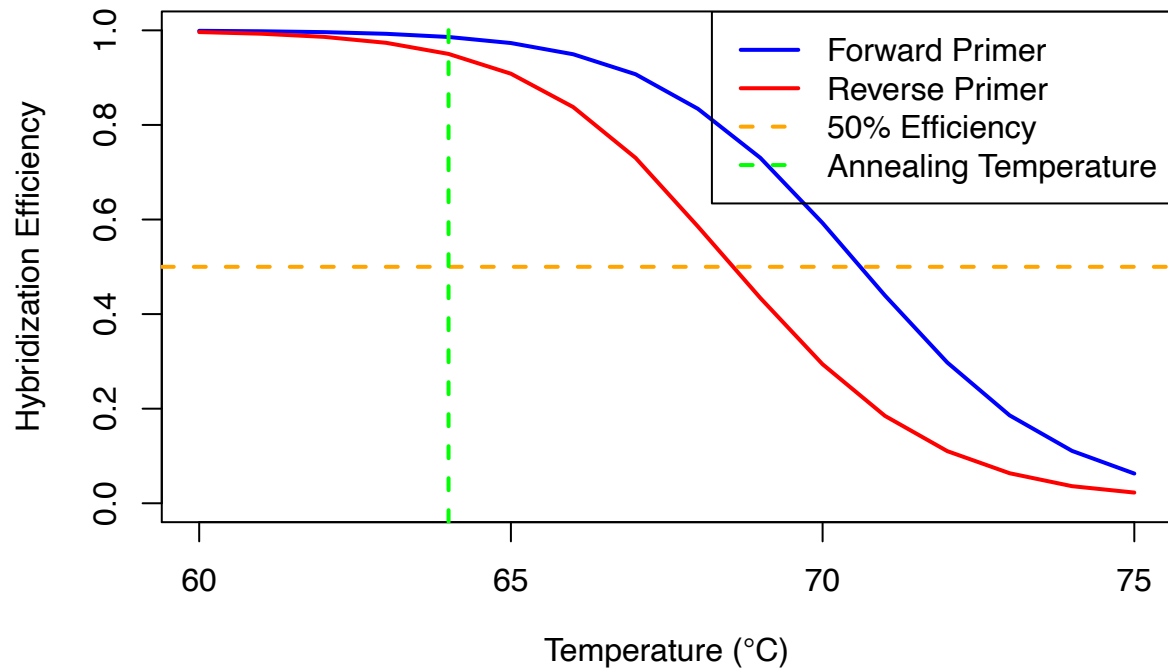
Denaturation Plot



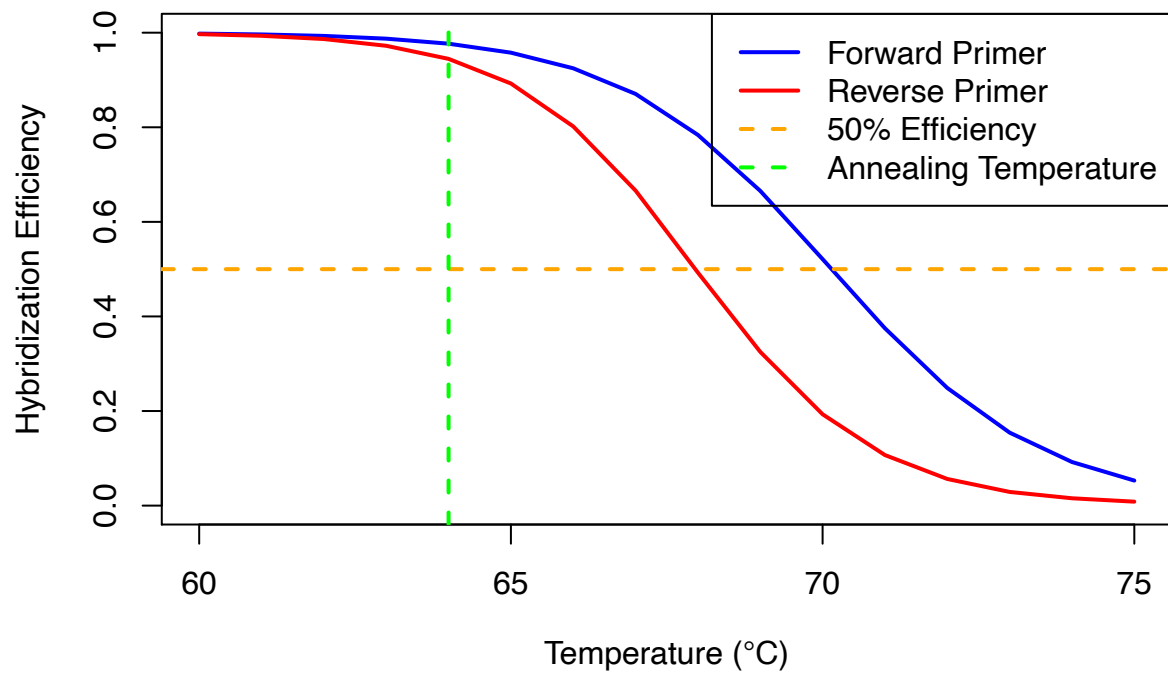
Denaturation Plot



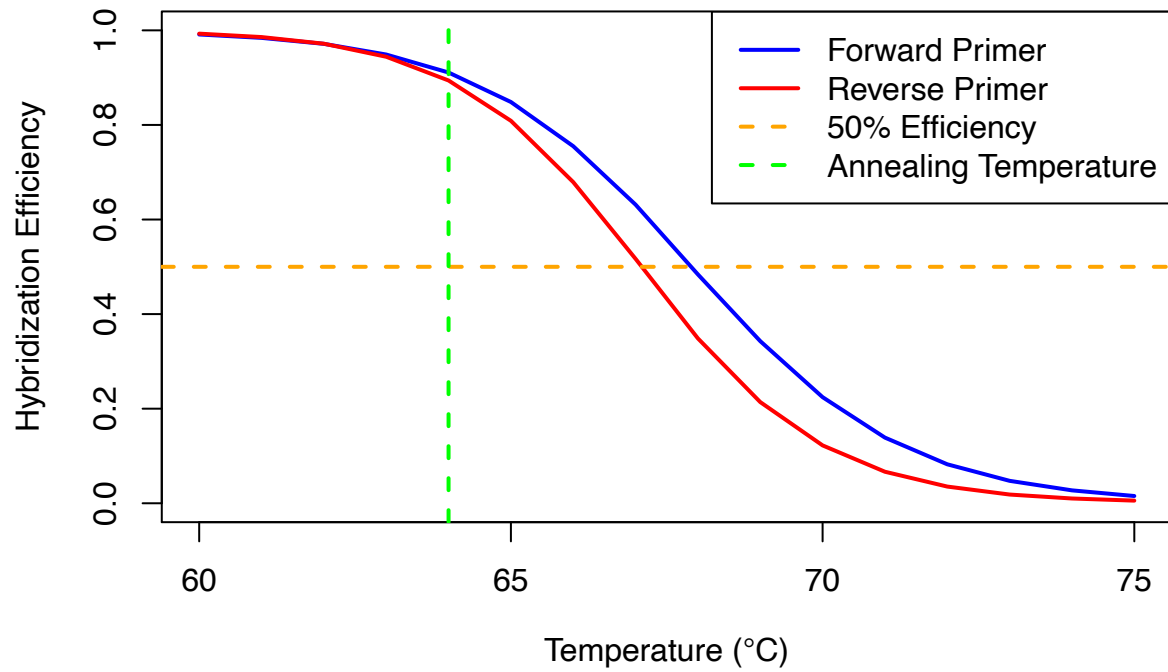
Denaturation Plot



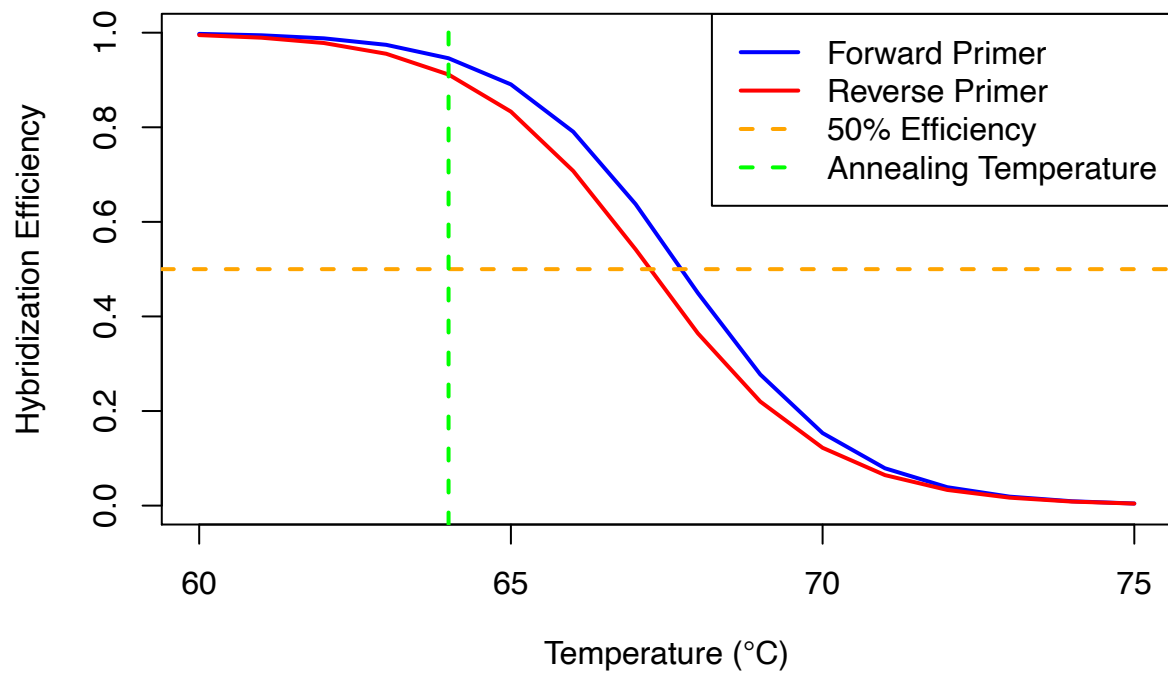
Denaturation Plot



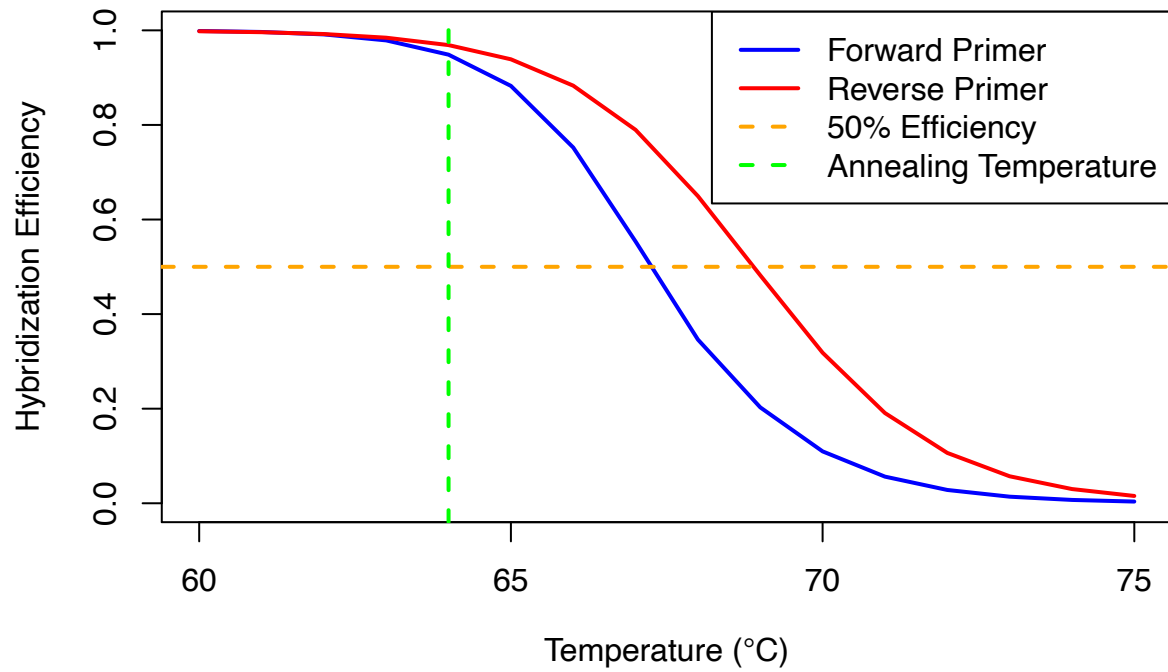
Denaturation Plot



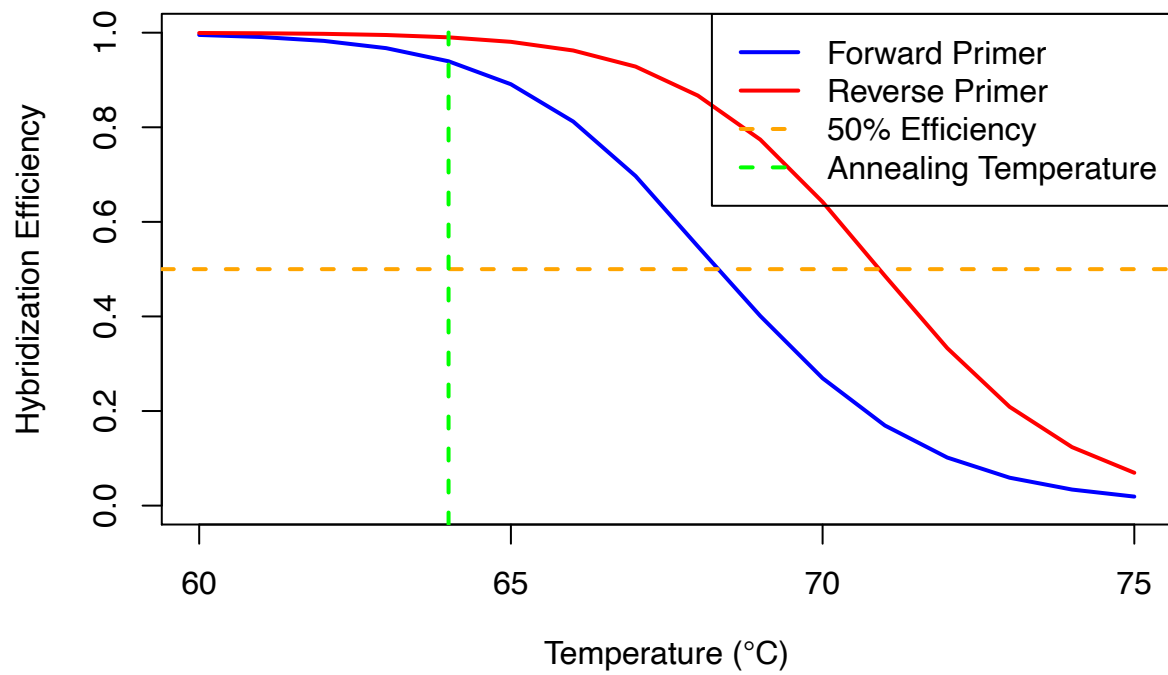
Denaturation Plot



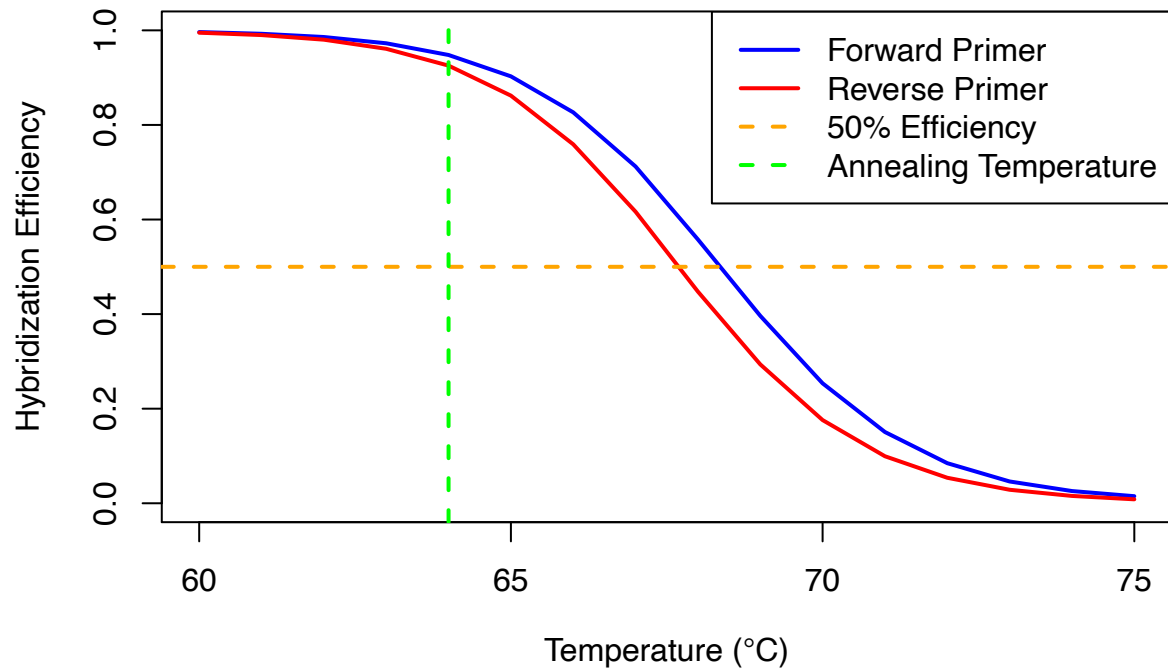
Denaturation Plot



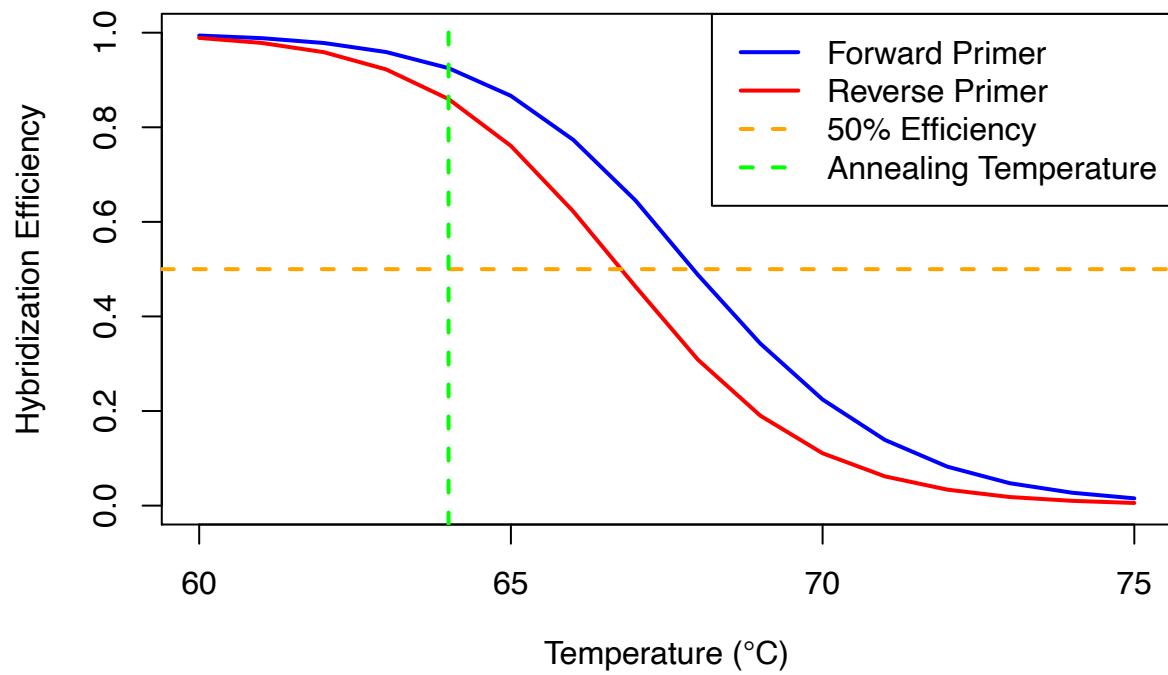
Denaturation Plot



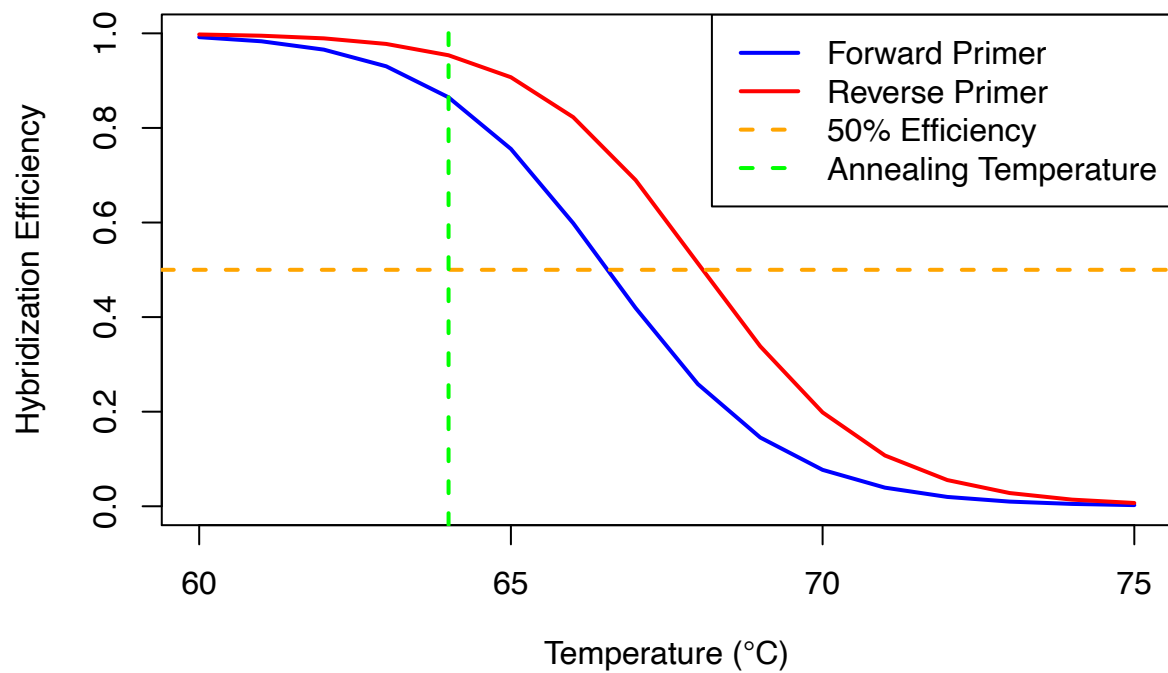
Denaturation Plot



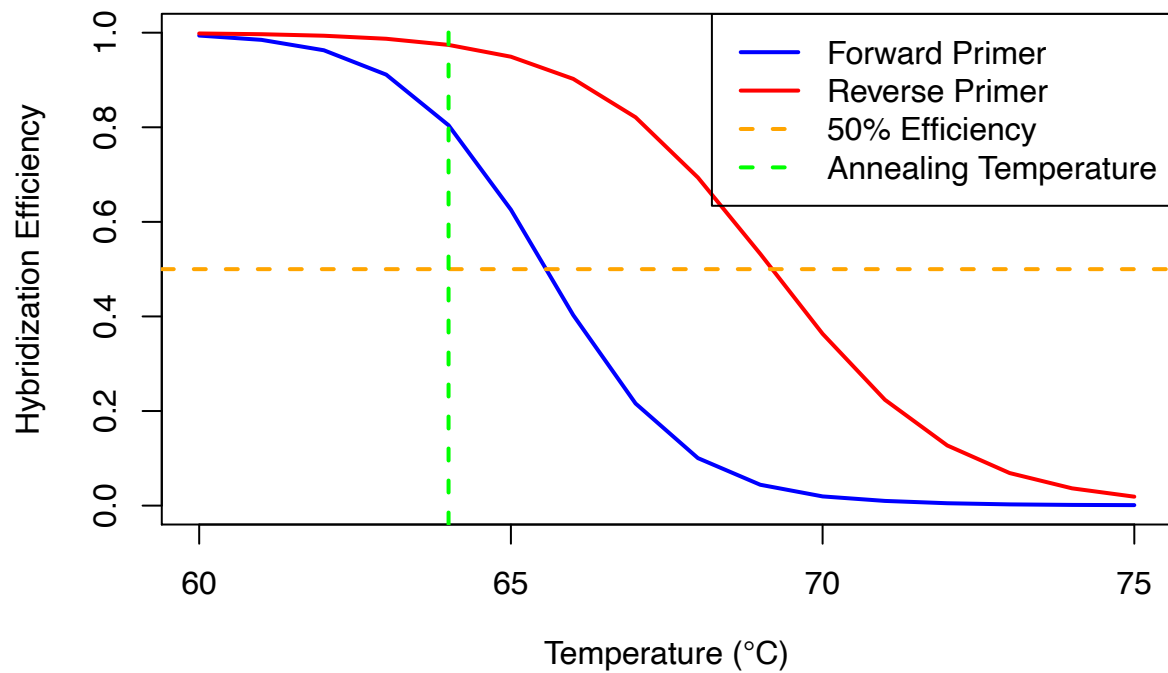
Denaturation Plot



Denaturation Plot



Denaturation Plot



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      CCAACGACGAGAGAAACACAA  ATGTCTTGCAATGTTGCCTTAGGT      0      0.2      0
## 2      CCAACGACGAGAGAAACACAAG  ATGTCTTGCAATGTTGCCTTAGGT      0      0.2      0
## 3      GCTTTGAGGATCCAACACGGC   GCAGTGAAGTGTTTCAGTTCGGT      0      0.2      0
## 4      GCTTTGAGGATCCAACACGGC   GTGTTTCAGTTCGGTGACAGAT      0      0.2      0
## 5      GCTTTGAGGATCCAACACGGC   GCAGTGAAGTGTTTCAGTTCGGTG      0      0.2      0
## 6      GCTTTGAGGATCCAACACGGC   AGTGTTTCAGTTCGGTGACAG      0      0.2      0

```

## 7	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCAGTTCGGTGC	0	0.2	0
## 8	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCGGTGCACAGA	0	0.2	0
## 9	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTCAGTTCGGTGCA	0	0.2	0
## 10	GCTTTGAGGATCCAACACGGC	GAAGTGTTCAGTTCGGTGCACA	0	0.2	0
## 11	TCGTGCTGCAACCGAGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2	0
## 12	TCGTGCTGCAACCGAGC	GTTGCCTTAGGTCCATGCATACTTA	0	0.2	0
## 13	CAGGAAMGACTCCAACGACGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2	0
## 14	CAGGAAMGACTCCAACGACGC	GTTGCCTTAGGTCCATGCATACTTA	0	0.2	0
## 15	GGAAMGACTCCAACGACGC	ATGTCTTGCAATGTTGCCTTAGGT	0	0.2	0
## 16	GGAAMGACTCCAACGACGC	GTTGCCTTAGGTCCATGCATACTTA	0	0.2	0
## 17	CCCCCCCCGCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2	0
## 18	CCCCCCCCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2	0
## 19	CCCCCCCCGCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2	0
## 20	CCCCCCCCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2	0
## 21	CCCCCCCCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2	0
## 22	CCCCCCCCGCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2	0
## 23	CCCCCCCCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2	0
## 24	CCCCCCCCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2	0
## 25	CCCCCCCCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2	0
## 26	CCCCCCCCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2	0
## 27	CCCCCCCCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2	0
## 28	TCTCCTGTACCTGGGCAATATGAT	TCYTCAACATGTCTGCTATACTGCT	0	0.2	0
## 29	TCTCCTGTACCTGGGCAATATGAT	CCTCAACATGTCTGCTATACTGCC	0	0.2	0
## 30	GCATGCTGCATGCCATAAATGTATA	TCYAATGTGTCTCCATACACAGAGT	0	0.2	0
## 31	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGT	0	0.2	0
## 32	TGCCGCCACGTCTAATGTTTC	GGGCACAGCCCCAAAATACATAACT	0	0.2	0
## 33	TGCCGCCACGTCTAATGTTTC	GGGCACAGCCCCAAAATACATAACTG	0	0.2	0
## 34	TGCCGCCACGTCTAATGTTTC	CAATAGCAGGGGCACAGCC	0	0.2	0
## 35	TGCCGCCACGTCTAATGTTTC	GGGGCACAGCCCCAAAATACATAAC	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
## 40	GATGTGAGAAACRCACCACAATACT	CACAGATCAGGTAGCTTGTAGGGT	0	0.2	0
## 41	GATGTGAGAAACRCACCACAATACT	AGTTCCGTGCACAGATCAGGT	0	0.2	0
## 42	GATGTGAGAAACRCACCACAATACT	GTGTTTCAGTTCGGTGCACAGAT	0	0.2	0
## 43	GATGTGAGAAACRCACCACAATACT	CTTGAGGGTCGCCGTGTTG	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	CAGTTCGGTGCACAGATCAGG	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	GTTTCAGTTCGGTGCACAGATCAG	0	0.2	0
## 52	GATGTGAGAAACRCACCACAATACT	ACAGATCAGGTAGCTTGTAGGGTC	0	0.2	0
## 53	GATGTGAGAAACRCACCACAATACT	TGTTTCAGTTCGGTGCACAGATC	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	GTGTTTCAGTTCGGTGCACAGA	0	0.2	0
## 58	GATGTGAGAAACRCACCACAATACT	GTTTCAGTTCGGTGCACAGATCA	0	0.2	0
## 59	TCTGAGGACGTTAGGGACAATGTG	GGCACAGCCCCAAAATACATAACTGT	0	0.2	0
## 60	TCTGAGGACGTTAGGGACAATGTG	GGGCACAGCCCCAAAATACATAACT	0	0.2	0

## 61	TCTGAGGACGTTAGGGACAATGTG	GGGCACAGCCCAAAATACATAACTG	0	0.2	0
## 62	TCTGAGGACGTTAGGGACAATGTG	CAATAGCAGGGGCACAGCC	0	0.2	0
## 63	TCTGAGGACGTTAGGGACAATGTG	GGGGCACAGCCCAAAATACATAAC	0	0.2	0
## 64	TCTGAGGACGTTAGGGACAATGTG	GCAGGGKYACAGCCCA	0	0.2	0
## 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
## 72	CGGCTGGTTTTATGTACAGGCTA	CGACCCTGTGTCTGTTGCATTTTC	0	0.2	0
## 73	ACTCTGTGTATGGAGACACATTGGA	GCACCGCAGGCACCTTATTAAT	0	0.2	0
## 74	ACTCTGTGTATGGAGACACATTGGA	GCACCGCAGGCACCTTATTA	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	GTGTTCAAGTTCCGTGCACAGAT	0	0.2	0
## 81	AGATGTGAGAAACRCACCACAAT	CTTGTAGGGTCGCCGTGTTG	0	0.2	0
## 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	AGATGTGAGAAACRCACCACAAT	GTAGCTTGTAGGGTCGCCG	0	0.2	0
## 88	AGATGTGAGAAACRCACCACAAT	GTTCCGTGCACAGATCAGGTAG	0	0.2	0
## 89	AGATGTGAGAAACRCACCACAAT	GTTCAAGTTCCGTGCACAGATCAG	0	0.2	0
## 90	AGATGTGAGAAACRCACCACAAT	AGTGTTCAAGTTCCGTGCACAG	0	0.2	0
## 91	AGATGTGAGAAACRCACCACAAT	ACAGATCAGGTAGCTTGTAGGGTC	0	0.2	0
## 92	AGATGTGAGAAACRCACCACAAT	TGTTCAAGTTCCGTGCACAGATC	0	0.2	0
## 93	AGATGTGAGAAACRCACCACAAT	AGTGAAGTGTTCAAGTTCCGTGC	0	0.2	0
## 94	AGATGTGAGAAACRCACCACAAT	TCAGGTAGCTTGTAGGGTCGC	0	0.2	0
## 95	AGATGTGAGAAACRCACCACAAT	AGGTAGCTTGTAGGGTCGCC	0	0.2	0
## 96	AGATGTGAGAAACRCACCACAAT	TGAAGTGTTCAAGTTCCGTGCAC	0	0.2	0
## 97	AGATGTGAGAAACRCACCACAAT	AGTTCCGTGCACAGATCAGGTA	0	0.2	0
## 98	AGATGTGAGAAACRCACCACAAT	GTGTTCAAGTTCCGTGCACAGA	0	0.2	0
## 99	AGATGTGAGAAACRCACCACAAT	GTTCAAGTTCCGTGCACAGATCA	0	0.2	0
## 100	AGATGTGAGAAACRCACCACAAT	GTGAAGTGTTCAAGTTCCGTGCA	0	0.2	0
##	similar_signatures	missing_signatures			
## 1		HPV16, HPV11, HPV4, HPV17			
## 2		HPV16, HPV11, HPV4, HPV17			
## 3		HPV16, HPV11, HPV4, HPV17			
## 4		HPV16, HPV11, HPV4, HPV17			
## 5		HPV16, HPV11, HPV4, HPV17			
## 6		HPV16, HPV11, HPV4, HPV17			
## 7		HPV16, HPV11, HPV4, HPV17			
## 8		HPV16, HPV11, HPV4, HPV17			
## 9		HPV16, HPV11, HPV4, HPV17			
## 10		HPV16, HPV11, HPV4, HPV17			
## 11		HPV16, HPV11, HPV4, HPV17			
## 12		HPV16, HPV11, HPV4, HPV17			
## 13		HPV16, HPV11, HPV4, HPV17			

## 14	HPV16, HPV11, HPV4, HPV17
## 15	HPV16, HPV11, HPV4, HPV17
## 16	HPV16, HPV11, HPV4, HPV17
## 17	HPV16, HPV11, HPV4, HPV17
## 18	HPV16, HPV11, HPV4, HPV17
## 19	HPV16, HPV11, HPV4, HPV17
## 20	HPV16, HPV11, HPV4, HPV17
## 21	HPV16, HPV11, HPV4, HPV17
## 22	HPV16, HPV11, HPV4, HPV17
## 23	HPV16, HPV11, HPV4, HPV17
## 24	HPV16, HPV11, HPV4, HPV17
## 25	HPV16, HPV11, HPV4, HPV17
## 26	HPV16, HPV11, HPV4, HPV17
## 27	HPV16, HPV11, HPV4, HPV17
## 28	HPV16, HPV11, HPV4, HPV17
## 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
## 35	HPV16, HPV11, HPV4, HPV17
## 36	HPV16, HPV11, HPV4, HPV17
## 37	HPV16, HPV11, HPV4, HPV17
## 38	HPV16, HPV11, HPV4, HPV17
## 39	HPV16, HPV11, HPV4, HPV17
## 40	HPV16, HPV11, HPV4, HPV17
## 41	HPV16, HPV11, HPV4, HPV17
## 42	HPV16, HPV11, HPV4, HPV17
## 43	HPV16, HPV11, HPV4, HPV17
## 44	HPV16, HPV11, HPV4, HPV17
## 45	HPV16, HPV11, HPV4, HPV17
## 46	HPV16, HPV11, HPV4, HPV17
## 47	HPV16, HPV11, HPV4, HPV17
## 48	HPV16, HPV11, HPV4, HPV17
## 49	HPV16, HPV11, HPV4, HPV17
## 50	HPV16, HPV11, HPV4, HPV17
## 51	HPV16, HPV11, HPV4, HPV17
## 52	HPV16, HPV11, HPV4, HPV17
## 53	HPV16, HPV11, HPV4, HPV17
## 54	HPV16, HPV11, HPV4, HPV17
## 55	HPV16, HPV11, HPV4, HPV17
## 56	HPV16, HPV11, HPV4, HPV17
## 57	HPV16, HPV11, HPV4, HPV17
## 58	HPV16, HPV11, HPV4, HPV17
## 59	HPV16, HPV11, HPV4, HPV17
## 60	HPV16, HPV11, HPV4, HPV17
## 61	HPV16, HPV11, HPV4, HPV17
## 62	HPV16, HPV11, HPV4, HPV17
## 63	HPV16, HPV11, HPV4, HPV17
## 64	HPV16, HPV11, HPV4, HPV17
## 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
## 71          HPV16, HPV11, HPV4, HPV17
## 72          HPV16, HPV11, HPV4, HPV17
## 73          HPV16, HPV11, HPV4, HPV17
## 74          HPV16, HPV11, HPV4, HPV17
## 75          HPV16, HPV11, HPV4, HPV17
## 76          HPV16, HPV11, HPV4, HPV17
## 77          HPV16, HPV11, HPV4, HPV17
## 78          HPV16, HPV11, HPV4, HPV17
## 79          HPV16, HPV11, HPV4, HPV17
## 80          HPV16, HPV11, HPV4, HPV17
## 81          HPV16, HPV11, HPV4, HPV17
## 82          HPV16, HPV11, HPV4, HPV17
## 83          HPV16, HPV11, HPV4, HPV17
## 84          HPV16, HPV11, HPV4, HPV17
## 85          HPV16, HPV11, HPV4, HPV17
## 86          HPV16, HPV11, HPV4, HPV17
## 87          HPV16, HPV11, HPV4, HPV17
## 88          HPV16, HPV11, HPV4, HPV17
## 89          HPV16, HPV11, HPV4, HPV17
## 90          HPV16, HPV11, HPV4, HPV17
## 91          HPV16, HPV11, HPV4, HPV17
## 92          HPV16, HPV11, HPV4, HPV17
## 93          HPV16, HPV11, HPV4, HPV17
## 94          HPV16, HPV11, HPV4, HPV17
## 95          HPV16, HPV11, HPV4, HPV17
## 96          HPV16, HPV11, HPV4, HPV17
## 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 <- 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  GCCCCCCTTTAGAACTTAAAAACACA  CCCCATAGGATCTGCAGACATTGT      0      0.2
## 2  GCCCCCCTTTAGAACTTAAAAACACA  CCCCATAGGATCTGCAGACATTG      0      0.2
## 3  GCCCCCCTTTAGAACTTAAAAACACA   TGAATCCCCATAAGGATCTGCAG      0      0.2
## 4      CCAACGACGCAGAGAAACACAA   GCTCGTCGGGCTGGTAAATGT      0      0.2
## 5      CCAACGACGCAGAGAAACACAA   GCTCGTCGGGCTGGTAAATG      0      0.2
## 6      CCAACGACGCAGAGAAACACAA  CGCTTAATTGCTCGTGACATAGAAG      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

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## 12	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGT CAT	0	0.2
## 13	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
## 14	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
## 15	GGTGCAGTTACCTGACCCAAATAAAT	CCCCTAAGGCCAACACCTAAAG	0	0.2
## 16	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT C	0	0.2
## 17	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGT CATC	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	GCCCTAAGGCCAACACC	0	0.2
## 23	GGTGCAGTTACCTGACCCAAATAAAT	TGACCACGGCCAATTTCCAC	0	0.2
## 24	GGTGCAGTTACCTGACCCAAATAAAT	CCMACACCTAAWGGCTGACCAC	0	0.2
## 25	GGTGCAGTTACCTGACCCAAATAAAT	TGCCCCTAAGGCCAACAC	0	0.2
## 26	GGTGCAGTTACCTGACCCAAATAAAT	GCCCTAAGGCCAACACCTA	0	0.2
## 27	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGT CA	0	0.2
## 28	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
## 29	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
## 30	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
## 31	GGTGCAGTTACCTGACCCAAATAAAT	GCCCTAAGGCCAACACCTAA	0	0.2
## 32	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
## 33	GGTGCAGTTACCTGACCCAAATAAAT	GCCCTAAGGCCAACACCTAAA	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	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGTG	0	0.2
## 41	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
## 42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
## 43	TCCCAGCAGTAAGCAACAATGG	ACAATAGCCTGTACATAAAACCAGCC	0	0.2
## 44	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
## 45	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
## 46	CCAACGACGCAGAGAAACACAAG	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 47	CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
## 48	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCA GTTCCGT	0	0.2
## 49	GCTTTGAGGATCCAACACGGC	GTGTTCA GTTCCGTGCACAGAT	0	0.2
## 50	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCA GTTCCGTG	0	0.2
## 51	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
## 52	GCTTTGAGGATCCAACACGGC	AGTGTTCA GTTCCGTGCACAG	0	0.2
## 53	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCA GTTCCGTGC	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	GTGTTCA GTTCCGTGCACAGA	0	0.2
## 56	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTCA GTTCCGTGCA	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GAAGTGTTCA GTTCCGTGCACA	0	0.2
## 58	TGTGCACGGA ACTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 59	TGTGCACGGA ACTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
## 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	CCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2

## 66	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 67	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 68	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
## 69	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 70	CCCCCCGCGCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 71	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
## 72	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 73	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 74	CCCCCCGCGCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 75	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 76	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 77	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 78	TGATCTGTGCACGGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 79	TGATCTGTGCACGGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 80	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 81	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	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
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2
## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAACCTAGTAGTTGGCGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAAACCTAGTAGTTGGCGGGG	0	0.2
## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTTC	0	0.2
## 93	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGAACACCAA	0	0.2
## 94	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGAACACCAAA	0	0.2
## 95	GCATGCTGCATGCCATAAATGTATA	GCACCGCAGGCACCTTATTAA	0	0.2
## 96	TGCCGCCACGTCTAATGTTTC	GCACAGCCCCAAAATACATAACTGTGT	0	0.2
## 97	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGT	0	0.2
## 98	TGCCGCCACGTCTAATGTTTC	GCCCCAAAATACATAACTGTGTCTGCT	0	0.2
## 99	TGCCGCCACGTCTAATGTTTC	GGGCACAGCCCCAAAATACATAACT	0	0.2
## 100	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGTG	0	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
## 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
## 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

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## 73	0	HPV16, HPV11, HPV4, HPV17	0
## 74	0	HPV16, HPV11, HPV4, HPV17	0
## 75	0	HPV16, HPV11, HPV4, HPV17	0
## 76	0	HPV16, HPV11, HPV4, HPV17	0
## 77	0	HPV16, HPV11, HPV4, HPV17	0
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## 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
## 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
## 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
##	fragments		
## 1	0		
## 2	0		
## 3	0		
## 4	0		
## 5	0		
## 6	0		
## 7	0		
## 8	0		
## 9	0		
## 10	0		
## 11	0		
## 12	0		
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## 14	0		
## 15	0		
## 16	0		
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## 18	0		
## 19	0		
## 20	0		
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## 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
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## 70	0
## 71	0
## 72	0
## 73	0
## 74	0
## 75	0
## 76	0
## 77	0
## 78	0
## 79	0

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## 80      0
## 81      0
## 82      0
## 83      0
## 84      0
## 85      0
## 86      0
## 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
## 100     0
```

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##
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```
## [[2]]
```

##	forward_primer	reverse_primer	score	coverage
## 1	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
## 2	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 3	CGGCGACCCTACAAGCTACC	CATTTATGGCATGCAGCATGCG	0	0.2
## 4	CGGCGACCCTACAAGCTACC	ACATTTATGGCATGCAGCATGC	0	0.2
## 5	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGTT	0	0.2
## 6	TCCCAGCAGTAAGCAACAATGG	AATCTACCATATCCGACCCTGTGT	0	0.2
## 7	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGT	0	0.2
## 8	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGT	0	0.2
## 9	TCCCAGCAGTAAGCAACAATGG	CTACCATATCCGACCCTGTGTCT	0	0.2
## 10	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGTG	0	0.2
## 11	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
## 12	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
## 13	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTGT	0	0.2
## 14	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
## 15	GCCCCCCTTTAGAACTTAAAAACACA	TGGAATCCCCATAAGGATCTGCAG	0	0.2
## 16	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATGT	0	0.2
## 17	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATG	0	0.2
## 18	CCAACGACGCAGAGAAACACAA	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 19	CCAACGACGCAGAGAAACACAA	GGCTCGTCGGGCTGGTAAA	0	0.2
## 20	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACTT	0	0.2
## 21	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT	0	0.2
## 22	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCT	0	0.2
## 23	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACT	0	0.2
## 24	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTGAT	0	0.2
## 25	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
## 26	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
## 27	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
## 28	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGTG	0	0.2
## 29	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTGATC	0	0.2
## 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	GGCATGGGAACTTTCAGTGTC	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	TCCAGCAGTAAGCAACAATGG	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	GCAGTGAAGTGTTTCAGTTCCGT	0	0.2
## 53	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGAT	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTTCAGTTCCGTG	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	AGTGTTTCAGTTCCGTGCACAG	0	0.2
## 56	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTTCAGTTCCGTGC	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGA	0	0.2
## 58	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTTCAGTTCCGTGCA	0	0.2
## 59	GCTTTGAGGATCCAACACGGC	GAAGTGTTTCAGTTCCGTGCACA	0	0.2
## 60	TGTGCACGGAAGTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 61	TGTGCACGGAAGTGAACACTTC	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	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
## 68	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 69	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 70	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
## 71	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 72	CCCCCCGCGCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 73	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
## 74	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 75	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 76	CCCCCCGCGCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 77	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 78	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 79	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 80	TGATCTGTGCACGGAAGTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 81	TGATCTGTGCACGGAAGTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 82	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 83	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	0.2
## 84	ACCTAAGGCAACATTGCAAGACATT	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2

## 85	ACCTAAGGCAACATTGCAAGACATT	GGCTCGTCGGGCTGGTAAA	0	0.2
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2
## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAACCTAGTAGTTGGCGGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAAACCTAGTAGTTGGCGGGGG	0	0.2
## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTTC	0	0.2
## 93	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAA	0	0.2
## 94	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAAAA	0	0.2
## 95	GCATGCTGCATGCCATAAAATGTATA	GCACCGCAGGCACCTTATTAA	0	0.2
## 96	TGCCGCCACGTCTAATGTTTC	GCACAGCCCCAAAATACATAACTGTGT	0	0.2
## 97	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGT	0	0.2
## 98	TGCCGCCACGTCTAATGTTTC	GCCCCAAAATACATAACTGTGTCTGCT	0	0.2
## 99	TGCCGCCACGTCTAATGTTTC	GGGCACAGCCCCAAAATACATAACT	0	0.2
## 100	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGTG	0	0.2
##	products similar_signatures	missing_signatures	enzyme	digest_score
## 1	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 2	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 3	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 4	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 5	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 6	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 7	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 8	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 9	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 10	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 11	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 12	0	HPV16, HPV11, HPV4, HPV17	AccI	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
## 28	0	HPV16, HPV11, HPV4, HPV17		0
## 29	0	HPV16, HPV11, HPV4, HPV17		0
## 30	0	HPV16, HPV11, HPV4, HPV17		0
## 31	0	HPV16, HPV11, HPV4, HPV17		0
## 32	0	HPV16, HPV11, HPV4, HPV17		0
## 33	0	HPV16, HPV11, HPV4, HPV17		0
## 34	0	HPV16, HPV11, HPV4, HPV17		0
## 35	0	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	
##	39	0	HPV16,	HPV11,	HPV4,	HPV17	
##	40	0	HPV16,	HPV11,	HPV4,	HPV17	
##	41	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	44	0	HPV16,	HPV11,	HPV4,	HPV17	
##	45	0	HPV16,	HPV11,	HPV4,	HPV17	
##	46	0	HPV16,	HPV11,	HPV4,	HPV17	
##	47	0	HPV16,	HPV11,	HPV4,	HPV17	
##	48	0	HPV16,	HPV11,	HPV4,	HPV17	
##	49	0	HPV16,	HPV11,	HPV4,	HPV17	
##	50	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	54	0	HPV16,	HPV11,	HPV4,	HPV17	
##	55	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	62	0	HPV16,	HPV11,	HPV4,	HPV17	
##	63	0	HPV16,	HPV11,	HPV4,	HPV17	
##	64	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	74	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	85	0	HPV16,	HPV11,	HPV4,	HPV17	
##	86	0	HPV16,	HPV11,	HPV4,	HPV17	
##	87	0	HPV16,	HPV11,	HPV4,	HPV17	
##	88	0	HPV16,	HPV11,	HPV4,	HPV17	
##	89	0	HPV16,	HPV11,	HPV4,	HPV17	
##	90	0	HPV16,	HPV11,	HPV4,	HPV17	
##	91	0	HPV16,	HPV11,	HPV4,	HPV17	

## 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	HPV16, HPV11, HPV4, HPV17	0
## 99	0	HPV16, HPV11, HPV4, HPV17	0
## 100	0	HPV16, HPV11, HPV4, HPV17	0
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## 4	4		
## 5	2		
## 6	2		
## 7	2		
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## 9	2		
## 10	2		
## 11	2		
## 12	2		
## 13	0		
## 14	0		
## 15	0		
## 16	0		
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## 22	0		
## 23	0		
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## 34	0		
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## 38	0		
## 39	0		
## 40	0		
## 41	0		
## 42	0		
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## 44	0		

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## 48	0
## 49	0
## 50	0
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## 52	0
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## 86	0
## 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
## 100     0
```

```
##
## [[3]]
```

##	forward_primer	reverse_primer	score	coverage
## 1	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTGT	0	0.2
## 2	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
## 3	GCCCCCCTTTAGAACTTAAAAACACA	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	GTGGCGGCATGGGAACCTT	0	0.2
## 9	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACCTTTCAGTGT	0	0.2
## 10	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCT	0	0.2
## 11	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACCT	0	0.2
## 12	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACCTTTCAGTGTCTAT	0	0.2
## 13	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
## 14	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
## 15	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
## 16	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACCTTTCAGTGTCT	0	0.2
## 17	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACCTTTCAGTGTCTATC	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	TGCCCCACTAAGGCCAACAC	0	0.2
## 26	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTA	0	0.2
## 27	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACCTTTCAGTGTCTA	0	0.2
## 28	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
## 29	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
## 30	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
## 31	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCTAA	0	0.2
## 32	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	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	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGTG	0	0.2
## 41	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
## 42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
## 43	TCCCAGCAGTAAGCAACAATGG	ACAATAGCCTGTACATAAAACCAGCC	0	0.2
## 44	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
## 45	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
## 46	CCAACGACGCAGAGAAACACAAG	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 47	CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
## 48	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTTCAGTTCCGT	0	0.2
## 49	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGAT	0	0.2

## 50	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTTCAGTTCCTG	0	0.2
## 51	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
## 52	GCTTTGAGGATCCAACACGGC	AGTGTTTCAGTTCCTGTCACAG	0	0.2
## 53	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTTCAGTTCCTGTC	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCTGTCACAGA	0	0.2
## 56	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTTCAGTTCCTGTC	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GAAGTGTTTCAGTTCCTGTCACA	0	0.2
## 58	TGTGCACGGAAGTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 59	TGTGCACGGAAGTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
## 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	CCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
## 66	CCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 67	CCCCCGCCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 68	CCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
## 69	CCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 70	CCCCCGCCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 71	CCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
## 72	CCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 73	CCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 74	CCCCCGCCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 75	CCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 76	CCCCCGCCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 77	CCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 78	TGATCTGTGCACGGAAGTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 79	TGATCTGTGCACGGAAGTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 80	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 81	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	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
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2
## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAACCTAGTAGTTGGCGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAACTAGTAGTTGGCGGGG	0	0.2
## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTTC	0	0.2
## 93	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAA	0	0.2
## 94	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAAA	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
## 1	0	HPV16, HPV11, HPV4, HPV17		0
## 2	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	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
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## 77	0	HPV16, HPV11, HPV4, HPV17	0
## 78	0	HPV16, HPV11, HPV4, HPV17	0
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## 85	0	HPV16, HPV11, HPV4, HPV17	0
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## 89	0	HPV16, HPV11, HPV4, HPV17	0
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## 95	0	HPV16, HPV11, HPV4, HPV17	0
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## 98	0	HPV16, HPV11, HPV4, HPV17	0
## 99	0	HPV16, HPV11, HPV4, HPV17	0
## 100	0	HPV16, HPV11, HPV4, HPV17	0
##	fragments		
## 1	0		
## 2	0		
## 3	0		
## 4	0		
## 5	0		
## 6	0		
## 7	0		
## 8	0		
## 9	0		

## 10	0
## 11	0
## 12	0
## 13	0
## 14	0
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## 16	0
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## 18	0
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## 55	0
## 56	0
## 57	0
## 58	0
## 59	0
## 60	0
## 61	0
## 62	0
## 63	0

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## 64      0
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## 66      0
## 67      0
## 68      0
## 69      0
## 70      0
## 71      0
## 72      0
## 73      0
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## 75      0
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## 79      0
## 80      0
## 81      0
## 82      0
## 83      0
## 84      0
## 85      0
## 86      0
## 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
## 100     0

```

```
##
```

```
## [[4]]
```

##	forward_primer	reverse_primer	score	coverage
## 1	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTGT	0	0.2
## 2	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
## 3	GCCCCCCTTTAGAACTTAAAAACACA	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	GGCATGGGAACTTTCAGTGT	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	GGCATGGGAACTTTCAGTGTC	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	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGTG	0	0.2
## 41	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
## 42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
## 43	TCCCAGCAGTAAGCAACAATGG	ACAATAGCCTGTACATAAAACCAGCC	0	0.2
## 44	CCAACGACGCAGAGAAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
## 45	CCAACGACGCAGAGAAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
## 46	CCAACGACGCAGAGAAAACACAAG	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 47	CCAACGACGCAGAGAAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
## 48	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTTCAGTTCCGT	0	0.2
## 49	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGAT	0	0.2
## 50	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTTCAGTTCCGTG	0	0.2
## 51	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
## 52	GCTTTGAGGATCCAACACGGC	AGTGTTCAGTTCCGTGCACAG	0	0.2
## 53	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTTCAGTTCCGTGC	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGA	0	0.2
## 56	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTTCAGTTCCGTGCA	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GAAGTGTTTCAGTTCCGTGCACA	0	0.2
## 58	TGTGCACGGAAGTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 59	TGTGCACGGAAGTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
## 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	CCCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
## 66	CCCCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 67	CCCCCCCGCCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 68	CCCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2

## 69	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 70	CCCCCCGCGCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 71	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
## 72	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 73	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 74	CCCCCCGCGCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 75	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 76	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 77	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 78	TGATCTGTGCACGGAAGTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 79	TGATCTGTGCACGGAAGTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 80	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 81	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	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
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2
## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAACCTAGTAGTTGGCGGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAAACCTAGTAGTTGGCGGGGG	0	0.2
## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTTC	0	0.2
## 93	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGAACACCAA	0	0.2
## 94	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGAACACCAAA	0	0.2
## 95	GCATGCTGCATGCCATAAATGTATA	GCACCGCAGGCACCTTATTAA	0	0.2
## 96	TGCCGCCACGTCTAATGTTTC	GCACAGCCCCAAAATACATAACTGTGT	0	0.2
## 97	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGT	0	0.2
## 98	TGCCGCCACGTCTAATGTTTC	GCCCCAAAATACATAACTGTGTCTGCT	0	0.2
## 99	TGCCGCCACGTCTAATGTTTC	GGGCACAGCCCCAAAATACATAACT	0	0.2
## 100	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGTG	0	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
## 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
## 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

56

## 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
## 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
## 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
##	fragments		
## 1	0		
## 2	0		
## 3	0		
## 4	0		
## 5	0		
## 6	0		
## 7	0		
## 8	0		
## 9	0		
## 10	0		
## 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		
## 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
## 81	0
## 82	0

```
## 83      0
## 84      0
## 85      0
## 86      0
## 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
## 100     0
```

```
##
```

```
## [[5]]
```

##	forward_primer	reverse_primer	score	coverage
## 1	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
## 2	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 3	CGGCGACCCCTACAAGCTACC	CATTTATGGCATGCAGCATGCG	0	0.2
## 4	CGGCGACCCCTACAAGCTACC	ACATTTATGGCATGCAGCATGC	0	0.2
## 5	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGTT	0	0.2
## 6	TCCCAGCAGTAAGCAACAATGG	AATCTACCATATCCGACCCTGTGT	0	0.2
## 7	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGT	0	0.2
## 8	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGT	0	0.2
## 9	TCCCAGCAGTAAGCAACAATGG	CTACCATATCCGACCCTGTGTCT	0	0.2
## 10	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGTG	0	0.2
## 11	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
## 12	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
## 13	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTGT	0	0.2
## 14	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
## 15	GCCCCCCTTTAGAACTTAAAAACACA	TGGAATCCCCATAAGGATCTGCAG	0	0.2
## 16	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATGT	0	0.2
## 17	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATG	0	0.2
## 18	CCAACGACGCAGAGAAACACAA	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 19	CCAACGACGCAGAGAAACACAA	GGCTCGTCGGGCTGGTAAA	0	0.2
## 20	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACTT	0	0.2
## 21	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT	0	0.2
## 22	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCT	0	0.2
## 23	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACT	0	0.2
## 24	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGT CAT	0	0.2
## 25	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
## 26	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
## 27	GGTGCAGTTACCTGACCCAAATAAAT	CCCCTAAGGCCAACACCTAAAG	0	0.2
## 28	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT C	0	0.2
## 29	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGT CATC	0	0.2
## 30	GGTGCAGTTACCTGACCCAAATAAAT	CCTAAWGGCTGACCACGGC	0	0.2
## 31	GGTGCAGTTACCTGACCCAAATAAAT	CCAATTTCCTACTCAACACAGGC	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	TCCAGCAGTAAGCAACAATGG	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	GCAGTGAAGTGTTTCAGTTCCGT	0	0.2
## 53	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGAT	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTTCAGTTCCGTG	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	AGTGTTTCAGTTCCGTGCACAG	0	0.2
## 56	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTTCAGTTCCGTGC	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGA	0	0.2
## 58	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTTCAGTTCCGTGCA	0	0.2
## 59	GCTTTGAGGATCCAACACGGC	GAAGTGTTTCAGTTCCGTGCACA	0	0.2
## 60	TGTGCACGGAAGTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 61	TGTGCACGGAAGTGAACACTTC	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	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
## 68	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 69	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 70	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
## 71	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 72	CCCCCCGCGCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 73	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
## 74	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 75	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 76	CCCCCCGCGCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 77	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 78	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 79	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 80	TGATCTGTGCACGGAAGTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 81	TGATCTGTGCACGGAAGTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 82	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 83	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	0.2
## 84	ACCTAAGGCAACATTGCAAGACATT	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 85	ACCTAAGGCAACATTGCAAGACATT	GGCTCGTCGGGCTGGTAAA	0	0.2
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2

## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAACTAGTAGTTGGCGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAAACTAGTAGTTGGCGGGG	0	0.2
## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGAACACCAAAGTTC	0	0.2
## 93	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAA	0	0.2
## 94	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAAA	0	0.2
## 95	GCATGCTGCATGCCATAAATGTATA	GCACCGCAGGCACCTTATTAA	0	0.2
## 96	TGCCGCCACGTCTAATGTTTC	GCACAGCCCCAAAATACATAACTGTGT	0	0.2
## 97	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGT	0	0.2
## 98	TGCCGCCACGTCTAATGTTTC	GCCCAAAATACATAACTGTGTCTGCT	0	0.2
## 99	TGCCGCCACGTCTAATGTTTC	GGGCACAGCCCCAAAATACATAACT	0	0.2
## 100	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGTG	0	0.2
##	products similar_signatures	missing_signatures	enzyme	digest_score
## 1	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 2	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 3	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 4	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 5	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 6	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 7	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 8	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 9	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 10	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 11	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 12	0	HPV16, HPV11, HPV4, HPV17	AccI	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
## 28	0	HPV16, HPV11, HPV4, HPV17		0
## 29	0	HPV16, HPV11, HPV4, HPV17		0
## 30	0	HPV16, HPV11, HPV4, HPV17		0
## 31	0	HPV16, HPV11, HPV4, HPV17		0
## 32	0	HPV16, HPV11, HPV4, HPV17		0
## 33	0	HPV16, HPV11, HPV4, HPV17		0
## 34	0	HPV16, HPV11, HPV4, HPV17		0
## 35	0	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	
##	42	0	HPV16,	HPV11,	HPV4,	HPV17	
##	43	0	HPV16,	HPV11,	HPV4,	HPV17	
##	44	0	HPV16,	HPV11,	HPV4,	HPV17	
##	45	0	HPV16,	HPV11,	HPV4,	HPV17	
##	46	0	HPV16,	HPV11,	HPV4,	HPV17	
##	47	0	HPV16,	HPV11,	HPV4,	HPV17	
##	48	0	HPV16,	HPV11,	HPV4,	HPV17	
##	49	0	HPV16,	HPV11,	HPV4,	HPV17	
##	50	0	HPV16,	HPV11,	HPV4,	HPV17	
##	51	0	HPV16,	HPV11,	HPV4,	HPV17	
##	52	0	HPV16,	HPV11,	HPV4,	HPV17	
##	53	0	HPV16,	HPV11,	HPV4,	HPV17	
##	54	0	HPV16,	HPV11,	HPV4,	HPV17	
##	55	0	HPV16,	HPV11,	HPV4,	HPV17	
##	56	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	59	0	HPV16,	HPV11,	HPV4,	HPV17	
##	60	0	HPV16,	HPV11,	HPV4,	HPV17	
##	61	0	HPV16,	HPV11,	HPV4,	HPV17	
##	62	0	HPV16,	HPV11,	HPV4,	HPV17	
##	63	0	HPV16,	HPV11,	HPV4,	HPV17	
##	64	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	66	0	HPV16,	HPV11,	HPV4,	HPV17	
##	67	0	HPV16,	HPV11,	HPV4,	HPV17	
##	68	0	HPV16,	HPV11,	HPV4,	HPV17	
##	69	0	HPV16,	HPV11,	HPV4,	HPV17	
##	70	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	74	0	HPV16,	HPV11,	HPV4,	HPV17	
##	75	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	81	0	HPV16,	HPV11,	HPV4,	HPV17	
##	82	0	HPV16,	HPV11,	HPV4,	HPV17	
##	83	0	HPV16,	HPV11,	HPV4,	HPV17	
##	84	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	86	0	HPV16,	HPV11,	HPV4,	HPV17	
##	87	0	HPV16,	HPV11,	HPV4,	HPV17	
##	88	0	HPV16,	HPV11,	HPV4,	HPV17	
##	89	0	HPV16,	HPV11,	HPV4,	HPV17	
##	90	0	HPV16,	HPV11,	HPV4,	HPV17	
##	91	0	HPV16,	HPV11,	HPV4,	HPV17	
##	92	0	HPV16,	HPV11,	HPV4,	HPV17	
##	93	0	HPV16,	HPV11,	HPV4,	HPV17	
##	94	0	HPV16,	HPV11,	HPV4,	HPV17	

## 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
##	fragments		
## 1	4		
## 2	4		
## 3	4		
## 4	4		
## 5	2		
## 6	2		
## 7	2		
## 8	2		
## 9	2		
## 10	2		
## 11	2		
## 12	2		
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## 37	0		
## 38	0		
## 39	0		
## 40	0		
## 41	0		
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## 43	0		
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## 45	0		
## 46	0		
## 47	0		

## 48	0
## 49	0
## 50	0
## 51	0
## 52	0
## 53	0
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## 56	0
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## 82	0
## 83	0
## 84	0
## 85	0
## 86	0
## 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
## 100	0
##	


```

## [[6]]
##          forward_primer          reverse_primer score coverage
## 1  GCCCCCTTTAGAACTTAAAAACACA CCCATAAGGATCTGCAGACATTTGT      0      0.2
## 2  GCCCCCTTTAGAACTTAAAAACACA CCCATAAGGATCTGCAGACATTTG      0      0.2
## 3  GCCCCCTTTAGAACTTAAAAACACA  TGAATCCCCATAAGGATCTGCAG      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      GTGGCGGCATGGGAACCT      0      0.2
## 9  GGTGCAGTTACCTGACCCAAATAAAT      CGGCATGGGAACTTTCAGTGT      0      0.2
## 10 GGTGCAGTTACCTGACCCAAATAAAT      GCCCACTAAGGCCAACACCT      0      0.2
## 11 GGTGCAGTTACCTGACCCAAATAAAT      GTGGCGGCATGGGAACCT      0      0.2
## 12 GGTGCAGTTACCTGACCCAAATAAAT      GGCATGGGAACTTTCAGTGTCTAT      0      0.2
## 13 GGTGCAGTTACCTGACCCAAATAAAT      CACCTAAWGGCTGACCACGG      0      0.2
## 14 GGTGCAGTTACCTGACCCAAATAAAT      CMACACCTAAWGGCTGACCACG      0      0.2
## 15 GGTGCAGTTACCTGACCCAAATAAAT      CCCACTAAGGCCAACACCTAAAG      0      0.2
## 16 GGTGCAGTTACCTGACCCAAATAAAT      CGGCATGGGAACTTTCAGTGTCT      0      0.2
## 17 GGTGCAGTTACCTGACCCAAATAAAT      GGCATGGGAACTTTCAGTGTCTATC      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      GGCATGGGAACTTTCAGTGTCTA      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      CCATATCCGACCCTGTGTCTGT      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      TCCCAGCAGTAAGCAACAATGG      TGAAATCTACCATATCCGACCCTGTG      0      0.2
## 41      TCCCAGCAGTAAGCAACAATGG      ACCATATCCGACCCTGTGTCTG      0      0.2
## 42      TCCCAGCAGTAAGCAACAATGG      CGACCCTGTGTCTGTGTCATTTTC      0      0.2
## 43      TCCCAGCAGTAAGCAACAATGG      ACAATAGCCTGTACATAAAACCAGCC      0      0.2
## 44      CCAACGACGCAGAGAAACACAAG      GCTCGTCGGGCTGGTAAATGT      0      0.2
## 45      CCAACGACGCAGAGAAACACAAG      GCTCGTCGGGCTGGTAAATG      0      0.2
## 46      CCAACGACGCAGAGAAACACAAG      CGCTTAATTGCTCGTGACATAGAAGG      0      0.2
## 47      CCAACGACGCAGAGAAACACAAG      GGCTCGTCGGGCTGGTAAA      0      0.2
## 48      GCTTTGAGGATCCAACACGGC      GCAGTGAAGTGTTTCAGTTCCGT      0      0.2
## 49      GCTTTGAGGATCCAACACGGC      GTGTTTCAGTTCCGTGCACAGAT      0      0.2
## 50      GCTTTGAGGATCCAACACGGC      GCAGTGAAGTGTTTCAGTTCCGTG      0      0.2
## 51      GCTTTGAGGATCCAACACGGC      CATTTATGGCATGCAGCATGCG      0      0.2
## 52      GCTTTGAGGATCCAACACGGC      AGTGTTTCAGTTCCGTGCACAG      0      0.2

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## 53	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCAGTTCGGTGC	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCGGTGCACAGA	0	0.2
## 56	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTCAGTTCGGTGC	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GAAGTGTTCAGTTCGGTGCACA	0	0.2
## 58	TGTGCACGGAAGTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 59	TGTGCACGGAAGTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
## 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	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
## 66	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 67	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 68	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
## 69	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 70	CCCCCCGCGCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 71	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
## 72	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 73	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 74	CCCCCCGCGCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 75	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 76	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 77	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 78	TGATCTGTGCACGGAAGTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 79	TGATCTGTGCACGGAAGTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 80	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 81	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	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
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2
## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAACAGTAGTTGGCGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAAACAGTAGTTGGCGGGG	0	0.2
## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTTC	0	0.2
## 93	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAA	0	0.2
## 94	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAA	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
## 1	0	HPV16, HPV11, HPV4, HPV17		0
## 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

## 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
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## 74	0	HPV16, HPV11, HPV4, HPV17	0
## 75	0	HPV16, HPV11, HPV4, HPV17	0
## 76	0	HPV16, HPV11, HPV4, HPV17	0
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## 83	0	HPV16, HPV11, HPV4, HPV17	0
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## 85	0	HPV16, HPV11, HPV4, HPV17	0
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## 87	0	HPV16, HPV11, HPV4, HPV17	0
## 88	0	HPV16, HPV11, HPV4, HPV17	0
## 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
## 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
##	fragments		
## 1	0		
## 2	0		
## 3	0		
## 4	0		
## 5	0		
## 6	0		
## 7	0		
## 8	0		
## 9	0		
## 10	0		
## 11	0		
## 12	0		

## 13	0
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## 16	0
## 17	0
## 18	0
## 19	0
## 20	0
## 21	0
## 22	0
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## 60	0
## 61	0
## 62	0
## 63	0
## 64	0
## 65	0
## 66	0

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## 67      0
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## 69      0
## 70      0
## 71      0
## 72      0
## 73      0
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## 78      0
## 79      0
## 80      0
## 81      0
## 82      0
## 83      0
## 84      0
## 85      0
## 86      0
## 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
## 100     0

```

```
##
```

```
## [[7]]
```

##	forward_primer	reverse_primer	score	coverage
## 1	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTGT	0	0.2
## 2	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
## 3	GCCCCCCTTTAGAACTTAAAAACACA	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	GGCATGGGAACTTTCAGTGT	0	0.2
## 13	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
## 14	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
## 15	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
## 16	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT	0	0.2
## 17	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGT	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	TGCCCCACTAAGGCCAACAC	0	0.2
## 26	GGTGCAGTTACCTGACCCAAATAAAT	GCCCCACTAAGGCCAACACCTA	0	0.2
## 27	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGTC	0	0.2
## 28	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
## 29	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
## 30	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
## 31	GGTGCAGTTACCTGACCCAAATAAAT	GCCCCACTAAKGCCMACACCTAA	0	0.2
## 32	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
## 33	GGTGCAGTTACCTGACCCAAATAAAT	GCCCCACTAAGGCCAACACCTAAA	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	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGTG	0	0.2
## 41	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
## 42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
## 43	TCCCAGCAGTAAGCAACAATGG	ACAATAGCCTGTACATAAAACCAGCC	0	0.2
## 44	CCAACGACGCAGAGAAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
## 45	CCAACGACGCAGAGAAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
## 46	CCAACGACGCAGAGAAAACACAAG	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 47	CCAACGACGCAGAGAAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
## 48	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTTCAGTTCCGT	0	0.2
## 49	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGAT	0	0.2
## 50	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTTCAGTTCCGTG	0	0.2
## 51	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
## 52	GCTTTGAGGATCCAACACGGC	AGTGTTTCAGTTCCGTGCACAG	0	0.2
## 53	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTTCAGTTCCGTGC	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	GTGTTTCAGTTCCGTGCACAGA	0	0.2
## 56	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTTCAGTTCCGTGCA	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GAAGTGTTTCAGTTCCGTGCACA	0	0.2
## 58	TGTGCACGGAAGTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 59	TGTGCACGGAAGTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
## 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	CCCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
## 66	CCCCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 67	CCCCCCCGCCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 68	CCCCCCCGCCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
## 69	CCCCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 70	CCCCCCCGCCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 71	CCCCCCCGCCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2

## 72	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 73	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 74	CCCCCCGCGCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 75	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 76	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 77	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 78	TGATCTGTGCACGGAAGTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 79	TGATCTGTGCACGGAAGTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 80	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 81	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	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
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2
## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAAGTAGTAGTTGGCGGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAAAGTAGTAGTTGGCGGGG	0	0.2
## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTTC	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
## 1	0	HPV16, HPV11, HPV4, HPV17		0
## 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
## 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

## 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
## 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
## 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
##	fragments		
## 1	0		
## 2	0		
## 3	0		
## 4	0		
## 5	0		
## 6	0		
## 7	0		
## 8	0		
## 9	0		
## 10	0		
## 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		
## 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
## 81	0
## 82	0
## 83	0
## 84	0
## 85	0

```
## 86      0
## 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
## 100     0
```

```
##
```

```
## [[8]]
```

##	forward_primer	reverse_primer	score	coverage
## 1	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
## 2	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 3	CGGCGACCCTACAAGCTACC	CATTTATGGCATGCAGCATGCG	0	0.2
## 4	CGGCGACCCTACAAGCTACC	ACATTTATGGCATGCAGCATGC	0	0.2
## 5	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGTT	0	0.2
## 6	TCCCAGCAGTAAGCAACAATGG	AATCTACCATATCCGACCCTGTGT	0	0.2
## 7	TCCCAGCAGTAAGCAACAATGG	CCATATCCGACCCTGTGTCTGT	0	0.2
## 8	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGT	0	0.2
## 9	TCCCAGCAGTAAGCAACAATGG	CTACCATATCCGACCCTGTGTCT	0	0.2
## 10	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGTG	0	0.2
## 11	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
## 12	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
## 13	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTGT	0	0.2
## 14	GCCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTTG	0	0.2
## 15	GCCCCCCTTTAGAACTTAAAAACACA	TGGAATCCCATAAGGATCTGCAG	0	0.2
## 16	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATGT	0	0.2
## 17	CCAACGACGCAGAGAAACACAA	GCTCGTCGGGCTGGTAAATG	0	0.2
## 18	CCAACGACGCAGAGAAACACAA	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 19	CCAACGACGCAGAGAAACACAA	GGCTCGTCGGGCTGGTAAA	0	0.2
## 20	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACTT	0	0.2
## 21	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT	0	0.2
## 22	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCT	0	0.2
## 23	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACT	0	0.2
## 24	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGT CAT	0	0.2
## 25	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
## 26	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
## 27	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
## 28	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACTTTCAGTGT C	0	0.2
## 29	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACTTTCAGTGT CATC	0	0.2
## 30	GGTGCAGTTACCTGACCCAAATAAAT	CCTAAWGGCTGACCACGGC	0	0.2
## 31	GGTGCAGTTACCTGACCCAAATAAAT	CCAATTTCCTACTCAACACAGGC	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	TGCCCCTAAGGCCAACAC	0	0.2
## 38	GGTGCAGTTACCTGACCCAAATAAAT	GCCCCTAAGGCCAACACCTA	0	0.2
## 39	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACCTTCAGTGTCA	0	0.2
## 40	GGTGCAGTTACCTGACCCAAATAAAT	CTGACCACGGCCAATTTCCA	0	0.2
## 41	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCA	0	0.2
## 42	GGTGCAGTTACCTGACCCAAATAAAT	GCCMACACCTAAWGGCTGACCA	0	0.2
## 43	GGTGCAGTTACCTGACCCAAATAAAT	GCCCCTAAGGCCAACACCTAA	0	0.2
## 44	GGTGCAGTTACCTGACCCAAATAAAT	CACGGCCAATTTCCACTCCAA	0	0.2
## 45	GGTGCAGTTACCTGACCCAAATAAAT	GCCCCTAAGGCCAACACCTAAA	0	0.2
## 46	GCATGCTGCATGCCATAAATGTAT	GCACCGCAGGCACCTTATTAA	0	0.2
## 47	TCCAGCAGTAAGCAACAATGG	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	GCAGTGAAGTGTTCAAGTCCGT	0	0.2
## 53	GCTTTGAGGATCCAACACGGC	GTGTTCAAGTCCGTGCACAGAT	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAAGTCCGTG	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	AGTGTTCAAGTCCGTGCACAG	0	0.2
## 56	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCAAGTCCGTGC	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GTGTTCAAGTCCGTGCACAGA	0	0.2
## 58	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTCAAGTCCGTGCA	0	0.2
## 59	GCTTTGAGGATCCAACACGGC	GAAGTGTTCAAGTCCGTGCACA	0	0.2
## 60	TGTGCACGGAAGTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 61	TGTGCACGGAAGTGAACACTTC	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	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
## 68	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 69	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 70	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
## 71	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 72	CCCCCCGCGCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 73	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
## 74	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 75	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 76	CCCCCCGCGCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 77	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 78	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 79	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 80	TGATCTGTGCACGGAAGTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 81	TGATCTGTGCACGGAAGTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 82	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 83	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	0.2
## 84	ACCTAAGGCAACATTGCAAGACATT	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 85	ACCTAAGGCAACATTGCAAGACATT	GGCTCGTCGGGCTGGTAAA	0	0.2
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2
## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAACTAGTAGTTGGCGGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAAACTAGTAGTTGGCGGGG	0	0.2

## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTTC	0	0.2
## 93	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAA	0	0.2
## 94	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAAA	0	0.2
## 95	GCATGCTGCATGCCATAAATGTATA	GCACCGCAGGCACCTTATTAA	0	0.2
## 96	TGCCGCCACGTCTAATGTTTC	GCACAGCCCCAAAATACATAACTGTGT	0	0.2
## 97	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGT	0	0.2
## 98	TGCCGCCACGTCTAATGTTTC	GGCCAAAATACATAACTGTGTCTGCT	0	0.2
## 99	TGCCGCCACGTCTAATGTTTC	GGGCACAGCCCCAAAATACATAACT	0	0.2
## 100	TGCCGCCACGTCTAATGTTTC	GGCACAGCCCCAAAATACATAACTGTG	0	0.2
##	products similar_signatures	missing_signatures	enzyme	digest_score
## 1	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 2	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 3	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 4	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 5	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 6	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 7	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 8	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 9	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 10	0	HPV16, HPV11, HPV4, HPV17	AccI	0
## 11	0	HPV16, HPV11, HPV4, HPV17	AccI	0
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## 15	0	HPV16, HPV11, HPV4, HPV17		0
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## 18	0	HPV16, HPV11, HPV4, HPV17		0
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## 20	0	HPV16, HPV11, HPV4, HPV17		0
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## 23	0	HPV16, HPV11, HPV4, HPV17		0
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## 28	0	HPV16, HPV11, HPV4, HPV17		0
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## 43	0	HPV16, HPV11, HPV4, HPV17		0

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##	97	0	HPV16,	HPV11,	HPV4,	HPV17	

## 98	0	HPV16, HPV11, HPV4, HPV17	0
## 99	0	HPV16, HPV11, HPV4, HPV17	0
## 100	0	HPV16, HPV11, HPV4, HPV17	0
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## 1	4		
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## 5	2		
## 6	2		
## 7	2		
## 8	2		
## 9	2		
## 10	2		
## 11	2		
## 12	2		
## 13	0		
## 14	0		
## 15	0		
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## 42	0		
## 43	0		
## 44	0		
## 45	0		
## 46	0		
## 47	0		
## 48	0		
## 49	0		
## 50	0		


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## 51      0
## 52      0
## 53      0
## 54      0
## 55      0
## 56      0
## 57      0
## 58      0
## 59      0
## 60      0
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## 90      0
## 91      0
## 92      0
## 93      0
## 94      0
## 95      0
## 96      0
## 97      0
## 98      0
## 99      0
## 100     0
##
## [[9]]
##          forward_primer      reverse_primer score coverage
## 1  GCCCCCTTTAGAACTTAAAAACACA CCCCATAGGATCTGCAGACATTGT      0      0.2

```

## 2	GCCCCCTTTAGAACTTAAAAACACA	CCCCATAAGGATCTGCAGACATTG	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	GTGGCGGCATGGGAACCT	0	0.2
## 9	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACCTTCAGTGT	0	0.2
## 10	GGTGCAGTTACCTGACCCAAATAAAT	GCCCACTAAGGCCAACACCT	0	0.2
## 11	GGTGCAGTTACCTGACCCAAATAAAT	GTGGCGGCATGGGAACCT	0	0.2
## 12	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACCTTCAGTGTCTAT	0	0.2
## 13	GGTGCAGTTACCTGACCCAAATAAAT	CACCTAAWGGCTGACCACGG	0	0.2
## 14	GGTGCAGTTACCTGACCCAAATAAAT	CMACACCTAAWGGCTGACCACG	0	0.2
## 15	GGTGCAGTTACCTGACCCAAATAAAT	CCCACTAAGGCCAACACCTAAAG	0	0.2
## 16	GGTGCAGTTACCTGACCCAAATAAAT	CGGCATGGGAACCTTCAGTGTCT	0	0.2
## 17	GGTGCAGTTACCTGACCCAAATAAAT	GGCATGGGAACCTTCAGTGTCTATC	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	GGCATGGGAACCTTCAGTGTCTA	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	CACGGCCAATTTCCACTCCA	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	TCCCAGCAGTAAGCAACAATGG	TGAAATCTACCATATCCGACCCTGTG	0	0.2
## 41	TCCCAGCAGTAAGCAACAATGG	ACCATATCCGACCCTGTGTCTG	0	0.2
## 42	TCCCAGCAGTAAGCAACAATGG	CGACCCTGTGTCTGTTGCATTTTC	0	0.2
## 43	TCCCAGCAGTAAGCAACAATGG	ACAATAGCCTGTACATAAAACCAGCC	0	0.2
## 44	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATGT	0	0.2
## 45	CCAACGACGCAGAGAAACACAAG	GCTCGTCGGGCTGGTAAATG	0	0.2
## 46	CCAACGACGCAGAGAAACACAAG	CGCTTAATTGCTCGTGACATAGAAGG	0	0.2
## 47	CCAACGACGCAGAGAAACACAAG	GGCTCGTCGGGCTGGTAAA	0	0.2
## 48	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAAGTCCGT	0	0.2
## 49	GCTTTGAGGATCCAACACGGC	GTGTTCAAGTCCGTGCACAGAT	0	0.2
## 50	GCTTTGAGGATCCAACACGGC	GCAGTGAAGTGTTCAAGTCCGTG	0	0.2
## 51	GCTTTGAGGATCCAACACGGC	CATTTATGGCATGCAGCATGCG	0	0.2
## 52	GCTTTGAGGATCCAACACGGC	AGTGTTCAAGTCCGTGCACAG	0	0.2
## 53	GCTTTGAGGATCCAACACGGC	AGTGAAGTGTTCAAGTCCGTGC	0	0.2
## 54	GCTTTGAGGATCCAACACGGC	ACATTTATGGCATGCAGCATGC	0	0.2
## 55	GCTTTGAGGATCCAACACGGC	GTGTTCAAGTCCGTGCACAGA	0	0.2

## 56	GCTTTGAGGATCCAACACGGC	GTGAAGTGTTTCAGTTCCGTGCA	0	0.2
## 57	GCTTTGAGGATCCAACACGGC	GAAGTGTTTCAGTTCCGTGCACA	0	0.2
## 58	TGTGCACGGAAGTGAACACTTC	CATTTATGGCATGCAGCATGCG	0	0.2
## 59	TGTGCACGGAAGTGAACACTTC	ACATTTATGGCATGCAGCATGC	0	0.2
## 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	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGT	0	0.2
## 66	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCAT	0	0.2
## 67	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCAT	0	0.2
## 68	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAAT	0	0.2
## 69	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCATC	0	0.2
## 70	CCCCCCGCGCAACTACTA	TCCTTATTTTCAGCYGGTGCAGC	0	0.2
## 71	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGC	0	0.2
## 72	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTA	0	0.2
## 73	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAATA	0	0.2
## 74	CCCCCCGCGCAACTACTA	CAGCATCCTTTTGACAGGTAATAGCA	0	0.2
## 75	CCCCCCGCGCAACTACTA	CCTTATTTTCAGCYGGTGCAGCA	0	0.2
## 76	CCCCCCGCGCAACTACTA	TTTCAGCYGGTGCAGCA	0	0.2
## 77	CCCCCCGCGCAACTACTA	GTGCAGCATCCTTTTGACAGGTAA	0	0.2
## 78	TGATCTGTGCACGGAAGTGAAC	CATTTATGGCATGCAGCATGCG	0	0.2
## 79	TGATCTGTGCACGGAAGTGAAC	ACATTTATGGCATGCAGCATGC	0	0.2
## 80	ACCTAAGGCAACATTGCAAGACATT	CATACACAACATTGTGTGACGTTGTG	0	0.2
## 81	ACCTAAGGCAACATTGCAAGACATT	GCTCGTCGGGCTGGTAAATG	0	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
## 86	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTT	0	0.2
## 87	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGT	0	0.2
## 88	TCTCCTGTACCTGGGCAATATGAT	AGTAGTTGGCGGGGGGG	0	0.2
## 89	TCTCCTGTACCTGGGCAATATGAT	CAAACCTAGTAGTTGGCGGGGG	0	0.2
## 90	TCTCCTGTACCTGGGCAATATGAT	CCAAACCTAGTAGTTGGCGGGGG	0	0.2
## 91	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAG	0	0.2
## 92	TCTCCTGTACCTGGGCAATATGAT	GGGGGGGGAACACCAAAGTTC	0	0.2
## 93	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAA	0	0.2
## 94	TCTCCTGTACCTGGGCAATATGAT	CGGGGGGGGAACACCAAA	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
## 1	0	HPV16, HPV11, HPV4, HPV17		0
## 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
## 8	0	HPV16, HPV11, HPV4, HPV17		0

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##	10	0	HPV16,	HPV11,	HPV4,	HPV17	
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##	51	0	HPV16,	HPV11,	HPV4,	HPV17	
##	52	0	HPV16,	HPV11,	HPV4,	HPV17	
##	53	0	HPV16,	HPV11,	HPV4,	HPV17	
##	54	0	HPV16,	HPV11,	HPV4,	HPV17	
##	55	0	HPV16,	HPV11,	HPV4,	HPV17	
##	56	0	HPV16,	HPV11,	HPV4,	HPV17	
##	57	0	HPV16,	HPV11,	HPV4,	HPV17	
##	58	0	HPV16,	HPV11,	HPV4,	HPV17	
##	59	0	HPV16,	HPV11,	HPV4,	HPV17	
##	60	0	HPV16,	HPV11,	HPV4,	HPV17	
##	61	0	HPV16,	HPV11,	HPV4,	HPV17	
##	62	0	HPV16,	HPV11,	HPV4,	HPV17	

## 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
## 74	0	HPV16, HPV11, HPV4, HPV17	0
## 75	0	HPV16, HPV11, HPV4, HPV17	0
## 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
## 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
## 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
##	fragments		
## 1	0		
## 2	0		
## 3	0		
## 4	0		
## 5	0		
## 6	0		
## 7	0		
## 8	0		
## 9	0		
## 10	0		
## 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
## 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
## 81      0
## 82      0
## 83      0
## 84      0
## 85      0
## 86      0
## 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
## 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)
```