

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 this package

```
devtools::install_github('Chebuu/HPV-Serovars')
library(HPVSerovars)
```

(Not run) This vignette is packaged and accessible via:

```
browseVignettes('HPVSerovars').
```

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')
```

Installing OpenPrimer Dependencies

From the [openPimer vignette](#):

openPrimeR requires external programs for some features, particularly for computing the physicochemical properties of primers. Please make sure you have the following tools installed on your system such that they are in your system's path:

[MELTING](#) (>= 5.1.1): For melting temperature computations. [ViennaRNA](#) (>= 2.2.4): For secondary structure prediction. [OligoArrayAux](#) (>= 3.8): For primer efficiency computations as performed by DECIPHER. [MAFFT](#) (>= 7.305): For computing multiple sequence alignments. [Pandoc](#) (>= 1.19.1): For creating PDF reports.

If you would like to be able to access the immunoglobulin repository IMGT from the openPrimeR Shiny app, you should additionally fulfill the following dependencies:

[PhantomJS](#) (>= 2.1): For headless website calls. [Python](#) (>=2.7.9) and the [selenium](#) (>=3.0.1) module: For data extraction scripts. openPrimeR will automatically check for all dependencies and inform you about any missing dependencies when the package is attached:

```
# library(openPrimeR)
```

Note that the tool is still functional if there are missing external programs. However, we recommend that all dependencies are fulfilled to guarantee the best user experience.

Install Bioconductor packages

<https://www.bioconductor.org/>

```
# 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")
```

Make alignment utils:

```
doAlignment <- function(xset) {
  useqs <- unique(xset)
  uidxs <- match(xset, useqs)
  aseqs <- AlignSeqs(useqs, verbose=F)
  aseqs[uidxs]
}
```

Quick-ref

Some references to remind me of packages, methods, etc.:

```
# CRAN
# https://rdrr.io/cran/dpcR/f/vignettes/overview.Rmd

# BIOC
# 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

# Other
# https://doi.org/10.1007/s13402-017-0331-y
```

Wiki Pheno Data

I copied the tables from [Wiki: Human_papillomavirus_infection](#) and included them in the R package assoc. w/ this document github.com/Chebuu/HPV-Serovars.

```
data(HPV.Sequelae)
data(HPV.GenitalCancerRisk)
```

The Wiki data contains phenotypic categorizations of several HPV strains. It's useful for testing.

```
HPV <- c(HPV.Sequelae, HPV.GenitalCancerRisk)
p.1 <- unique(unlist(HPV))

knitr::kable(
  sprintf('HPV-%s', sort(p.1)), col.names = '',
  caption = sprintf(
    'Unique HPV serotypes (N=%s) (Total=%s): ',
    length(p.1), length(HPV))
```

)
)

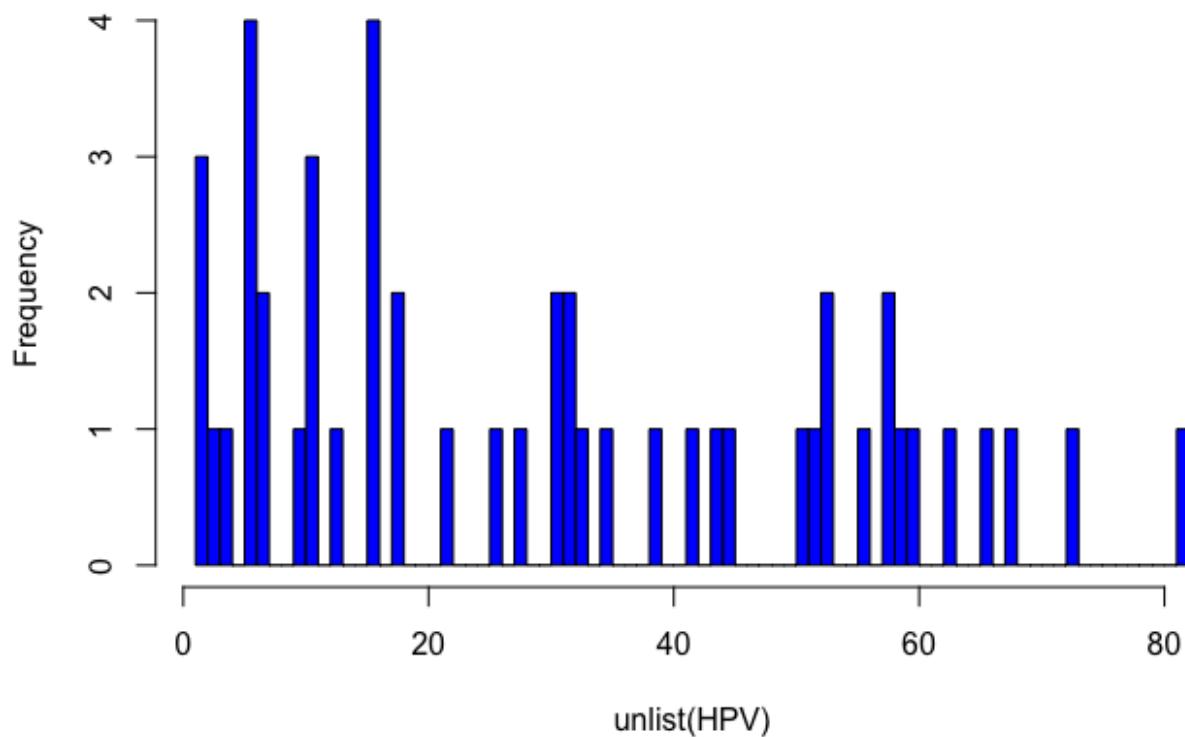
HPV-1
HPV-2
HPV-3
HPV-4
HPV-6
HPV-7
HPV-10
HPV-11
HPV-13
HPV-16
HPV-18
HPV-22
HPV-26
HPV-28
HPV-31
HPV-32
HPV-33
HPV-35
HPV-39
HPV-42
HPV-44
HPV-45
HPV-51
HPV-52

HPV-53
HPV-56
HPV-58
HPV-59
HPV-60
HPV-63
HPV-66
HPV-68
HPV-73
HPV-82

Unique HPV serotypes (N=34) (Total=13):

```
hist(unlist(HPV), max(unlist(HPV)), col='blue'); head(HPV, 4)
```

Histogram of unlist(HPV)



```
## `$Common warts`  
## [1] 2 7 22  
##  
## `$Plantar warts`  
## [1] 1 2 4 63  
##  
## `$Flat warts`  
## [1] 3 10 28  
##  
## `$Anogenital warts`  
## [1] 6 11 42 44
```

PaVE Data

Reference genomes for all serovars listed in `data(HPV.Sequela)` and `data(HPV.GenitalCancerRisk)` were selected from among the results of the following [PaVEPaVE](#) query:

```
https://pave.niaid.nih.gov/#search/search\_database/kw  
?dbNamespace=Genomes  
&includeNR=true  
&refCloneOnly=false  
&sort=Locus\_ID  
&sortType=true  
&page=600&start=1  
&text=Human&showTable=1  
&
```

```
library(dplyr)
```

```
##  
## Attaching package: 'dplyr'  
  
## The following objects are masked from 'package:stats':  
##  
##     filter, lag  
  
## The following objects are masked from 'package:base':  
##  
##     intersect, setdiff, setequal, union
```

```
library(tidyr)
library(stringr)

library(Biostrings)
```

```
## Loading required package: BiocGenerics

## Loading required package: parallel

##
## Attaching package: 'BiocGenerics'

## The following objects are masked from 'package:parallel':
## 
##     clusterApply, clusterApplyLB, clusterCall, clusterEvalQ,
##     clusterExport, clusterMap, parApply, parCapply, parLapply,
##     parLapplyLB, parRapply, parSapply, parSapplyLB

## The following objects are masked from 'package:dplyr':
## 
##     combine, intersect, setdiff, union

## The following objects are masked from 'package:stats':
## 
##     IQR, mad, sd, var, xtabs

## The following objects are masked from 'package:base':
## 
##     anyDuplicated, append, as.data.frame, basename, cbind, colnames,
##     dirname, do.call, duplicated, eval, evalq, Filter, Find, get, grep,
##     grepl, intersect, is.unsorted, lapply, Map, mapply, match, mget,
##     order, paste, pmax, pmax.int, pmin, pmin.int, Position, rank,
##     rbind, Reduce, rownames, sapply, setdiff, sort, table, tapply,
##     union, unique, unsplit, which, which.max, which.min

## Loading required package: S4Vectors

## Warning: package 'S4Vectors' was built under R version 3.6.3

## Loading required package: stats4

##
## Attaching package: 'S4Vectors'

## The following object is masked from 'package:tidyr':
## 
##     expand

## The following objects are masked from 'package:dplyr':
```

```
##  
##      first, rename  
  
## The following object is masked from 'package:base':  
##  
##      expand.grid  
  
## Loading required package: IRanges  
  
##  
## Attaching package: 'IRanges'  
  
## The following objects are masked from 'package:dplyr':  
##  
##      collapse, desc, slice  
  
## Loading required package: XVector  
  
##  
## Attaching package: 'Biostrings'  
  
## The following object is masked from 'package:base':  
##  
##      strsplit
```

```
library(DECIPHER)
```

```
## Loading required package: RSQLite
```

```
# data(PaVE.Wikiv)  
data(HPV.REF.PaVE.seqs)  
data(HPV.REF.PaVE.vars)  
  
testVars <- lapply(grep('[1-9]*', HPV.REF.PaVE.vars, value = T), function(x) {  
  sapply(HPV.Sequelae, function(y) any(x %in% y))  
})  
  
dbConn <- dbConnect(SQLite(), ':memory:')  
  
DECIPHER::Seqs2DB(HPV.REF.PaVE.seqs, 'XStringSet', dbConn, '')
```

```
## Adding 218 sequences to the database.  
##
```

```
## 218 total sequences in table Seqs.
## Time difference of 0.23 secs
```

```
DECIPHER::Add2DB(
  data.frame(
    # identifier = testVars
    identifier = lapply(HPV.REF.PaVE.vars, function(x) grep('[1-9]', x, perl =
  ),
  dbConn, verbose = F
)

# # DEL
# library(Biostrings)
# PaVE.Wikiv<-Biostrings::readDNAStringSet('../inst/extdata/HPV.REFS.PaVE.wikiv')
# usethis::use_data(PaVE.Wikiv)
#
# https://www.youtube.com/watch?v=zu8Z9-kebKQ&list=PLjixAZ027elDHGlQwfd06r7coj
#
# # END
```

NCBI Data

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

library(Biostrings)
library(DECIPHER)

library(HPVSerovars)
```

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>

"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.

```
library(HPSerovars)

data(Oral.L1.seqs)
data(Oral.L1.vars)

# load('../data/Oral.L1.seqs.rda')
# load('../data/Oral.L1.vars.rda')

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

# Oral.L1.seqs <- readDNAStringSet('../inst/extdata/HPV.oral.L1.fasta') %>%
# Oral.L1.vars <- read.csv('../inst/extdata/HPV.oral.L1.csv', stringsAsFactors = TRUE)
```

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

```
## Adding 31 sequences to the database.  
##  
## 31 total sequences in table Seqs.  
## Time difference of 0.04 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  
  
## Warning: Factors converted to character  
  
## 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  
  
## Warning: Factors converted to character  
  
## Expression:  
## update Seqs set identifier = :identifier where row_names = :row_names  
  
## Warning: Factors converted to character  
  
## Added to table Seqs: "GI" and "SVAR" and "ISO" and "GENE" and "identifier"  
##  
## Time difference of 0.05 secs
```

```
dbGetQuery(dbConn, "select * from Seqs") %>% head(4)
```

```
##   row_names identifier
## 1          1      HPV18
## 2          2      HPV18
## 3          3      HPV16
## 4          4      HPV18
##
## 1 gi|944543704|gb|KT365847.1| Human papillomavirus isolate HPV18-14 L1 prot
## 2 gi|944543703|gb|KT365846.1| Human papillomavirus isolate HPV18-13 L1 prot
## 3 gi|944543701|gb|KT365845.1| Human papillomavirus isolate HPV16-5 L1 prot
## 4 gi|944543699|gb|KT365844.1| Human papillomavirus isolate HPV18-12 L1 prot
##       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
)
```

```
## Warning in TileSeqs(dbFile = dbConn, minLength = 18, maxLength = 29, minCoverage = 0.8): Skipped due to multiple width sequences: HPV18
```

```
## Warning in TileSeqs(dbFile = dbConn, minLength = 18, maxLength = 29, minCoverage = 0.8): Skipped due to multiple width sequences: HPV16
```

```
## =====
```

```
## Warning in TileSeqs(dbFile = dbConn, minLength = 18, maxLength = 29, minCoverage = 0.8): Skipped due to multiple width sequences: HPV17
```

```
##
##
## Time difference of 2.95 secs
```

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

```
##  misprime      target_site
## 1 FALSE CATATTTATCATGCCAGCAGTTCTAGAC
## 2 FALSE AAGGTTTCAGCAAATCAGTACAGAGTACT
## 3 FALSE GGACACAACTAAATTGTGATGACCACA
## 4 FALSE AGTATTGGGACACAACTAAATTGTGAT
## 5 TRUE ATCCCACAAATGATAAAAAAATTGTGGTC
## 6 FALSE AGGCGGTCCCTTAGGAATAGGTGCTACTG
```

```
oligos.L1 <- DesignPrimers(
  tiles = tiles.L1,
  identifier = 'HPV4',
  worstScore = -1E3,
  maxPermutations = 5,
  minGroupCoverage = 0.85,
  minCoverage = 0.85,
  minLength = 20,
  maxLength = 28
)
```

```
##
## HPV4 (324 candidate primers):
## =====
## 
## Time difference of 5.7 secs
```

```
head(oligos.L1)
```

```
##   identifier start_forward start_reverse start_aligned_forward
## 3     HPV4          37           52            30
## 4     HPV4          37           53            31
## 5     HPV4          38           54            32
## 6     HPV4          38           55            33
## 7     HPV4          39           55            34
## 8     HPV4          40           55            35
##   start_aligned_reverse permutations_forward permutations_reverse score_for
## 3                  58                 1                 1
## 4                  59                 1                 1
## 5                  60                 1                 1
```

```

## 5          00          1          1
## 6          61          1          1
## 7          62          1          1
## 8          63          1          1
##   score_reverse      forward_primer.1 forward_primer.2 forward_primer.3
## 3          0 TGGTCCCAAAGGTTTCAGCAA <NA> <NA>
## 4          0 TGGTCCCAAAGGTTTCAGCAAAT <NA> <NA>
## 5          0 GGTCCCAAAGGTTTCAGCAAATC <NA> <NA>
## 6          0 GGTCCCAAAGGTTTCAGCAAATCA <NA> <NA>
## 7          0 GTCCCAAAGGTTTCAGCAAATCAG <NA> <NA>
## 8          0 TCCCAAAGGTTTCAGCAAATCAGT <NA> <NA>
##   forward_primer.4 forward_primer.5      reverse_primer.1 reverse_primer.
## 3          <NA>          <NA> GAAACCTTGGGACCACAATT <NA>
## 4          <NA>          <NA> TGAAACCTTGGGACCACAATT <NA>
## 5          <NA>          <NA> CTGAAACCTTGGGACCACAATT <NA>
## 6          <NA>          <NA> GCTGAAACCTTGGGACCACAATT <NA>
## 7          <NA>          <NA> GCTGAAACCTTGGGACCACAA <NA>
## 8          <NA>          <NA> GCTGAAACCTTGGGACCACAA <NA>
##   reverse_primer.3 reverse_primer.4 reverse_primer.5 forward_efficiency.1
## 3          <NA>          <NA> <NA> 0.8695543
## 4          <NA>          <NA> <NA> 0.8997148
## 5          <NA>          <NA> <NA> 0.9171716
## 6          <NA>          <NA> <NA> 0.9356067
## 7          <NA>          <NA> <NA> 0.8303409
## 8          <NA>          <NA> <NA> 0.9161453
##   forward_efficiency.2 forward_efficiency.3 forward_efficiency.4
## 3          NA          NA          NA
## 4          NA          NA          NA
## 5          NA          NA          NA
## 6          NA          NA          NA
## 7          NA          NA          NA
## 8          NA          NA          NA
##   forward_efficiency.5 reverse_efficiency.1 reverse_efficiency.2
## 3          NA          0.8433773 NA
## 4          NA          0.8369640 NA
## 5          NA          0.8697235 NA
## 6          NA          0.9333216 NA
## 7          NA          0.9122828 NA
## 8          NA          0.8831295 NA
##   reverse_efficiency.3 reverse_efficiency.4 reverse_efficiency.5
## 3          NA          NA          NA
## 4          NA          NA          NA
## 5          NA          NA          NA
## 6          NA          NA          NA
## 7          NA          NA          NA
## 8          NA          NA          NA
##   forward_coverage.1 forward_coverage.2 forward_coverage.3 forward_coverage.
## 3          1          NA          NA
## 4          1          NA          NA
## 5          1          NA          NA
## 6          1          NA          NA
## 7          1          NA          NA

```

```
## , 1 NA NA
## 8 1 NA NA
##   forward_coverage.5 reverse_coverage.1 reverse_coverage.2 reverse_coverage
## 3 NA 1 NA
## 4 NA 1 NA
## 5 NA 1 NA
## 6 NA 1 NA
## 7 NA 1 NA
## 8 NA 1 NA
##   reverse_coverage.4 reverse_coverage.5 mismatches_forward mismatches_rever
## 3 NA NA
## 4 NA NA
## 5 NA NA
## 6 NA NA
## 7 NA NA
## 8 NA NA
```

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 compliment of each primer pair (5) in each primer set (7).

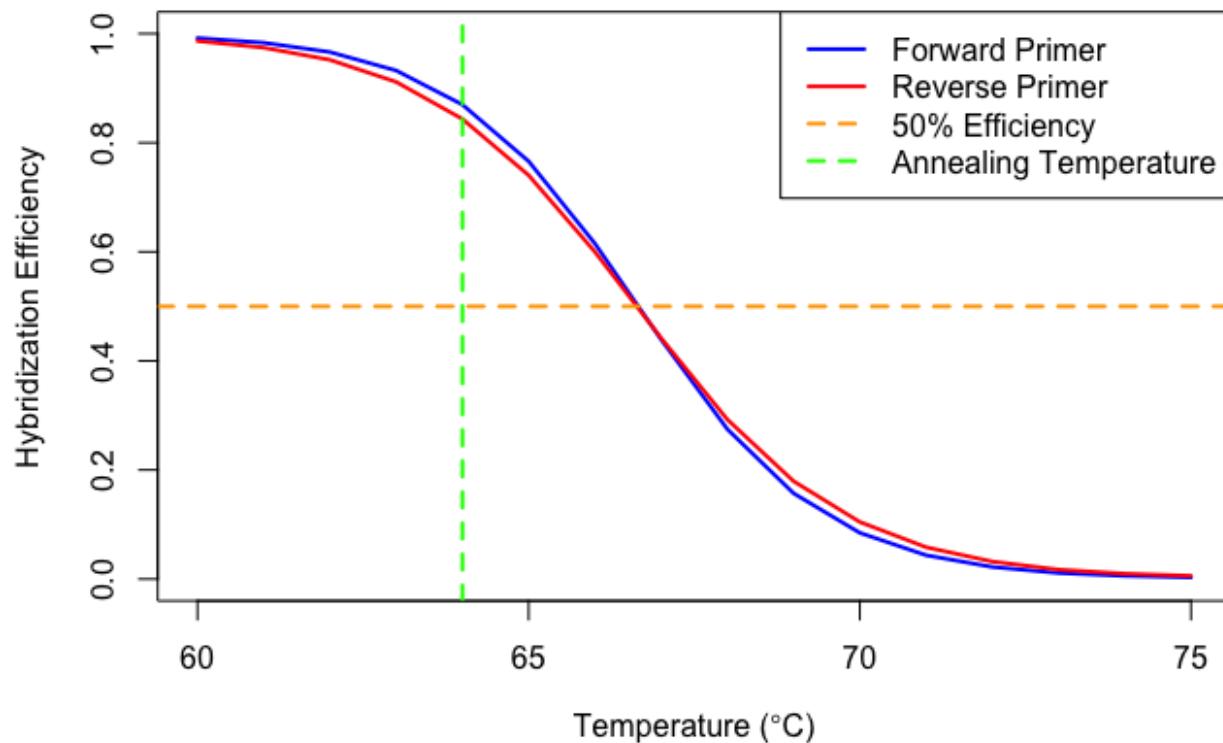
```
plotMeltCurves <- function(temp, effs) {
  plot(
    temp, effs[,1], ylim=c(0,1),
    ylab="Hybridization Efficiency",
    xlab=expression(paste("Temperature (", degree, "C)", sep="")),
    type="l", lwd=2, col="Blue", main="Denaturation Plot"
  )
  lines(temp, effs[,2], col="Red", lwd=2)
  abline(h=0.5, 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:
    fxn <- function(temp) CalculateEfficiencyPCR(primers, target, temp, P=P, i
    effs <- matrix(unlist(lapply(temps, fxn)), ncol=2, byrow=TRUE)
    if (doPlot) plotMeltCurves(temps, effs)
    list(temps = temps, effs = effs)
  }

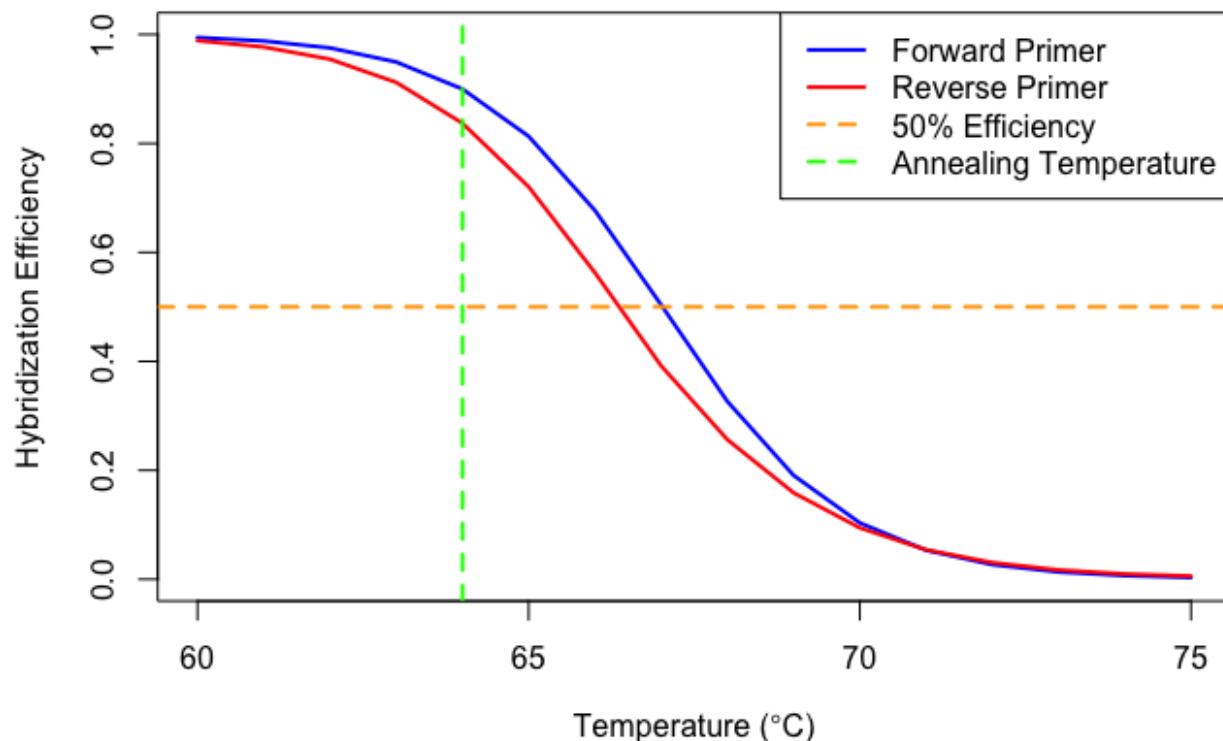
nsets <- nrow(oligos.L1)
npair <- ncol(oligos.L1)

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
      # # i --- It's supposed to be 70 x 17p --- ?
      # warning(sprintf('%s [iteration i=%s j=%s]', e, i, j))
    )
  
```

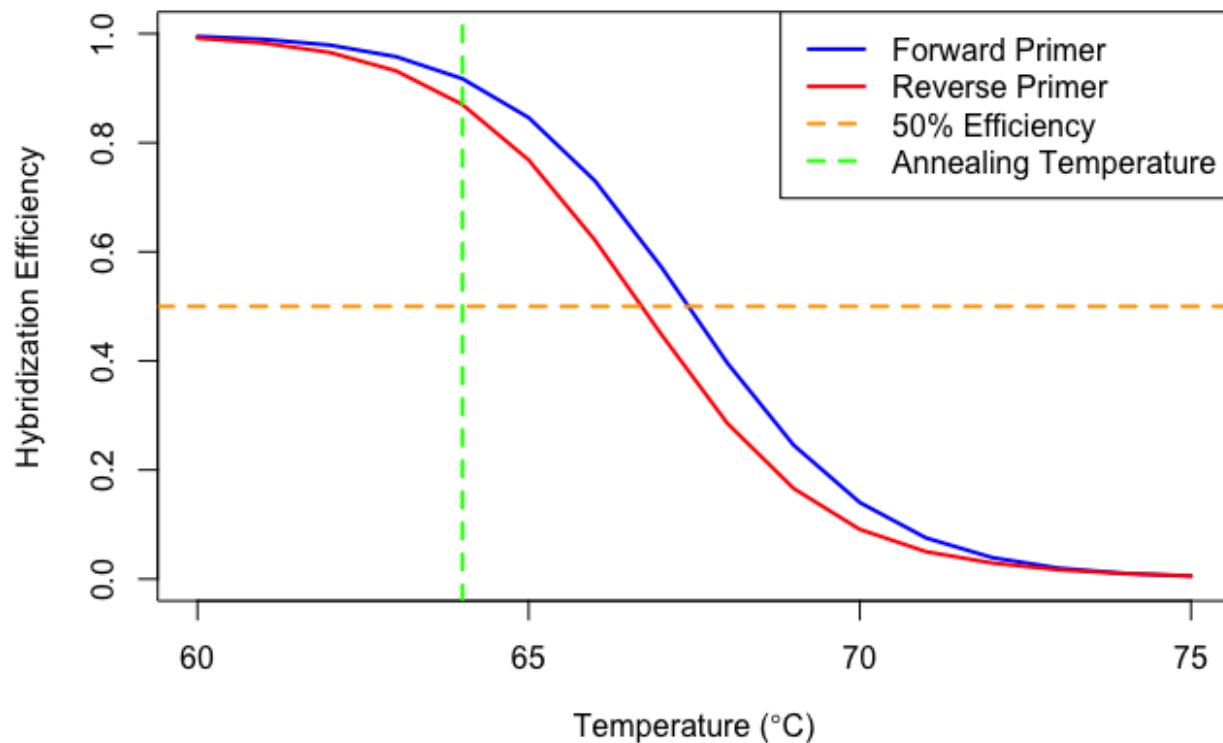
Denaturation Plot



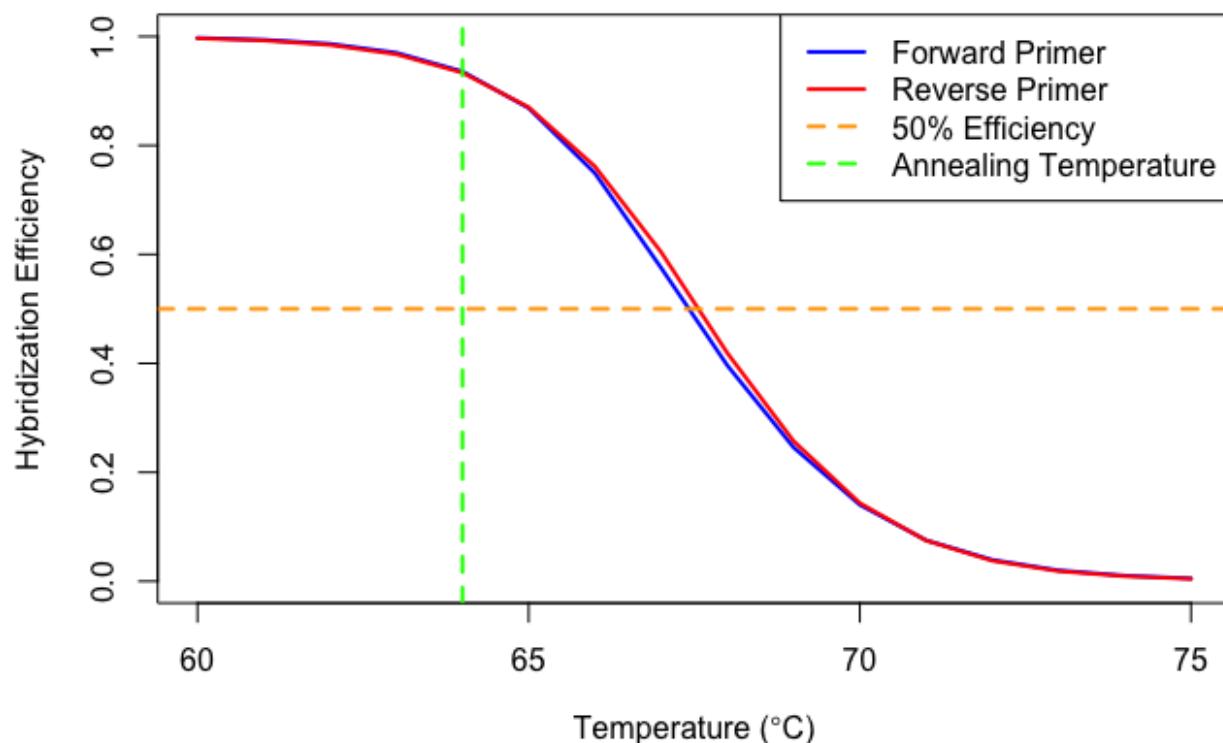
Denaturation Plot



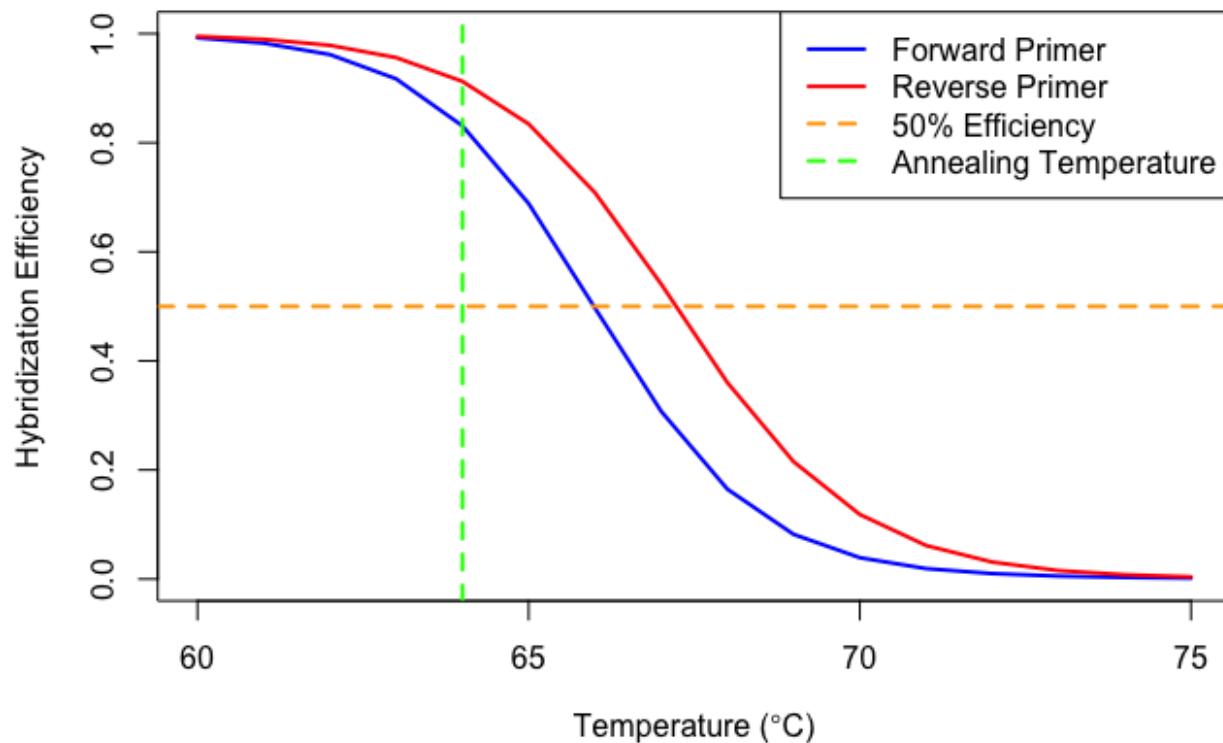
Denaturation Plot



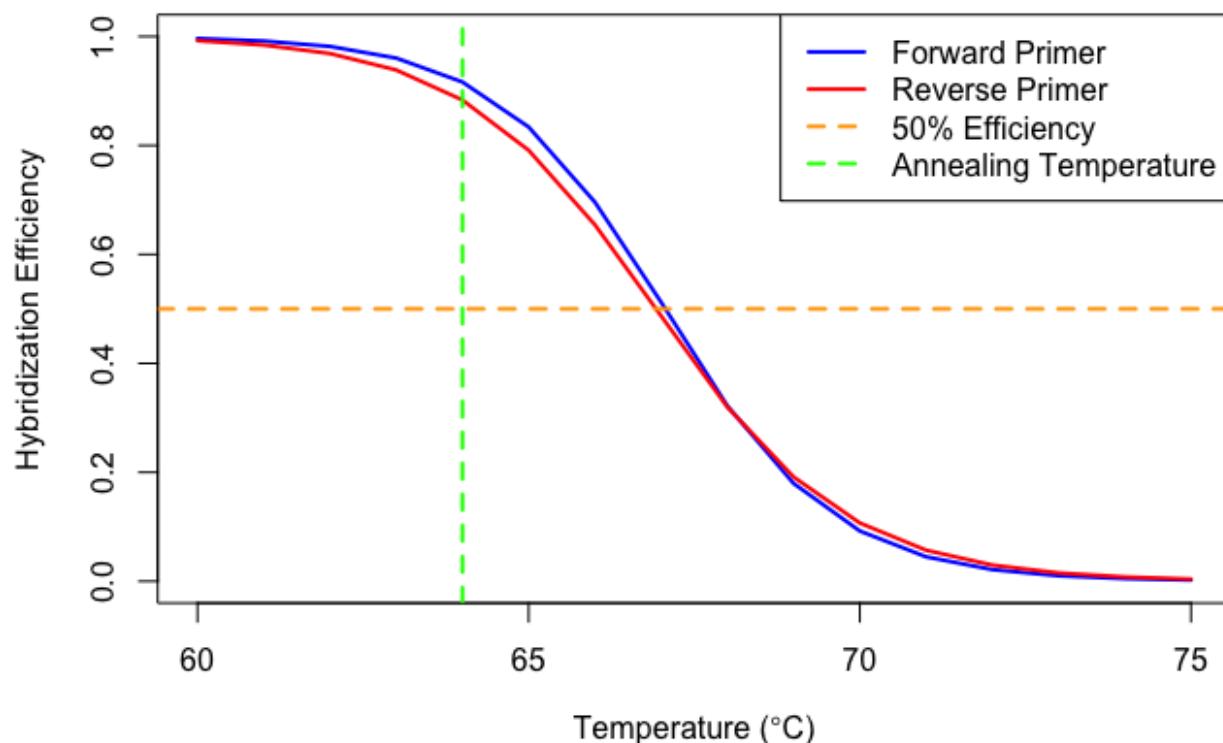
Denaturation Plot



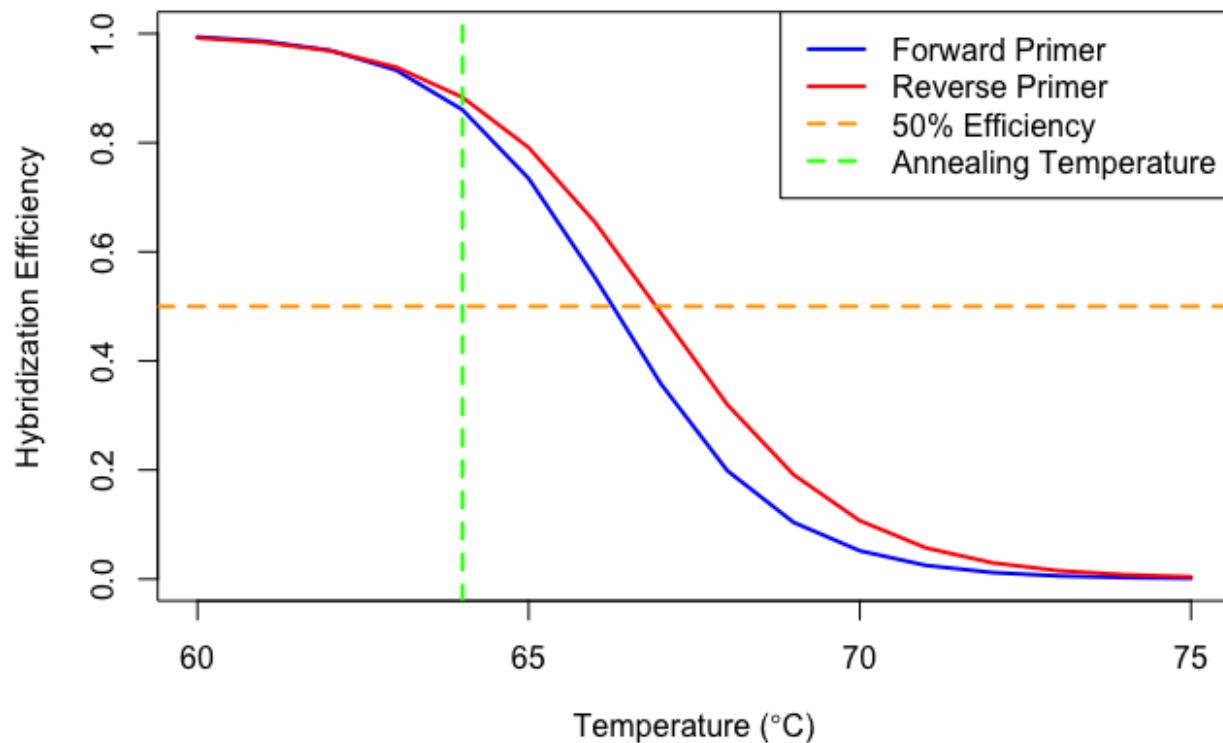
Denaturation Plot



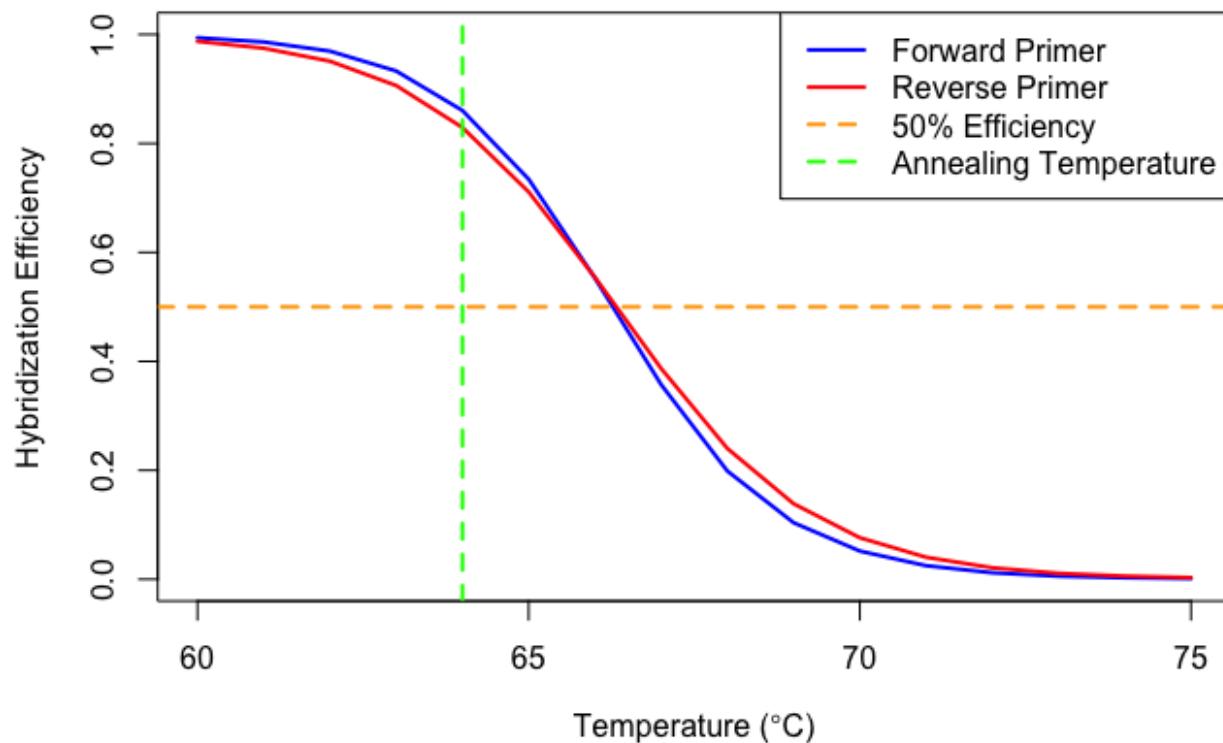
Denaturation Plot



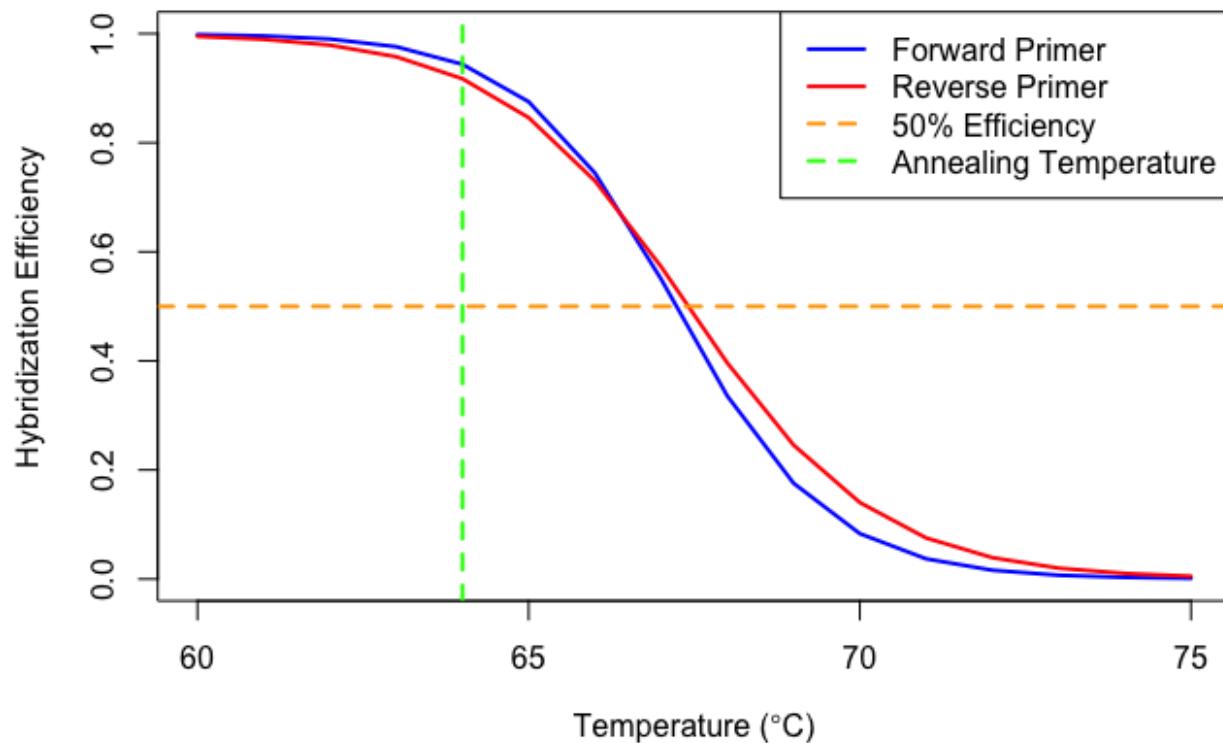
Denaturation Plot



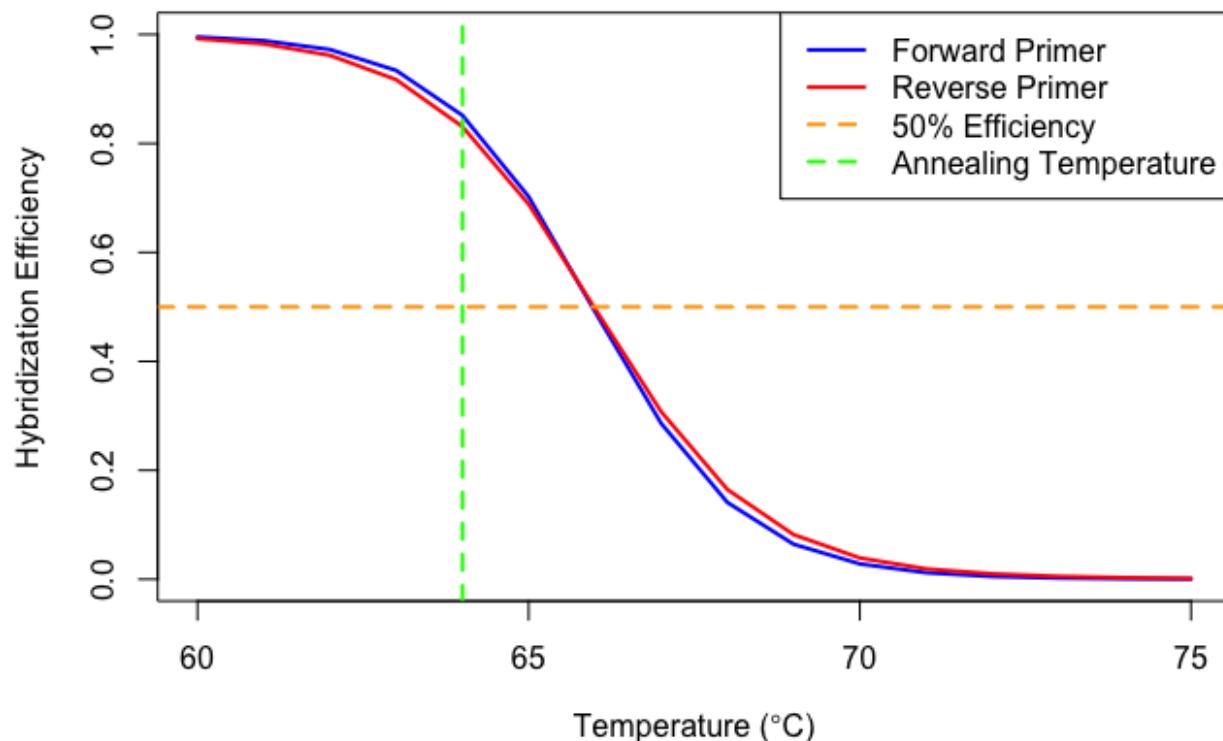
Denaturation Plot



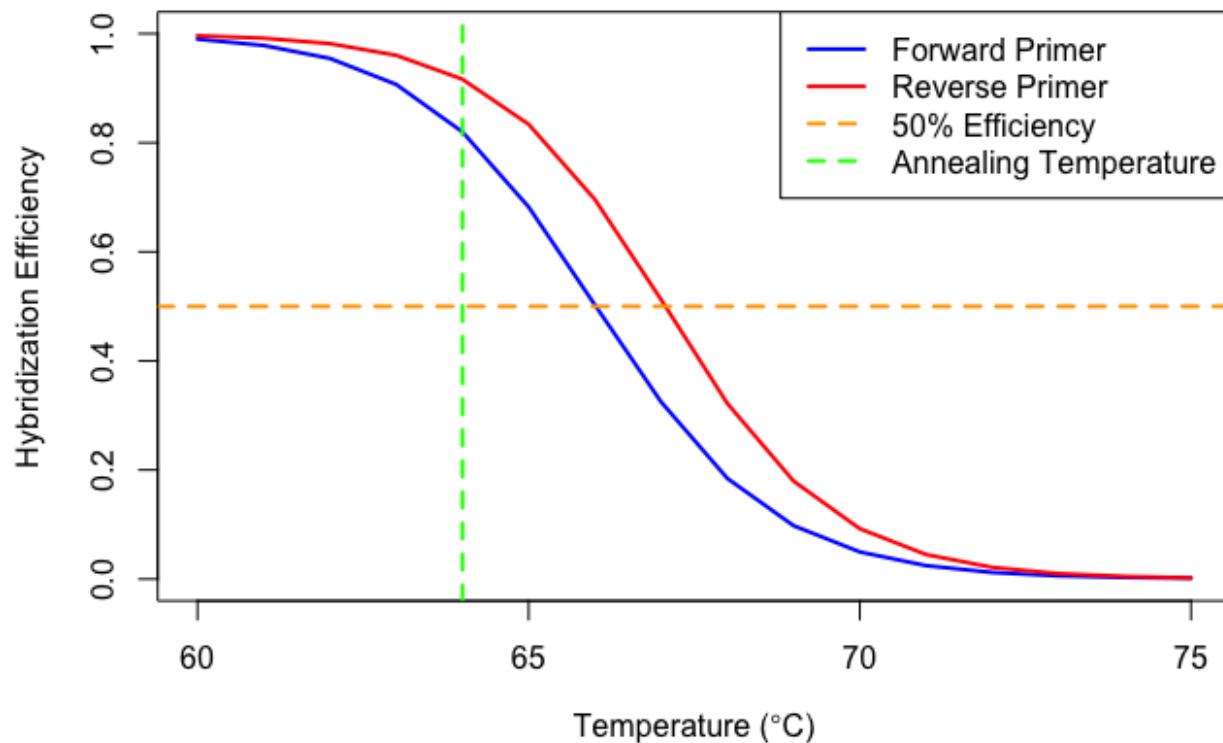
Denaturation Plot



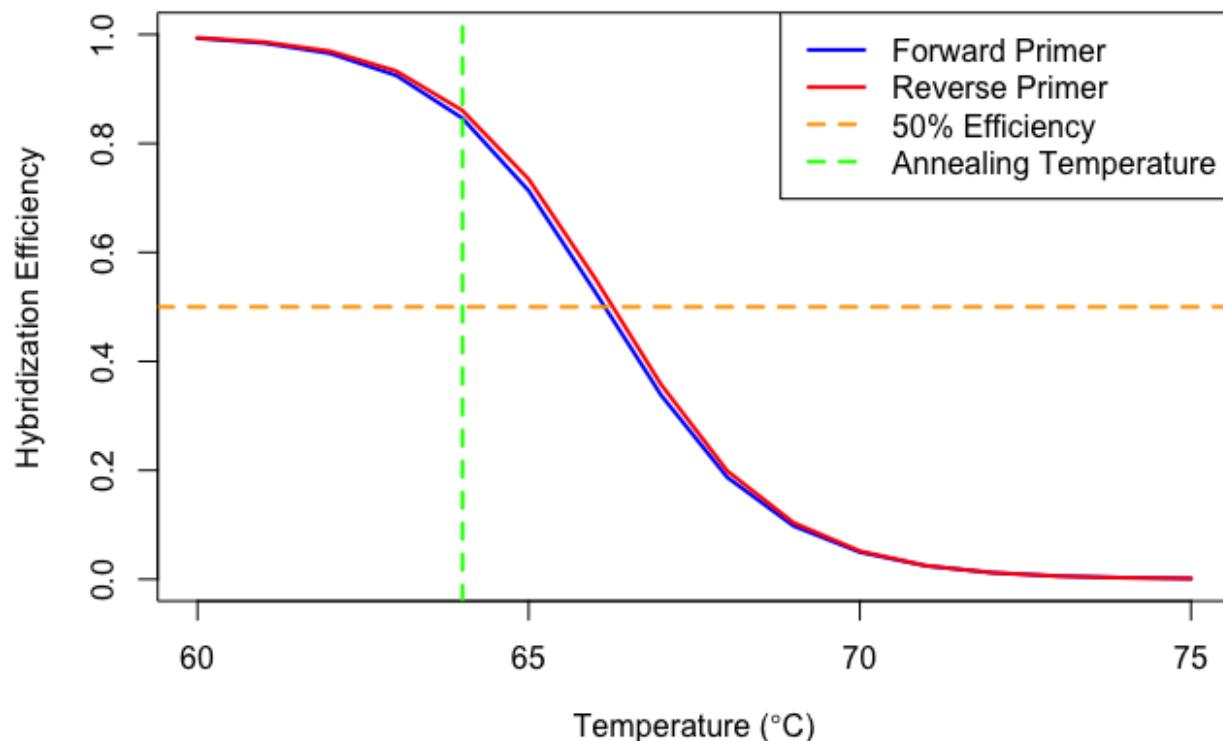
Denaturation Plot



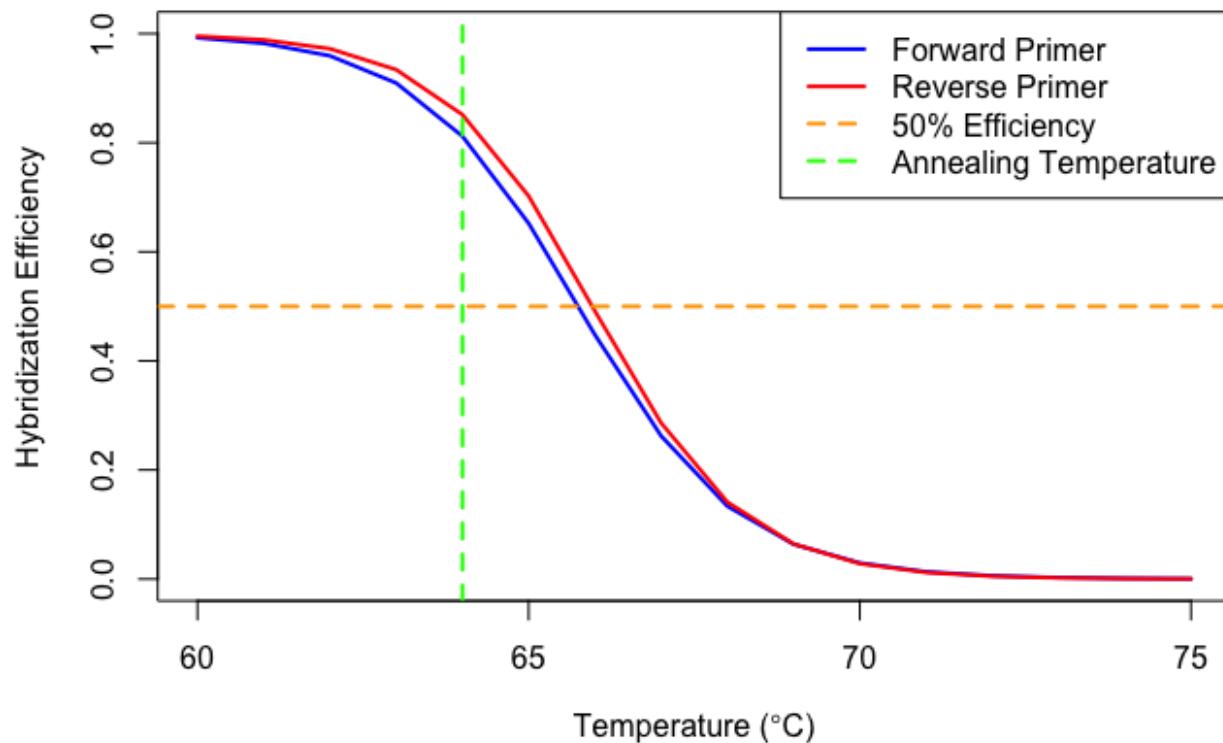
Denaturation Plot



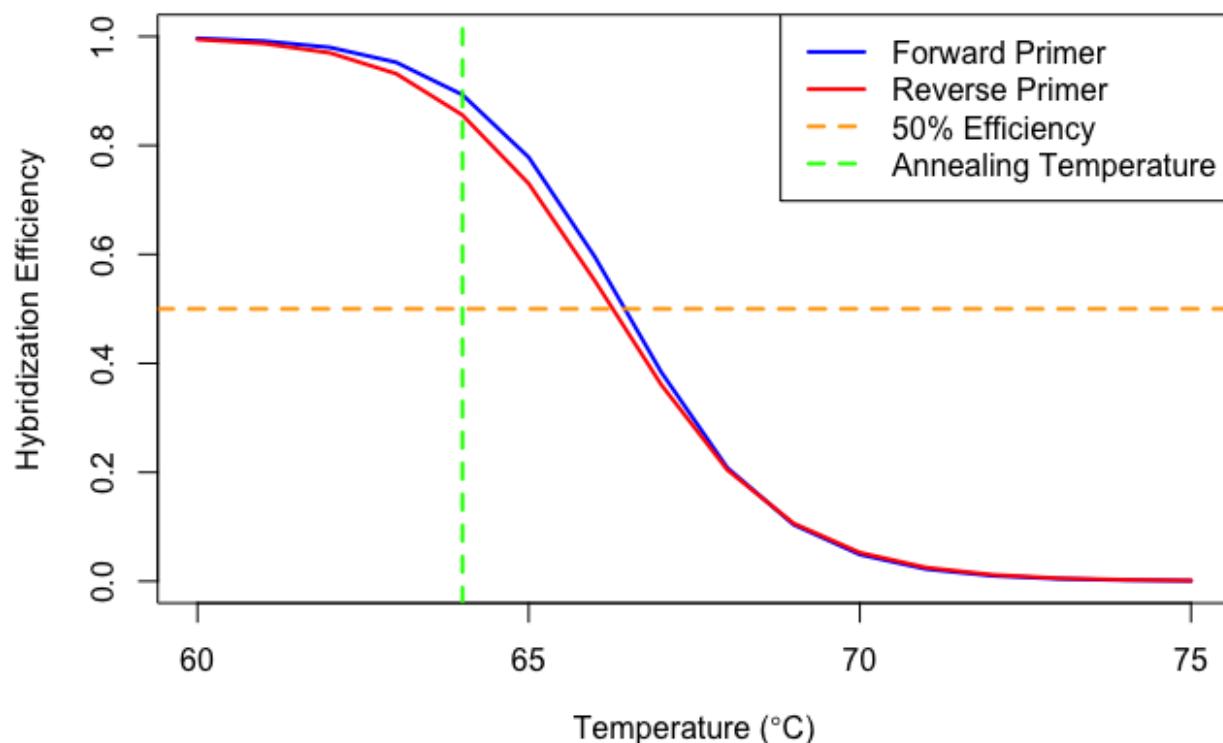
Denaturation Plot



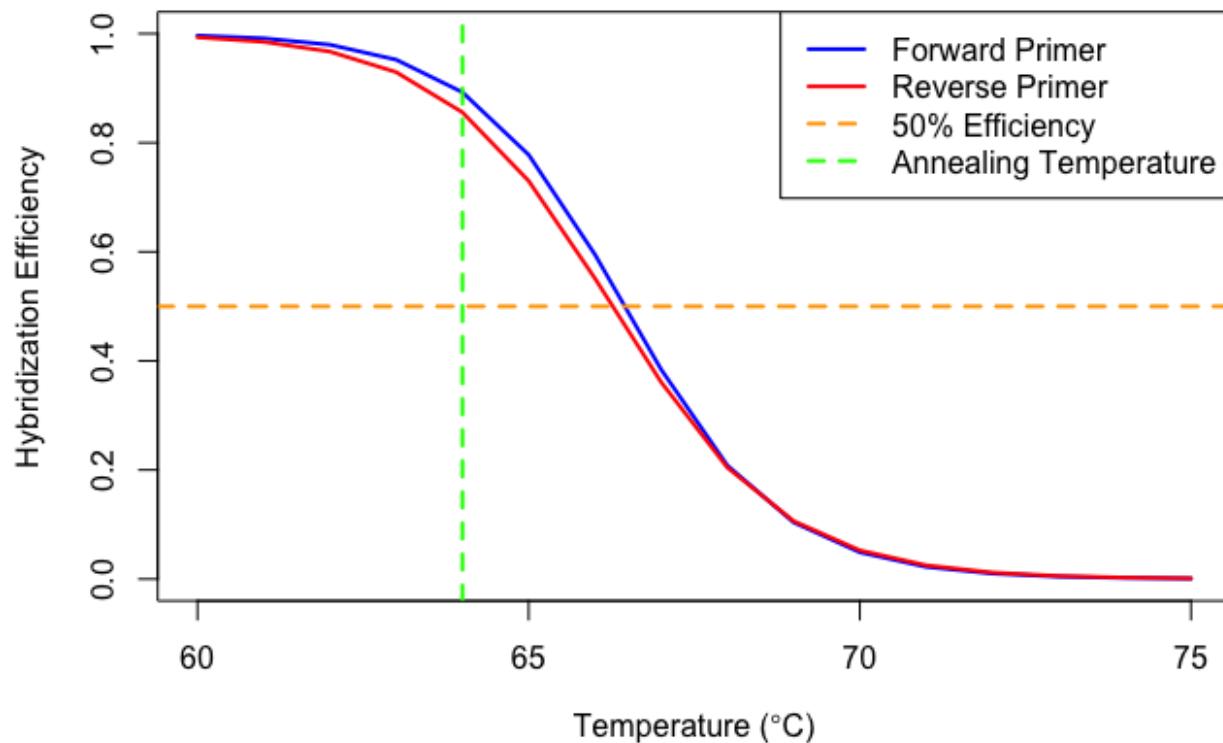
Denaturation Plot



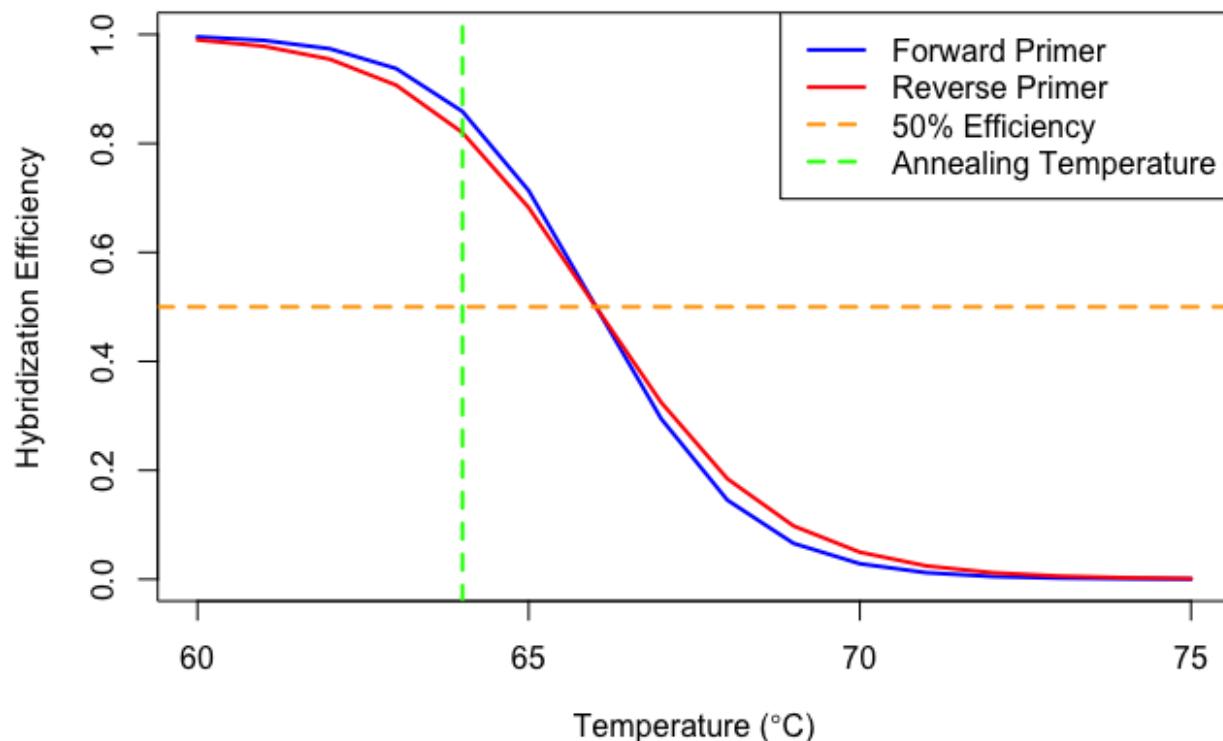
Denaturation Plot



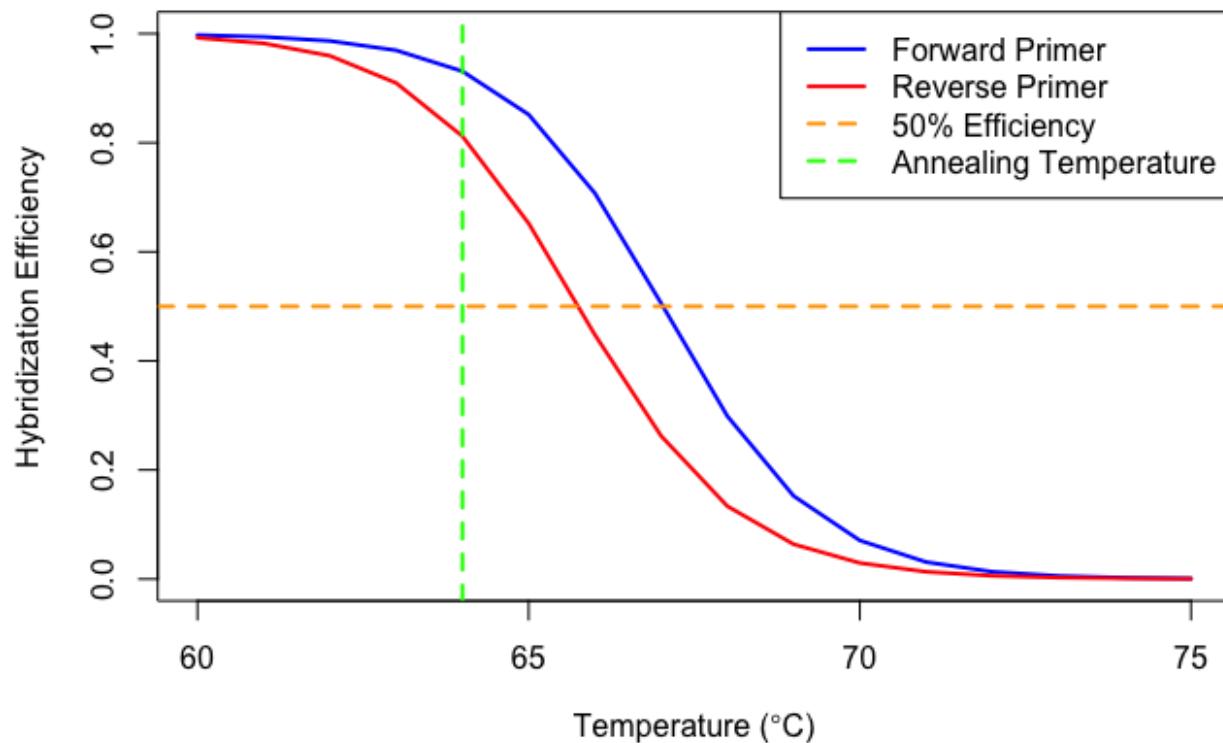
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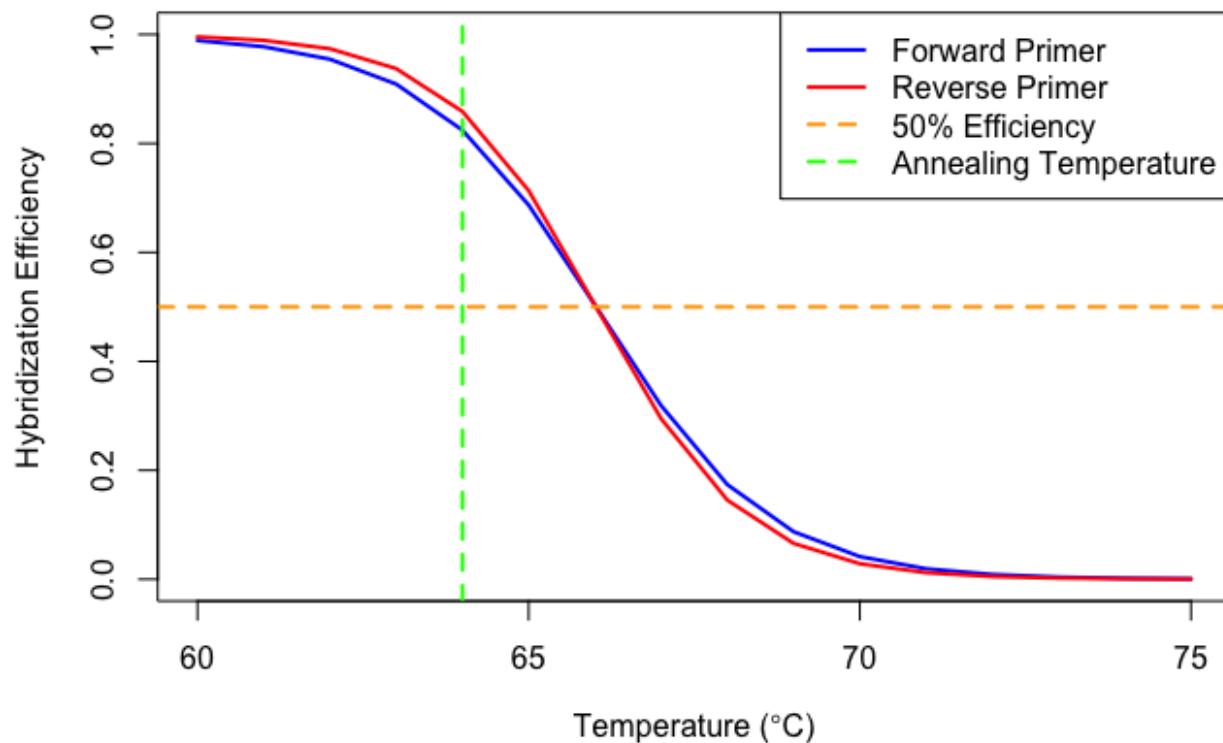
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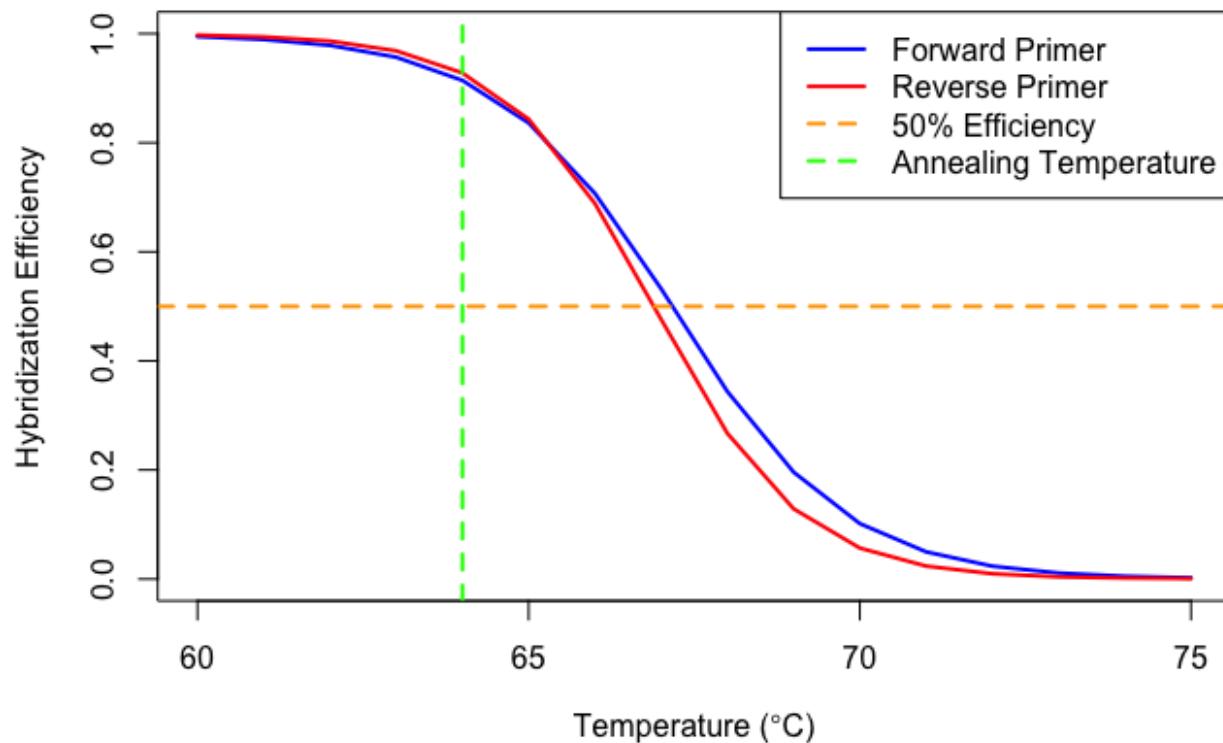
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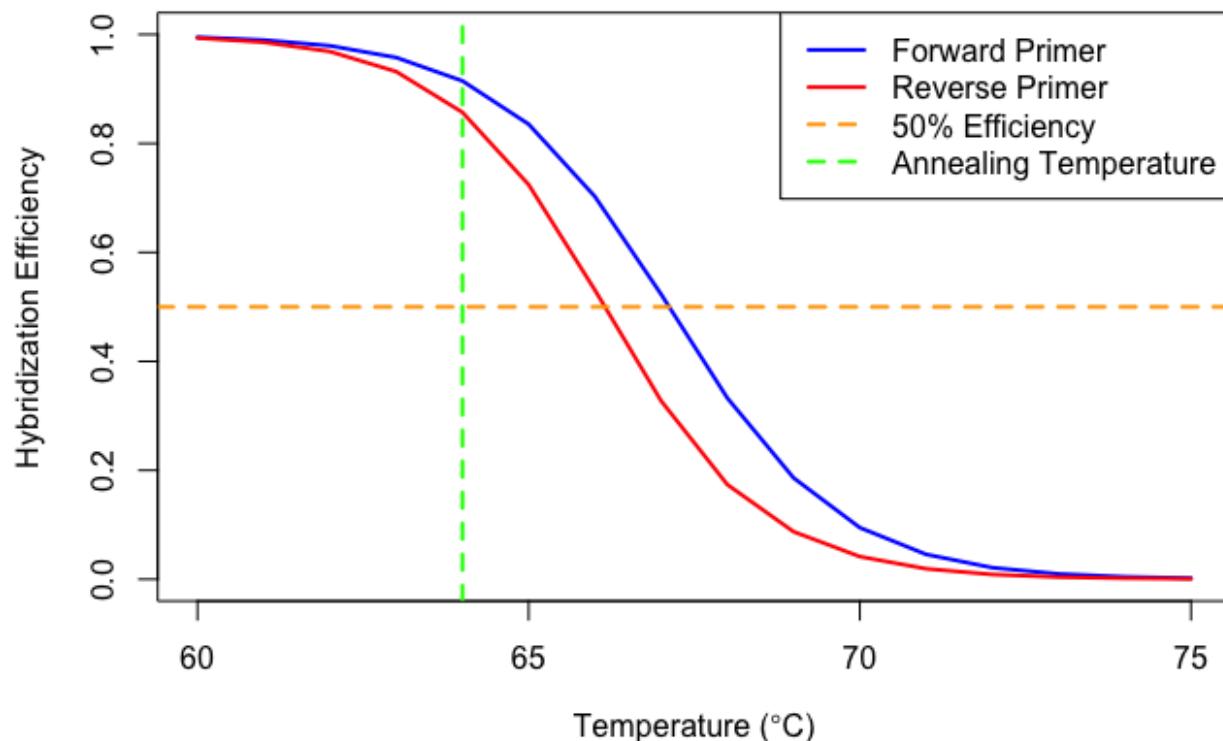
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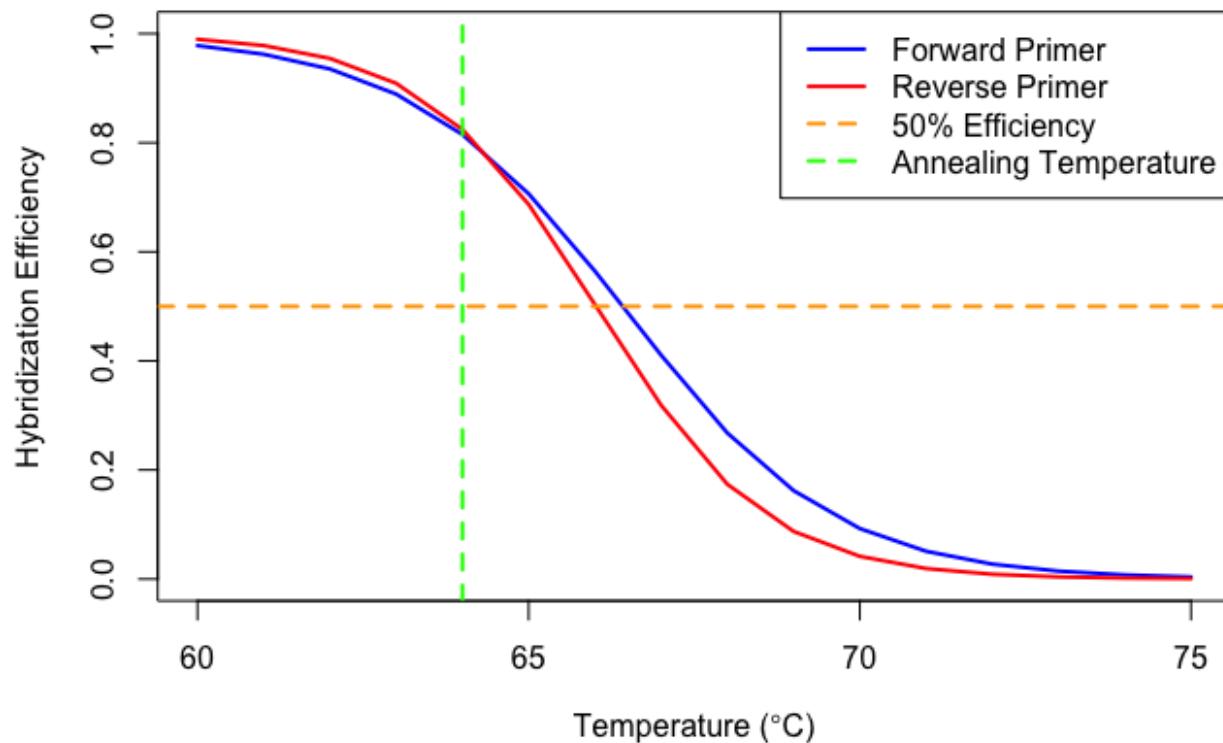
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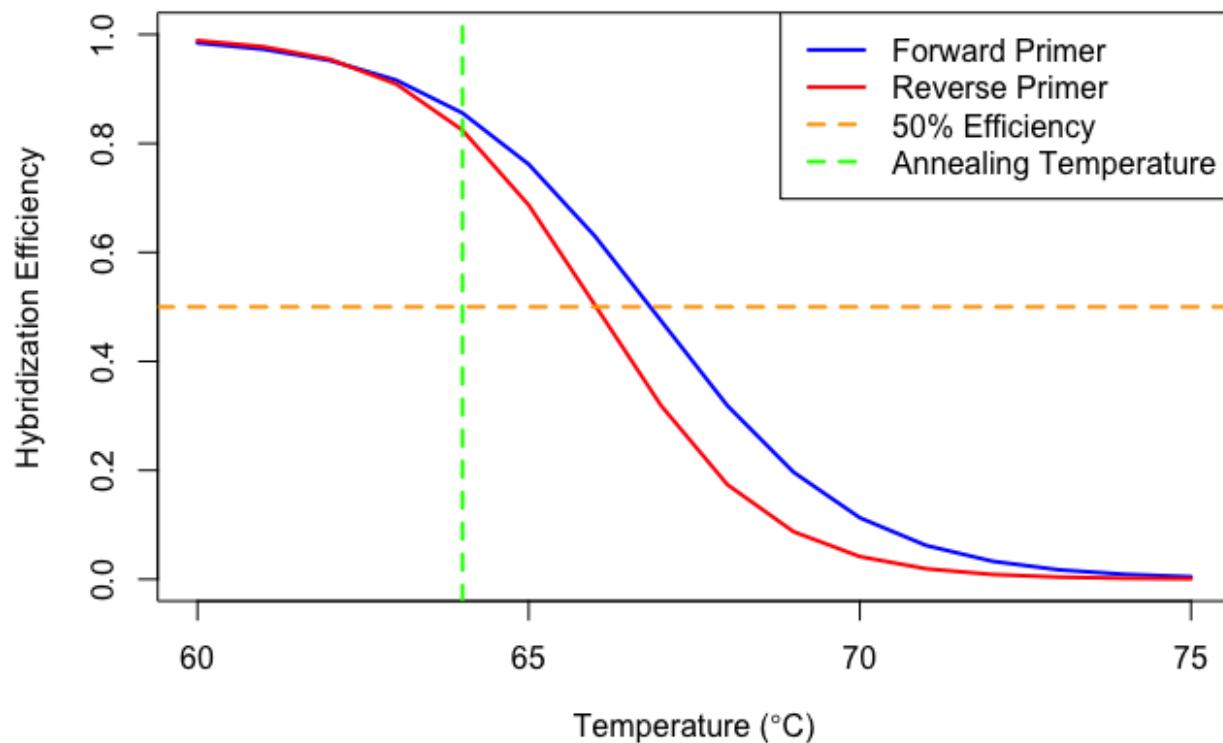
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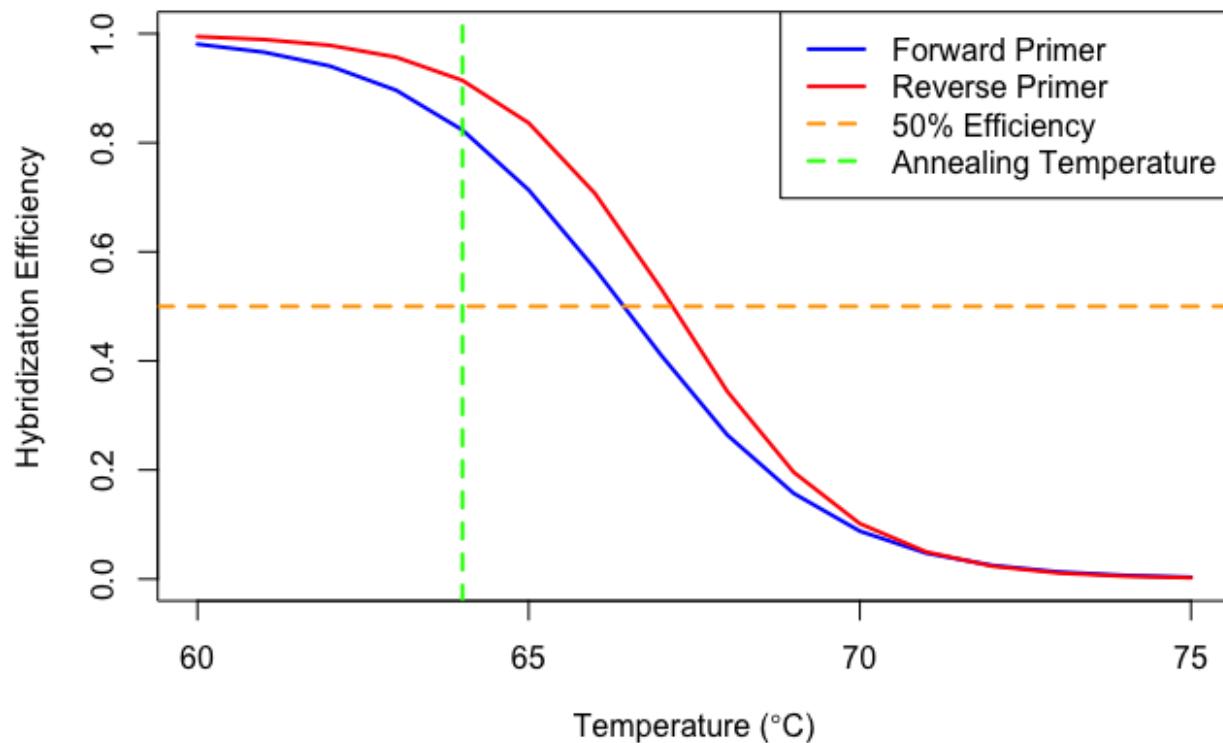
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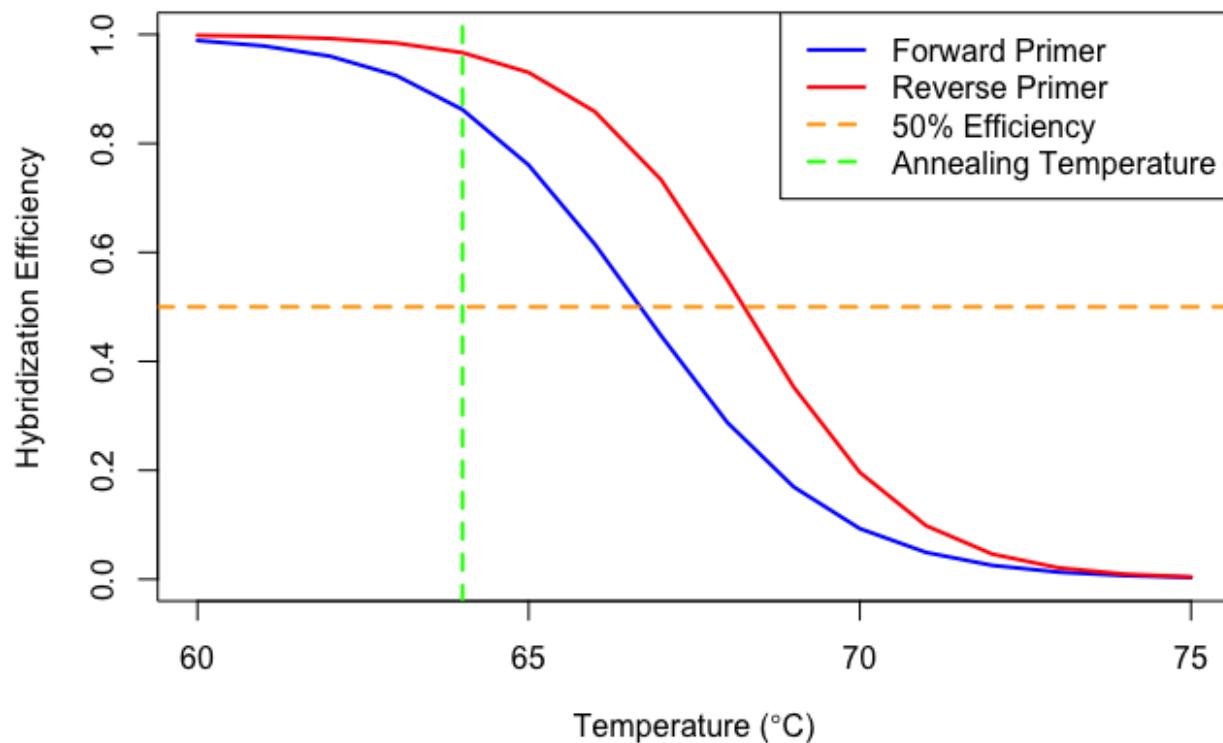
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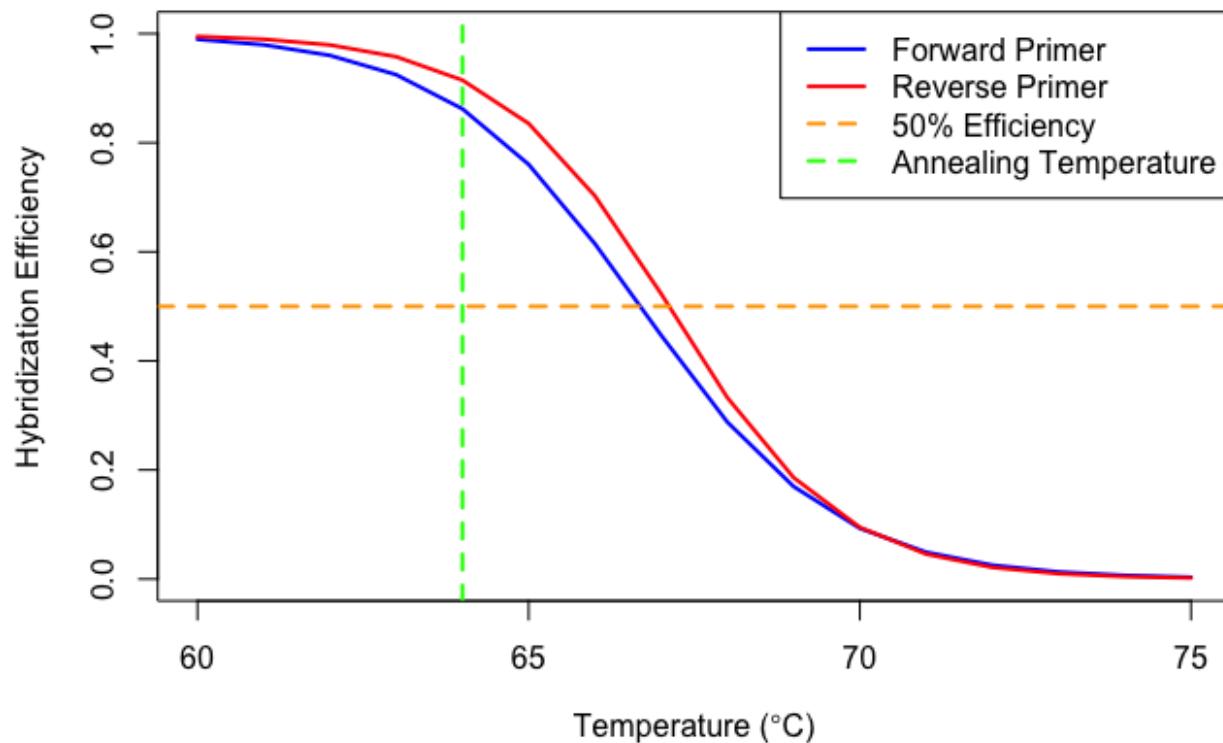
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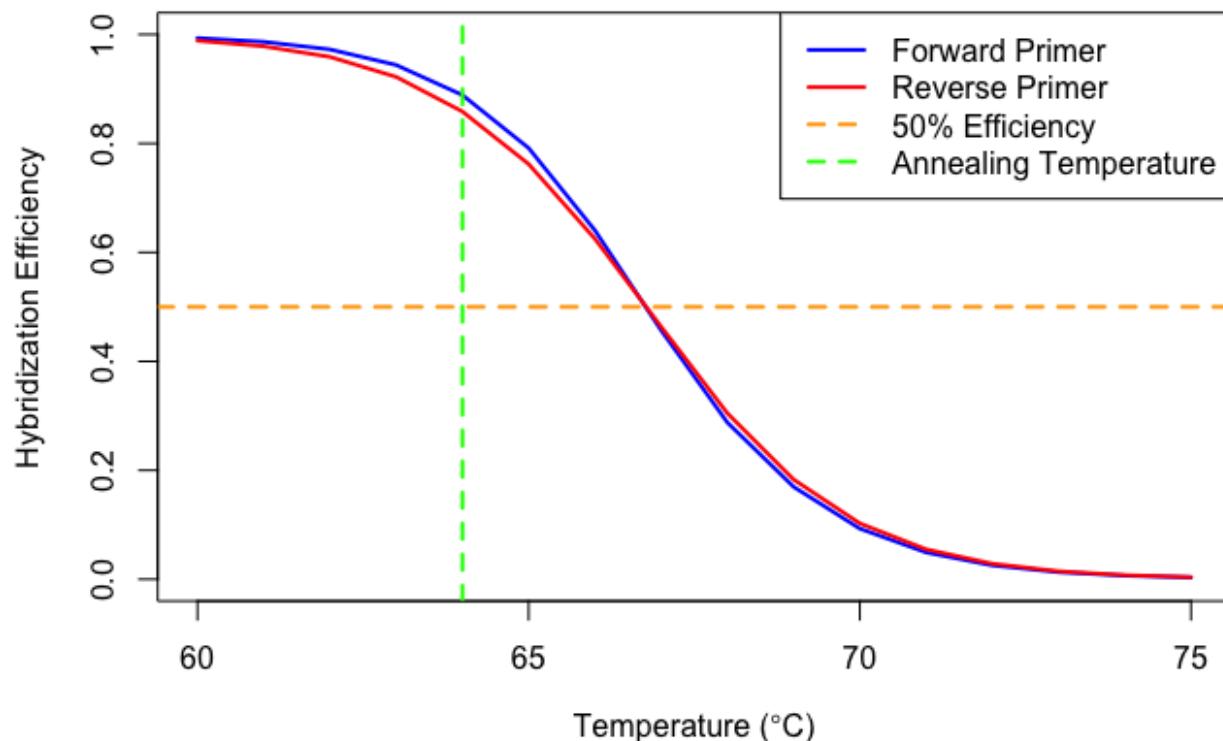
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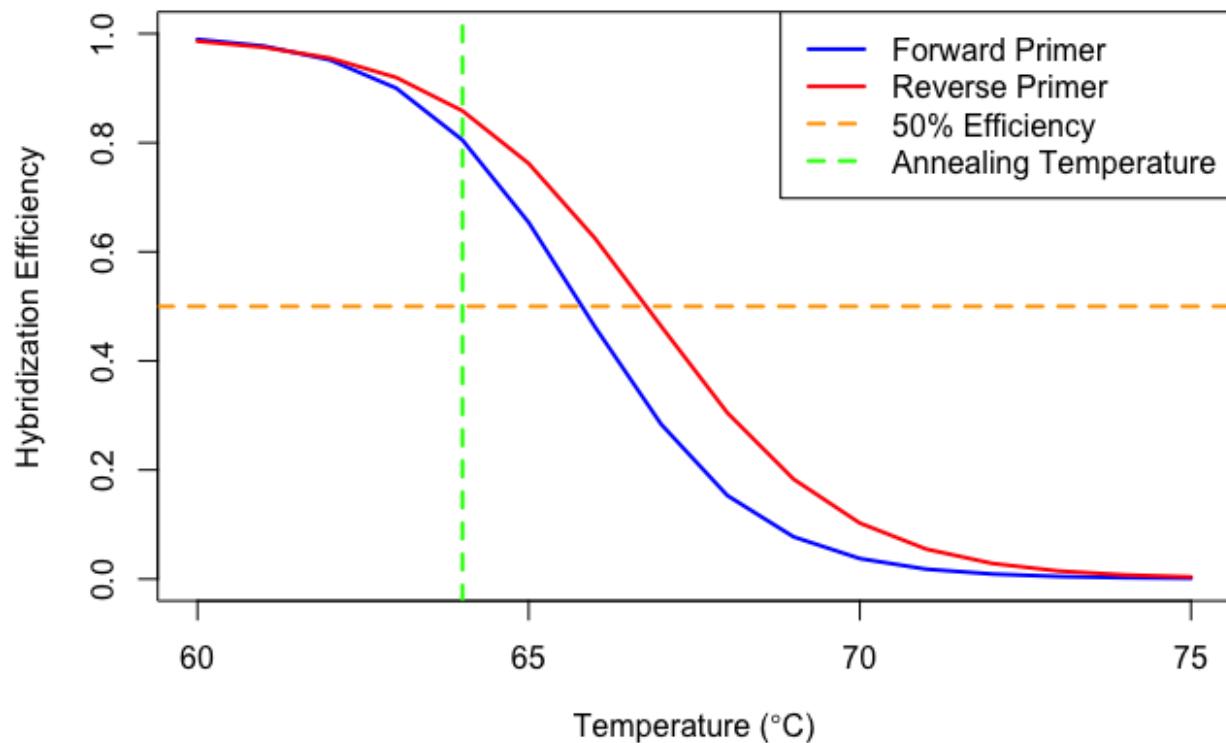
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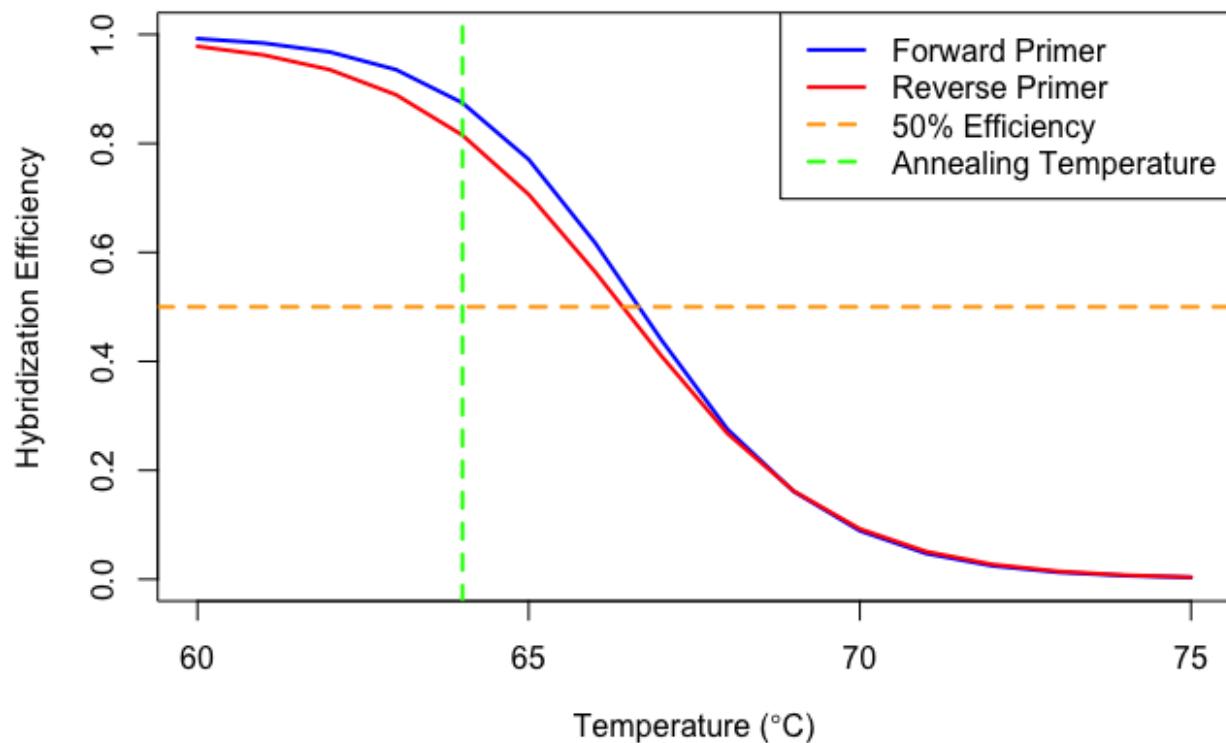
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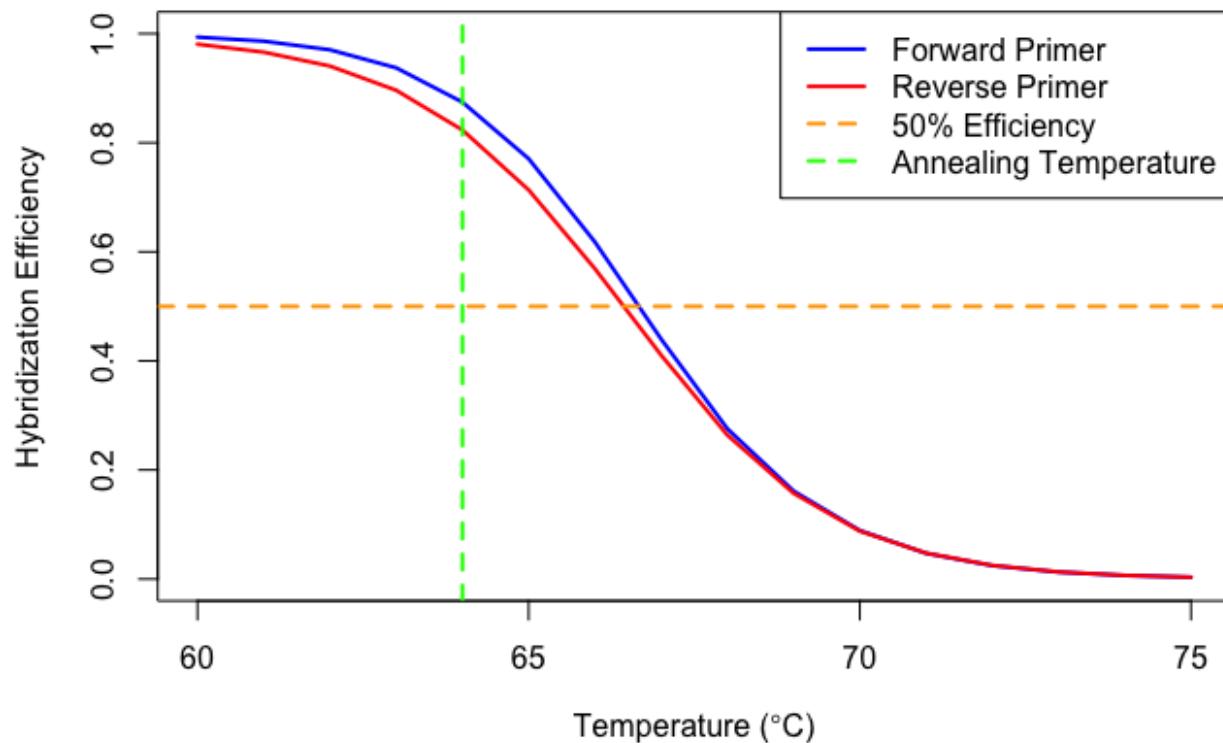
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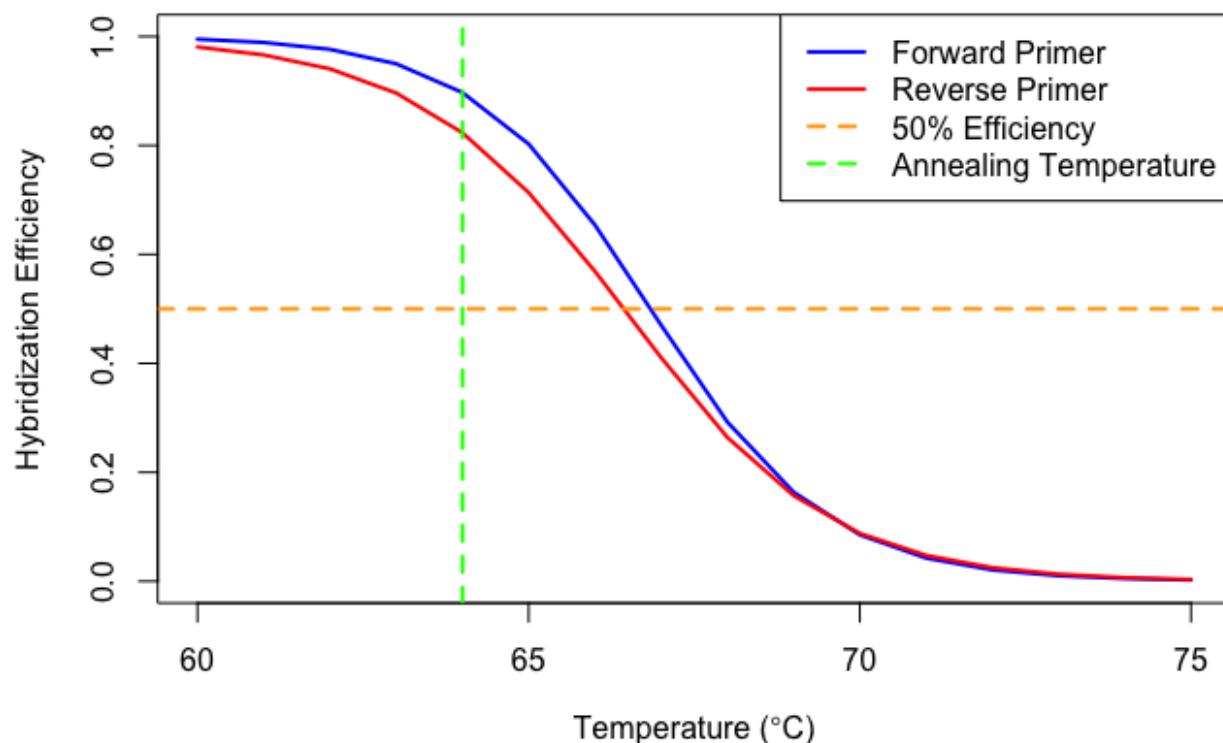
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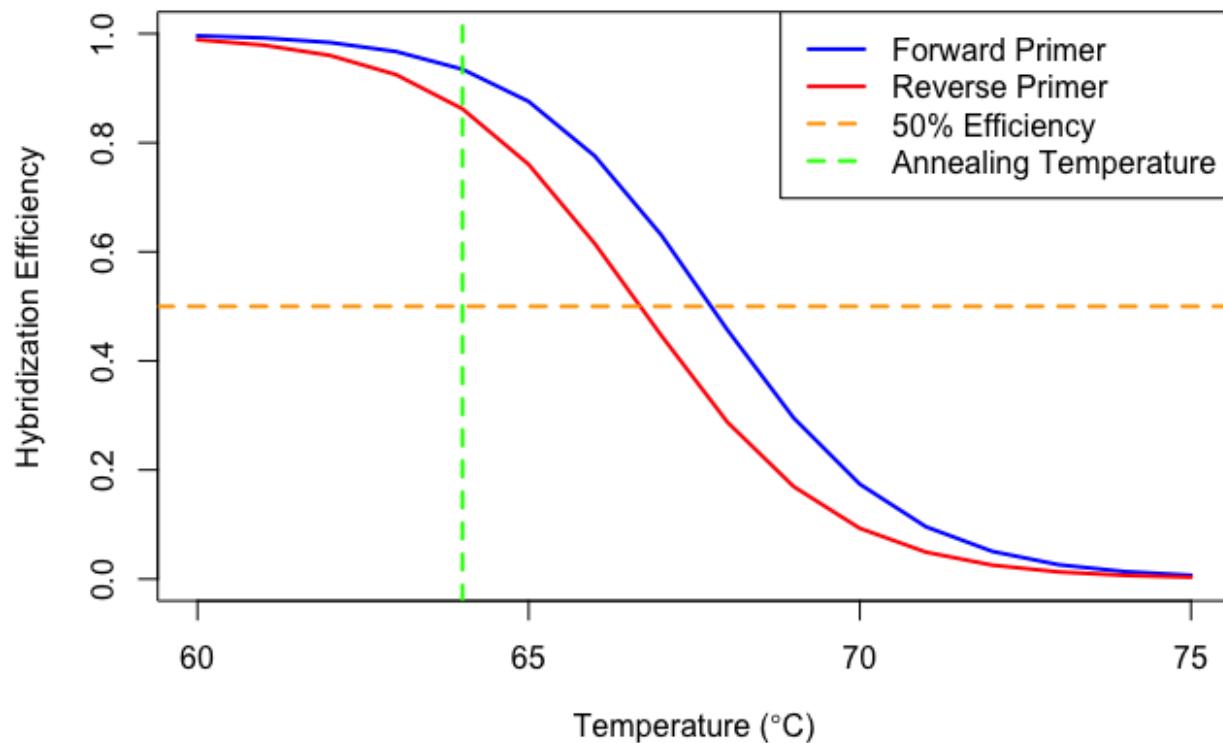
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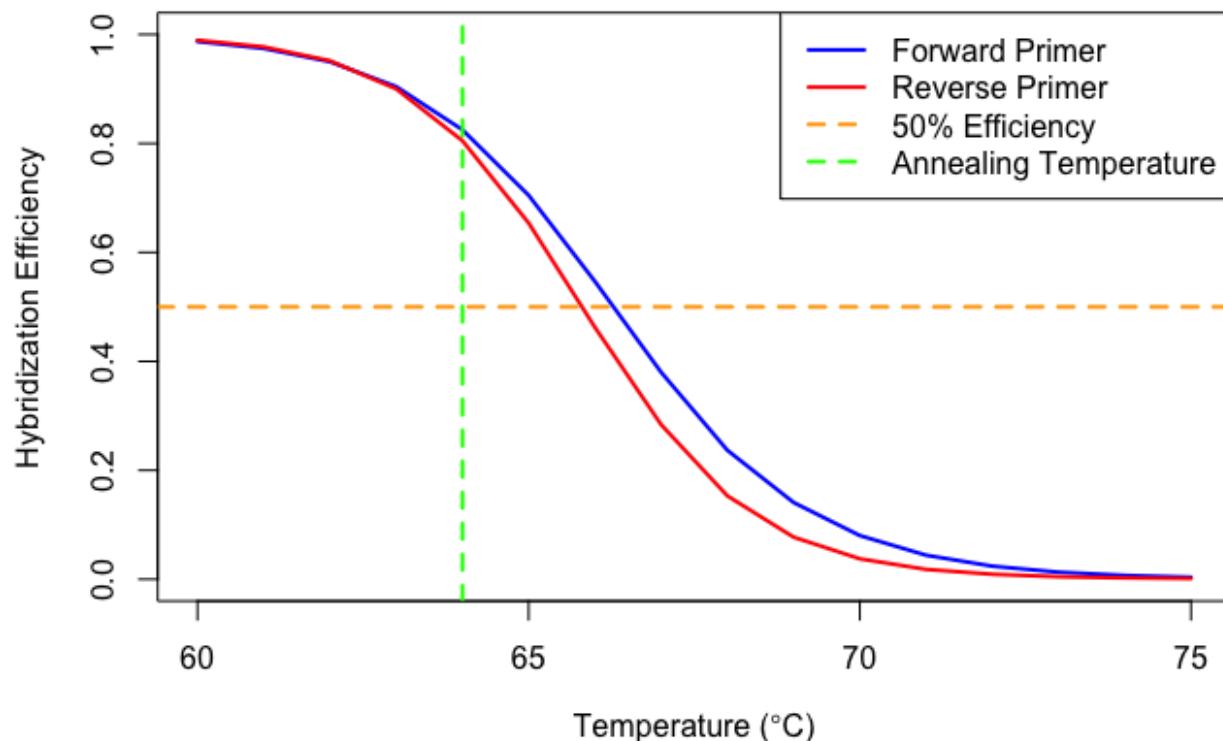
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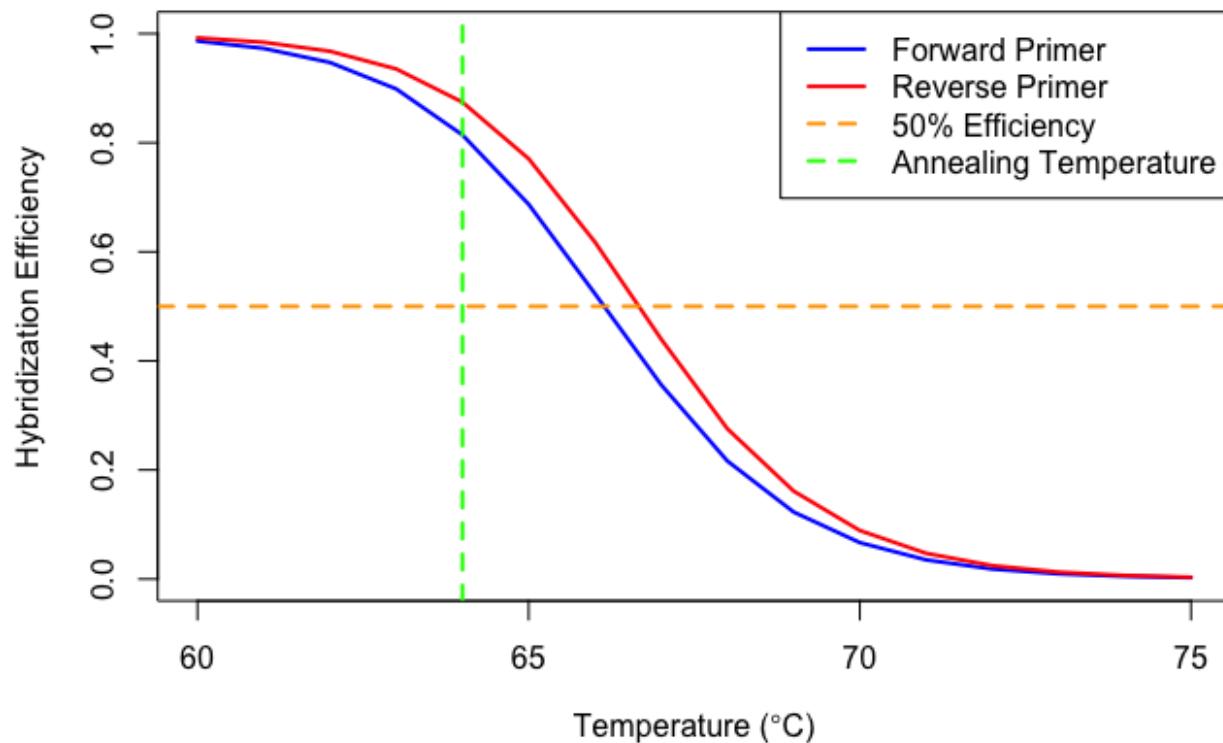
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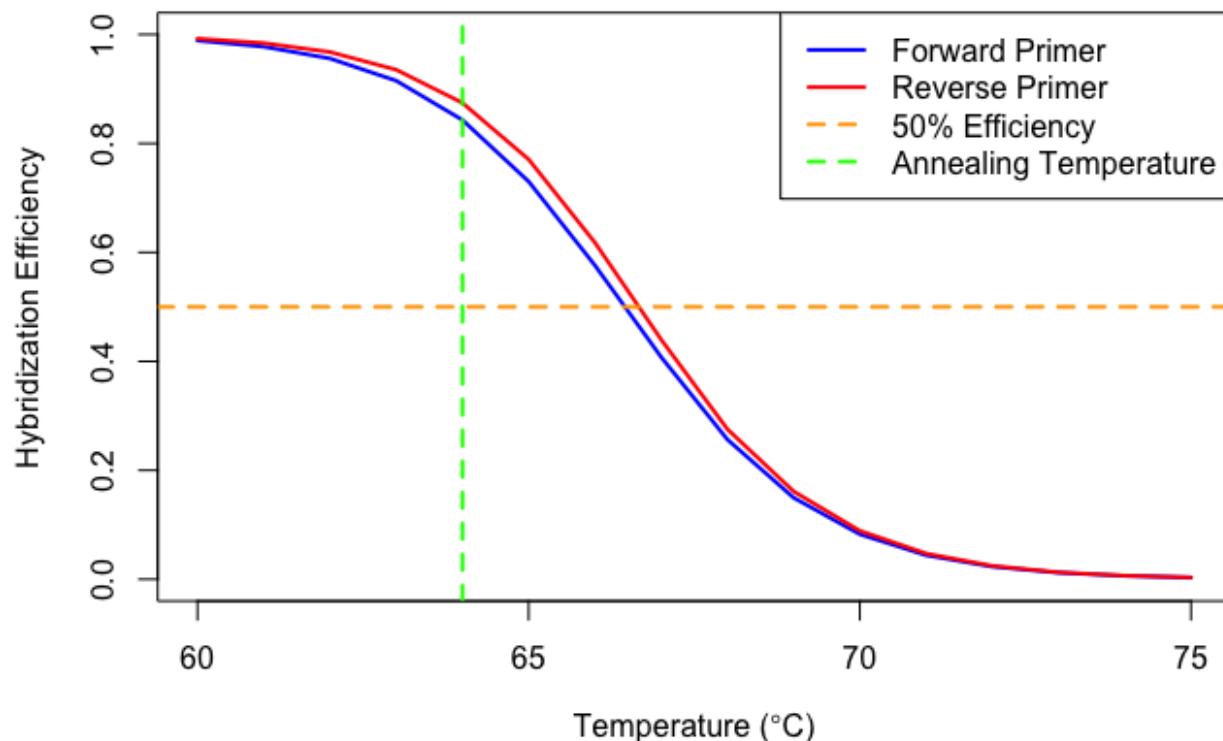
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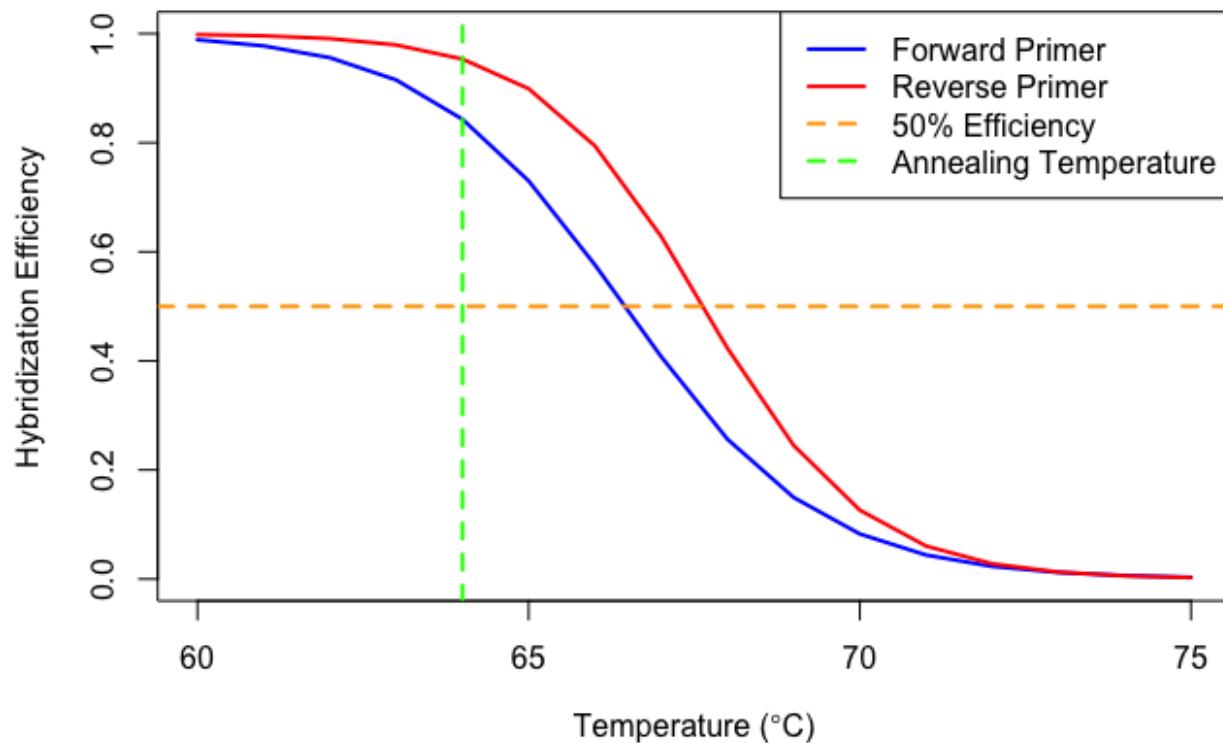
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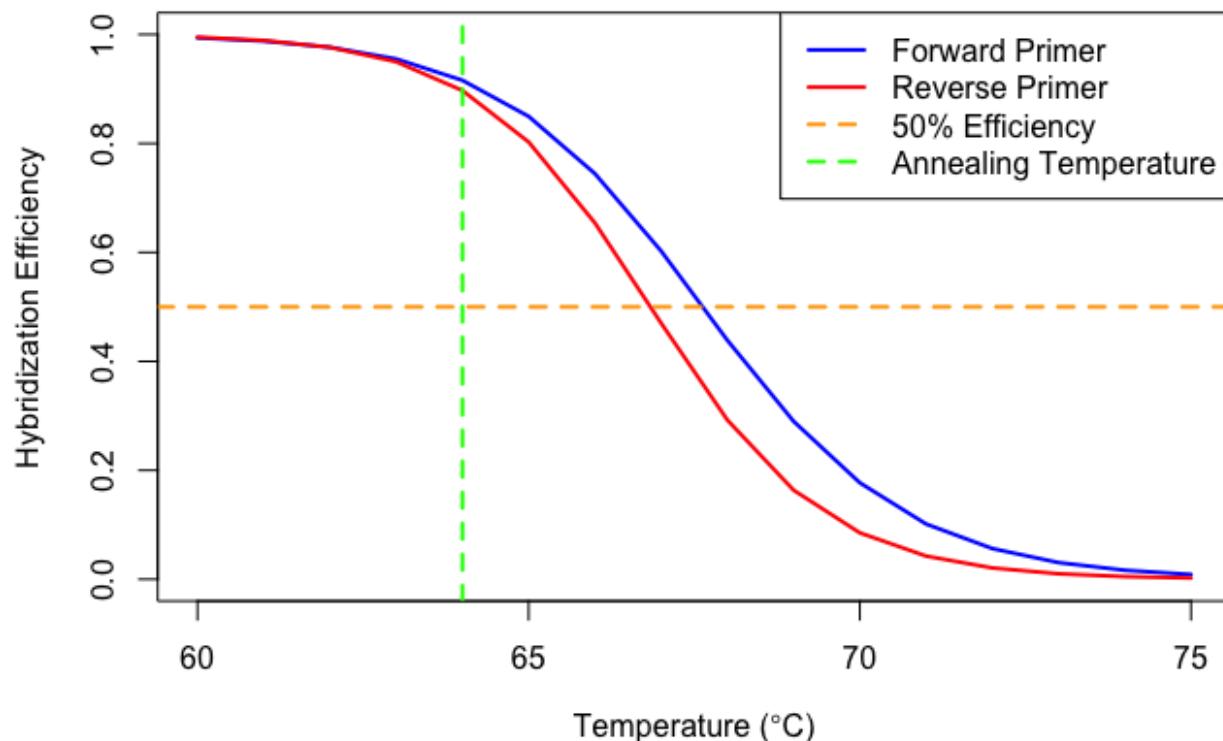
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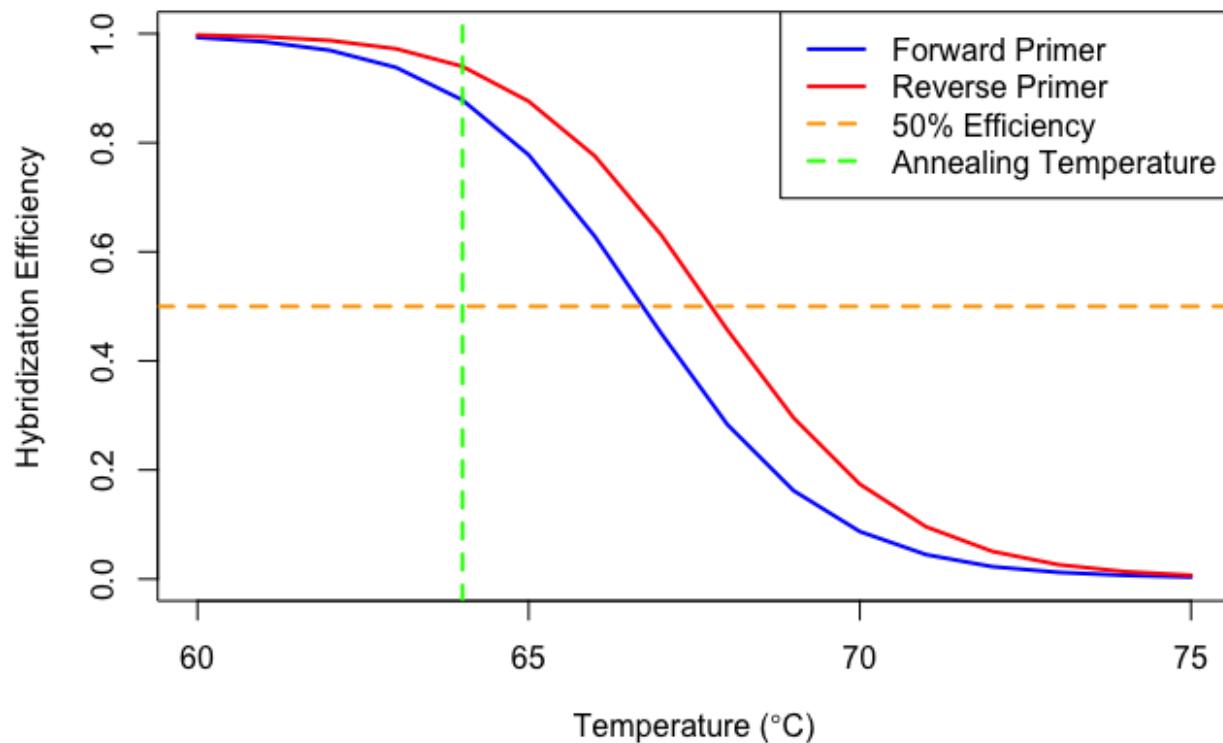
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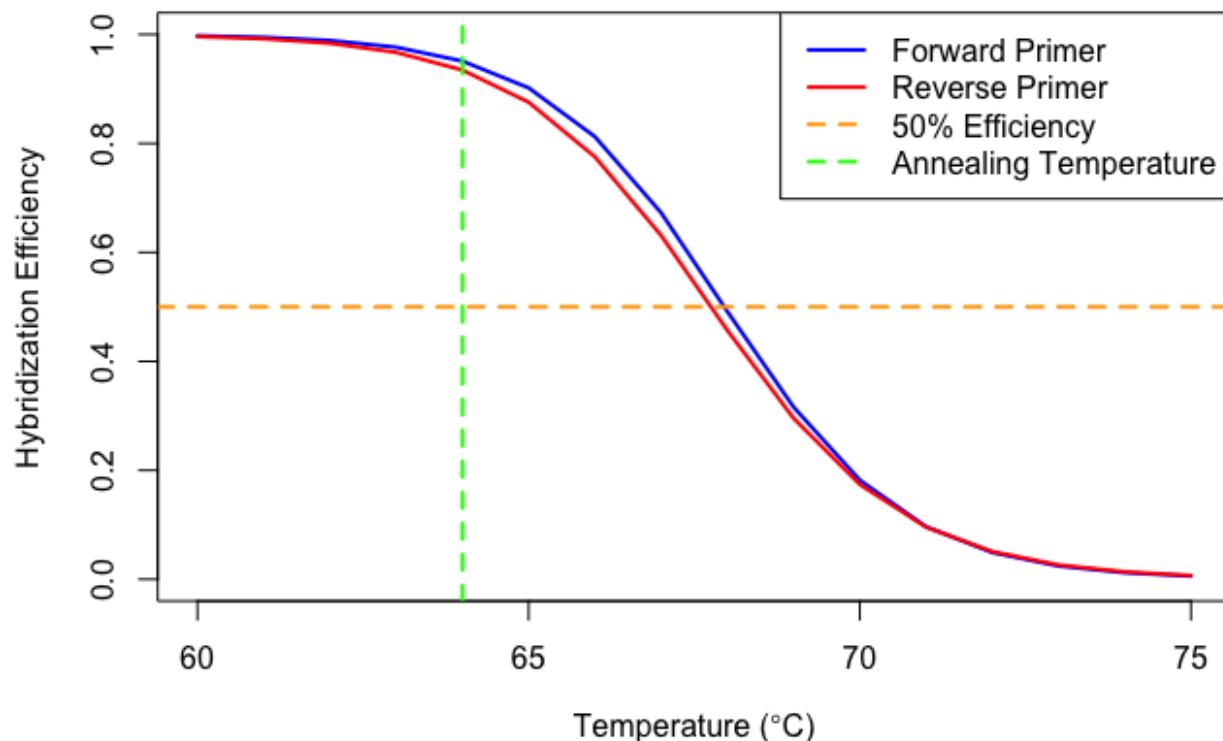
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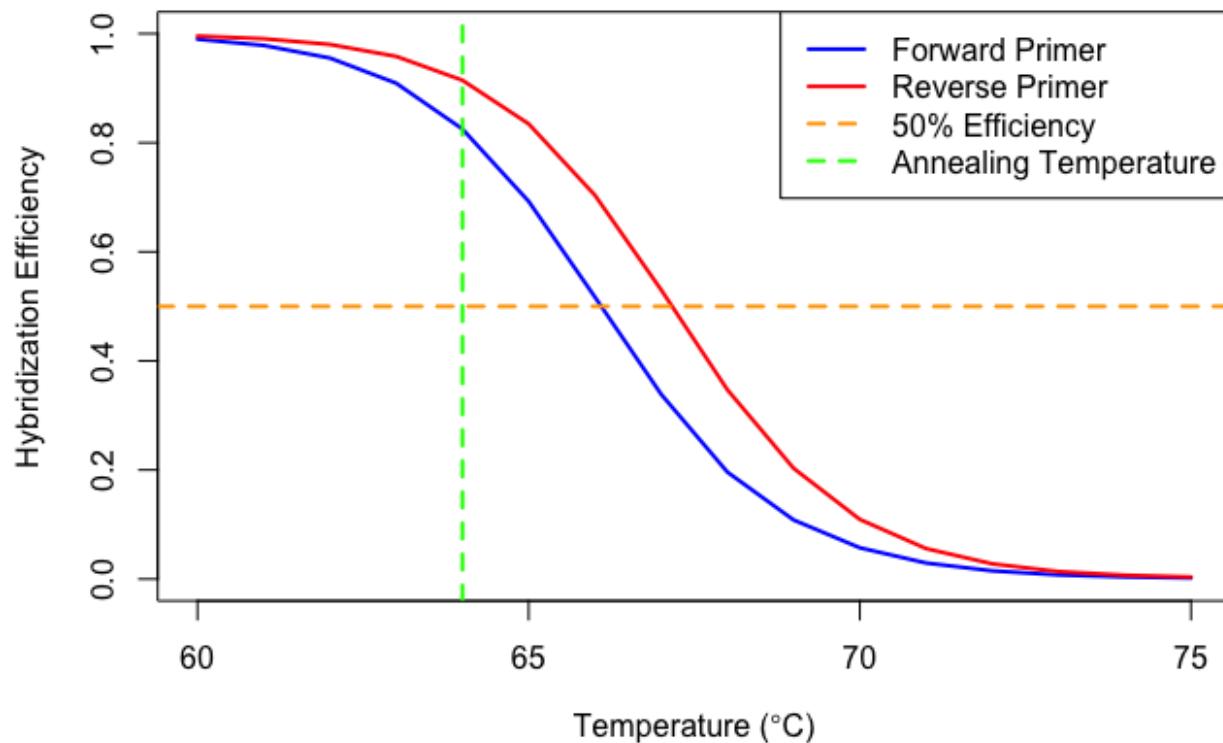
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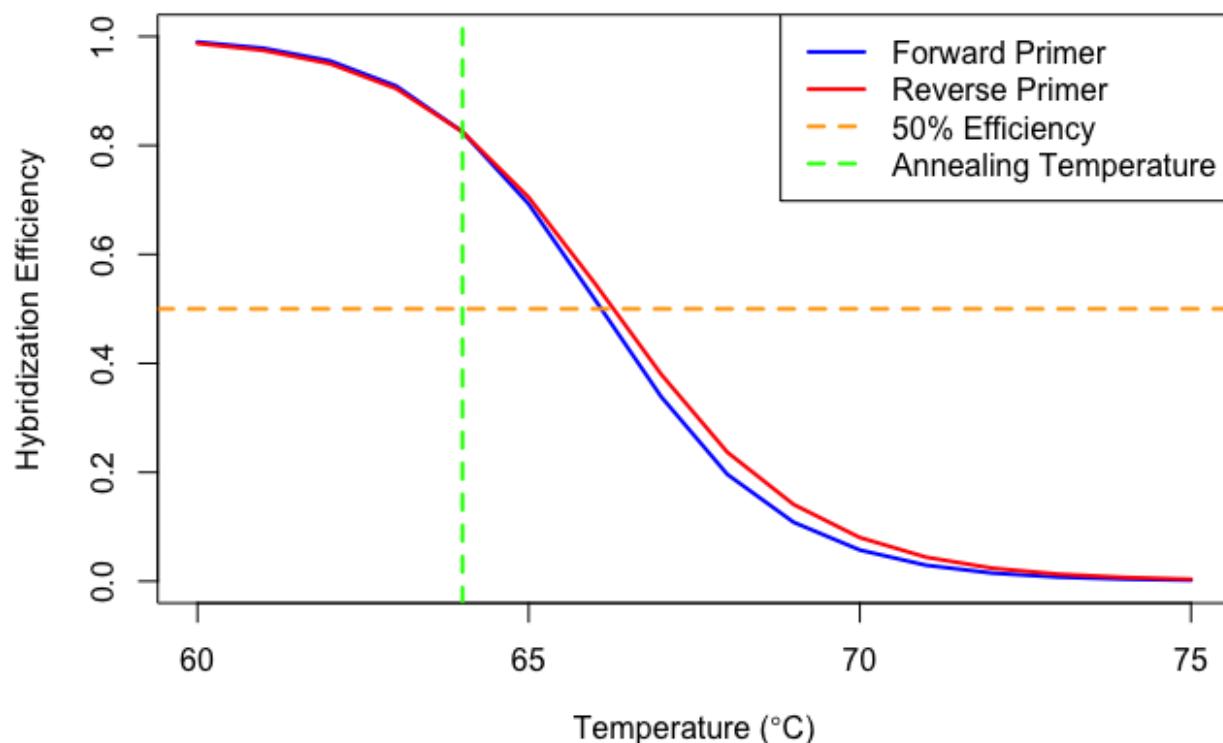
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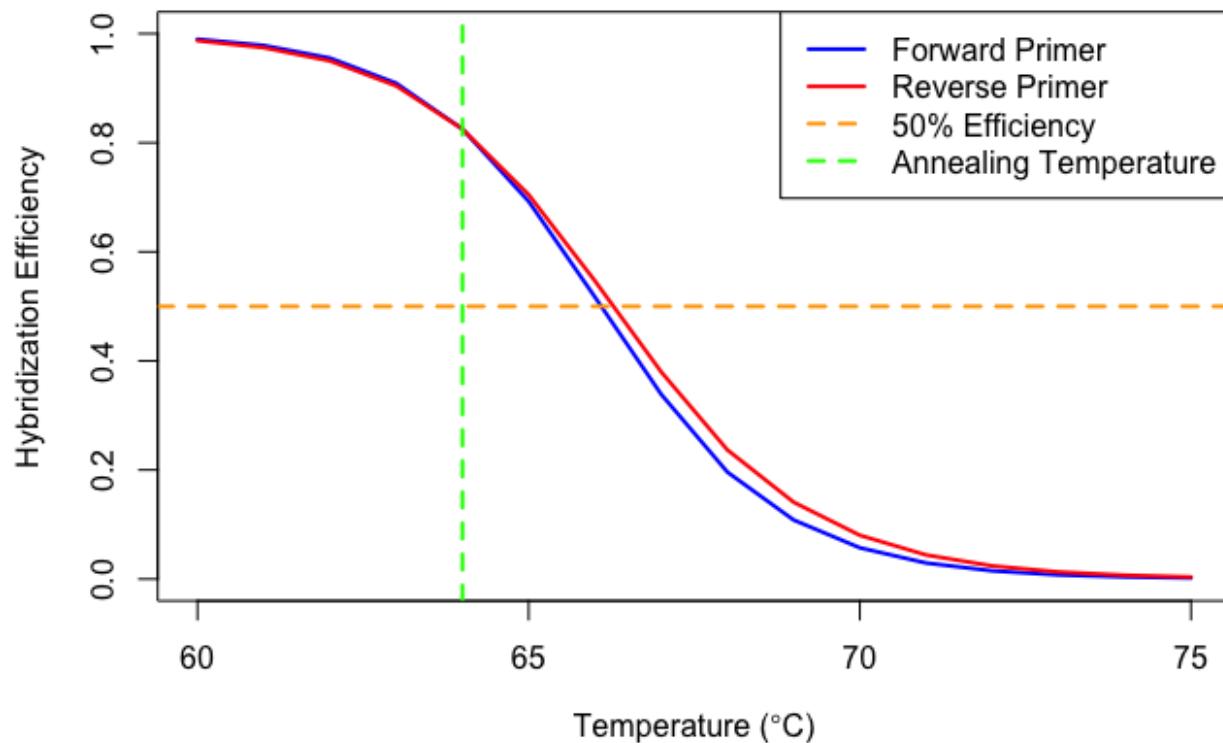
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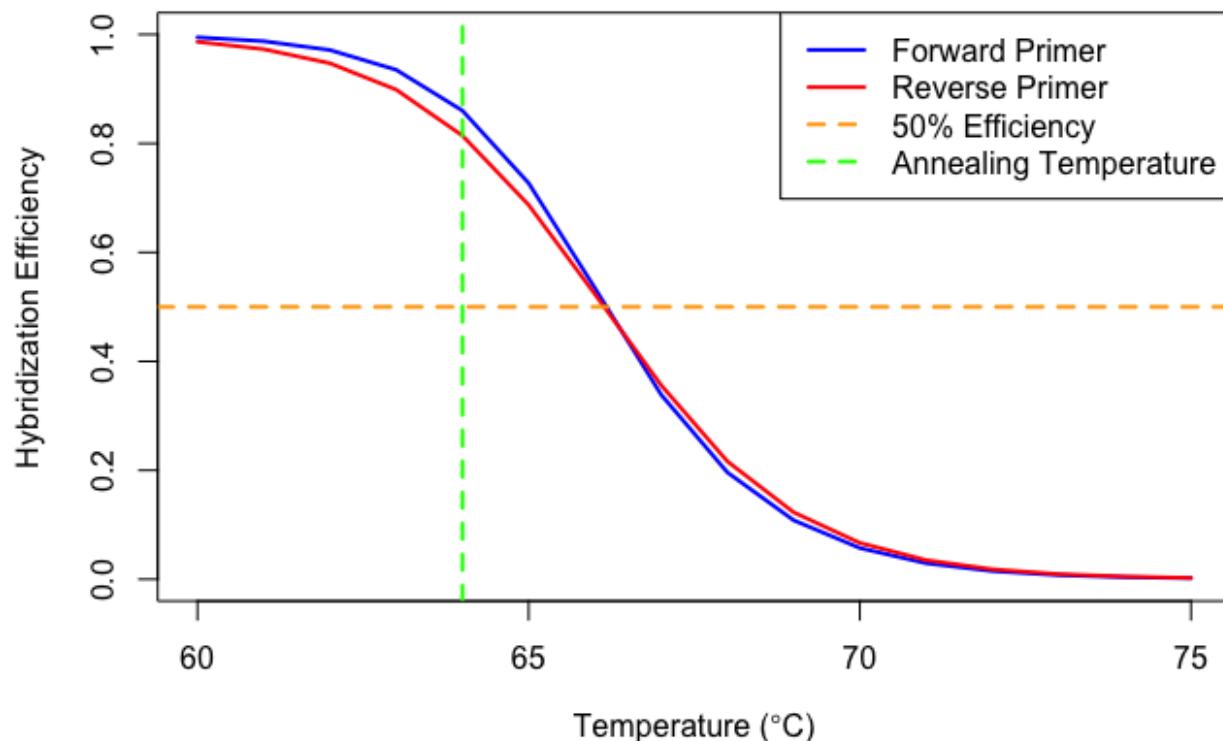
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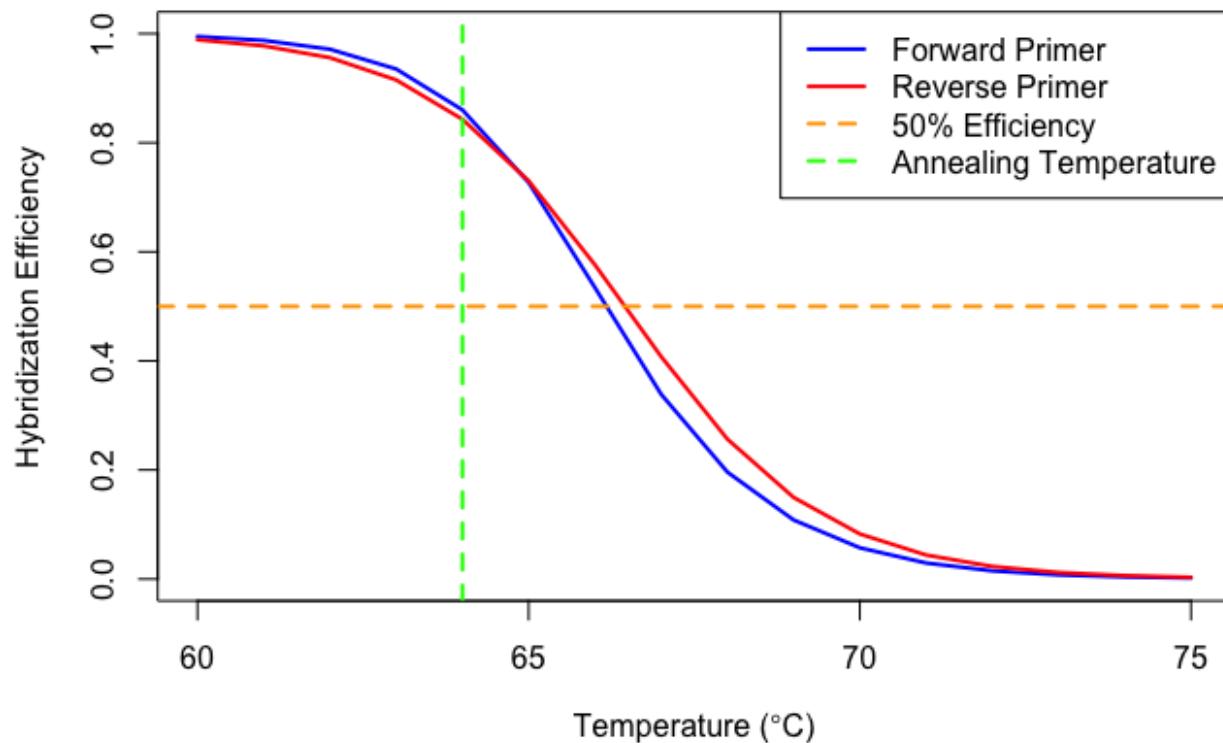
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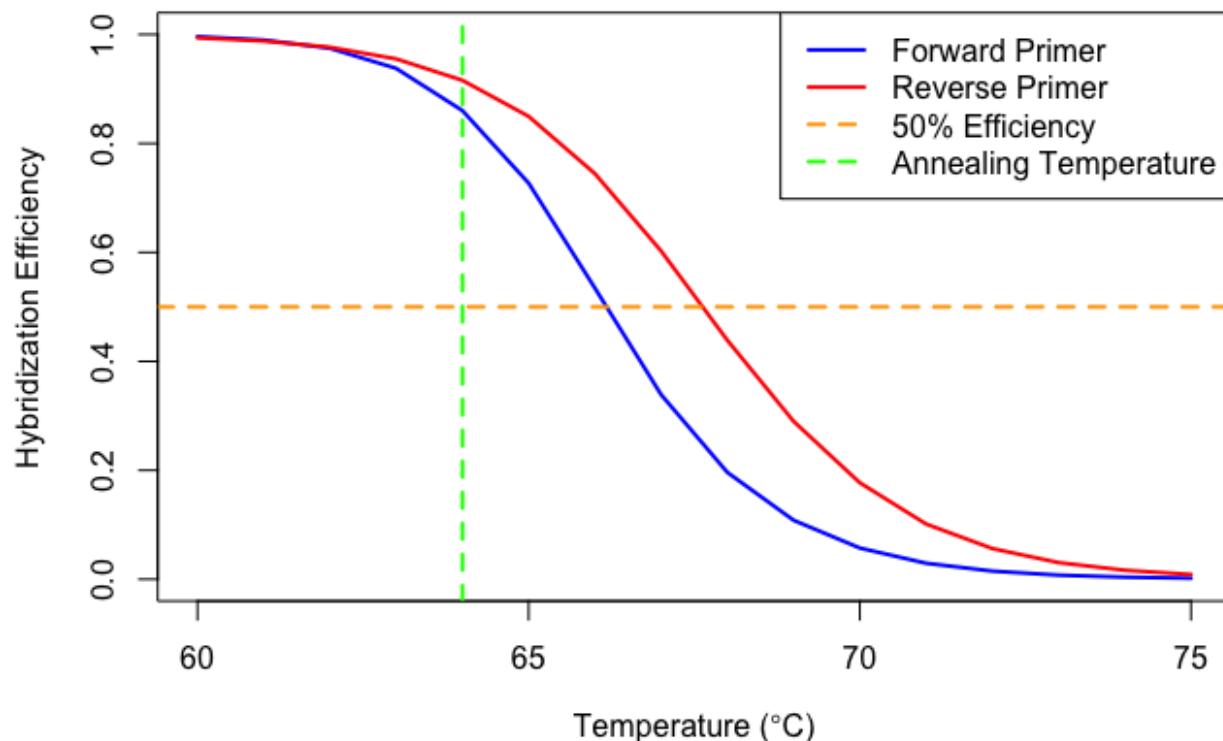
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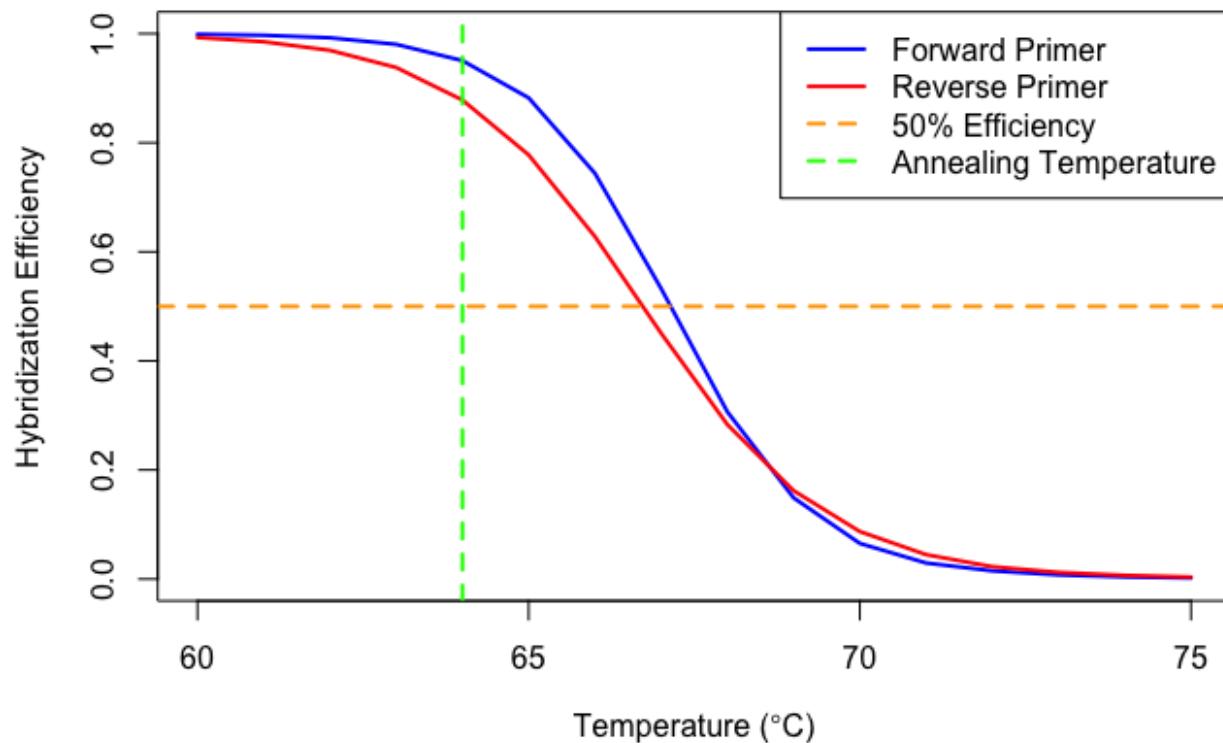
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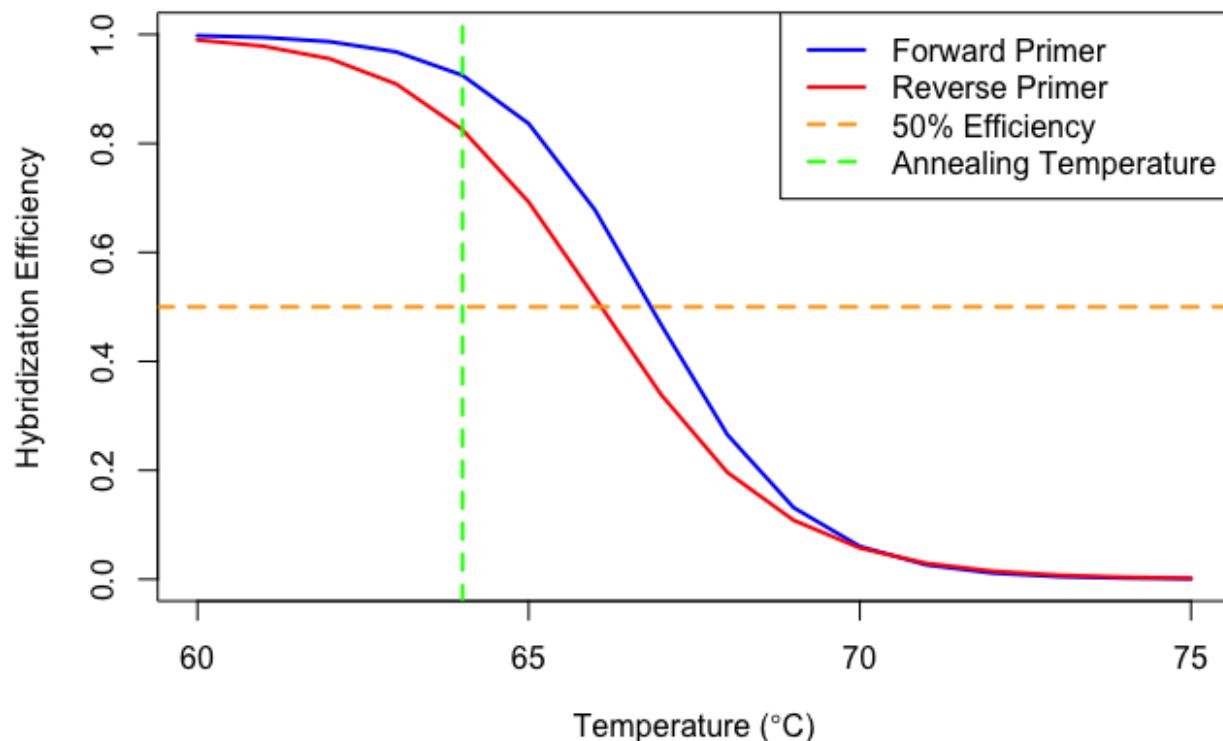
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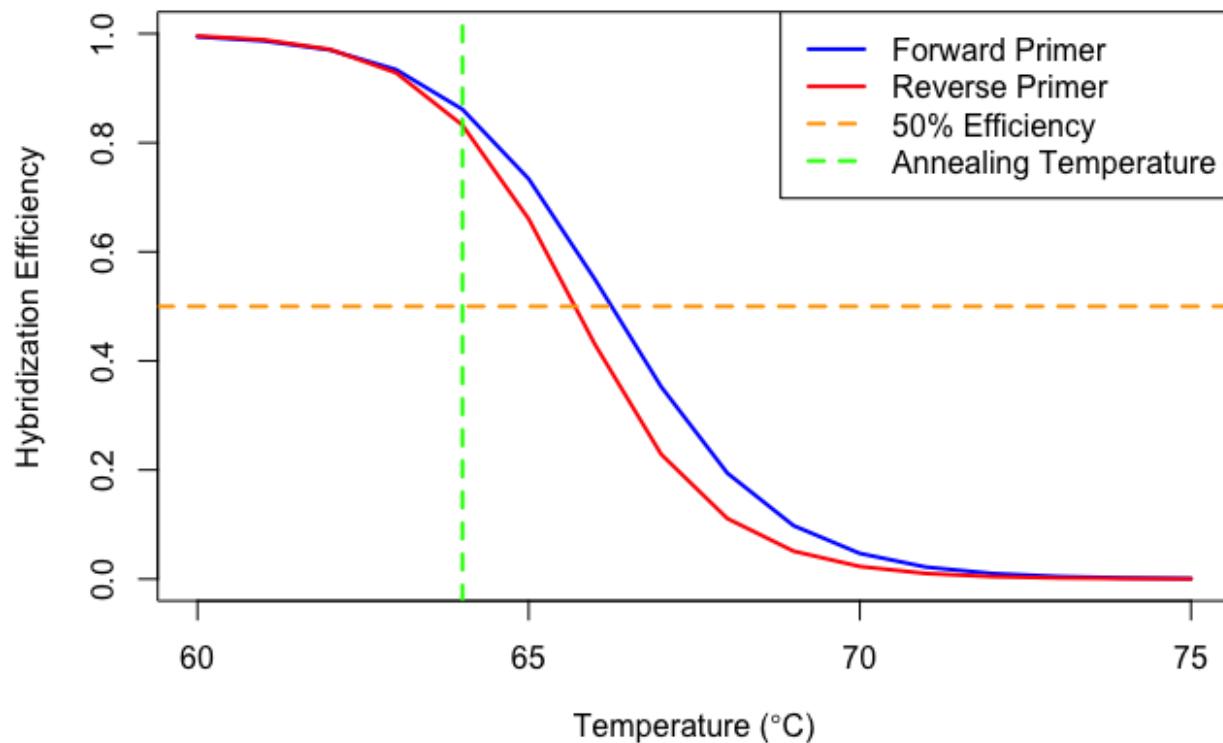
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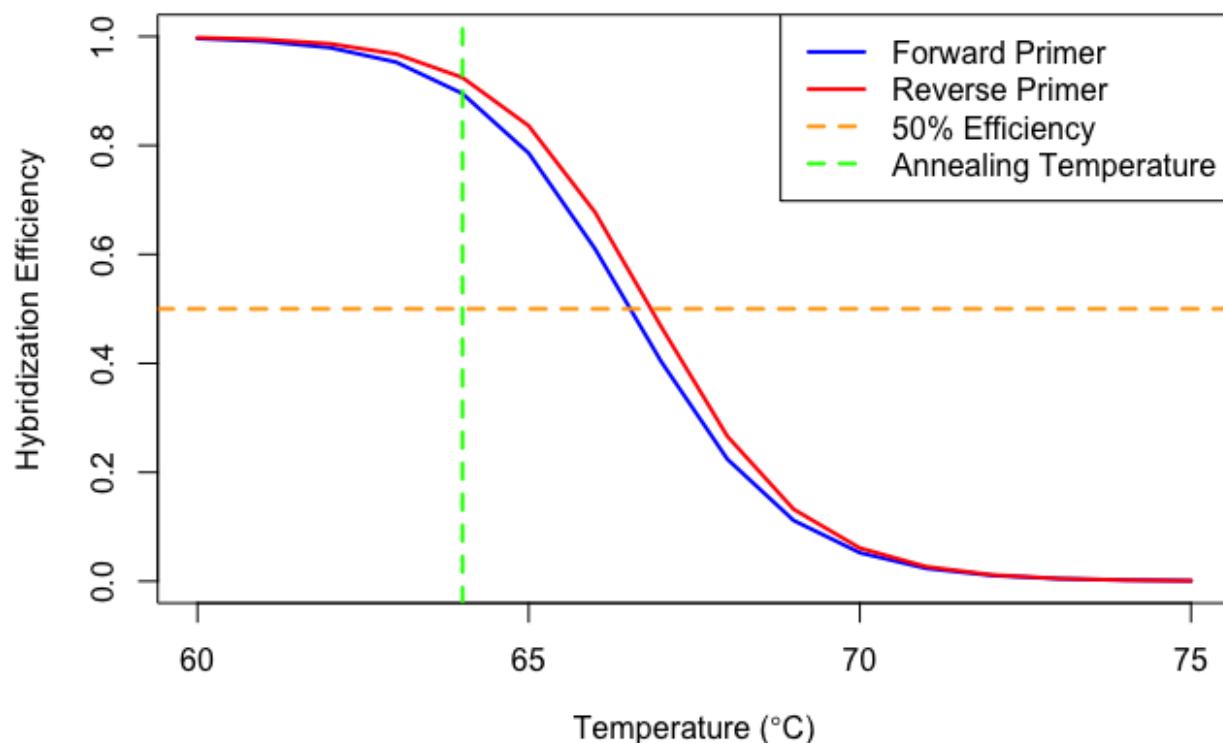
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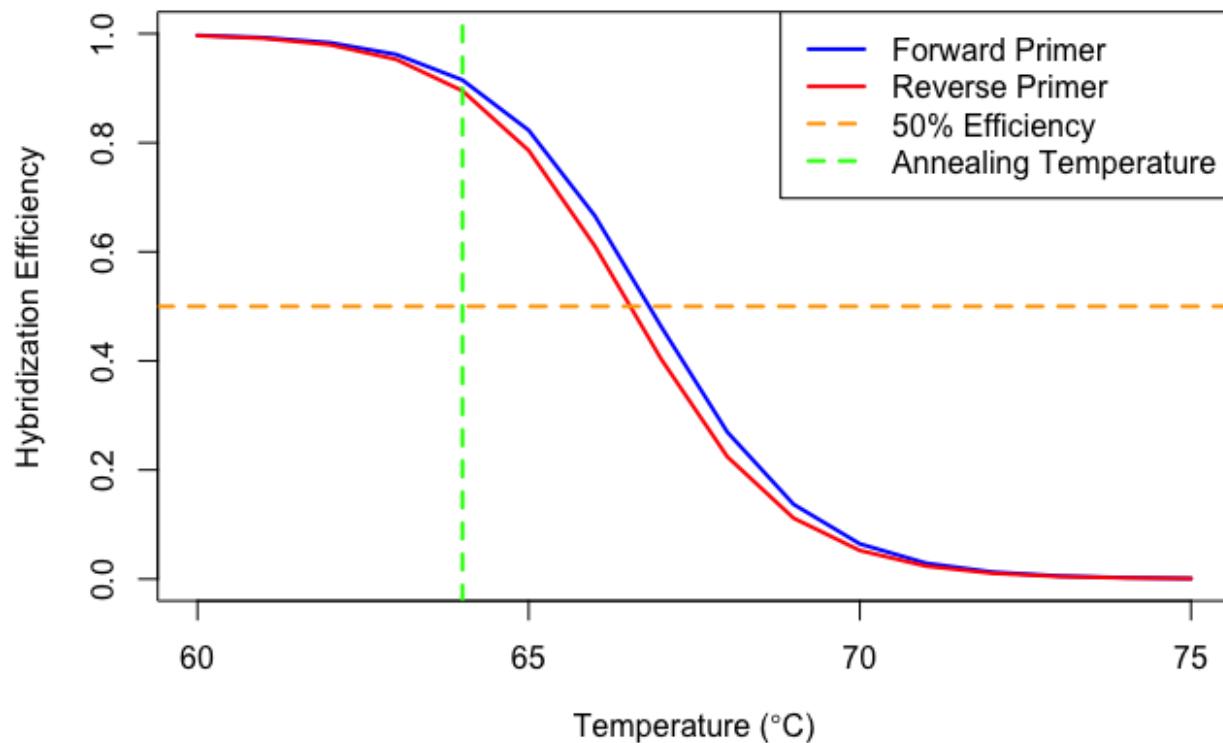
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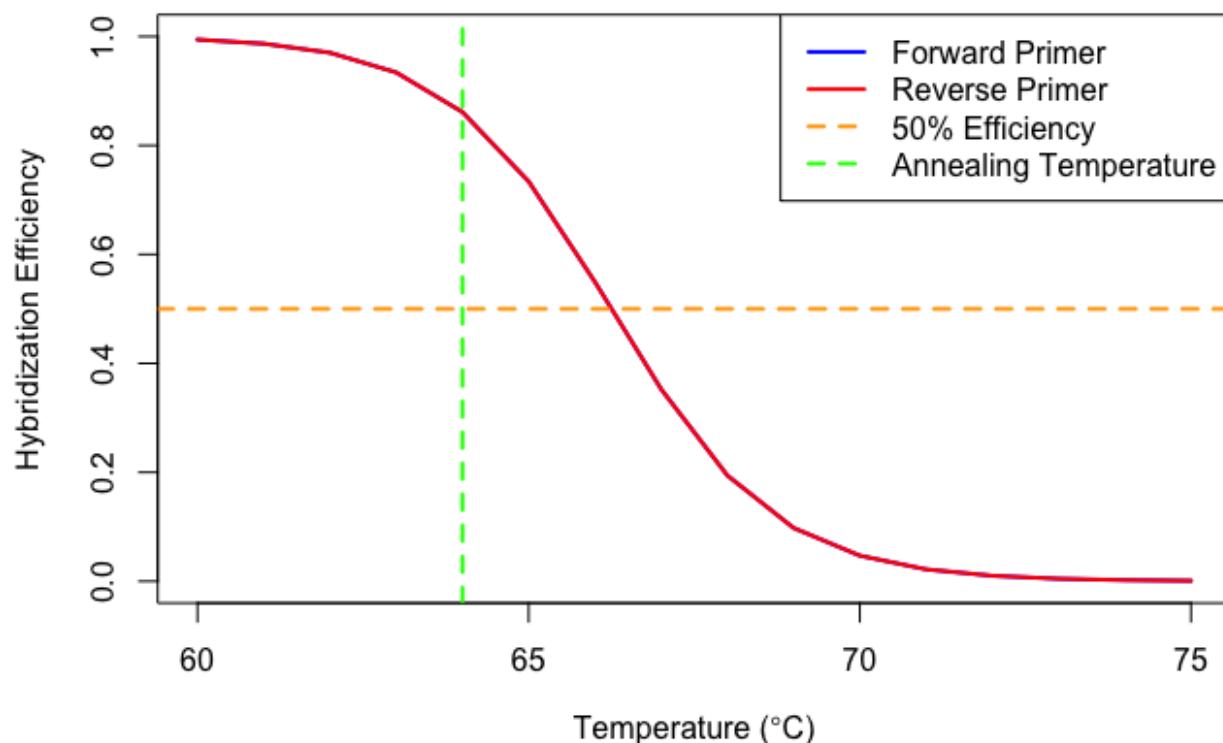
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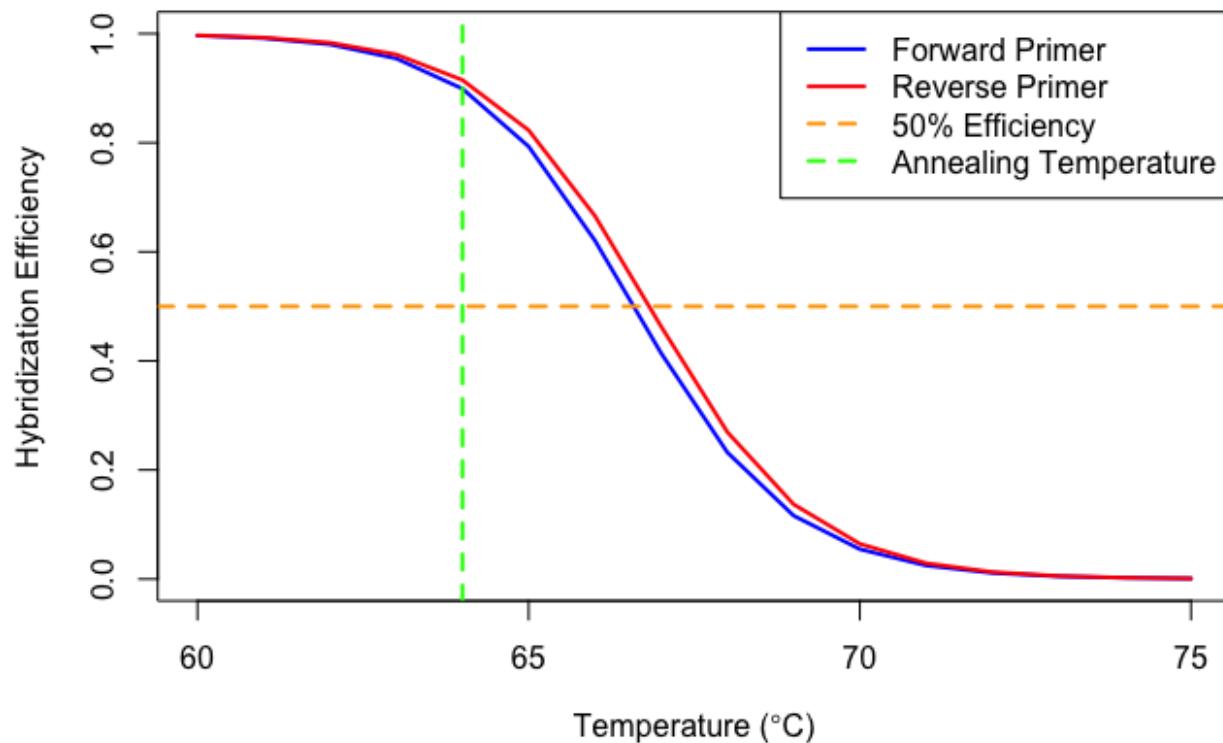
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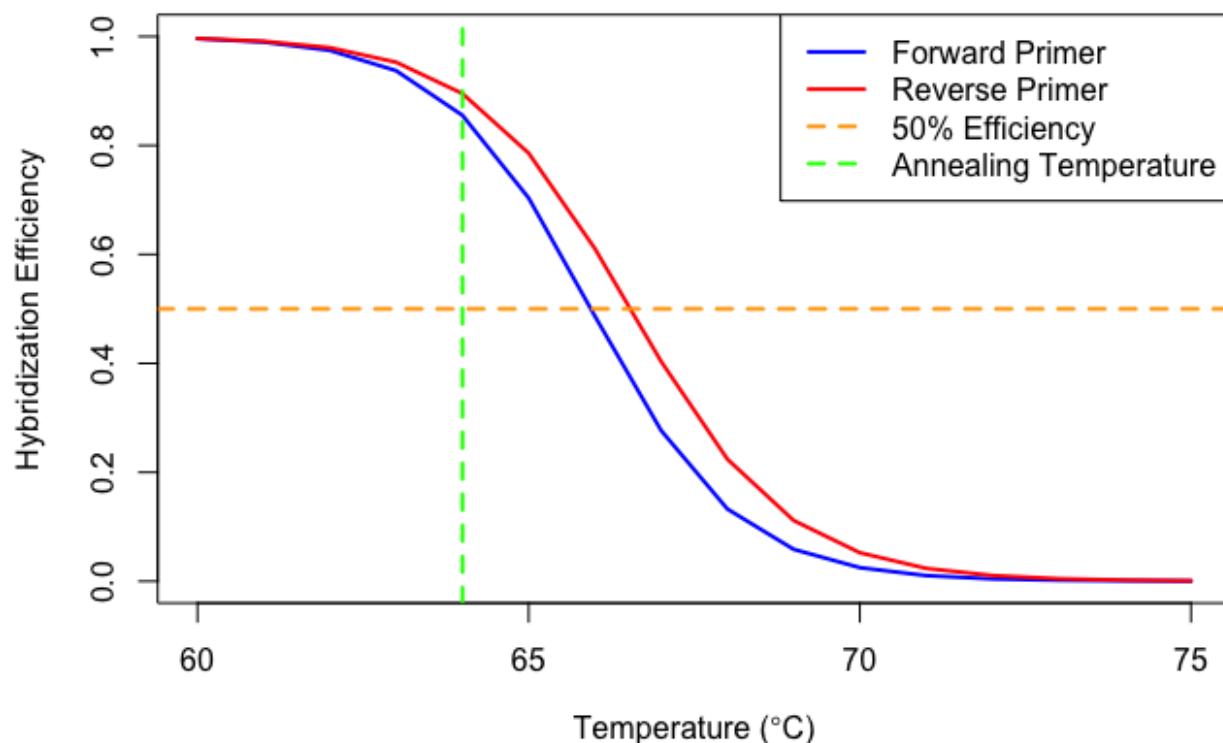
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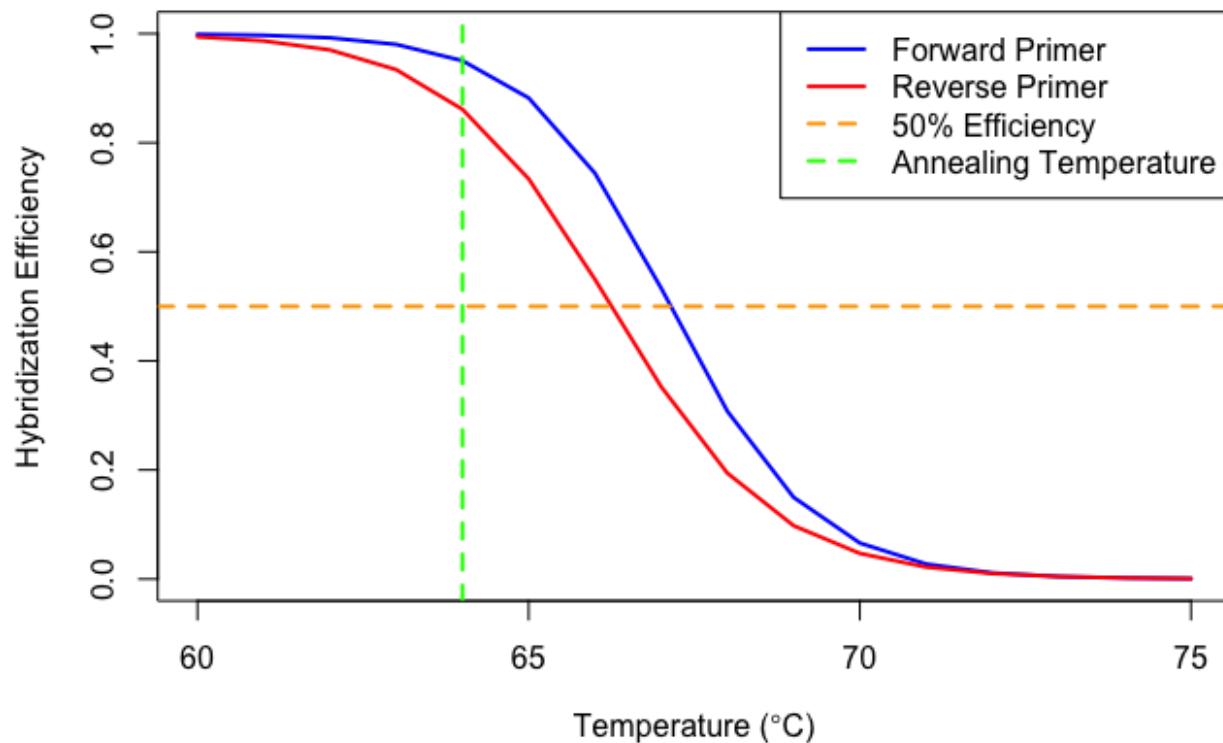
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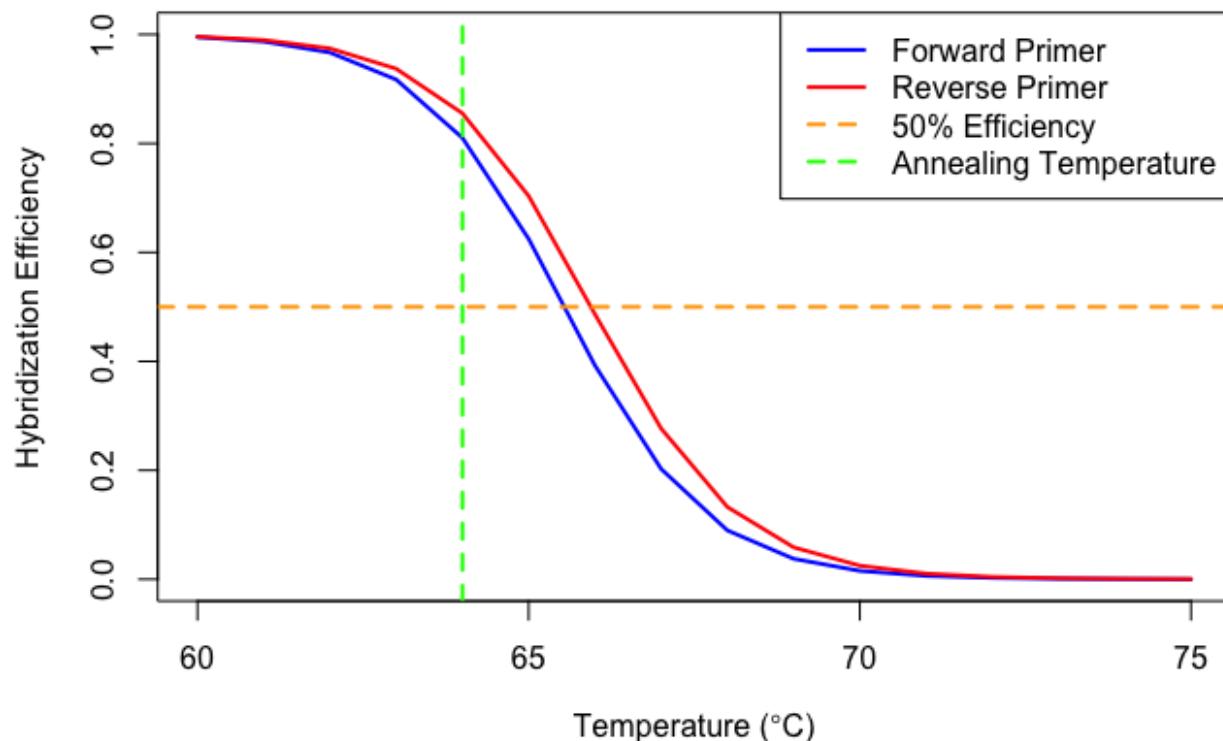
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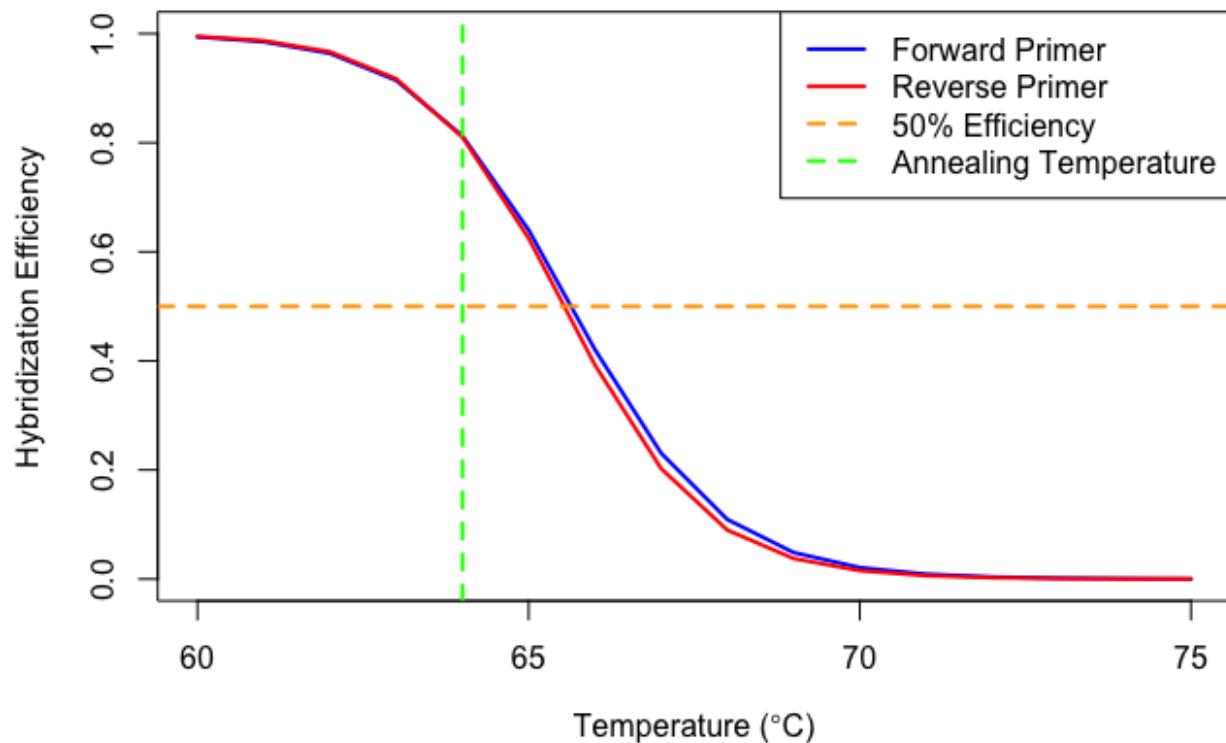
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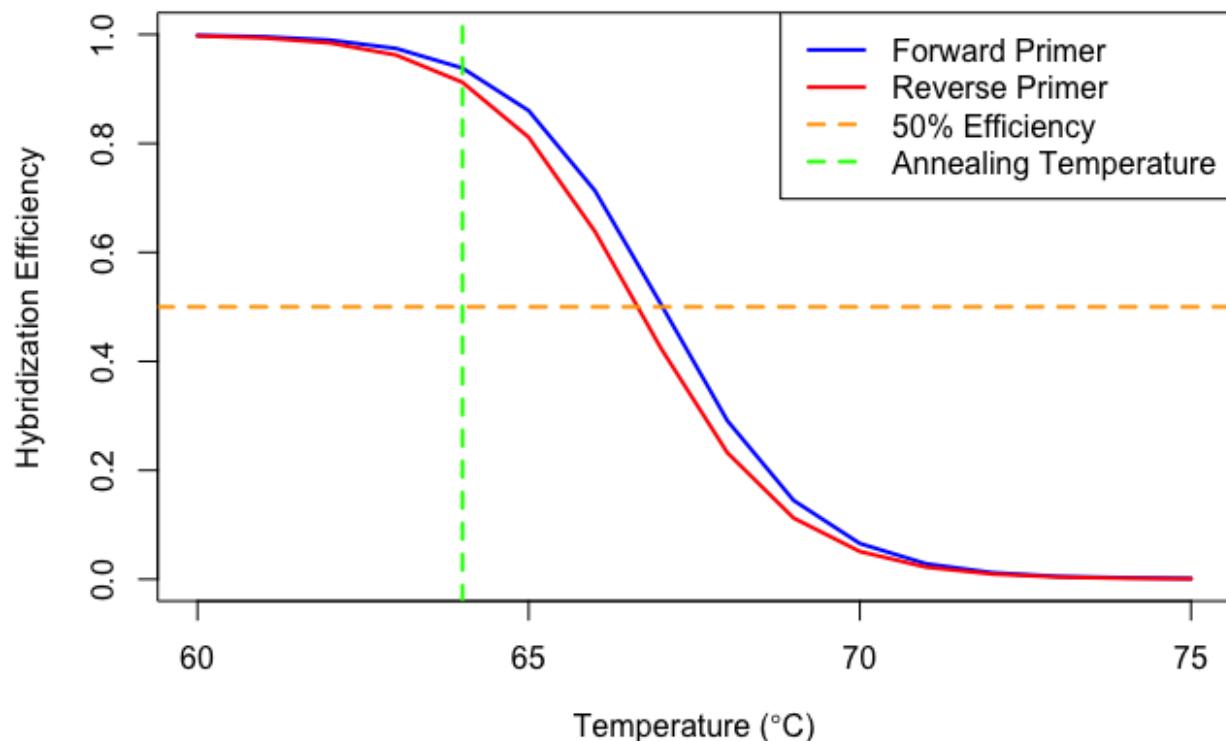
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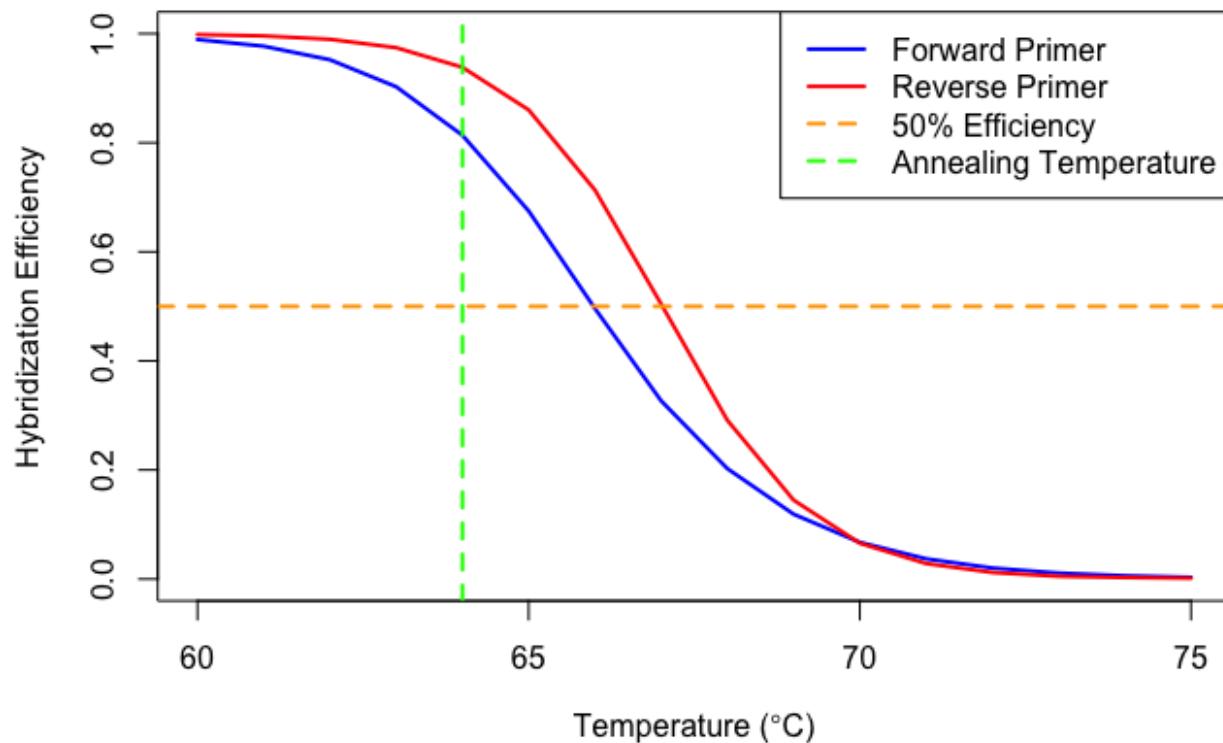
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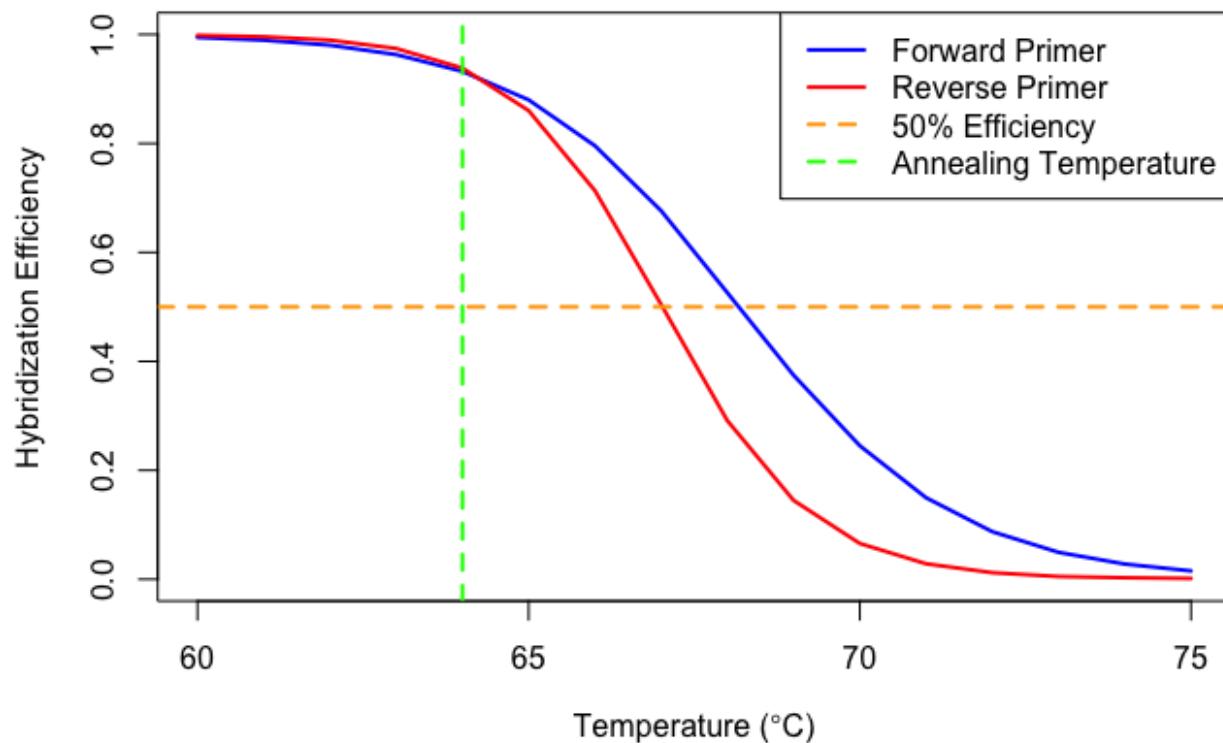
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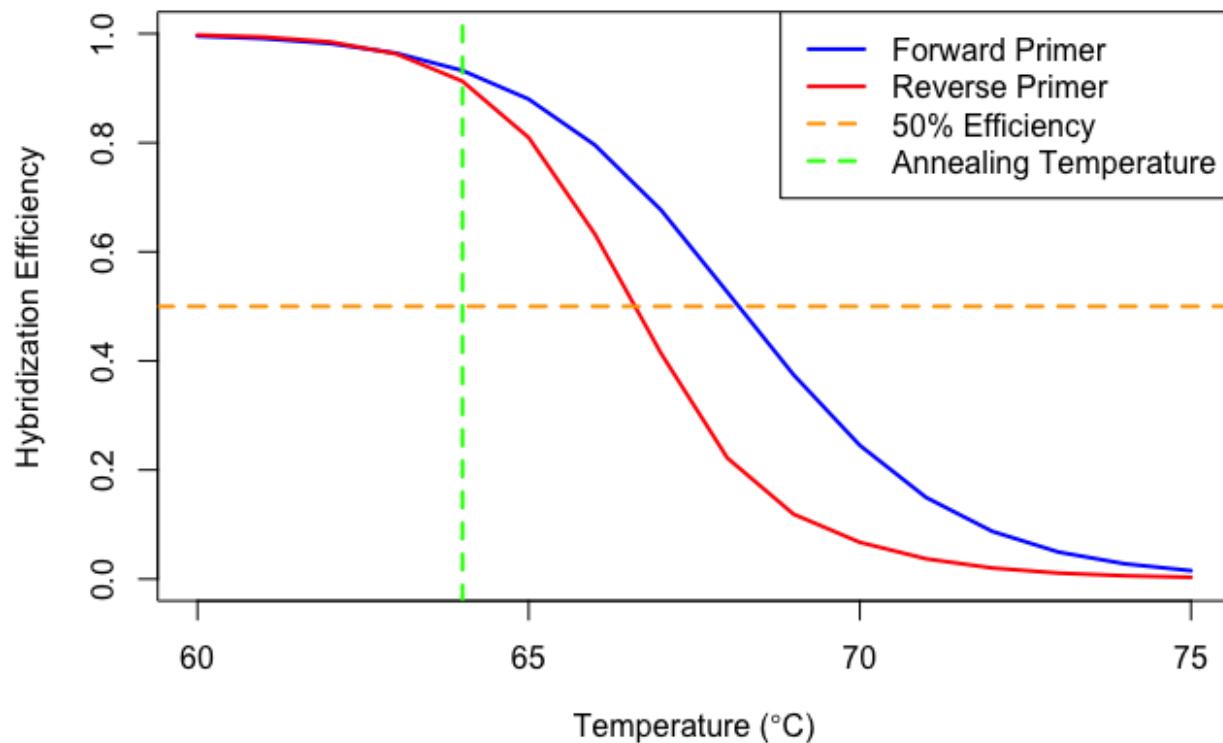
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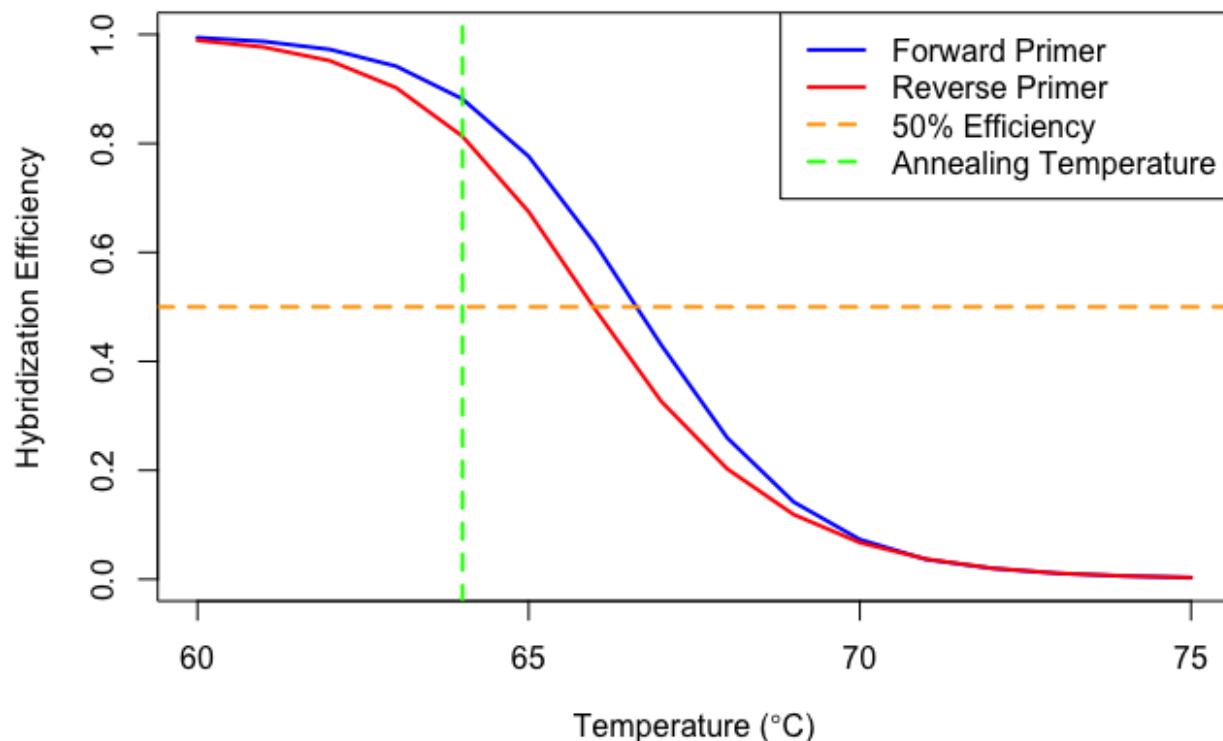
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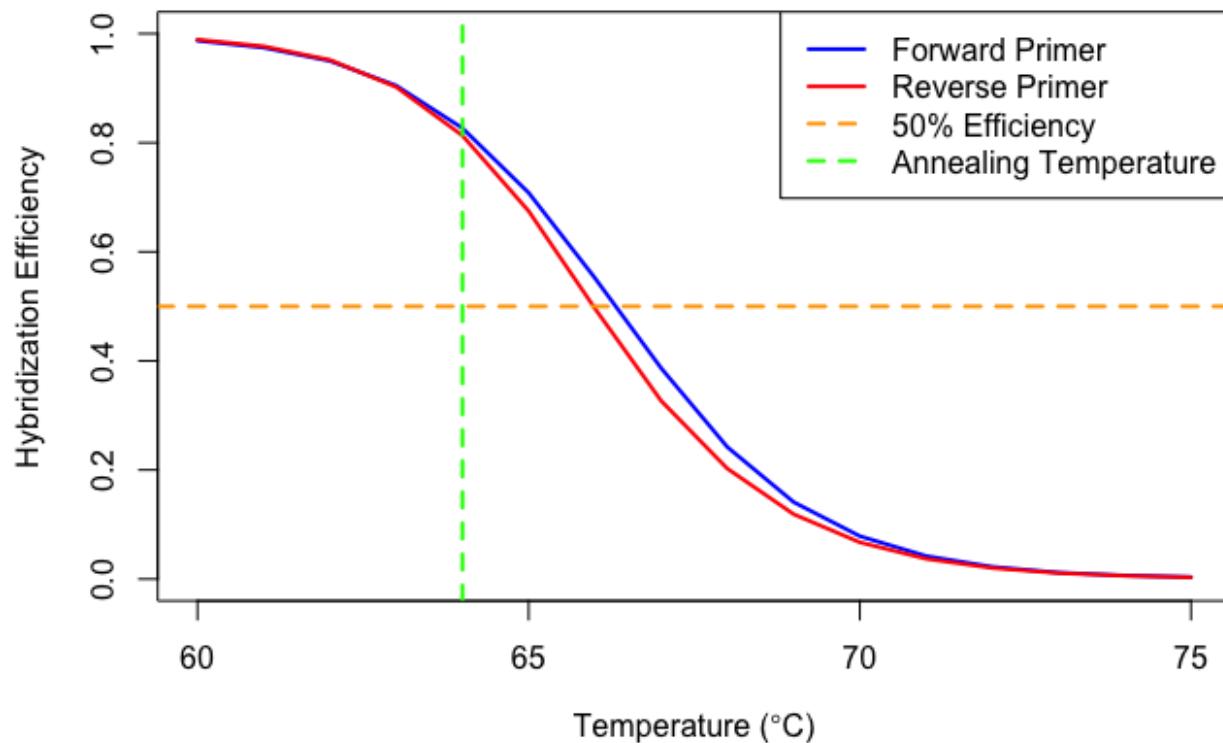
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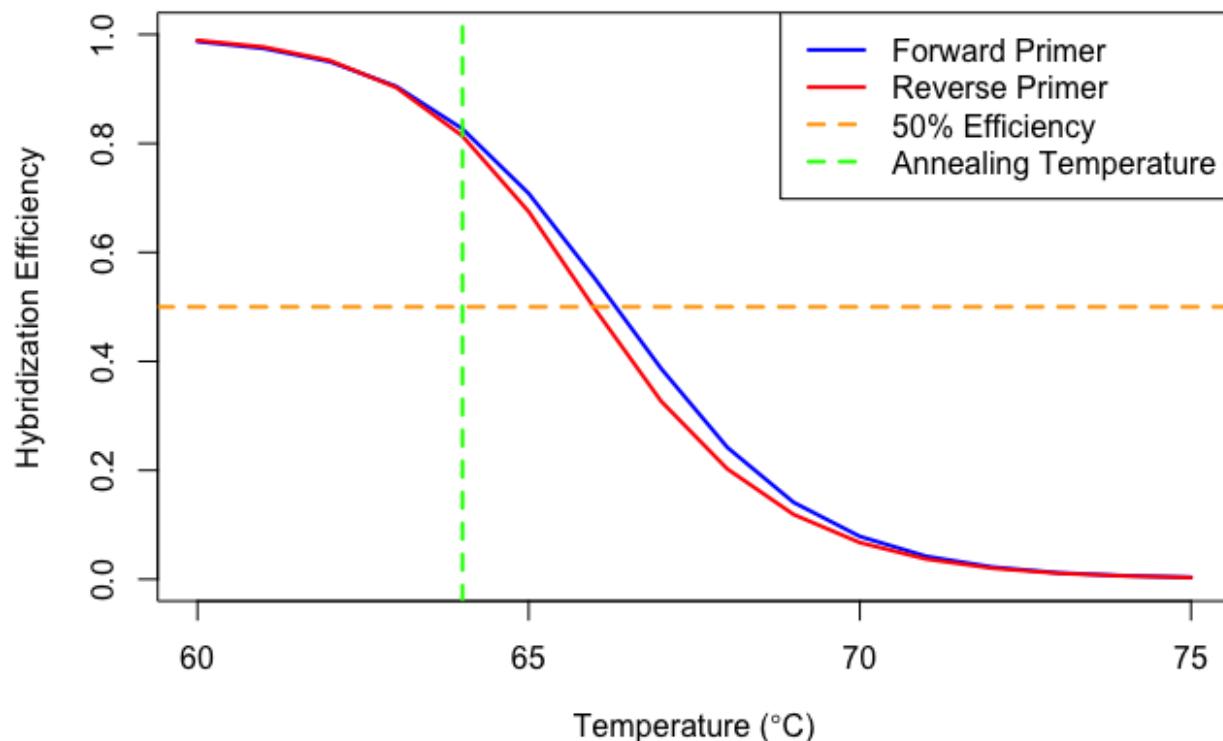
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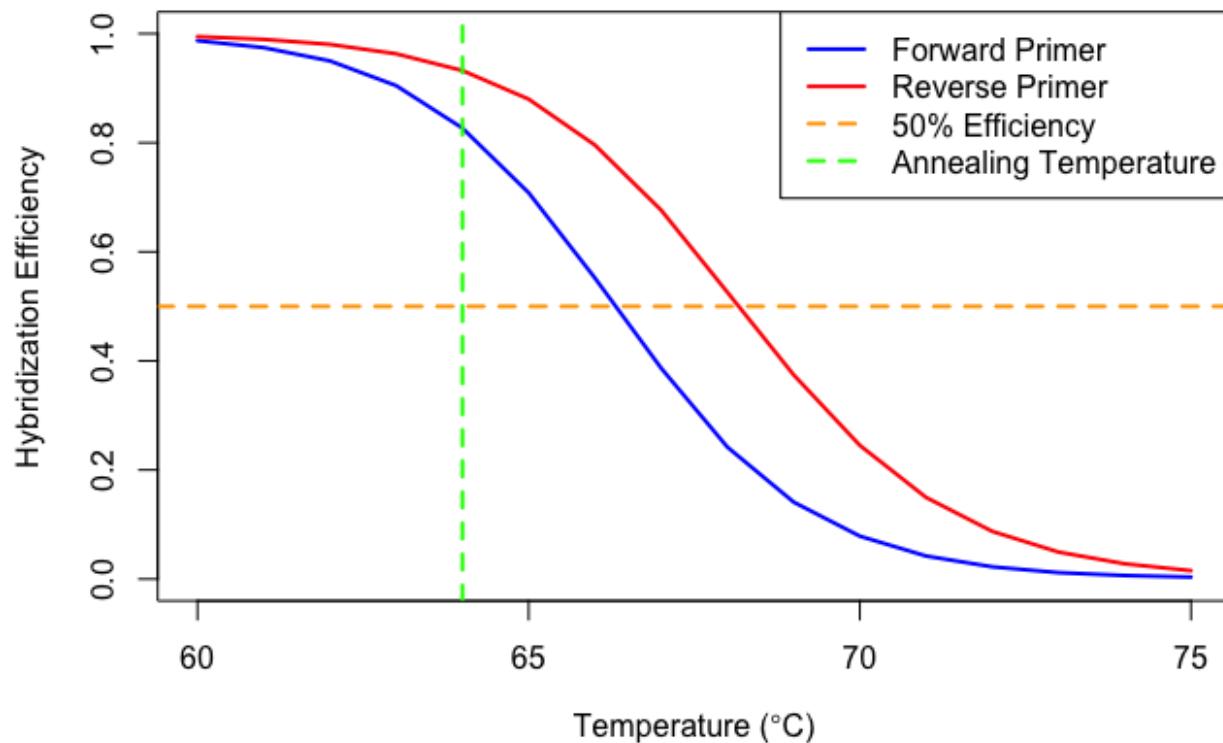
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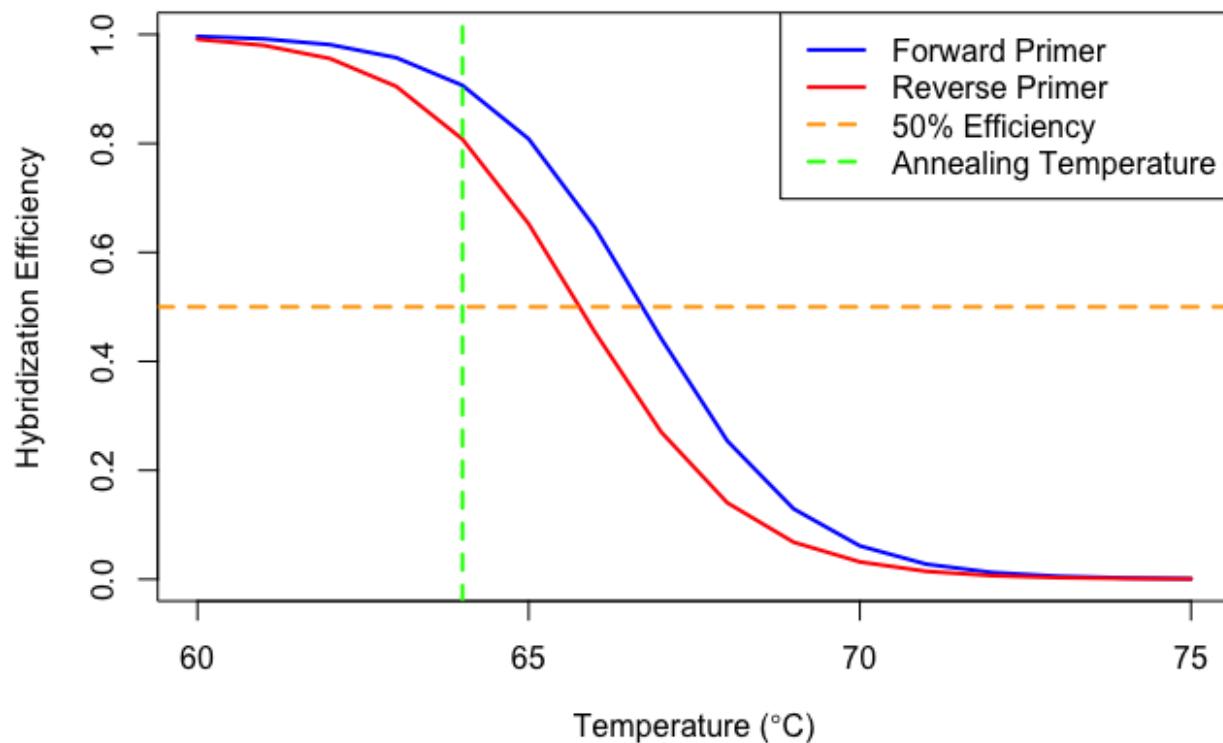
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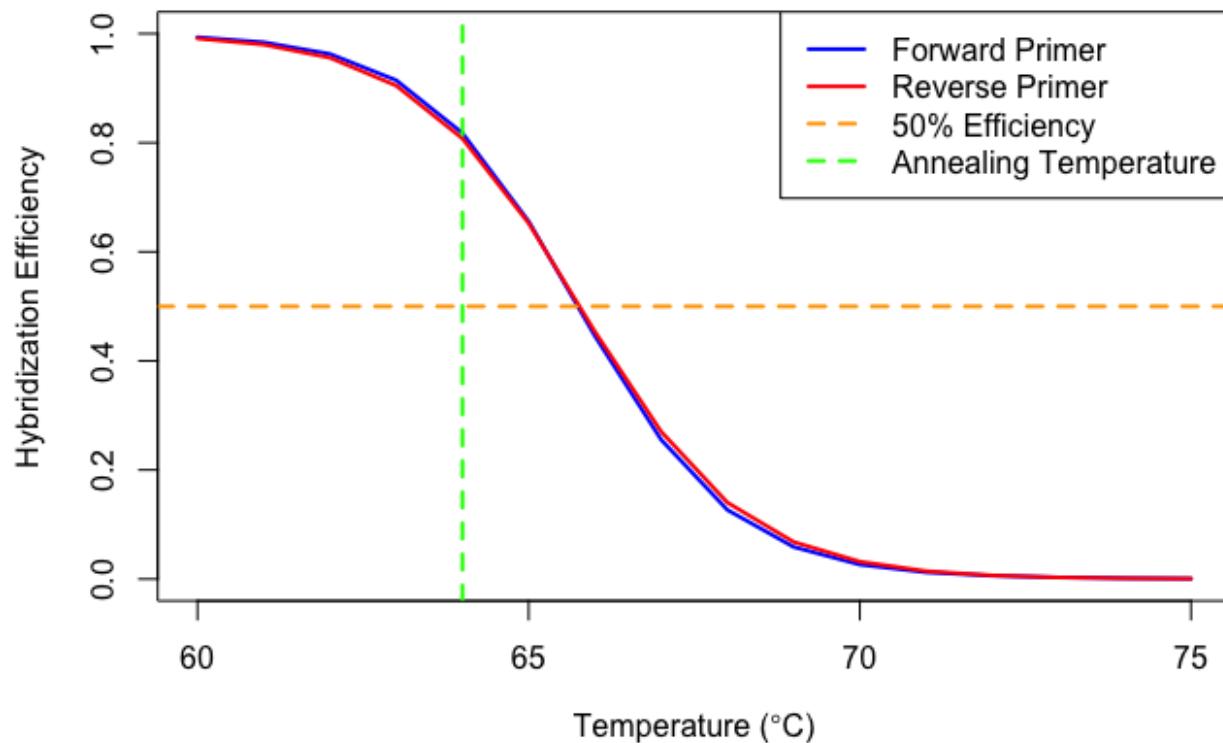
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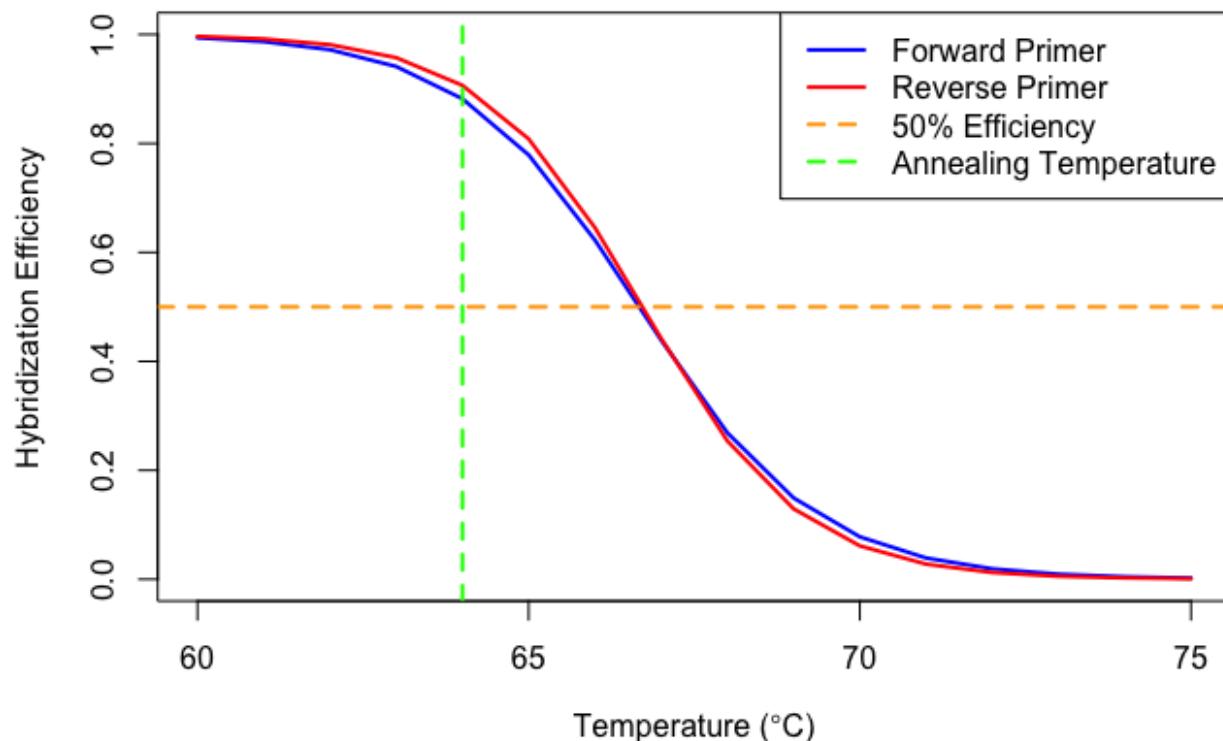
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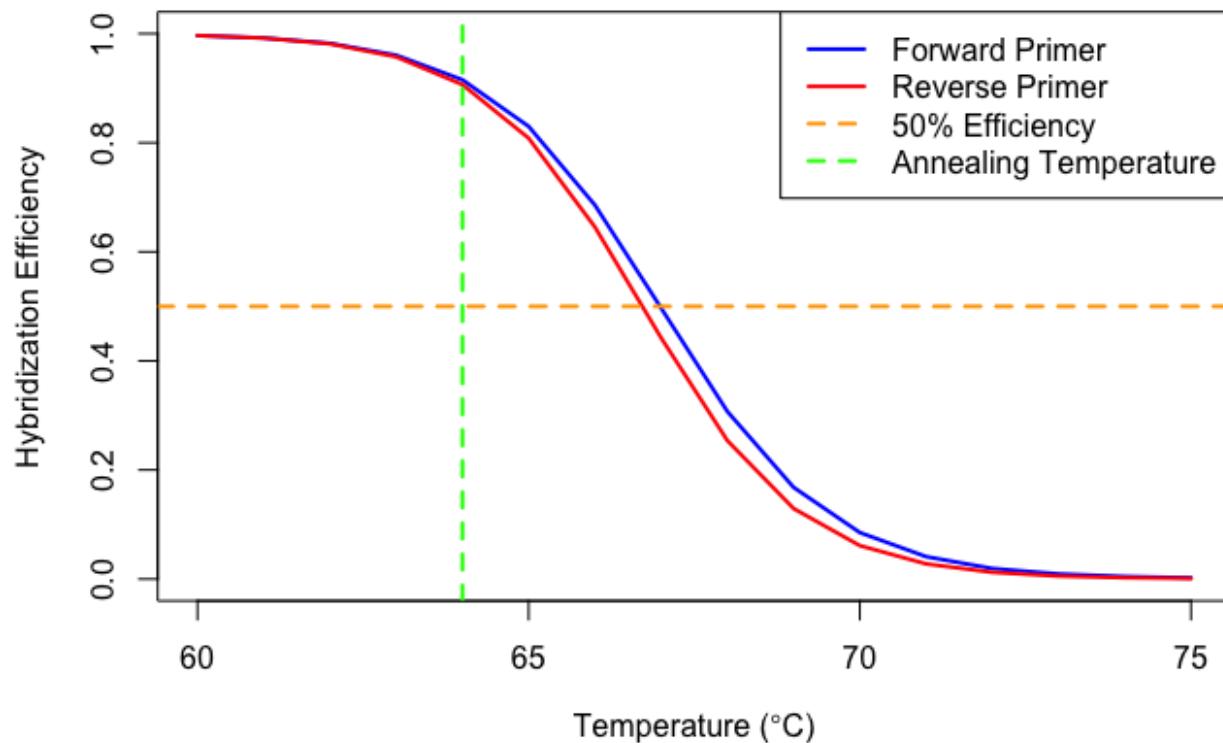
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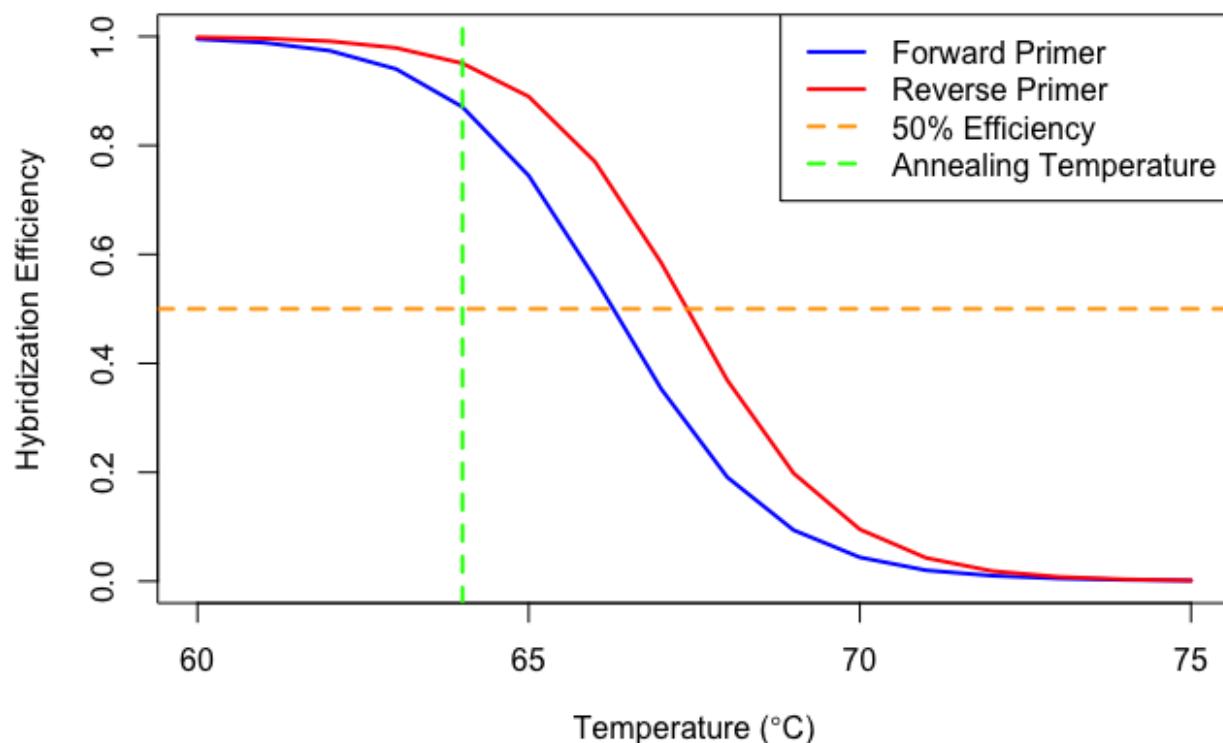
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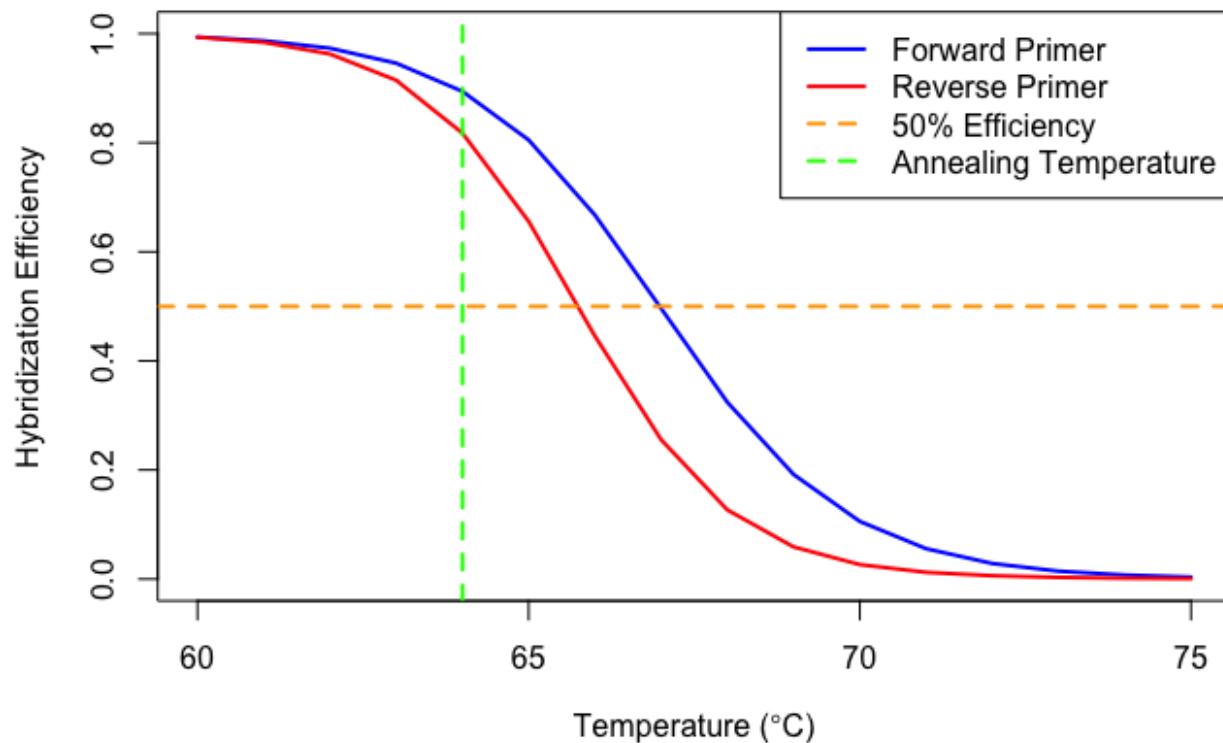
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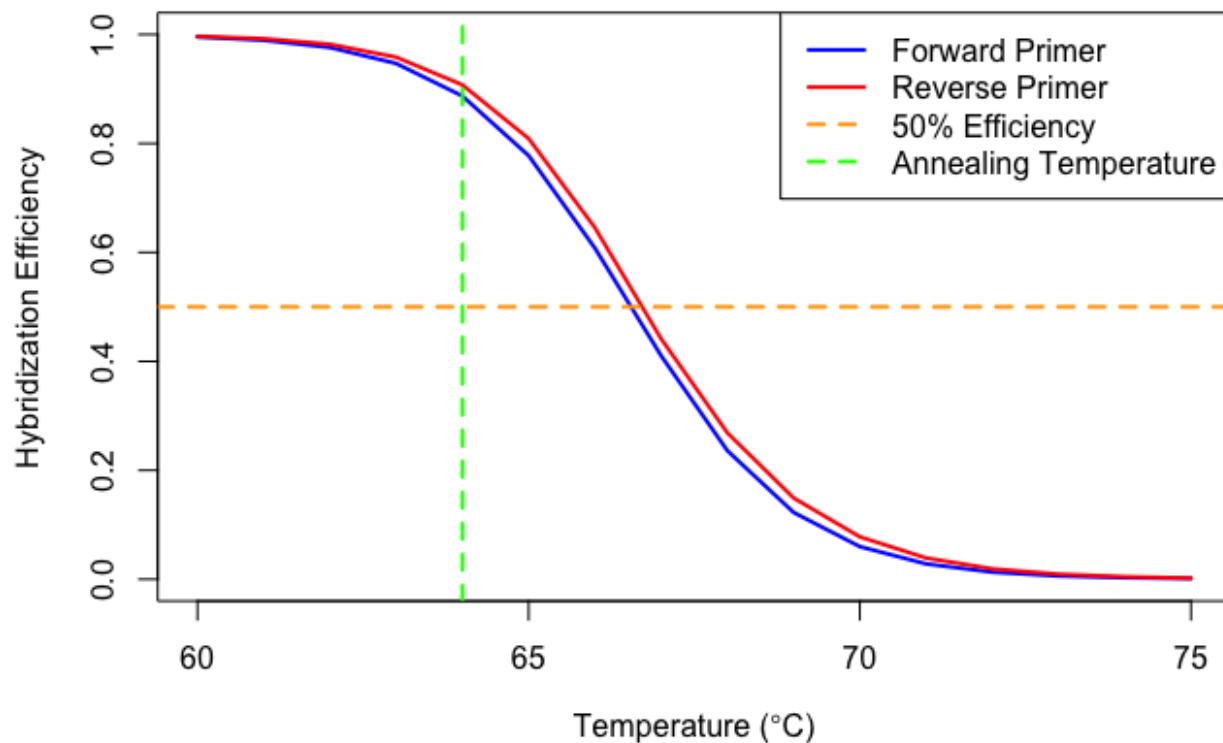
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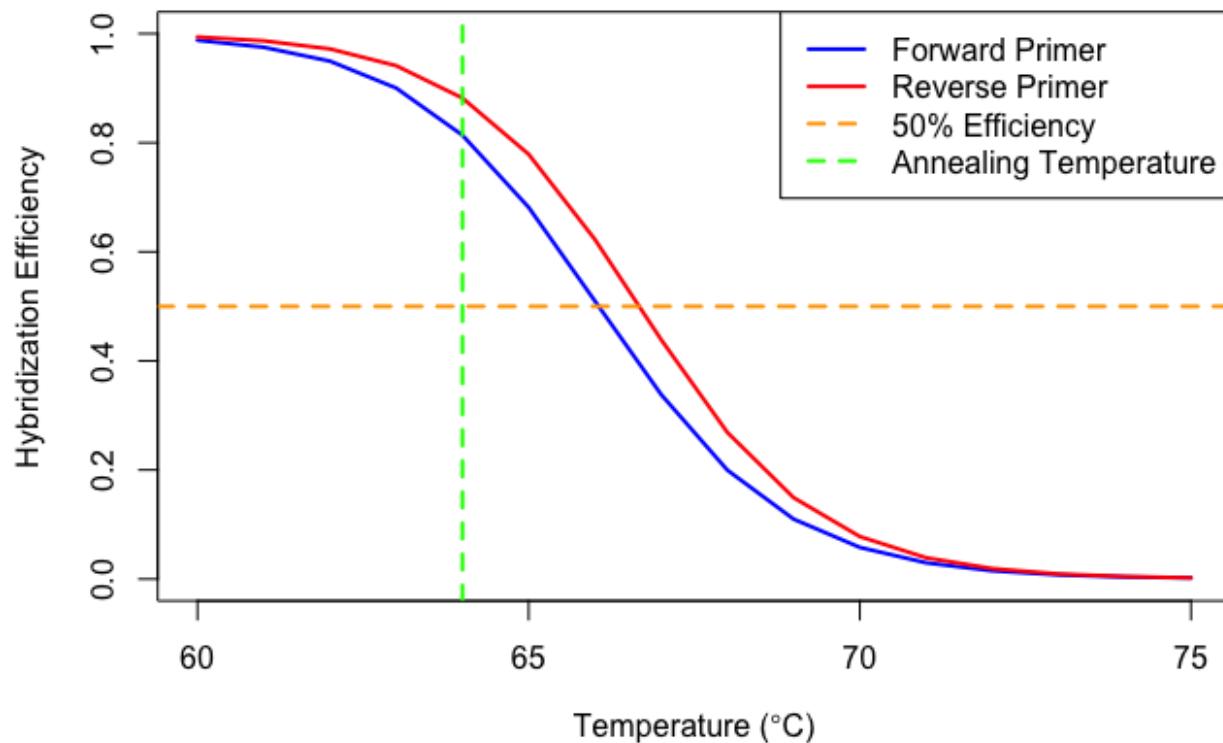
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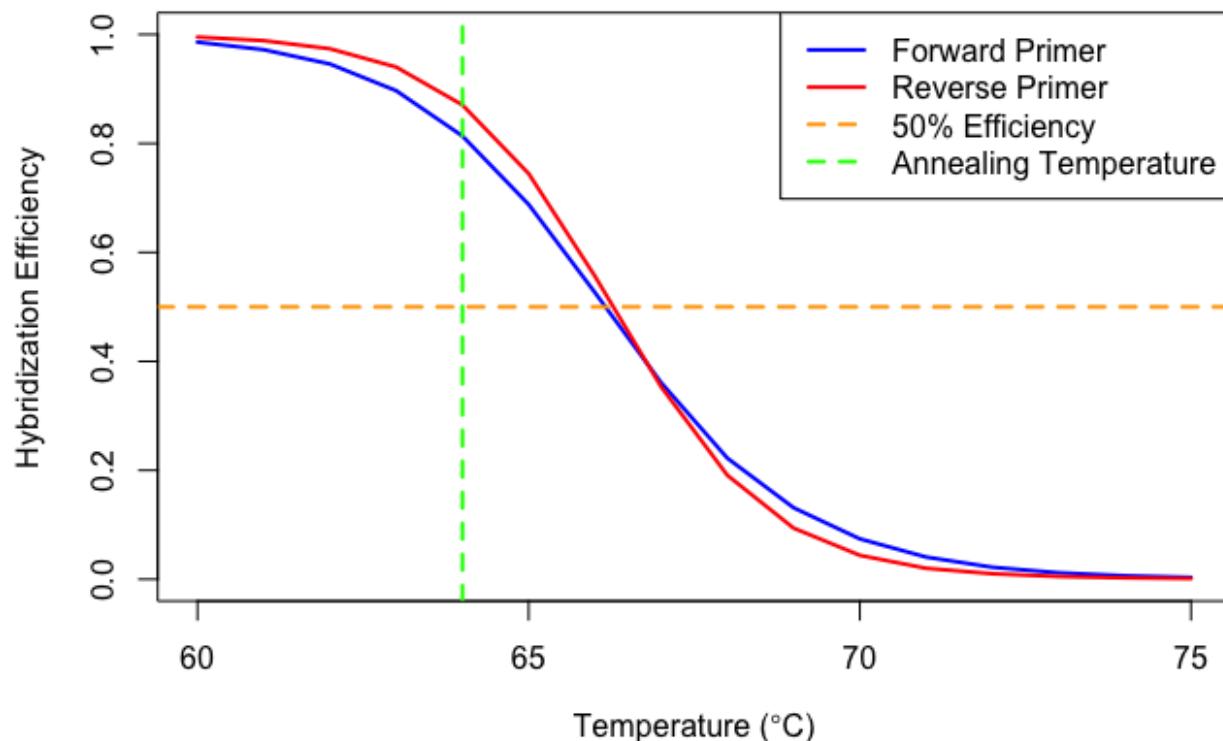
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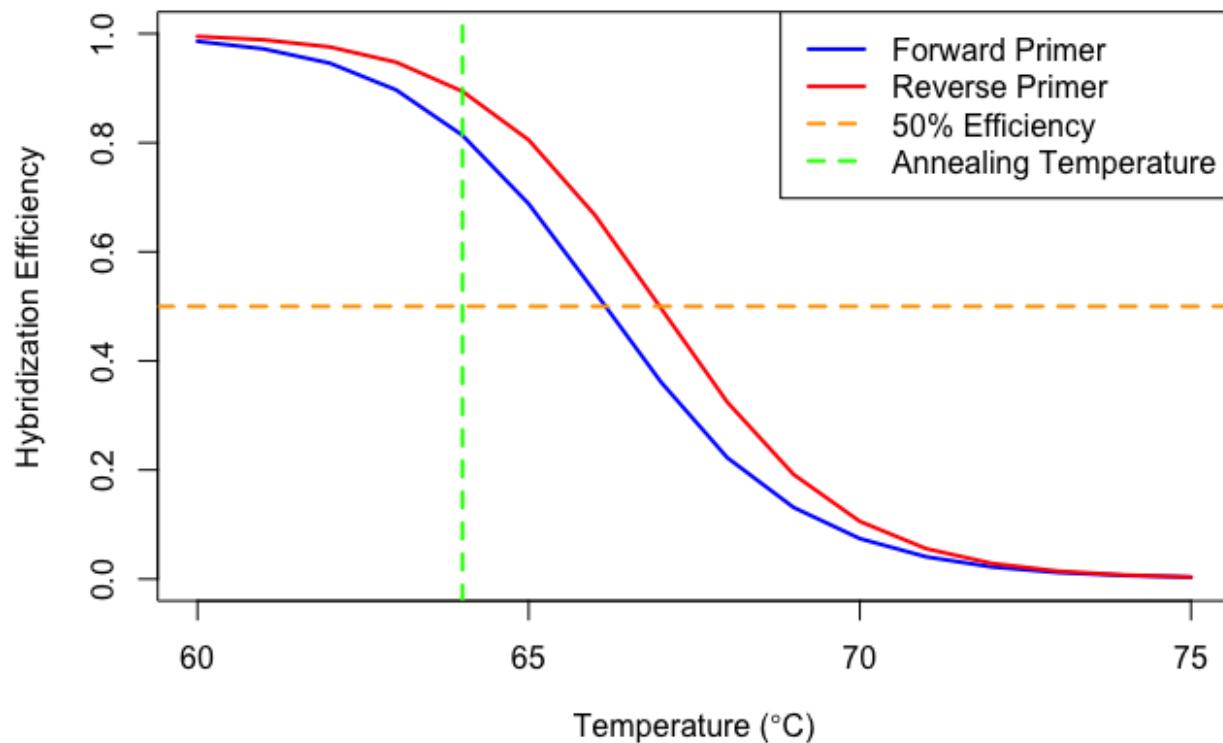
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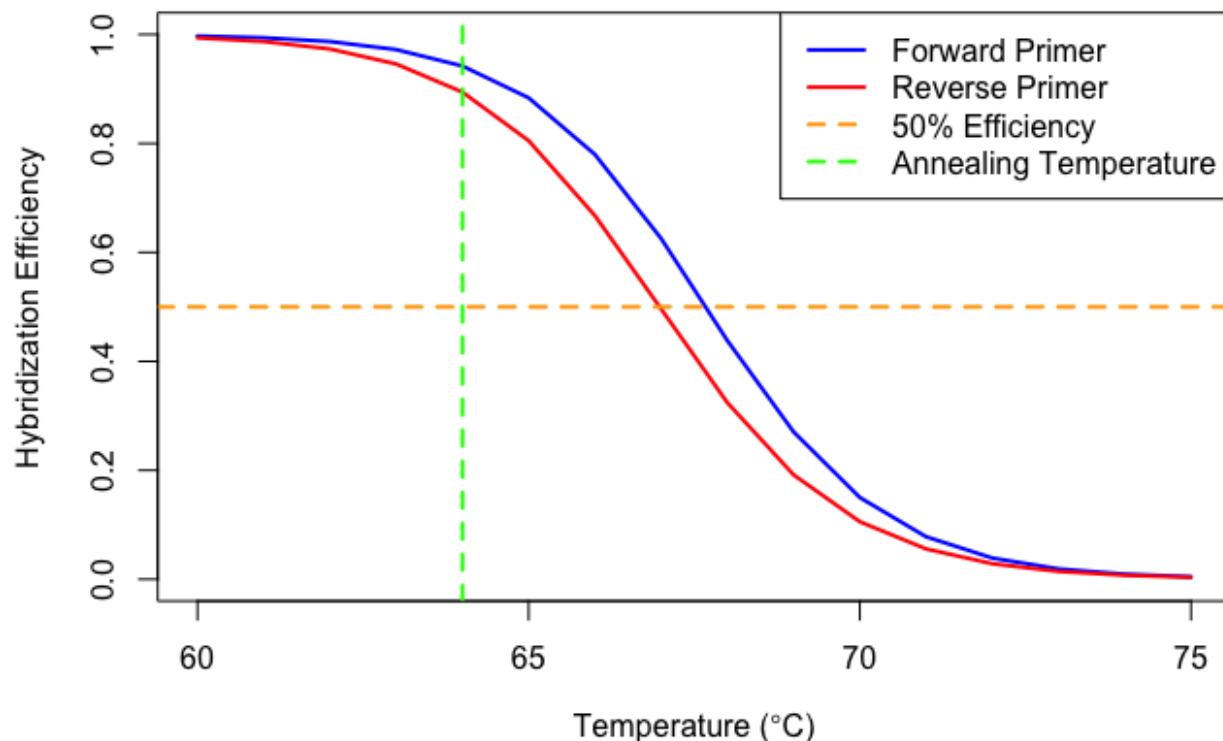
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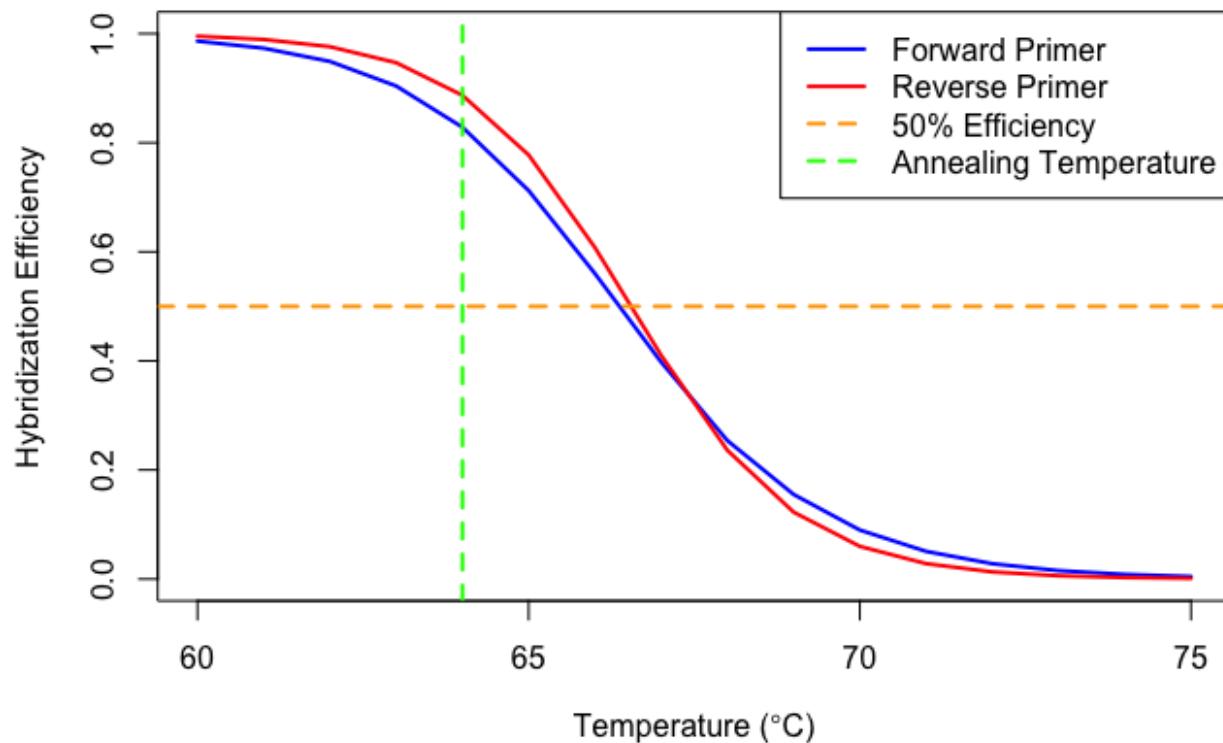
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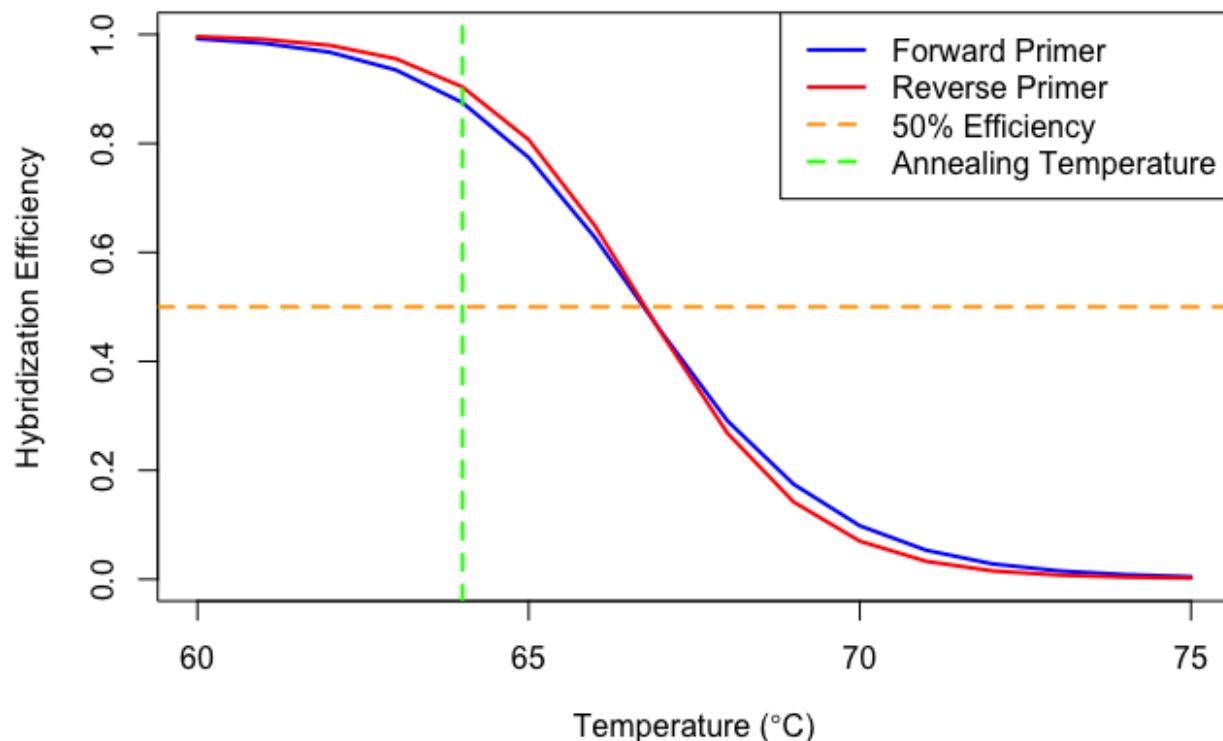
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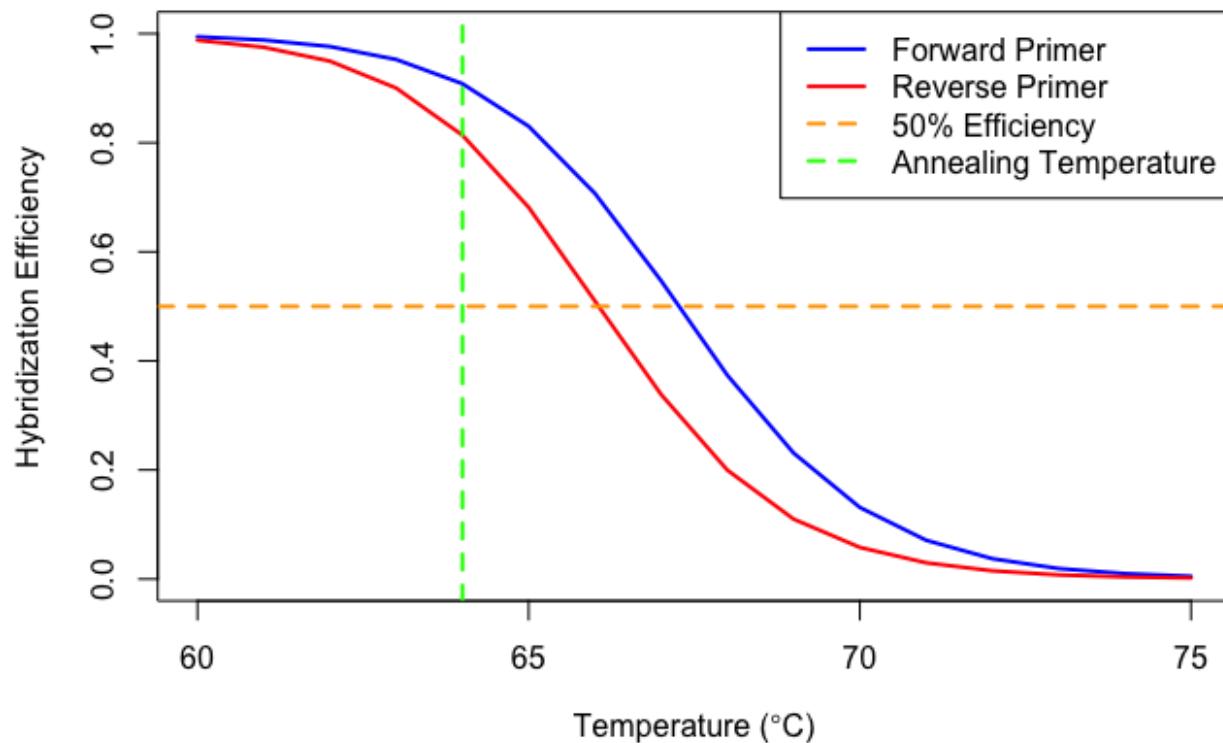
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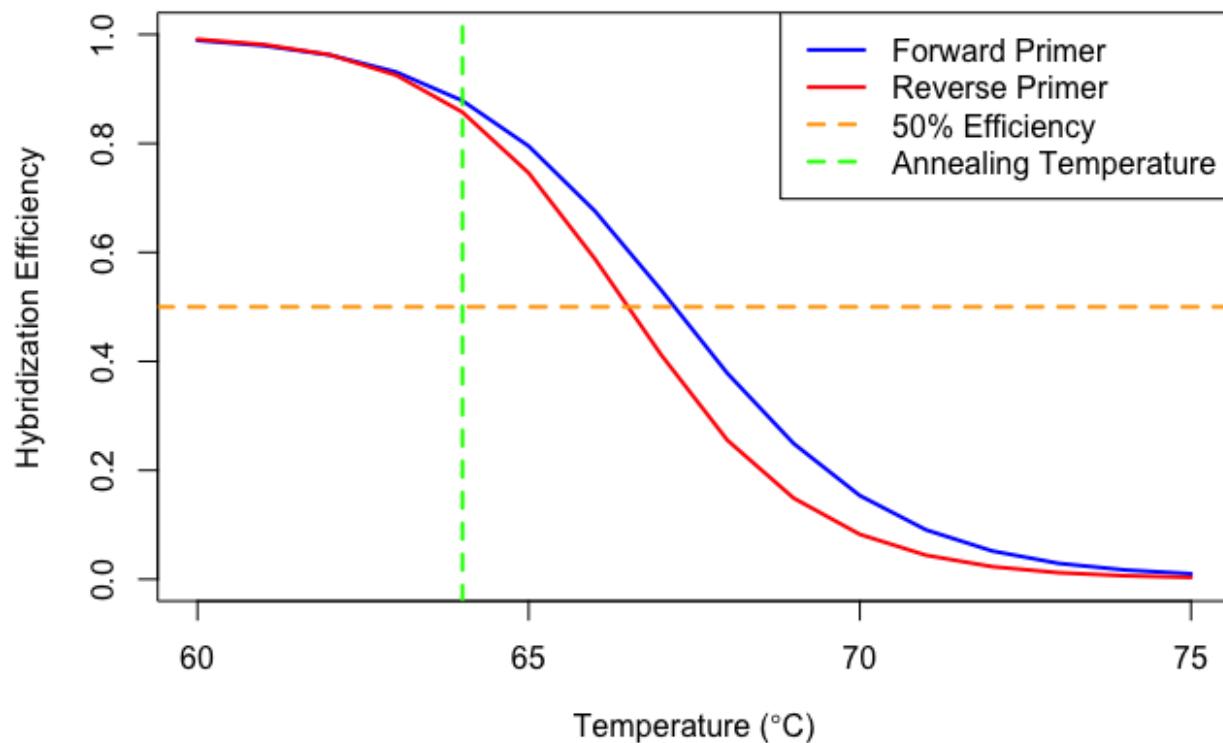
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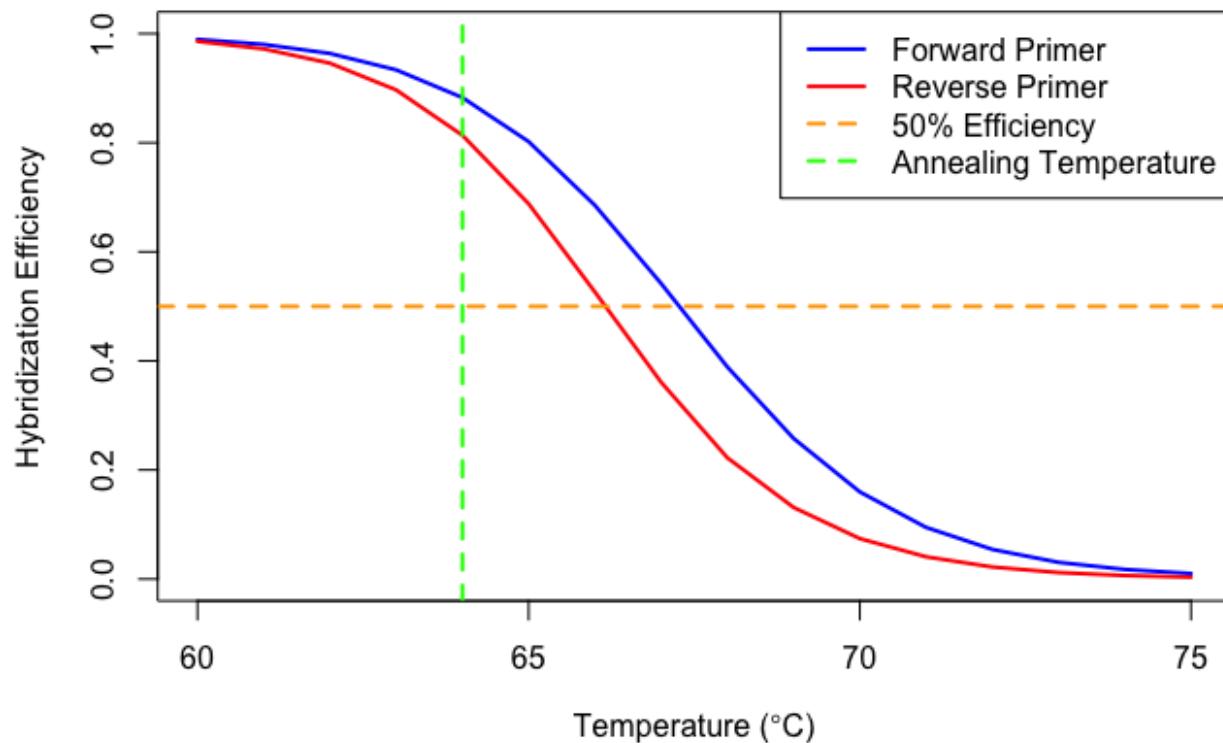
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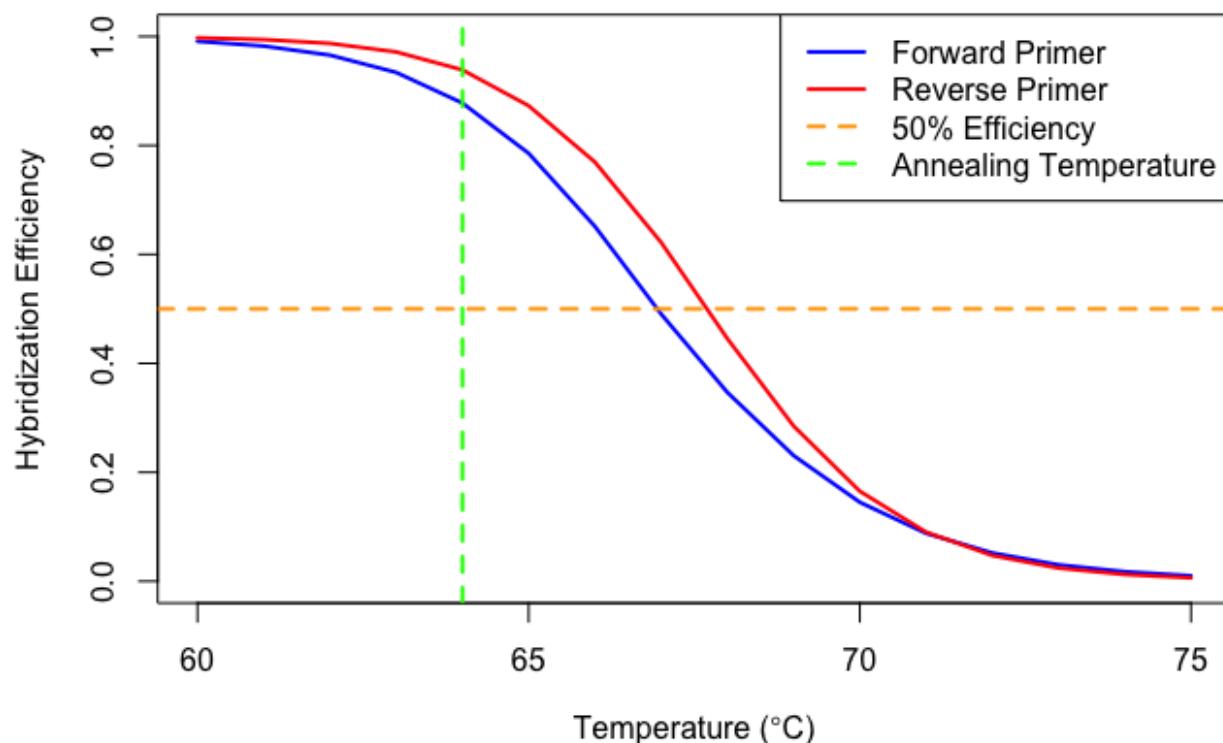
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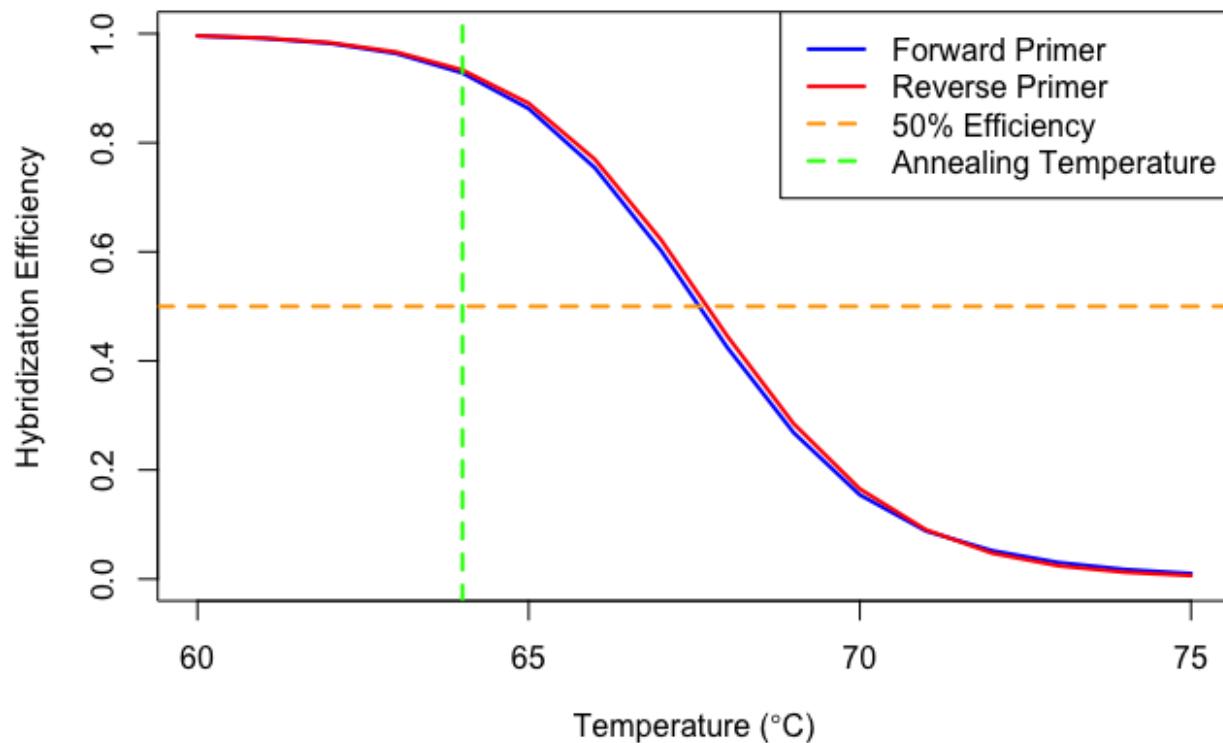
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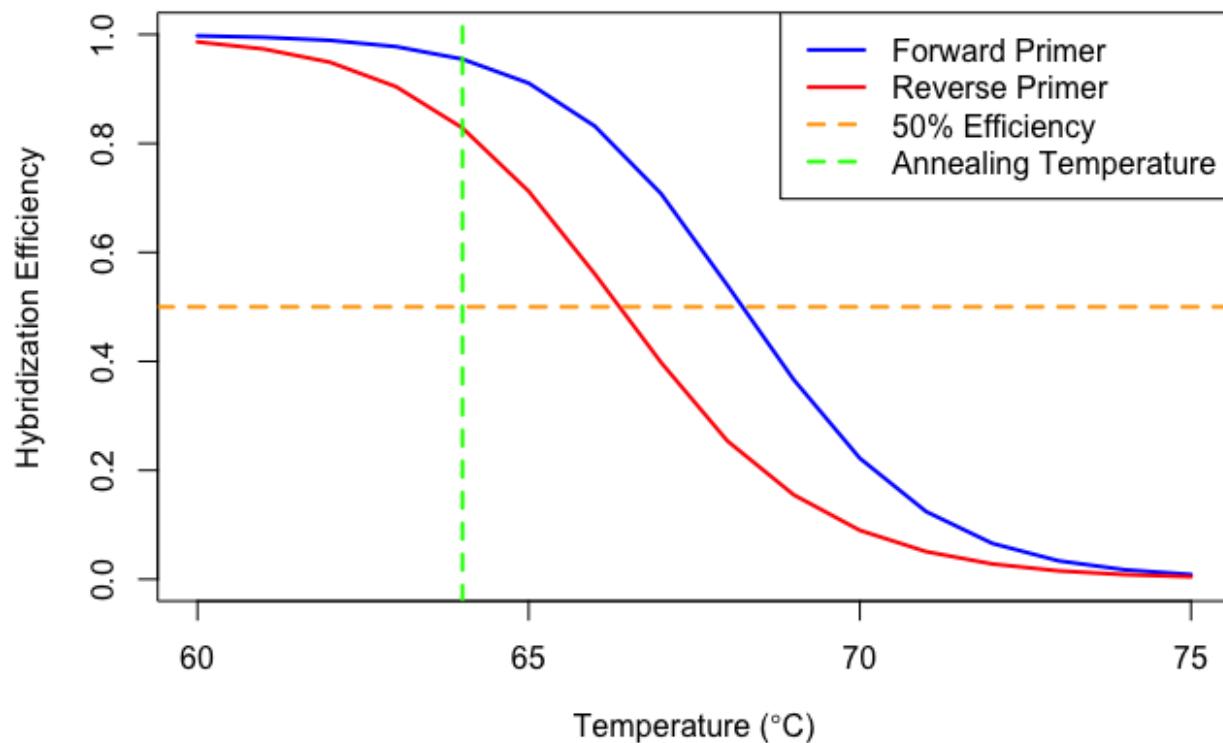
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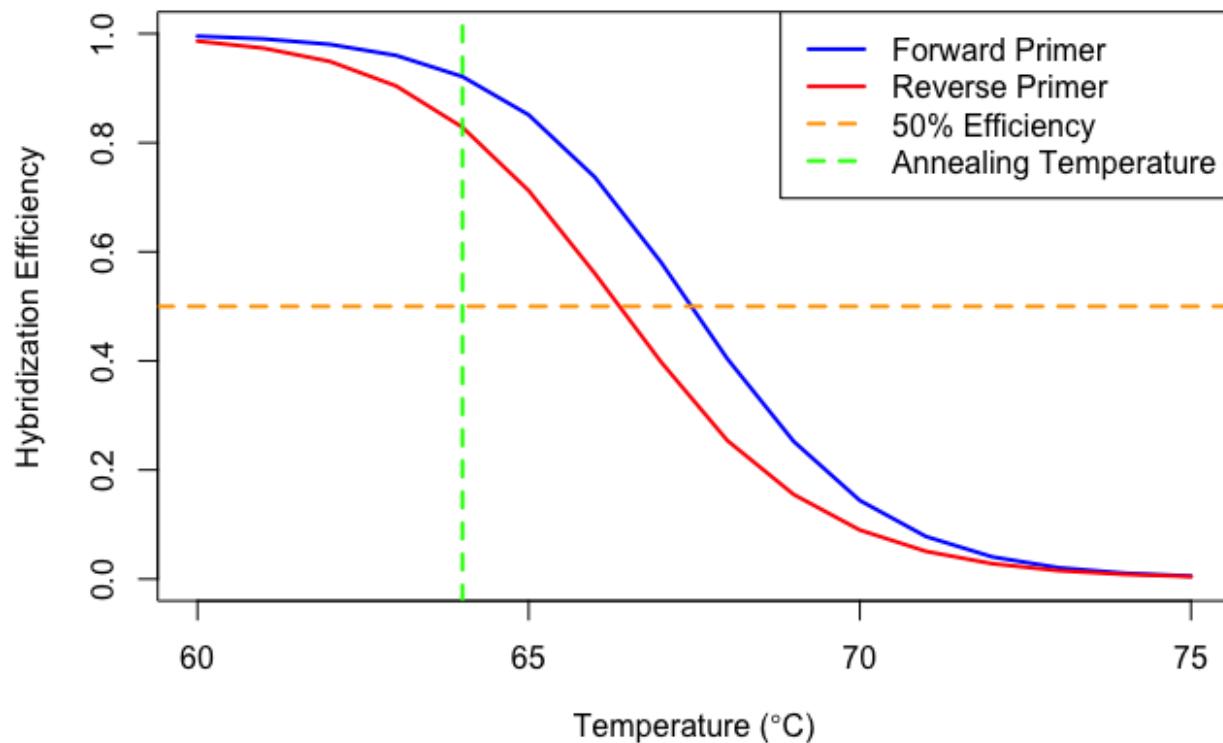
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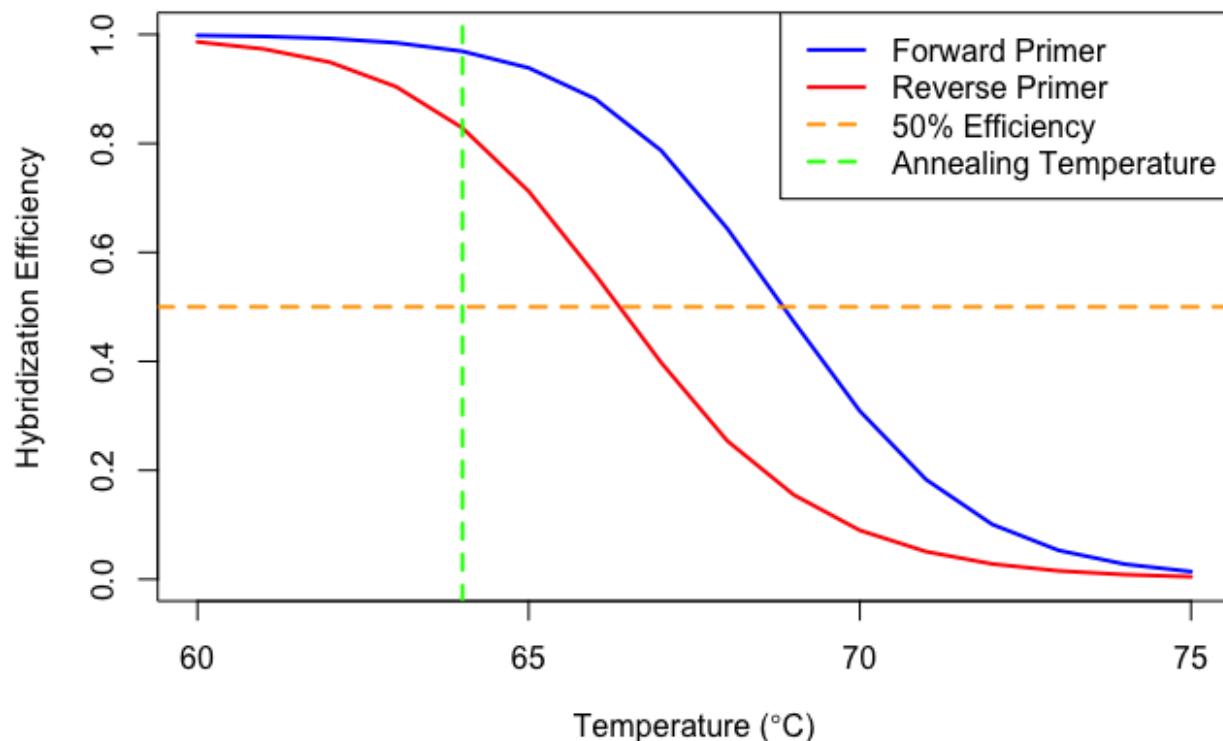
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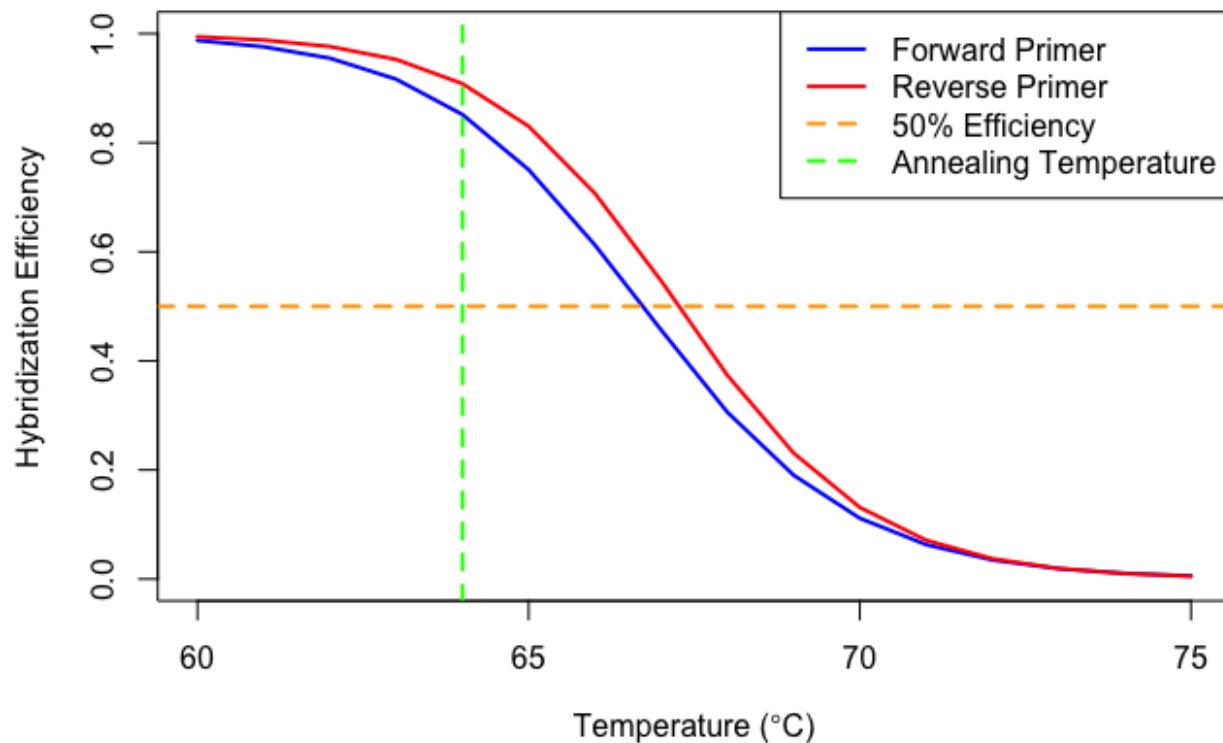
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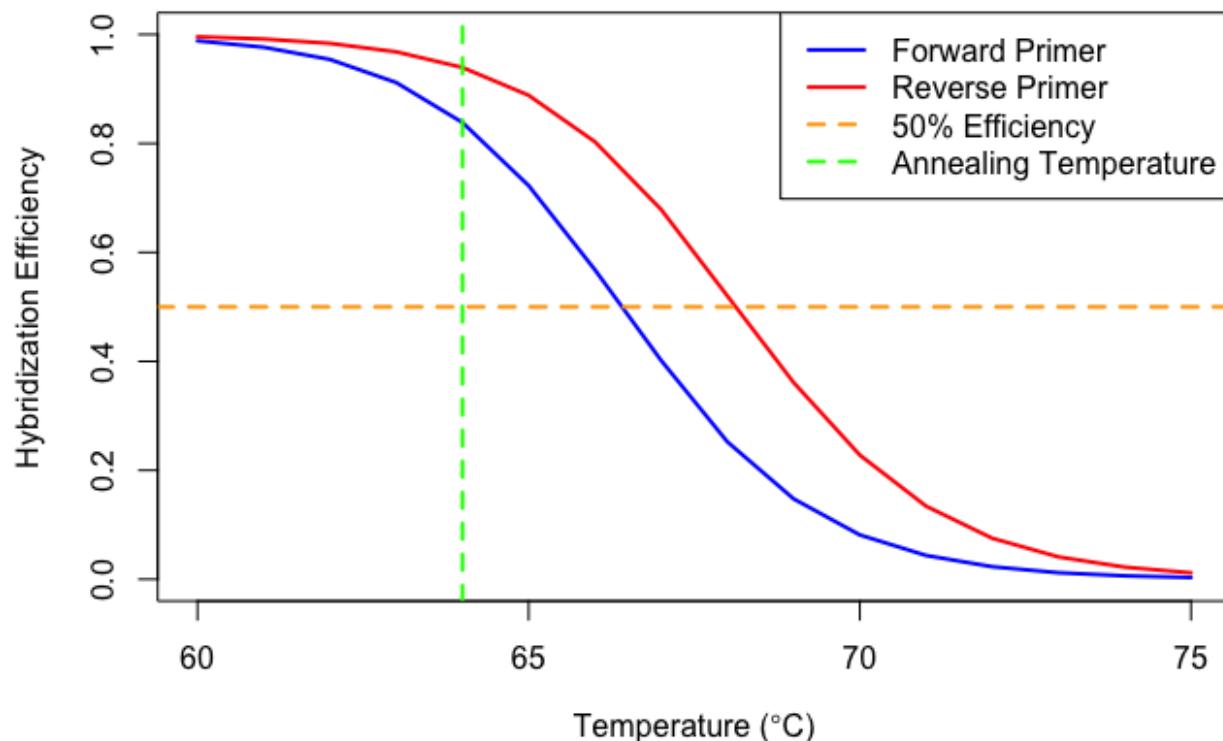
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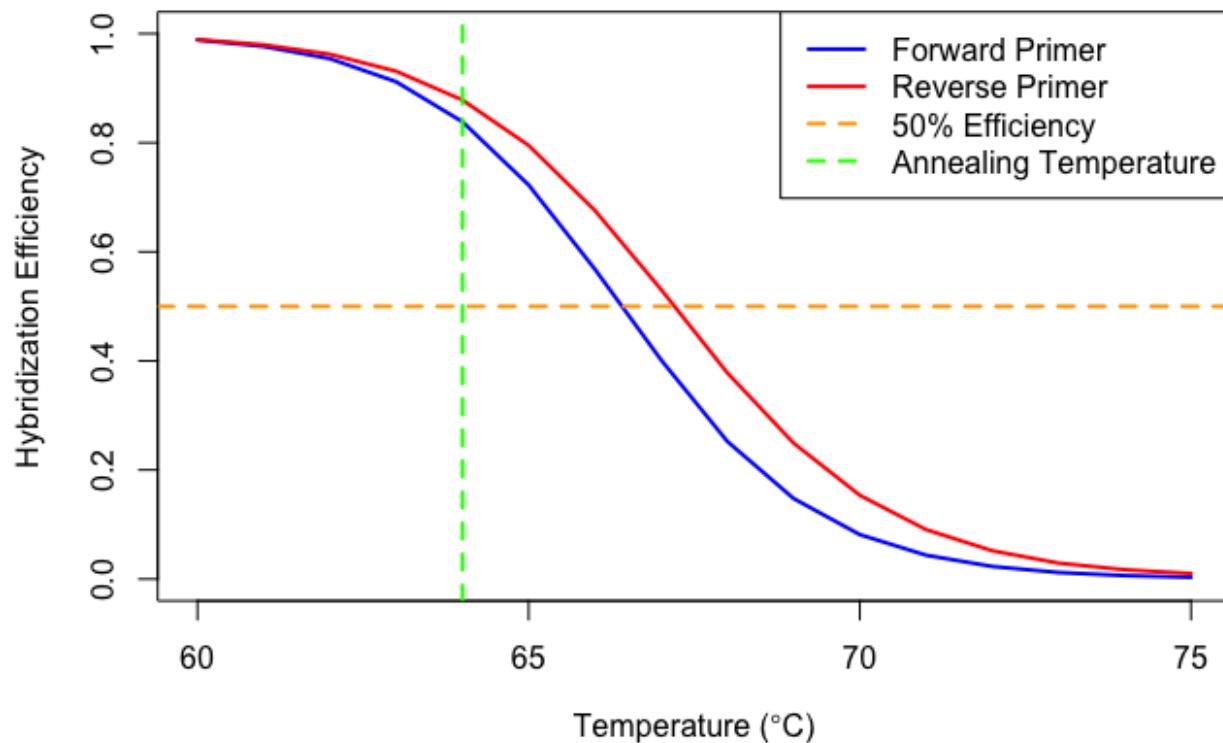
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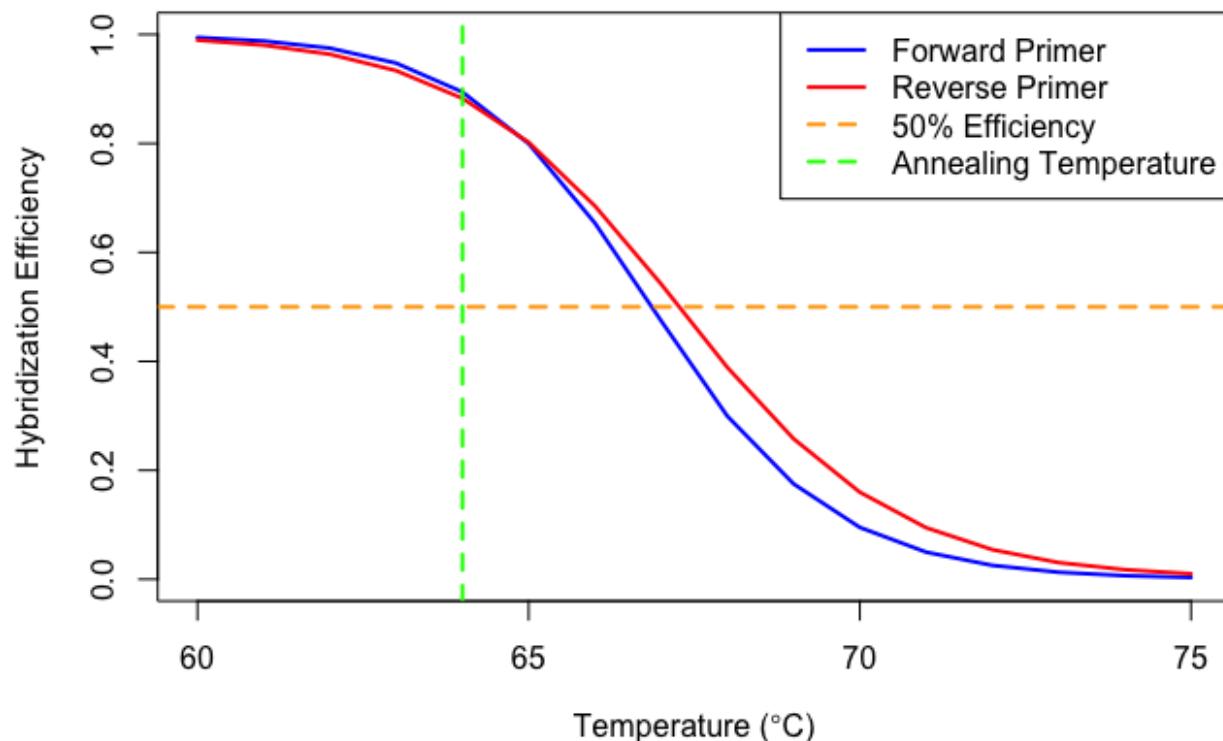
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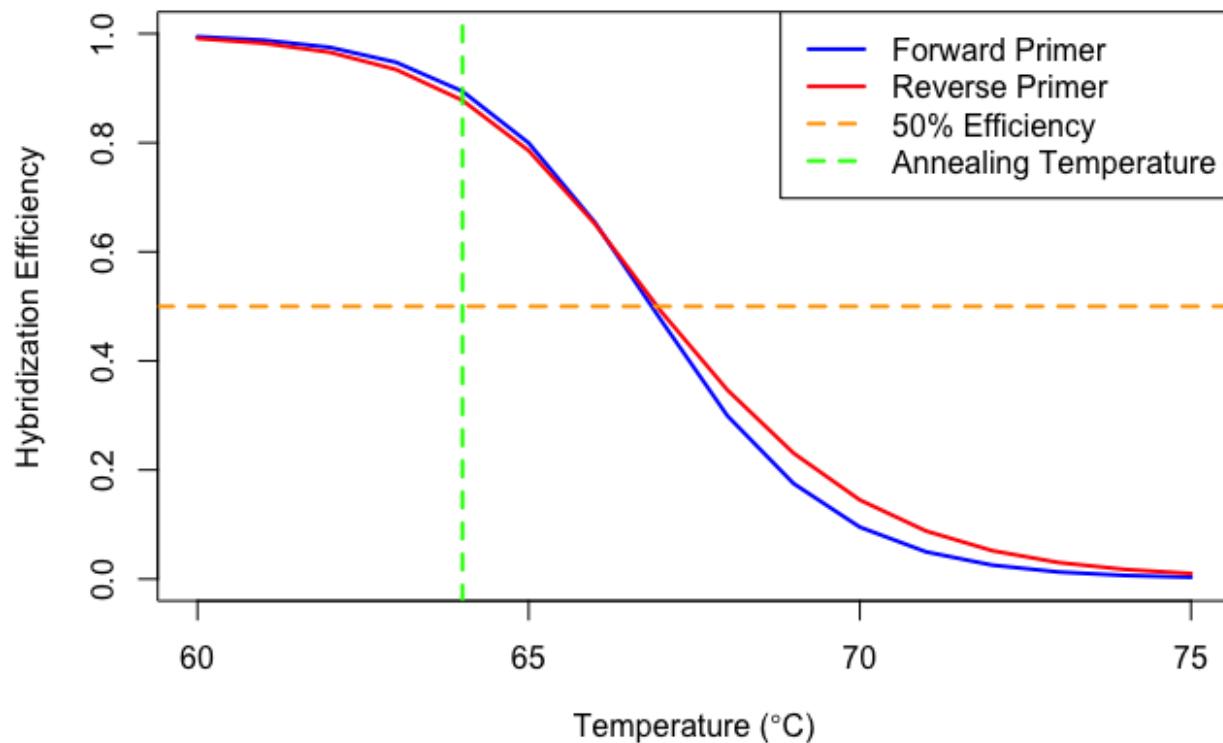
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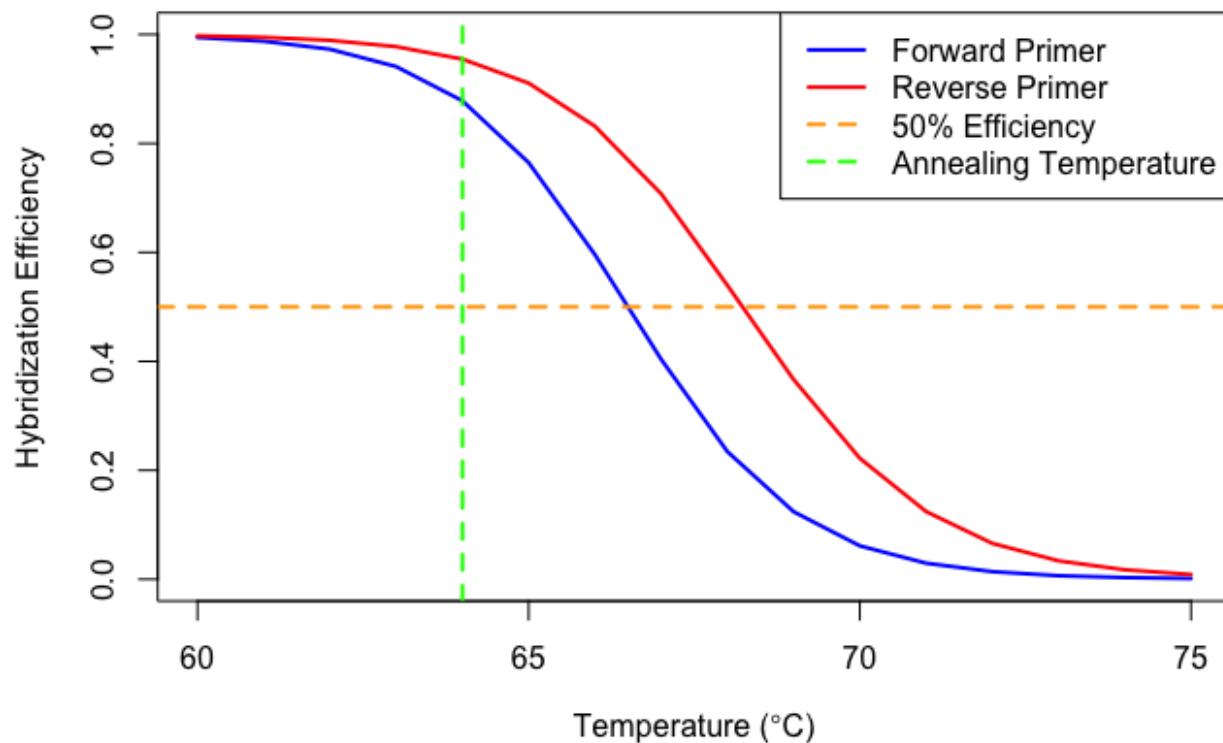
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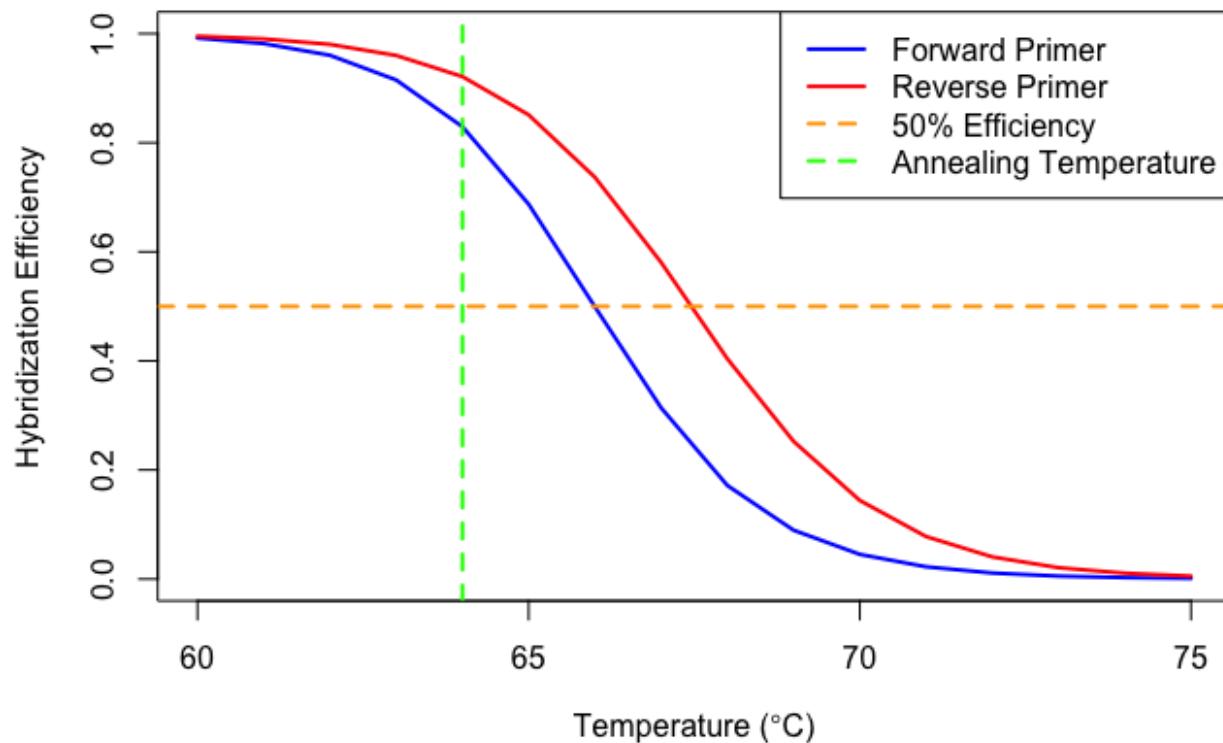
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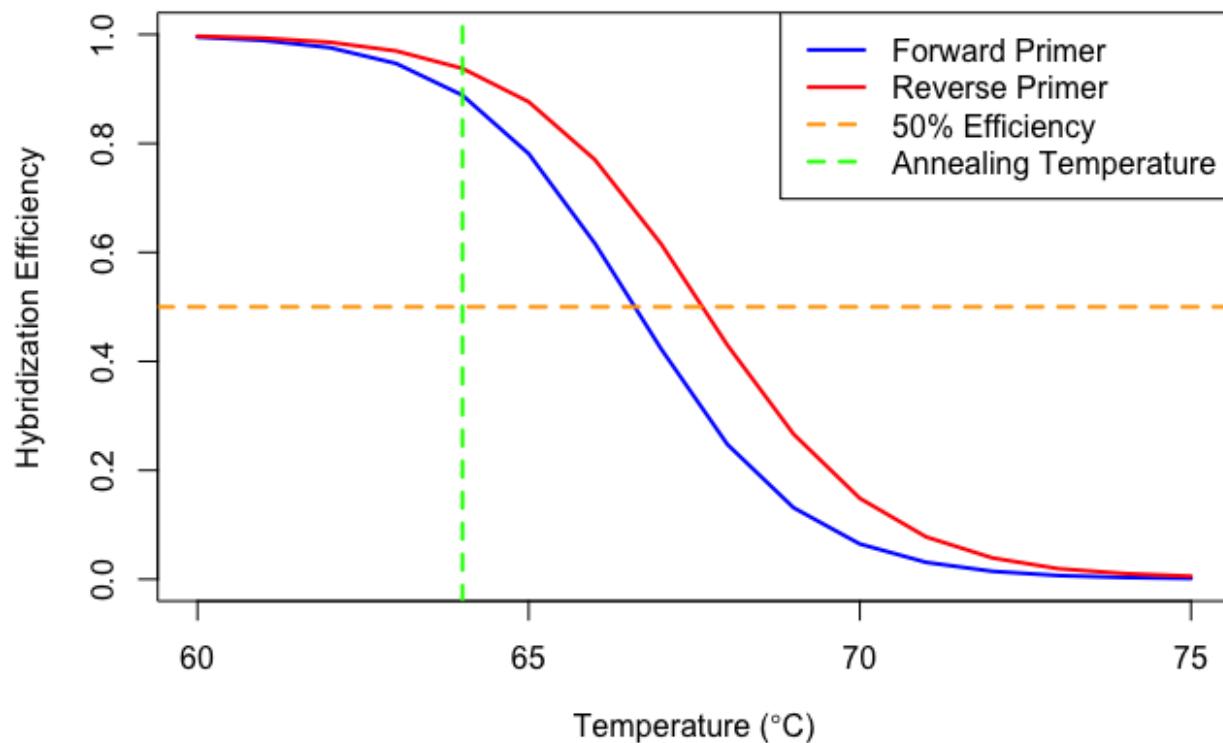
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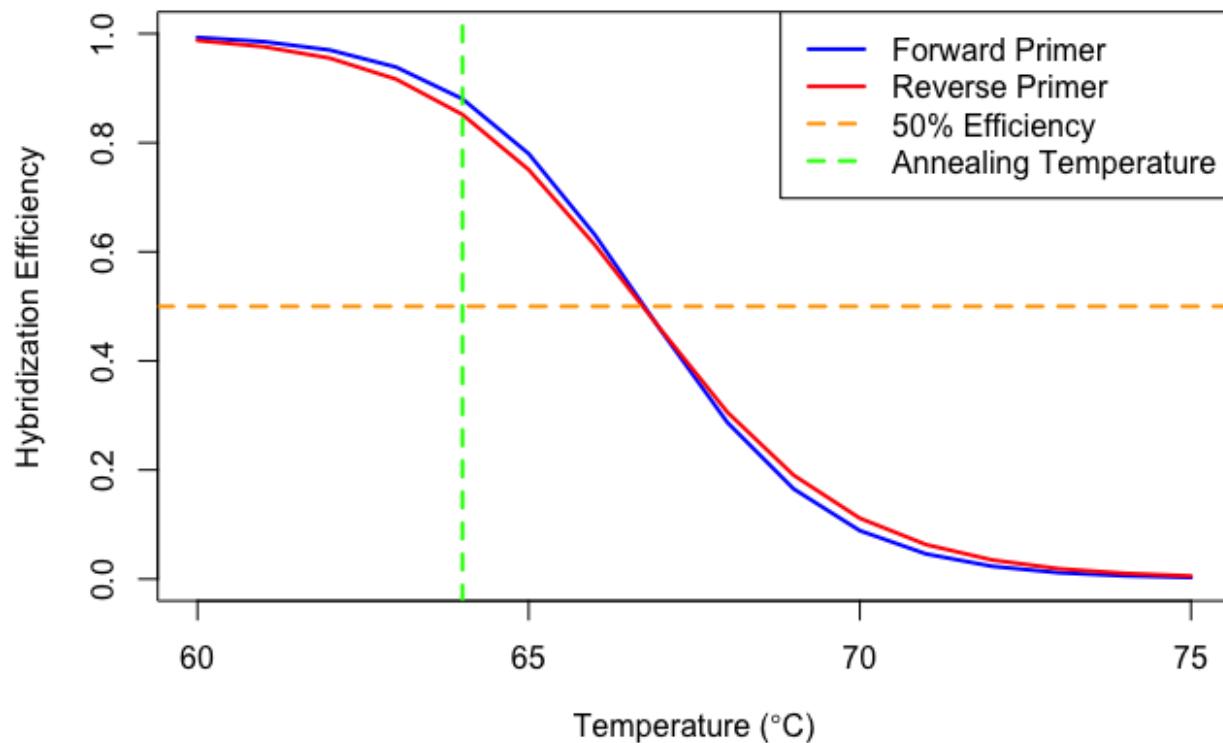
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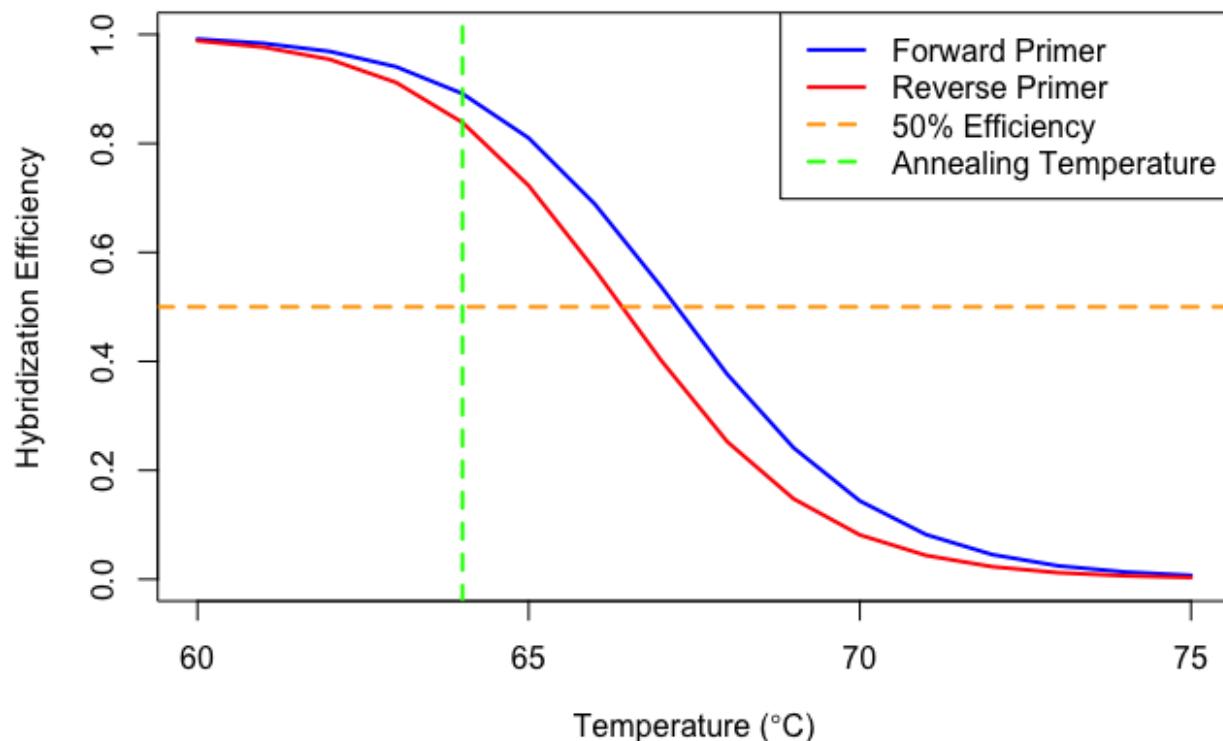
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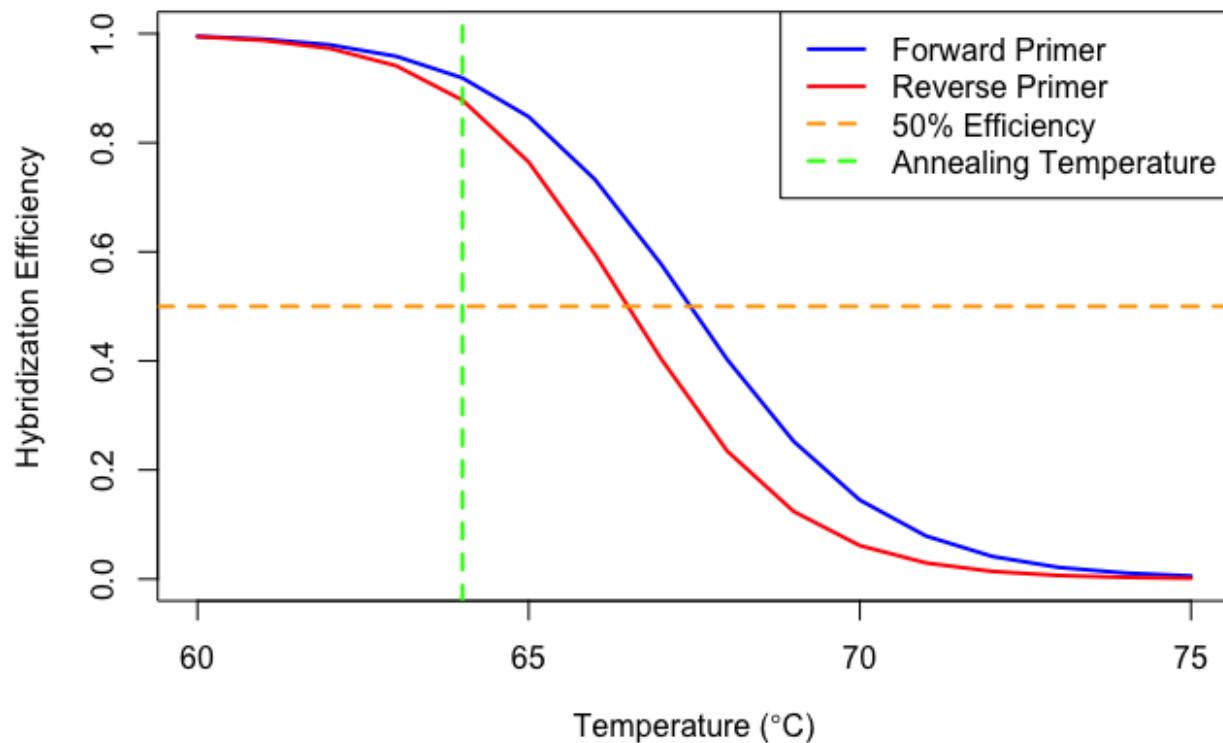
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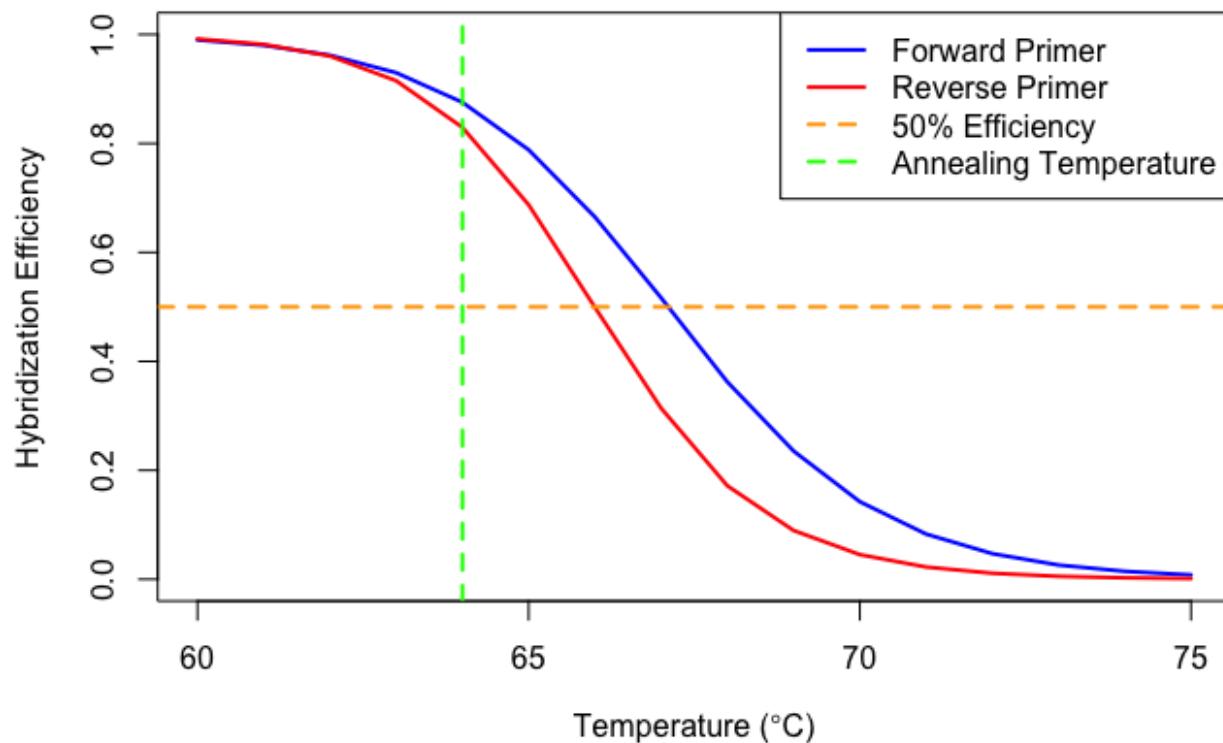
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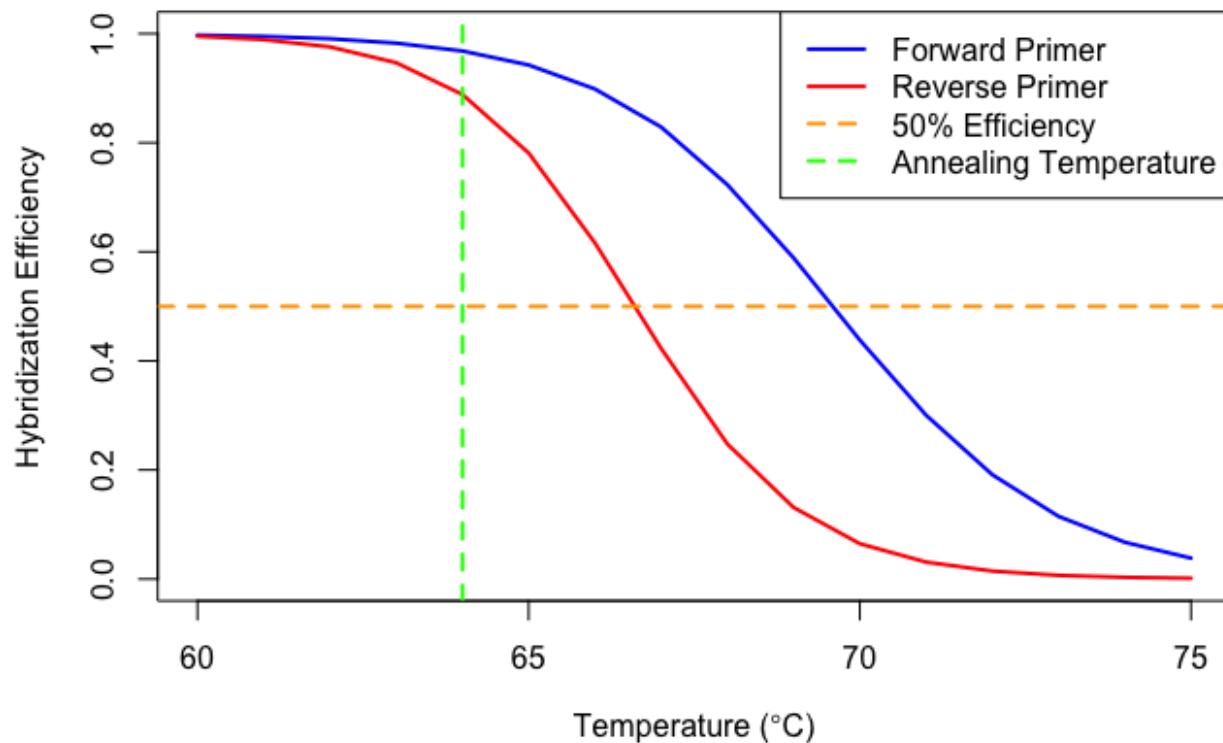
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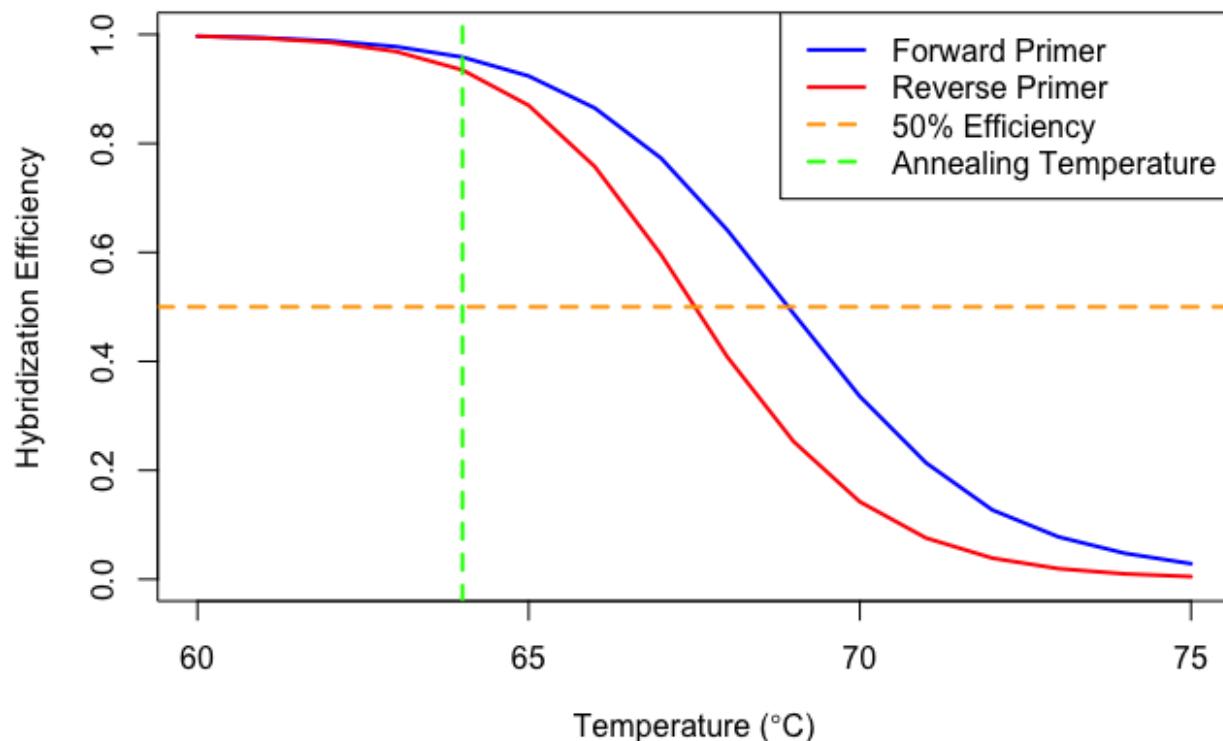
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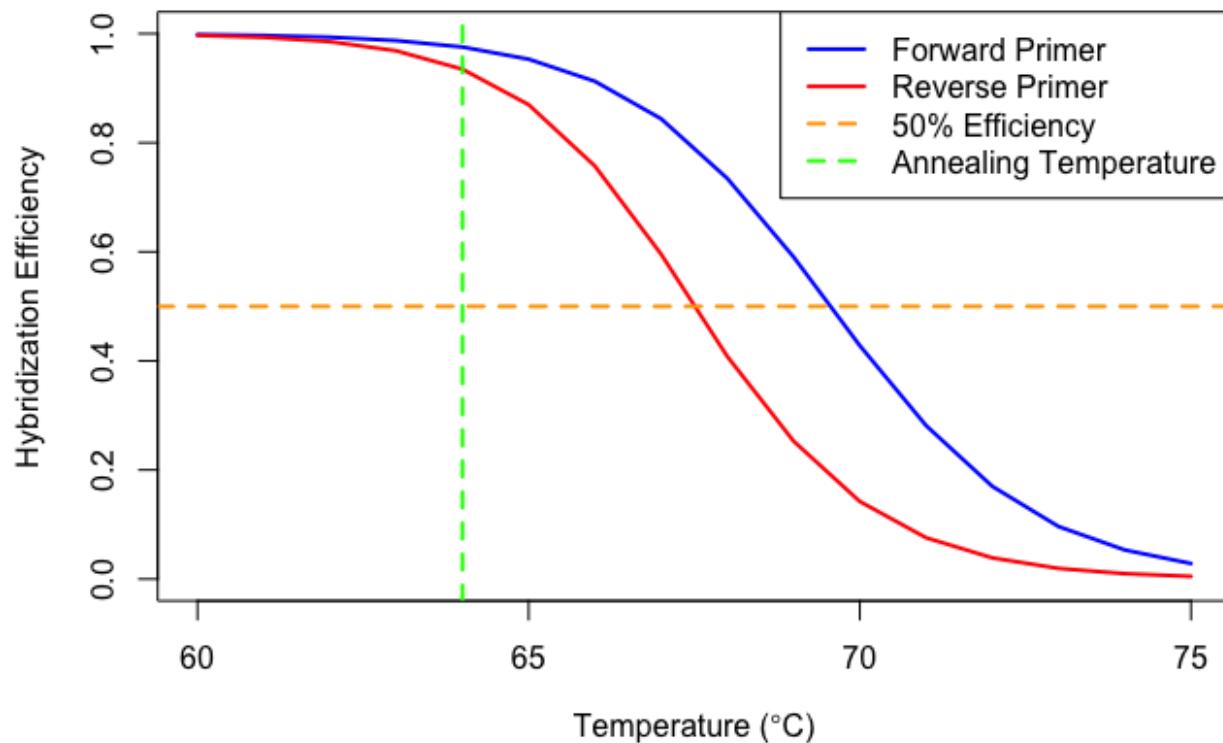
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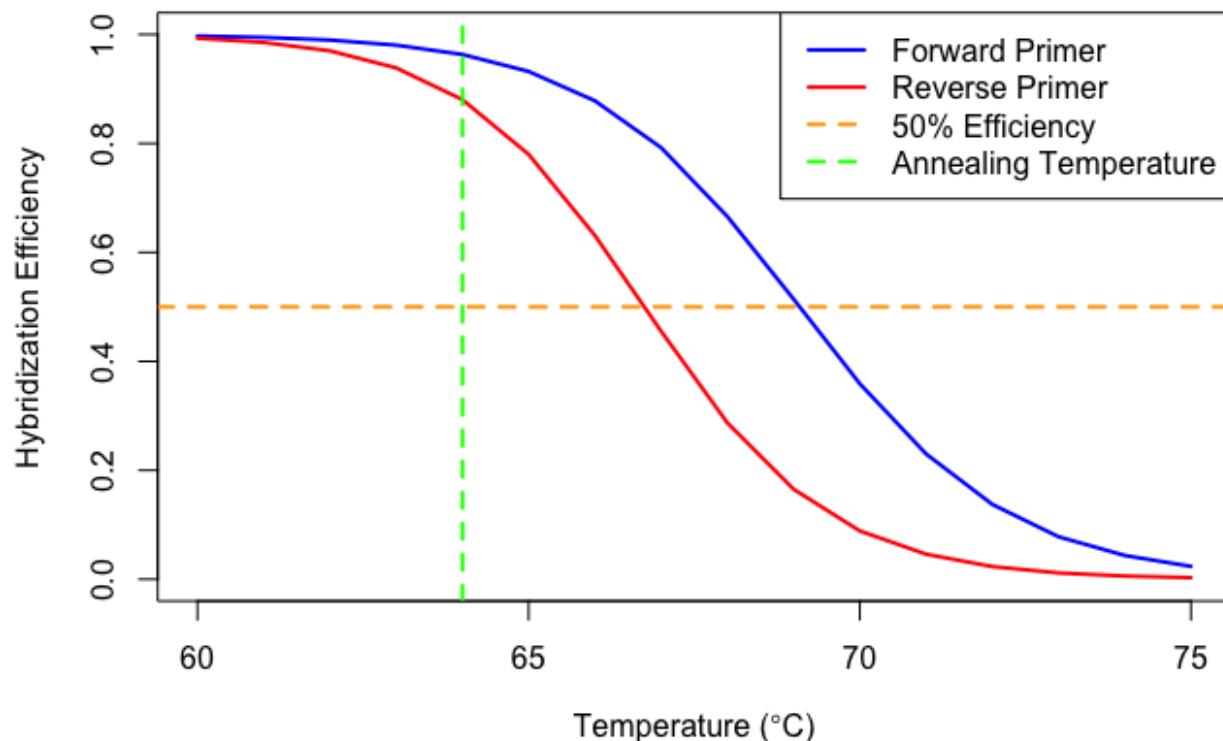
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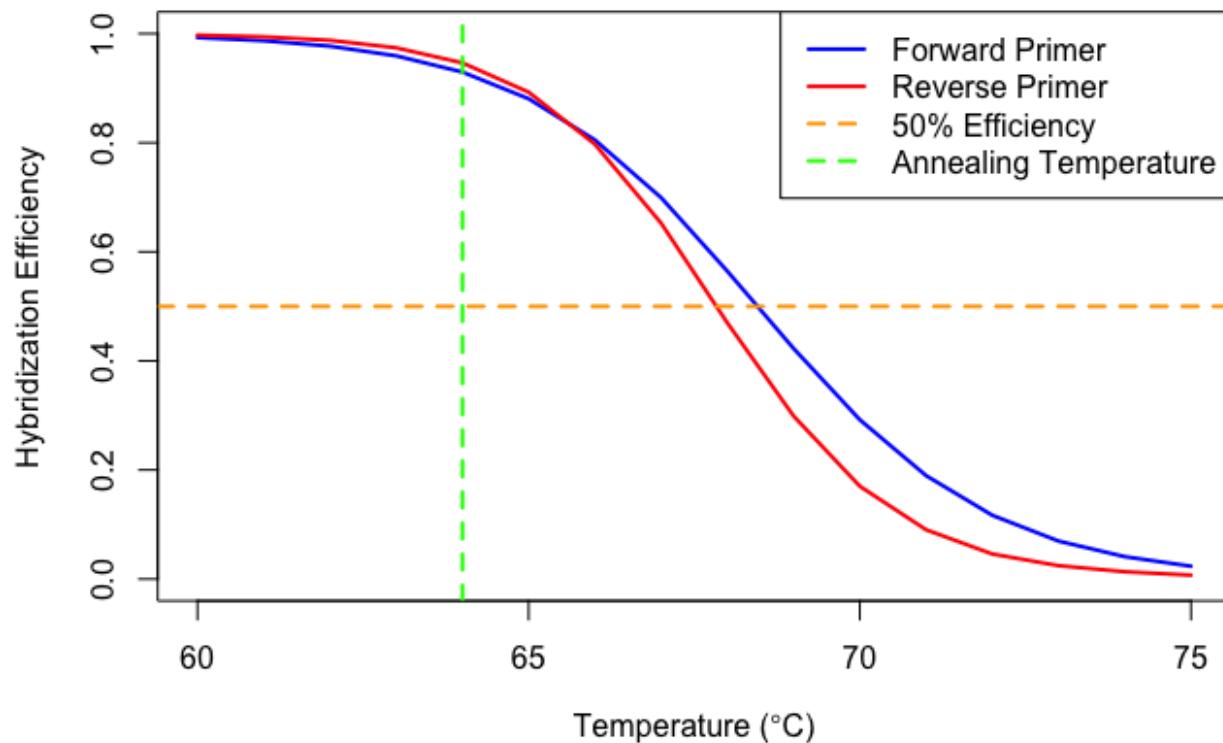
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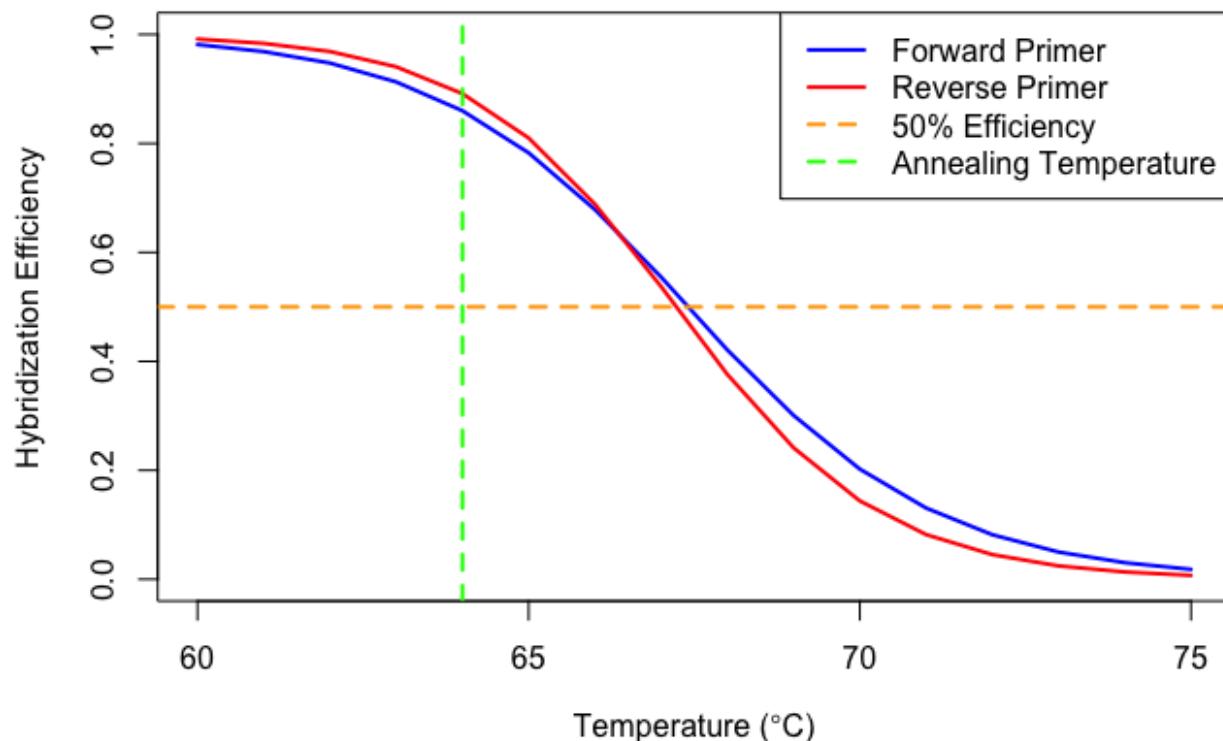
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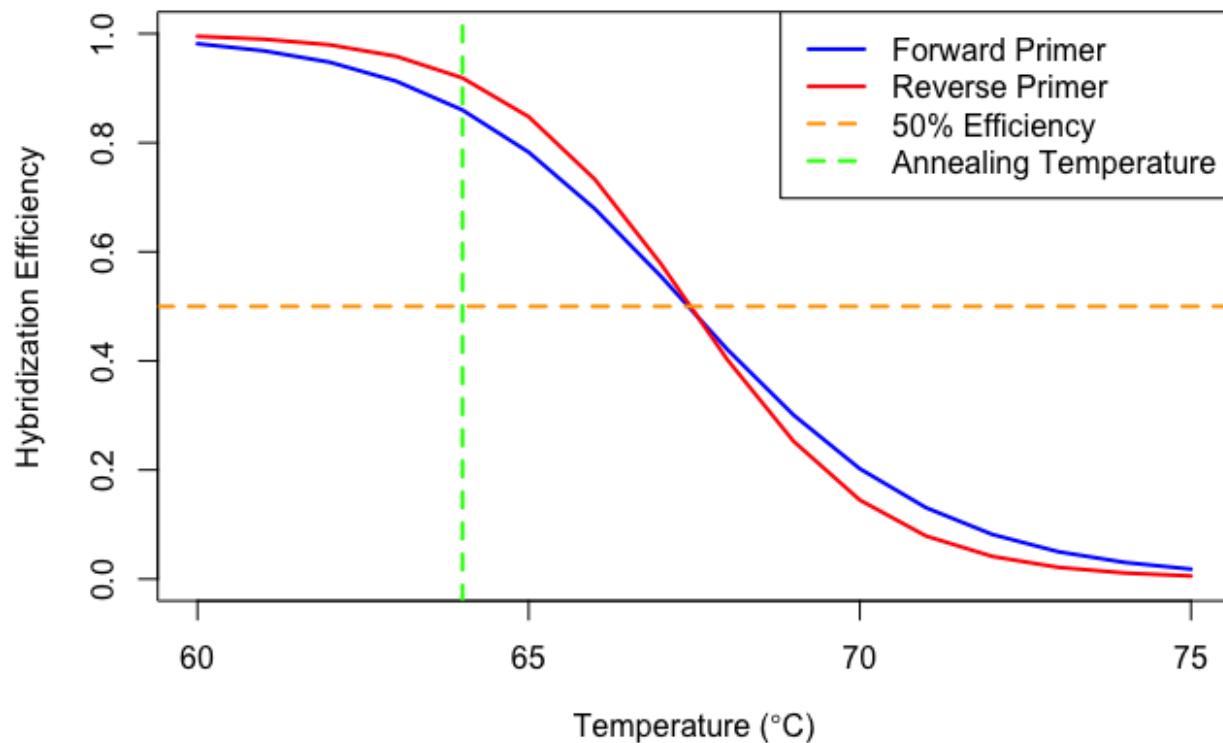
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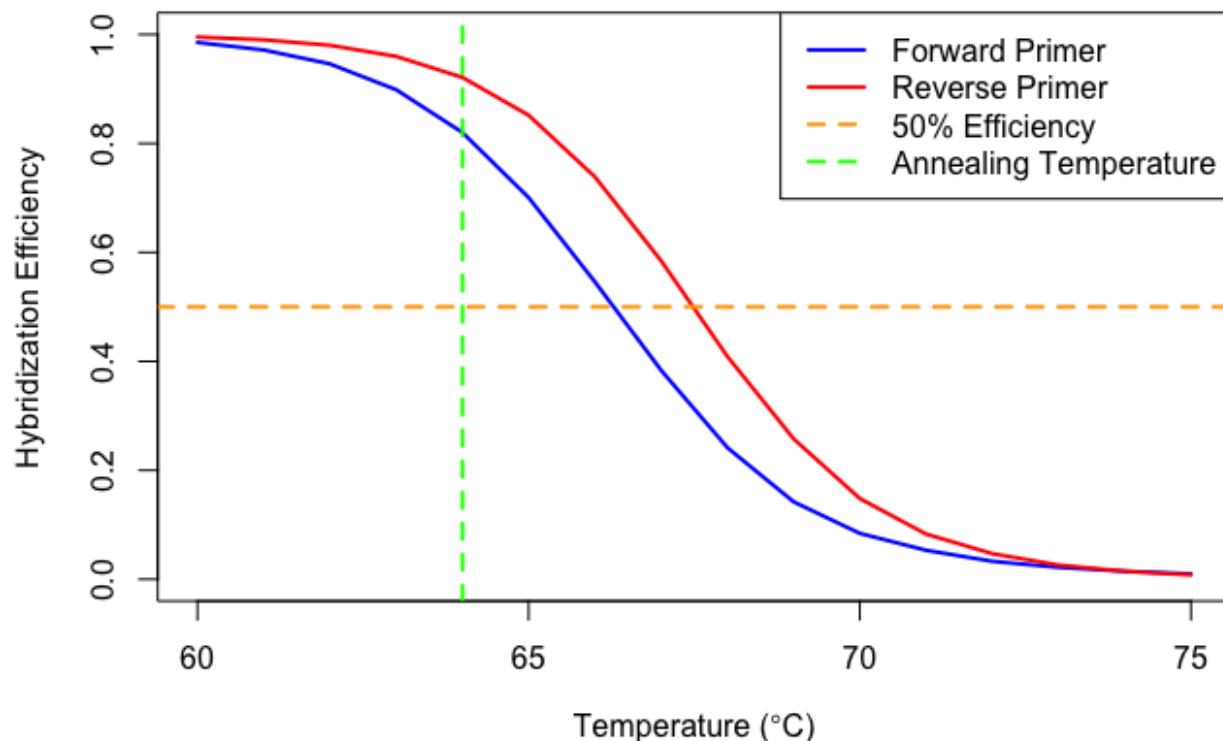
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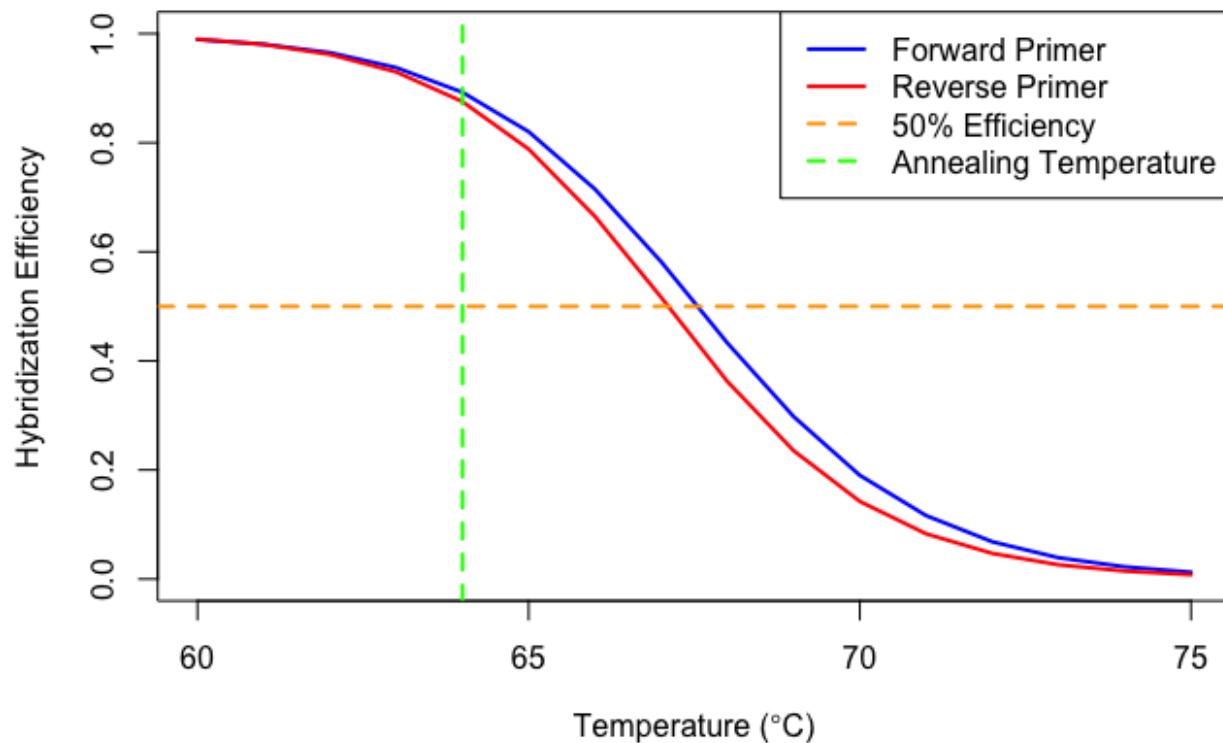
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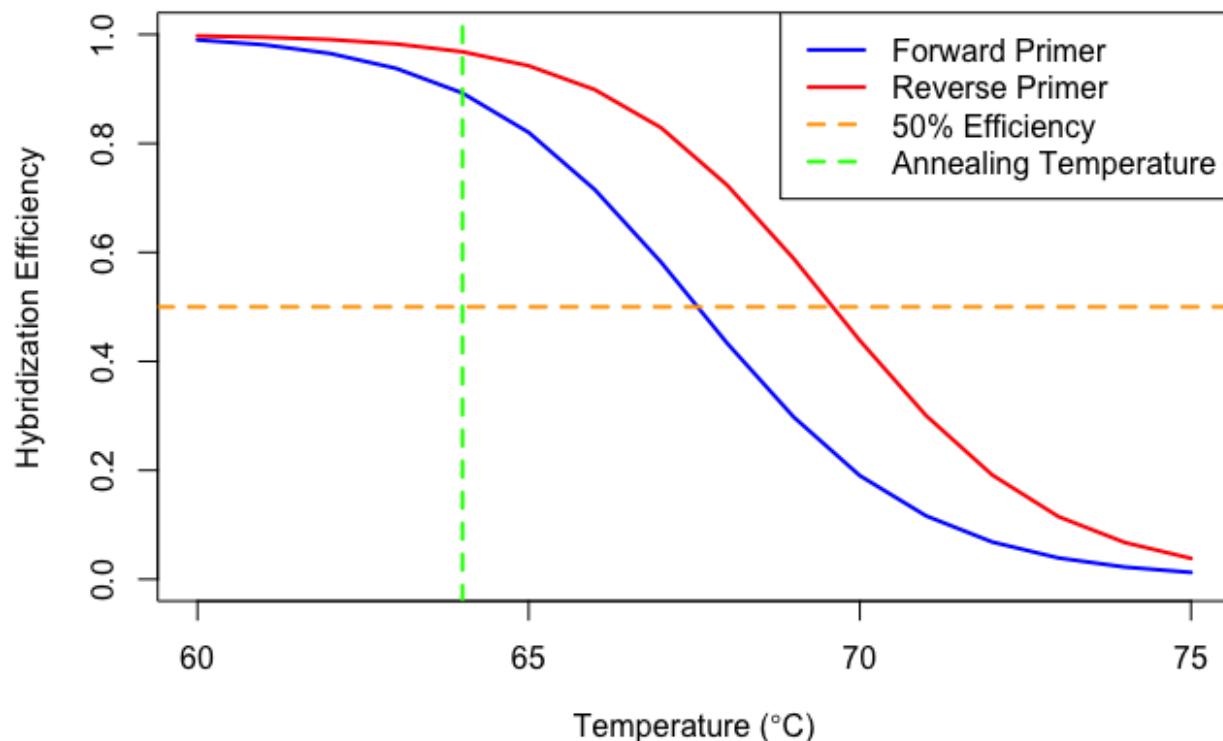
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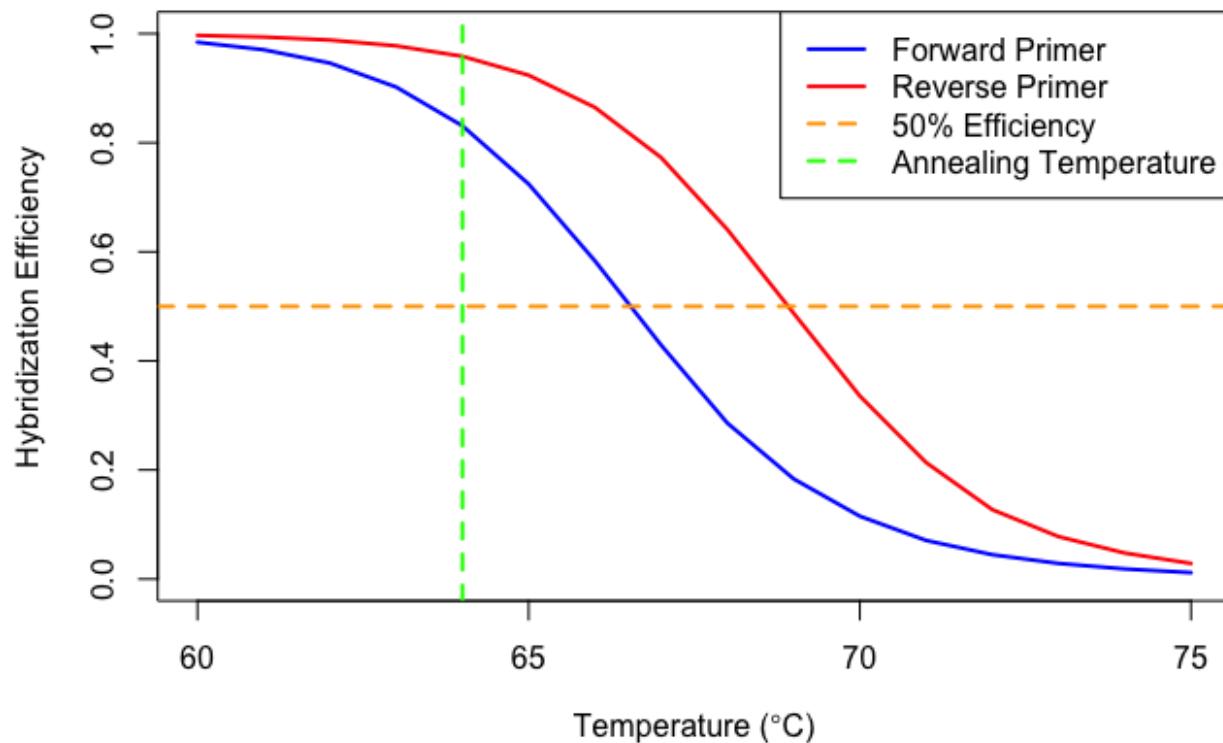
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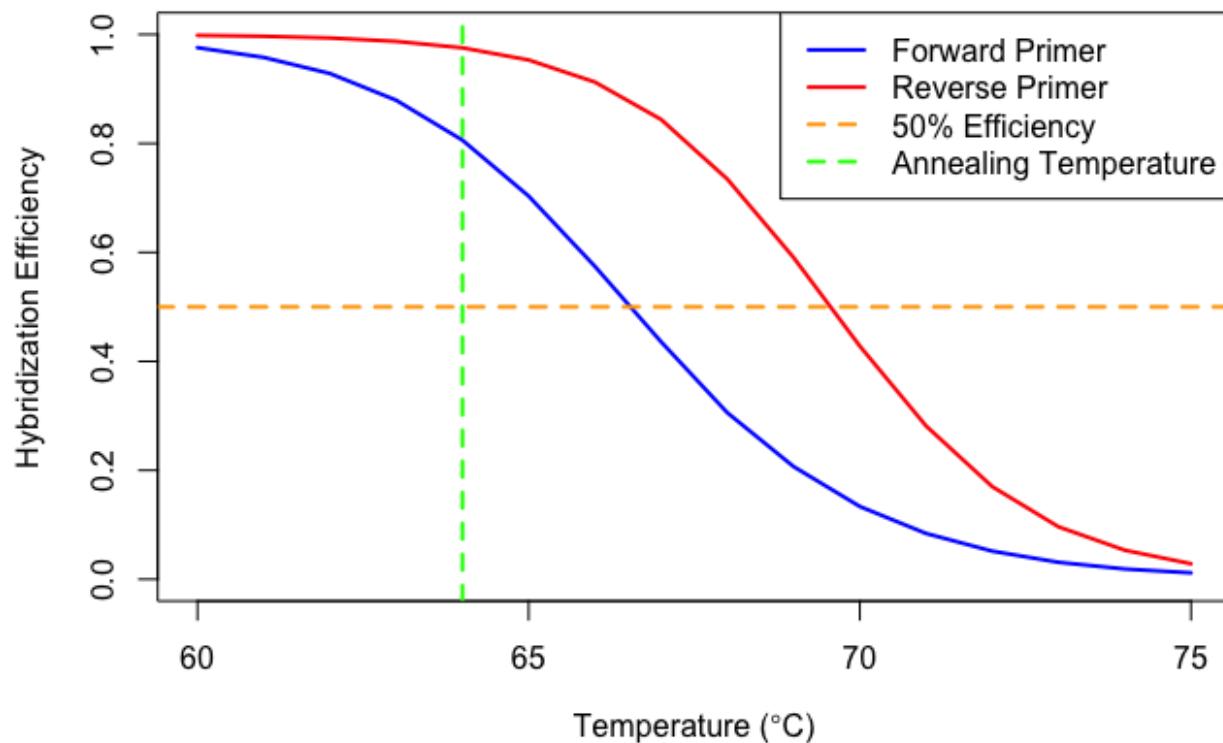
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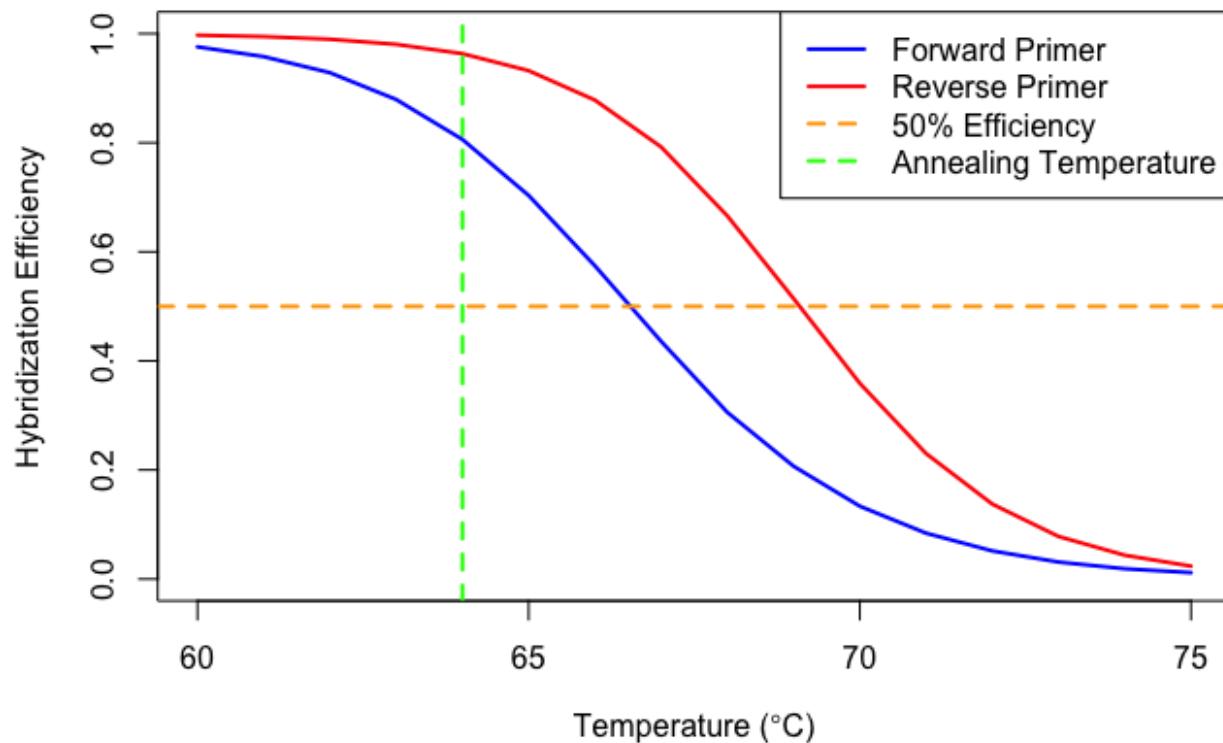
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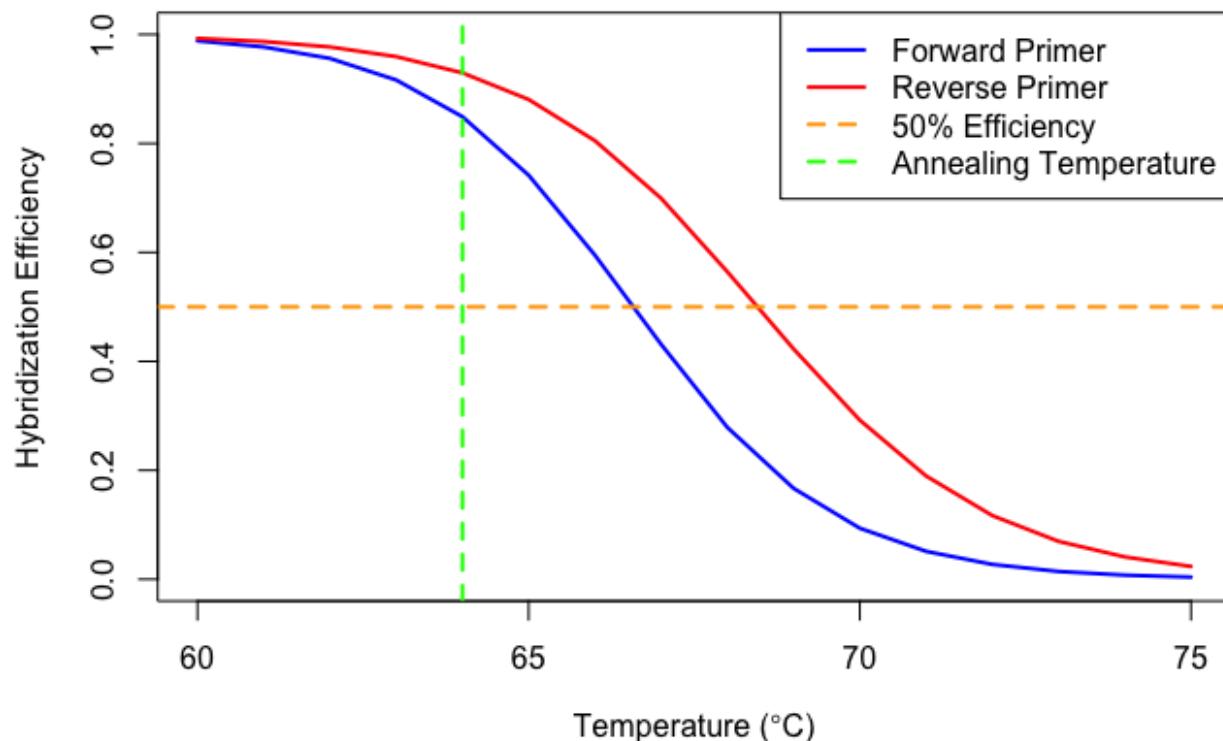
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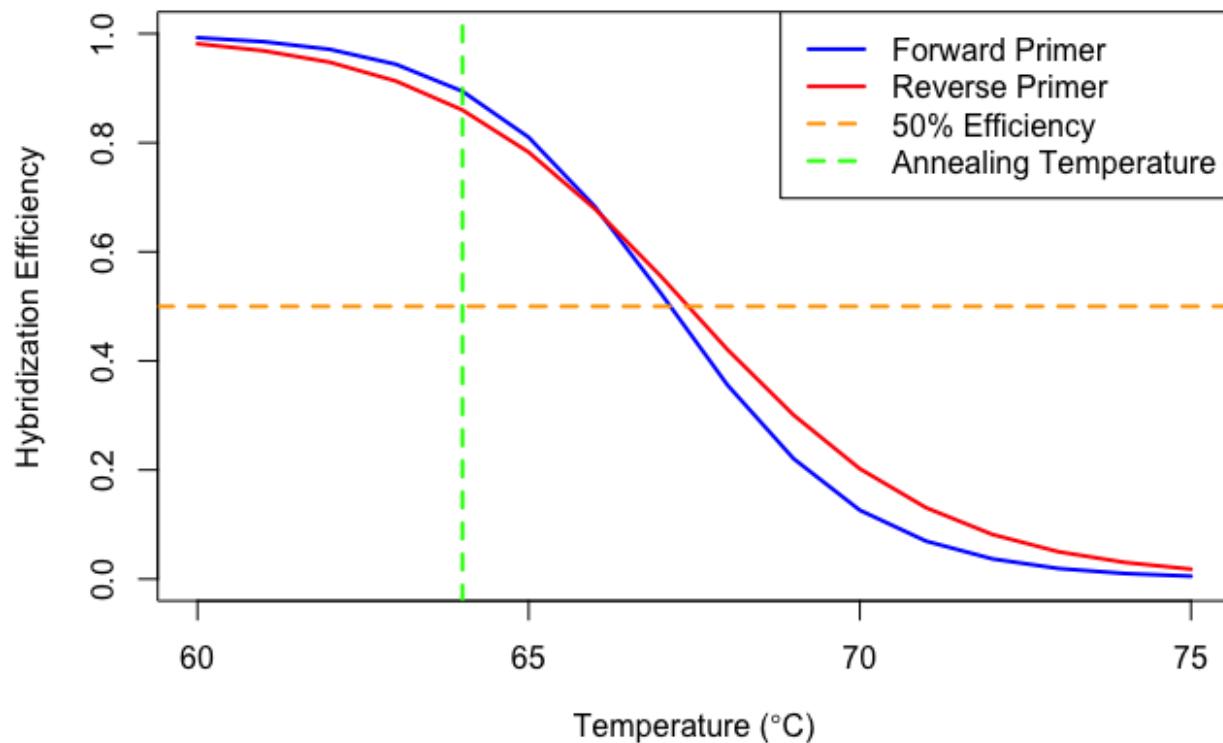
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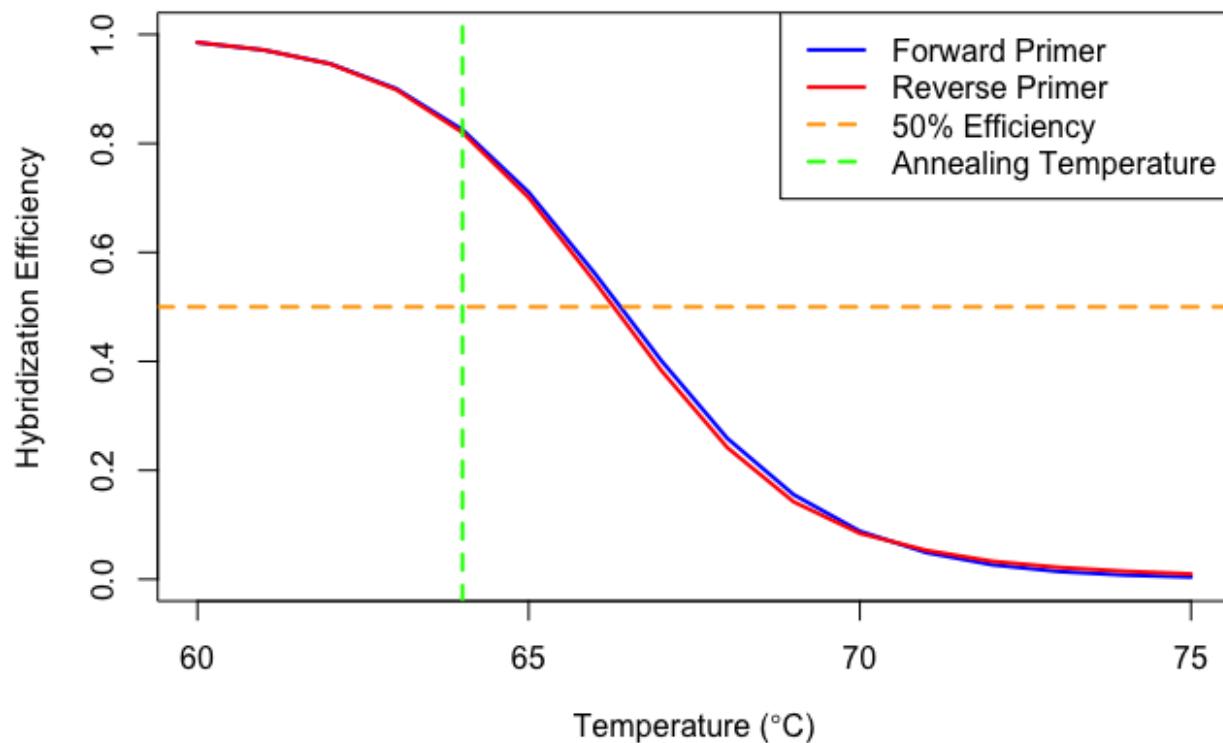
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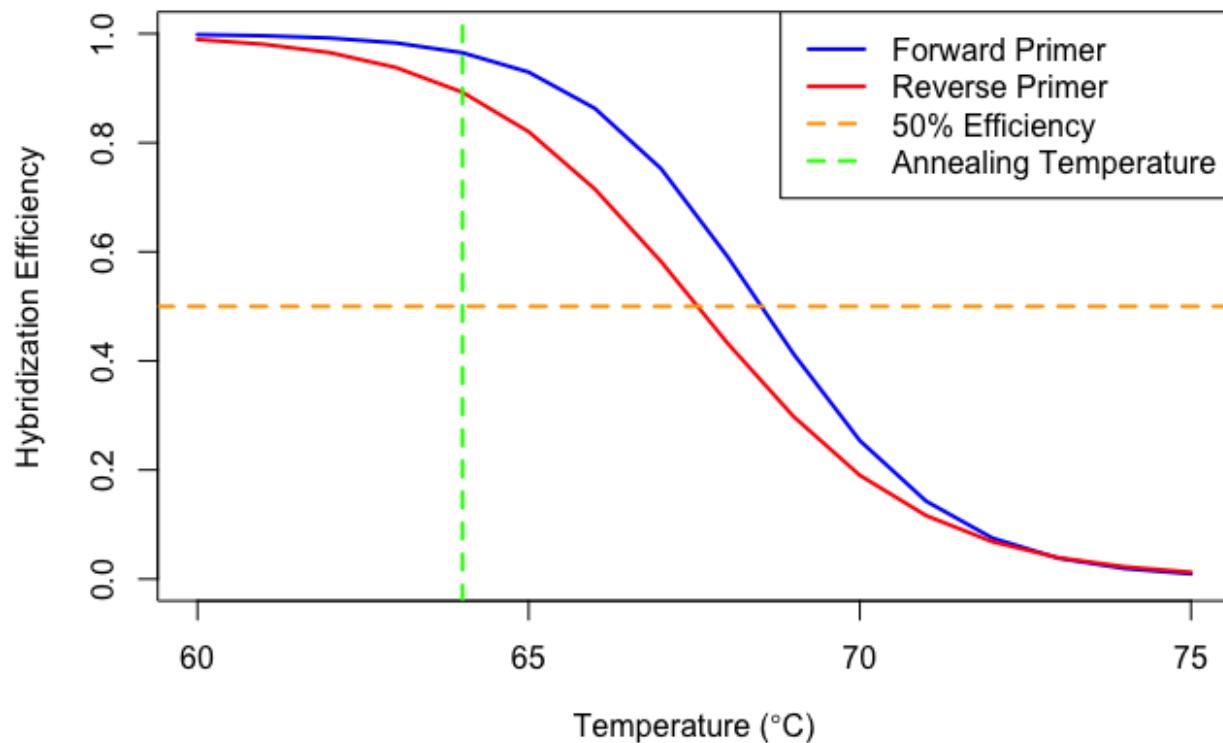
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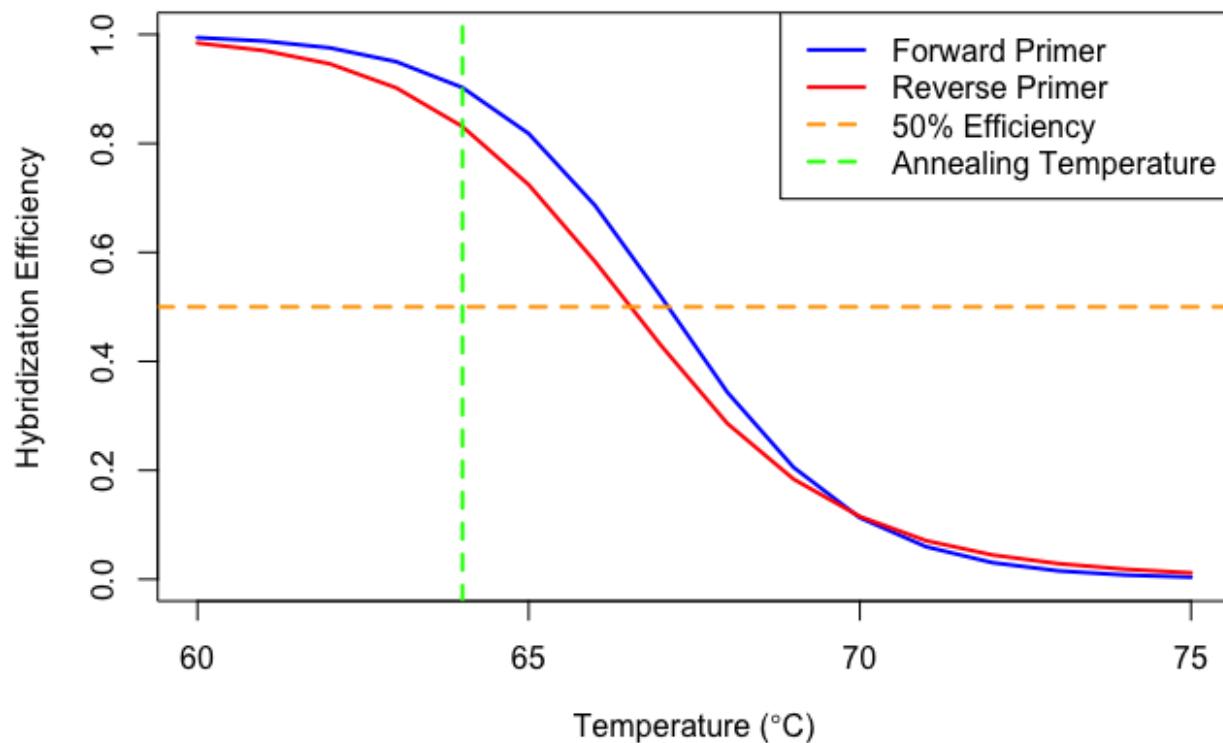
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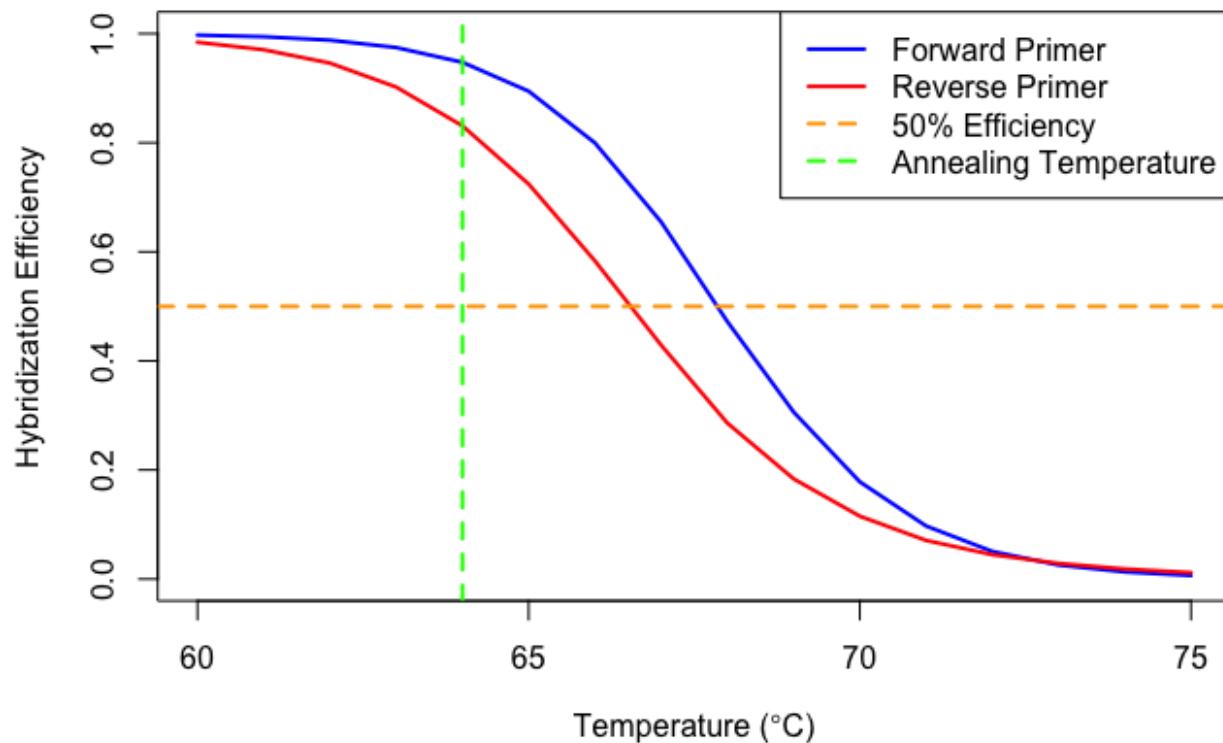
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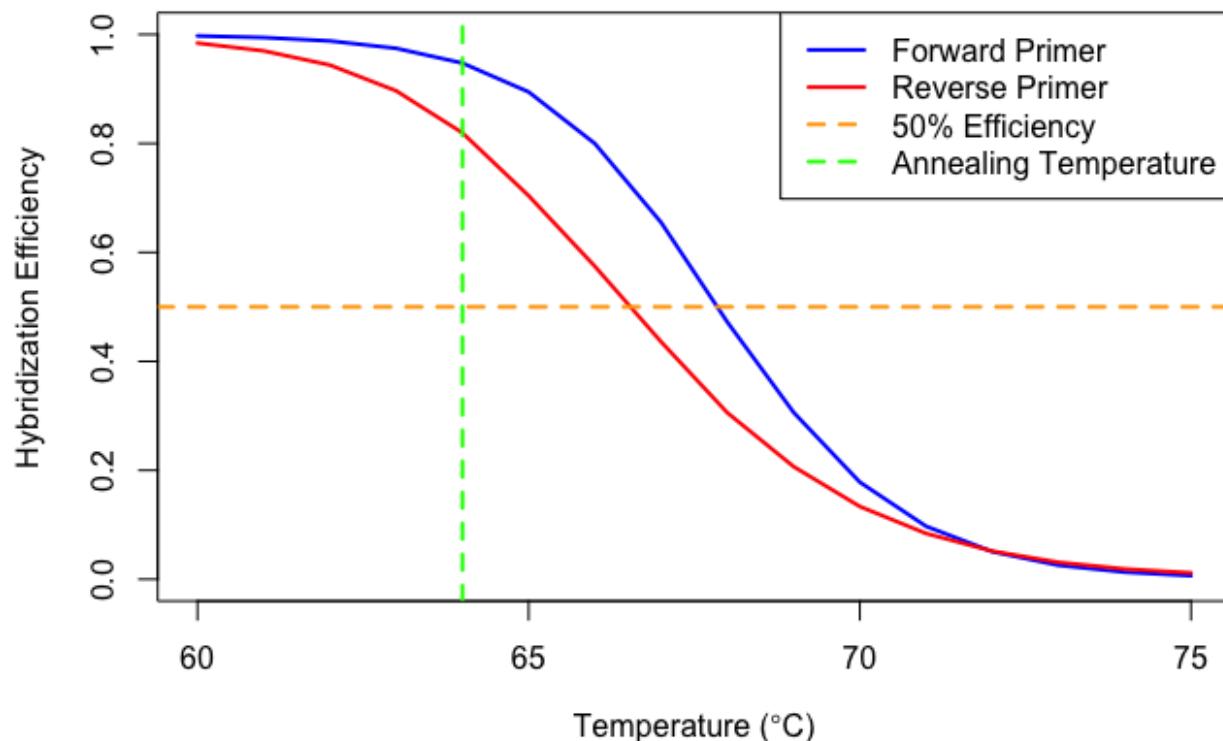
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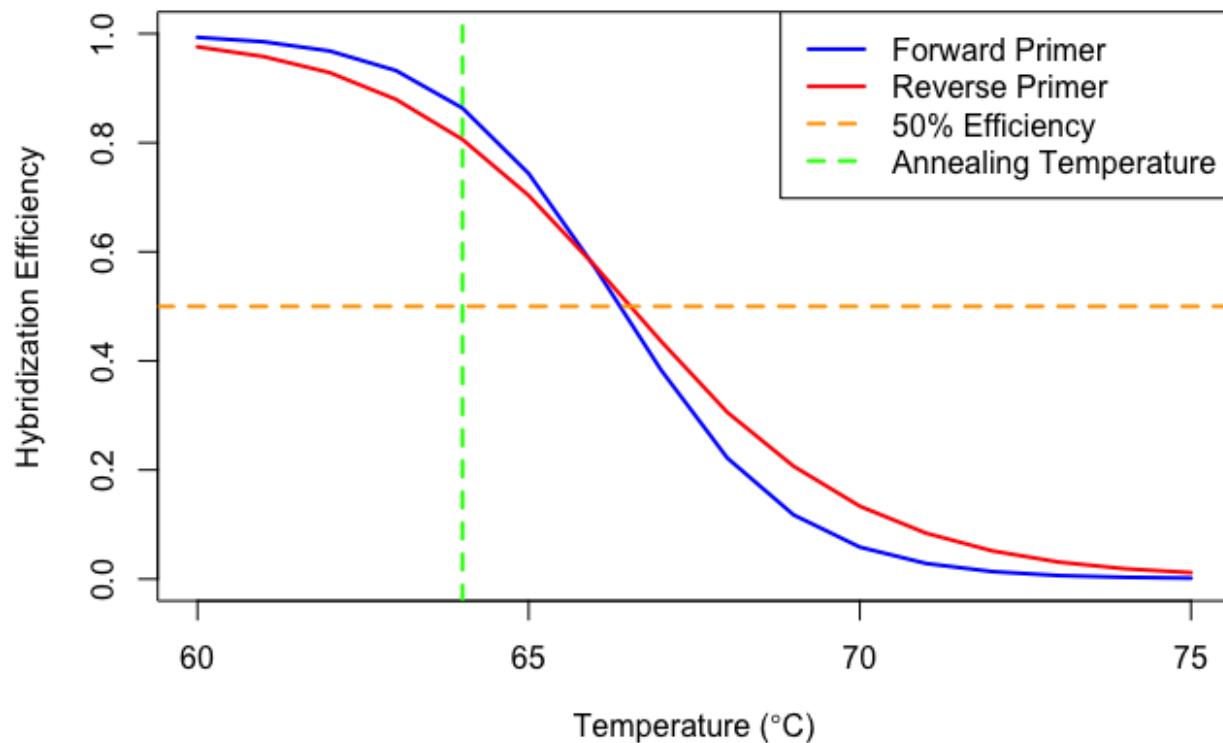
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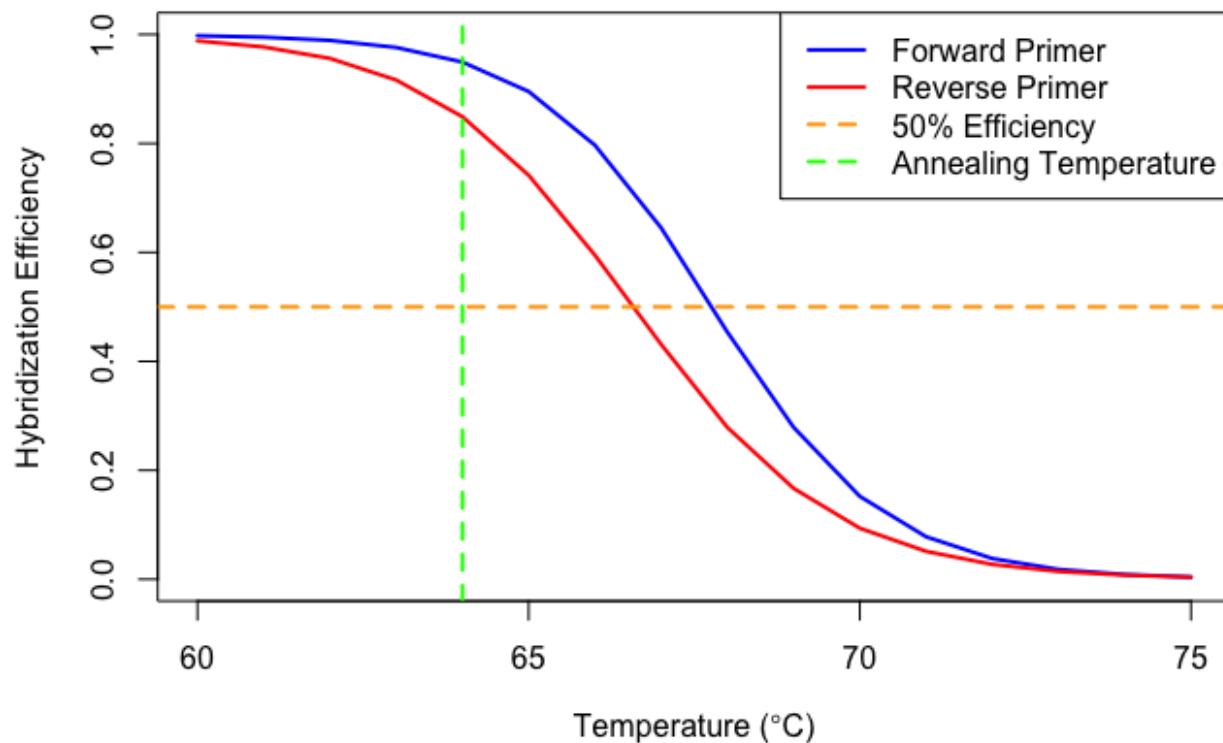
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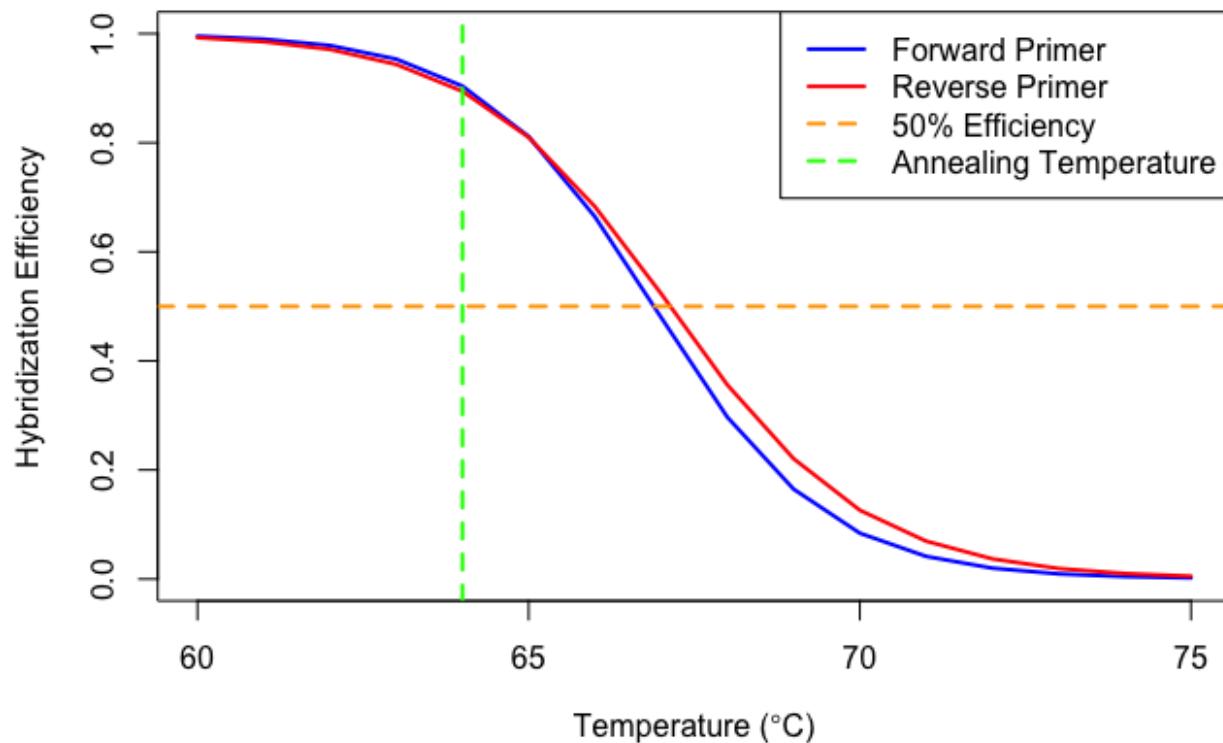
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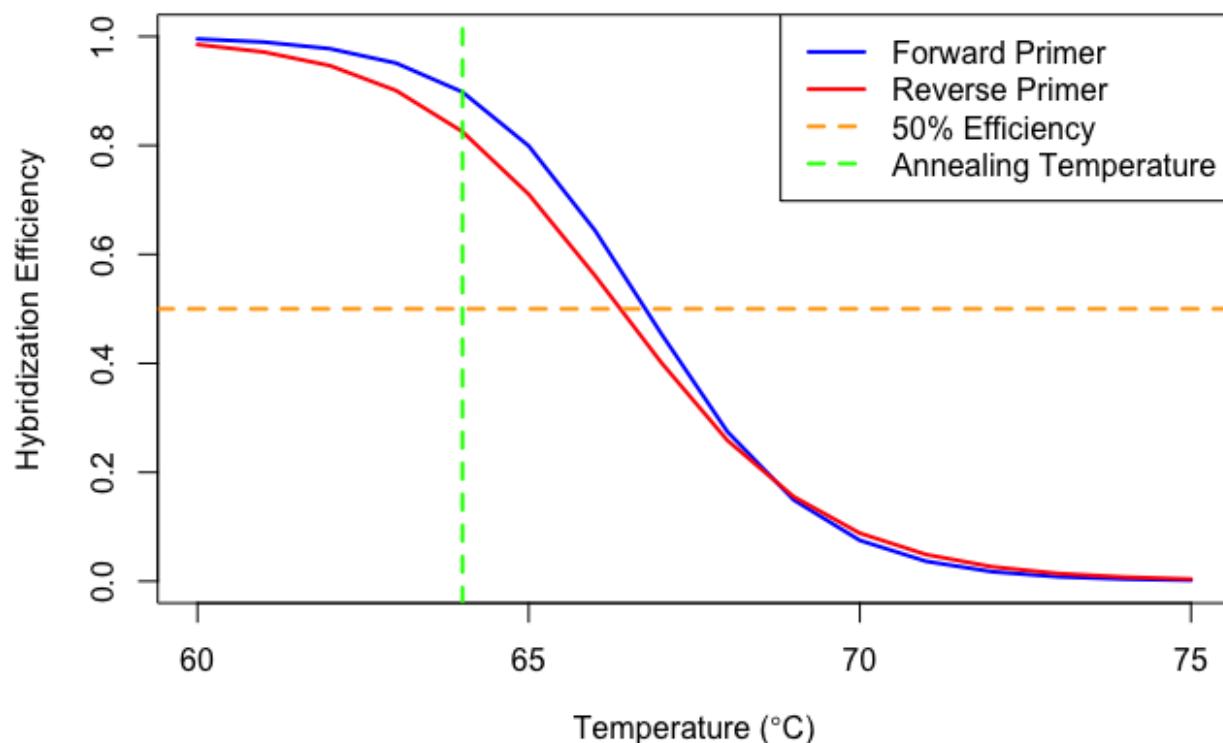
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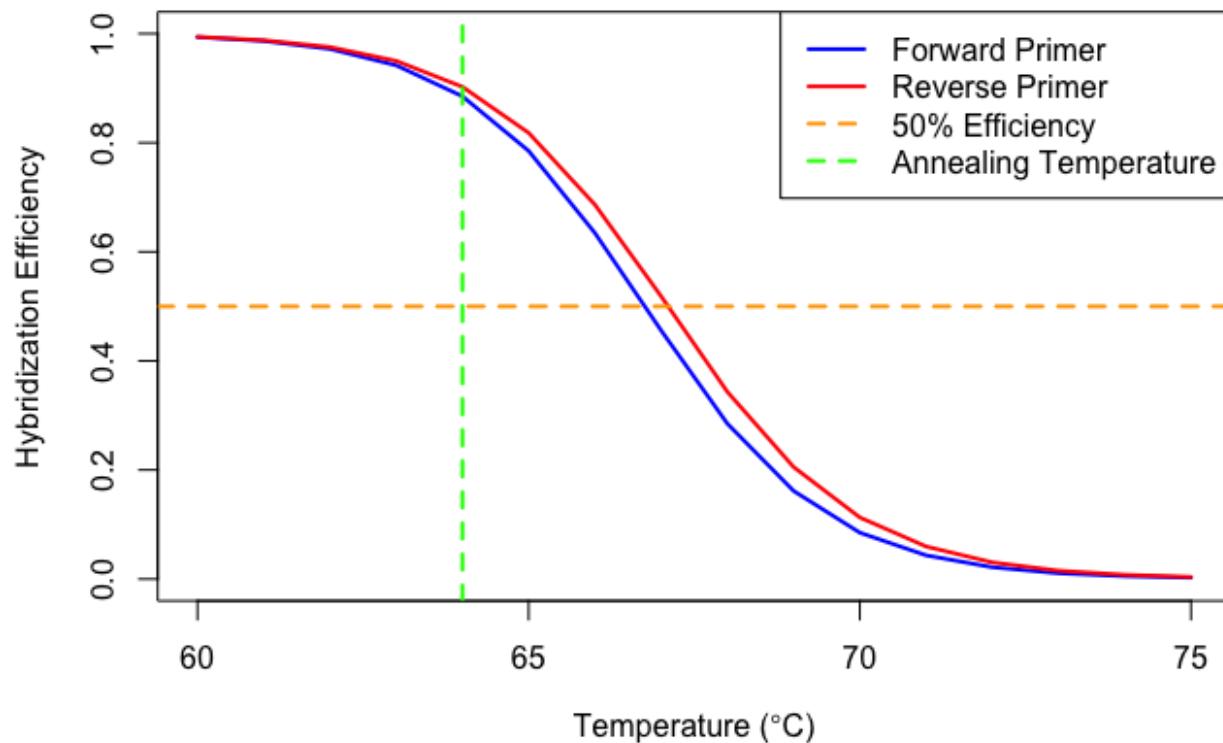
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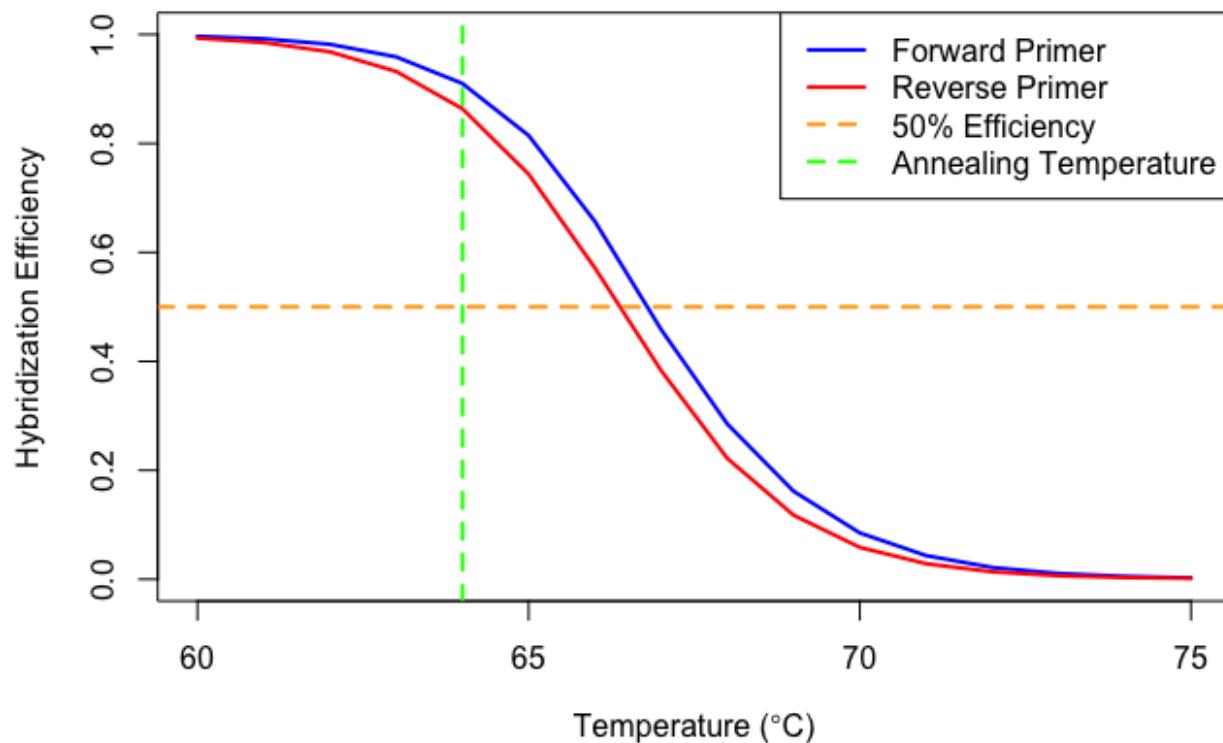
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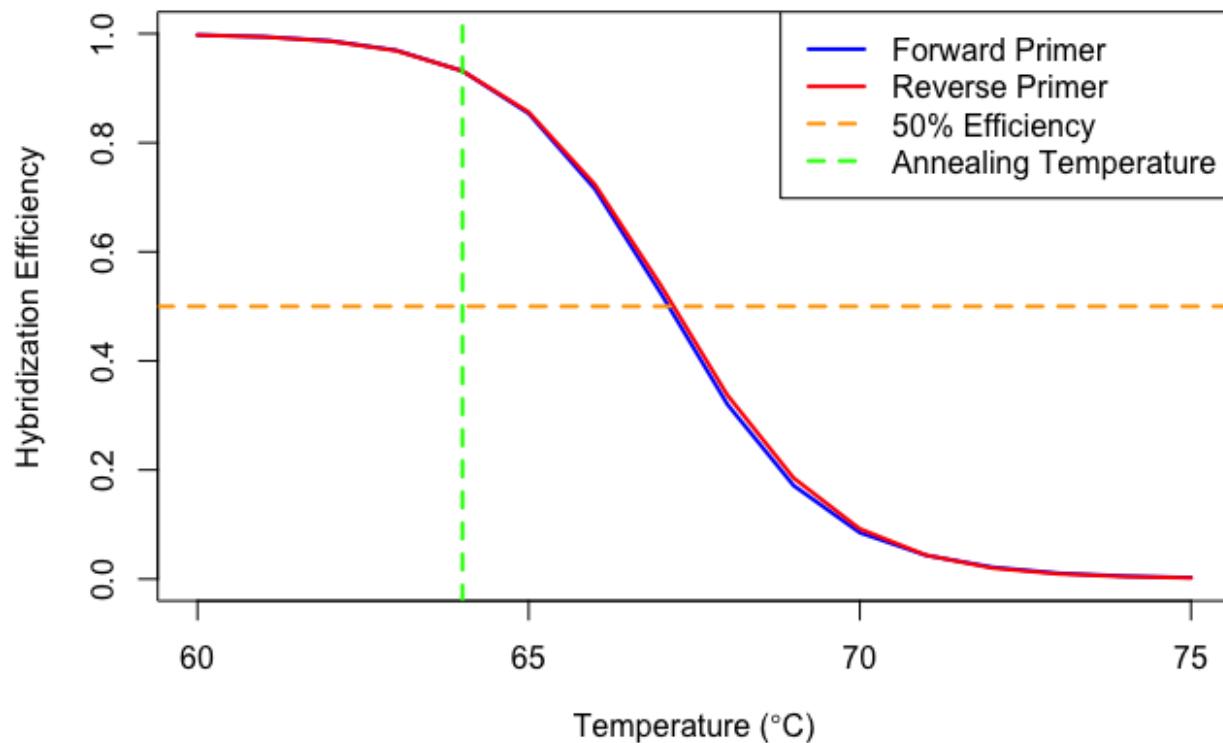
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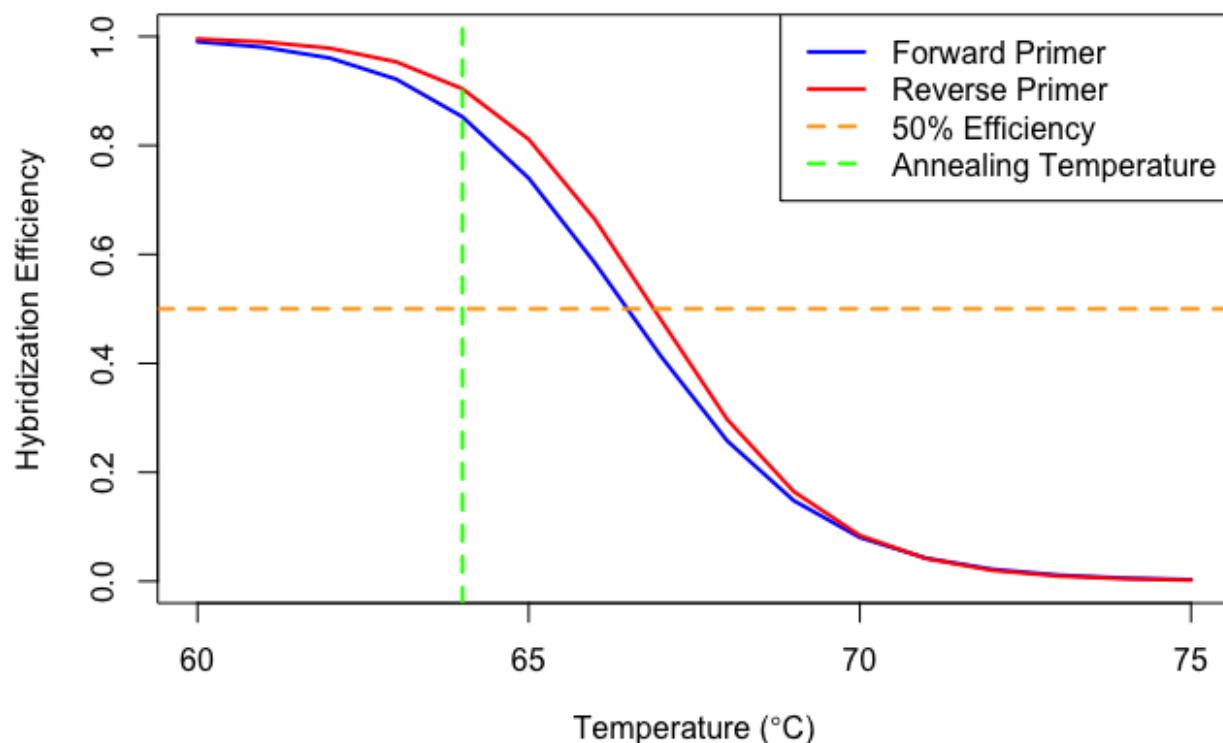
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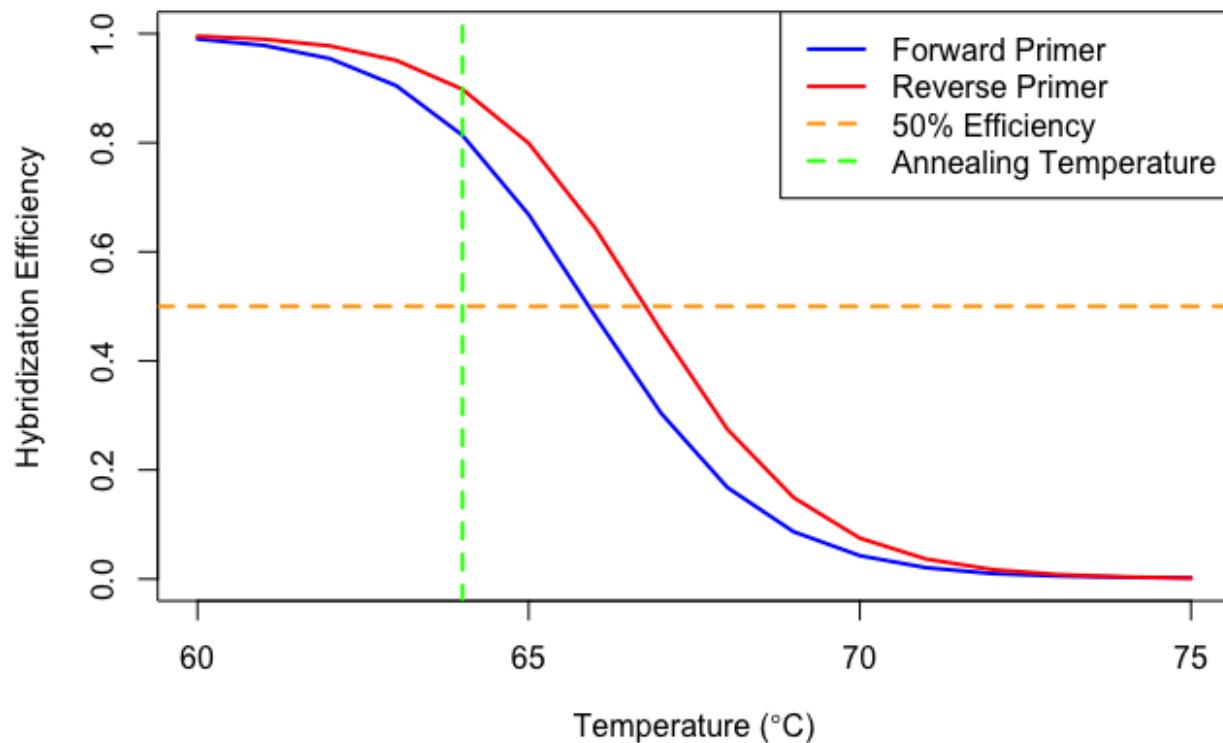
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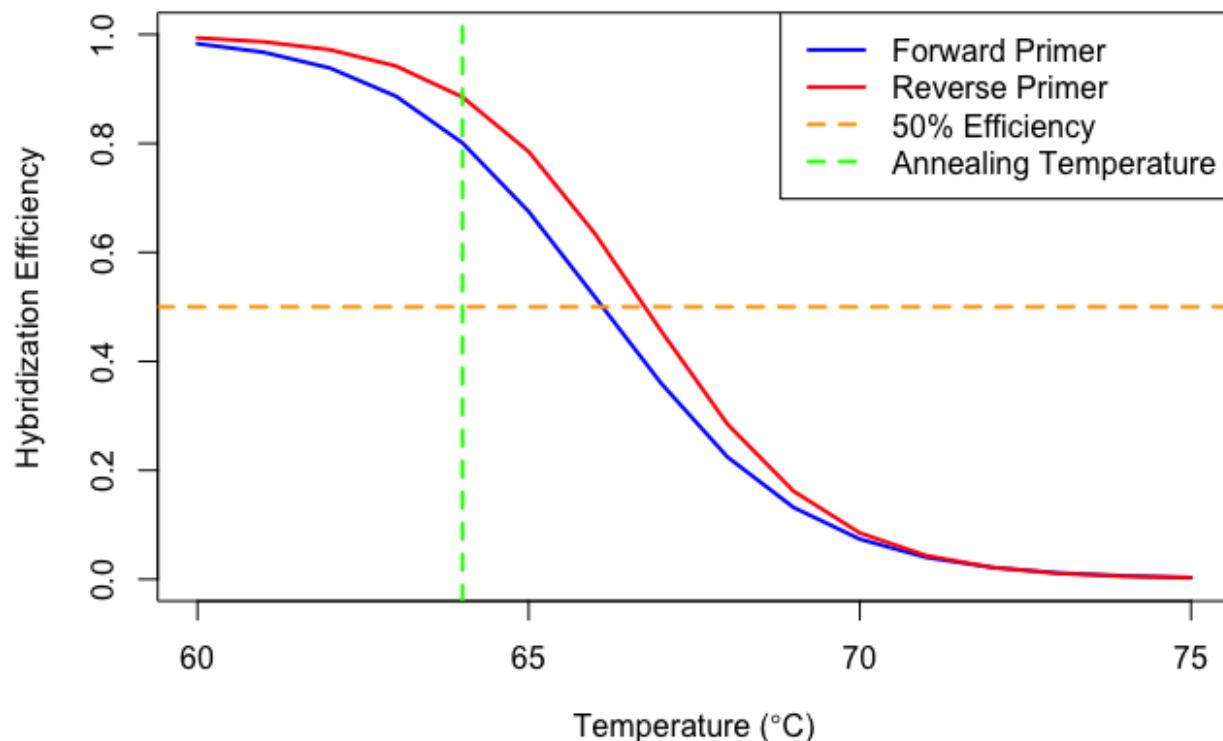
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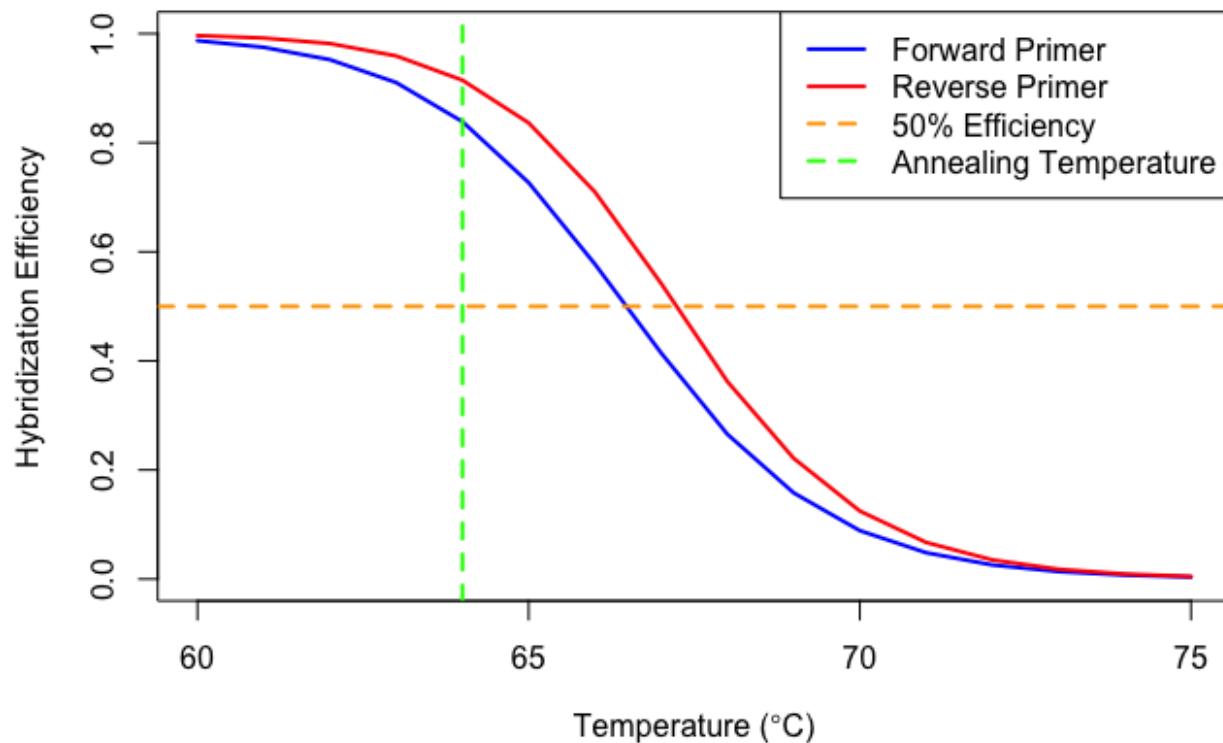
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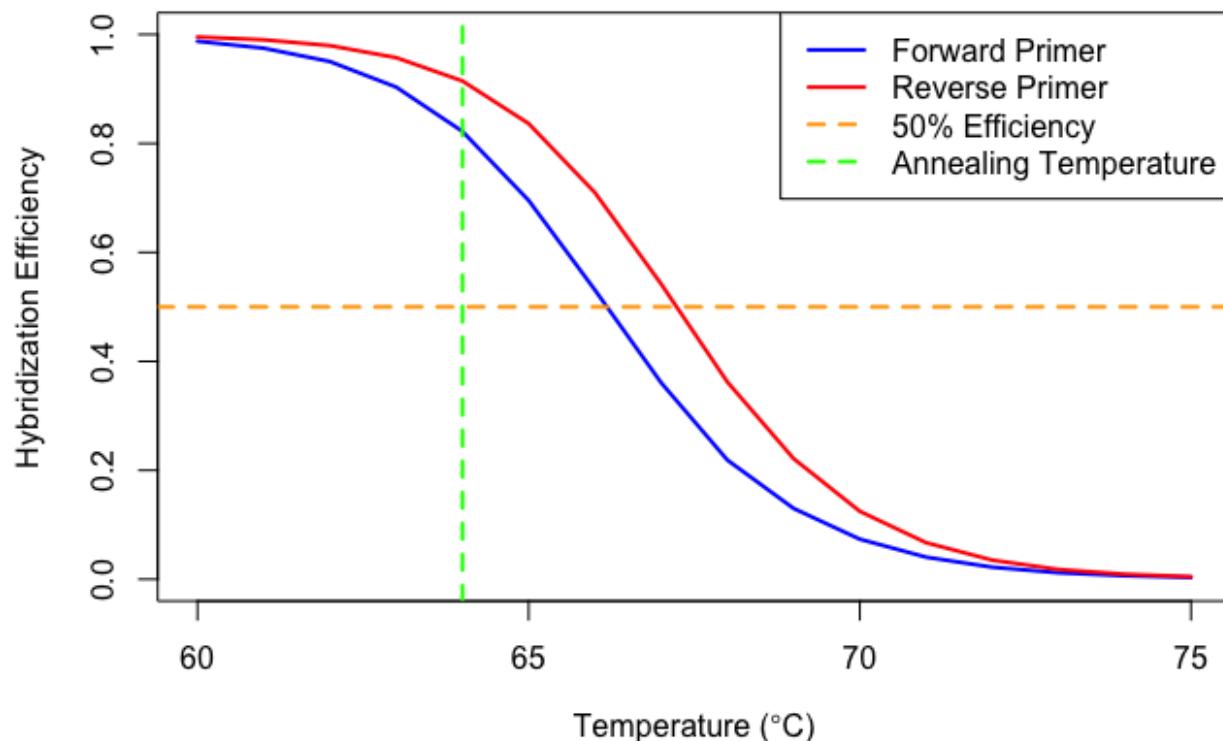
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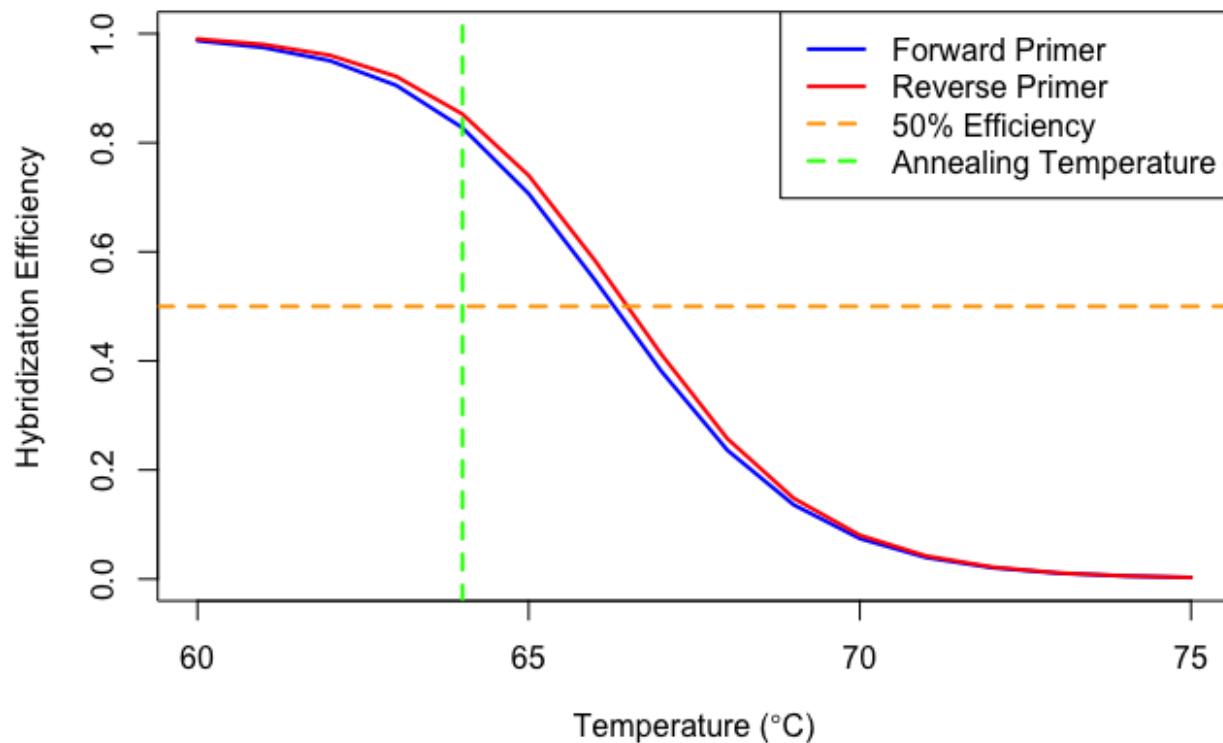
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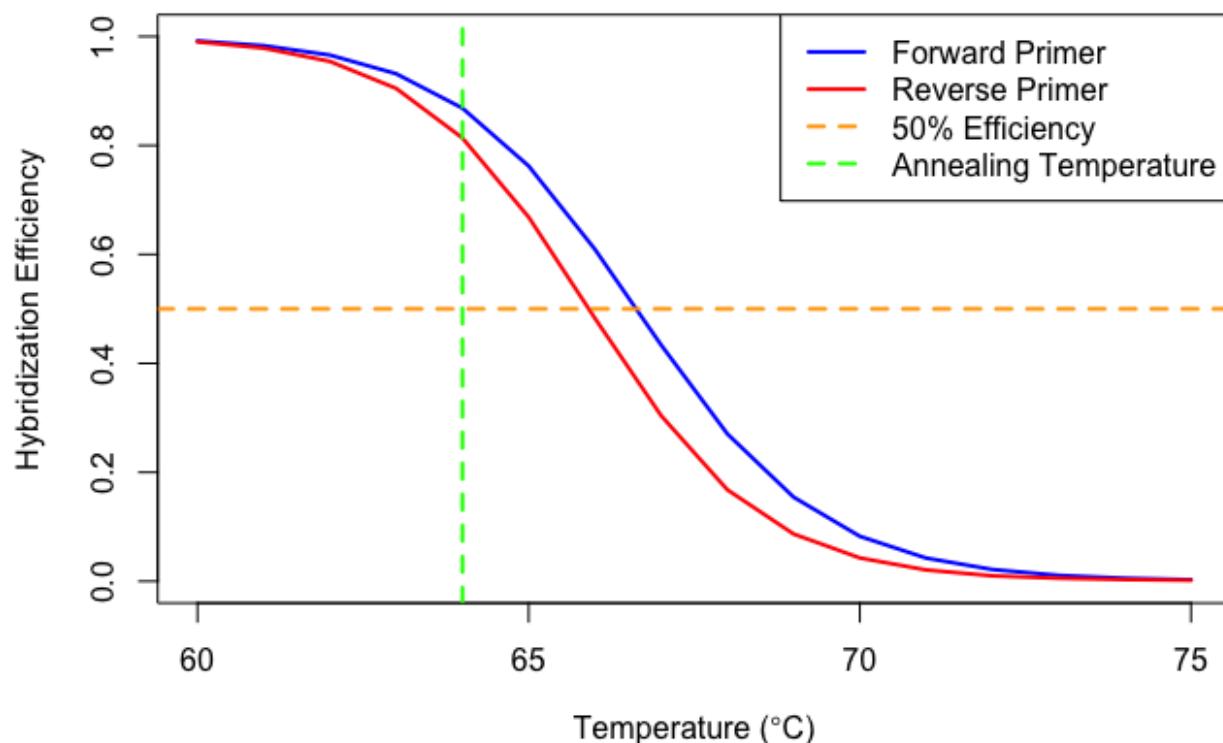
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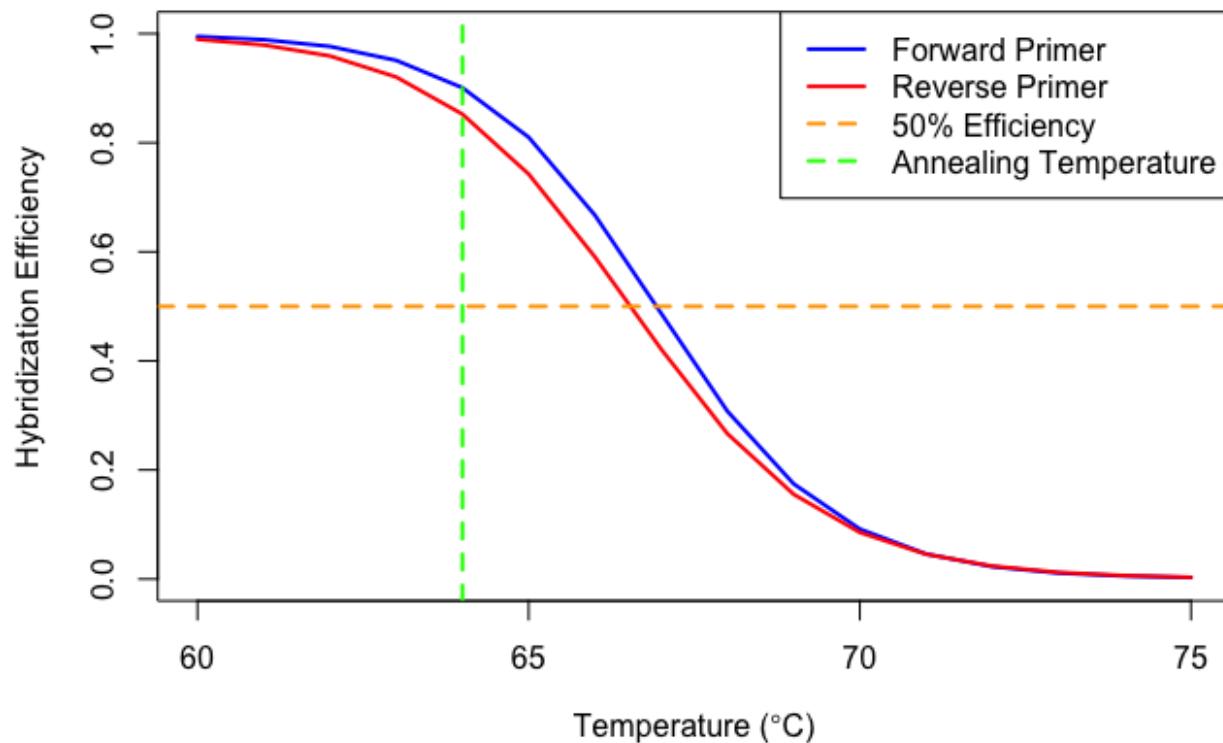
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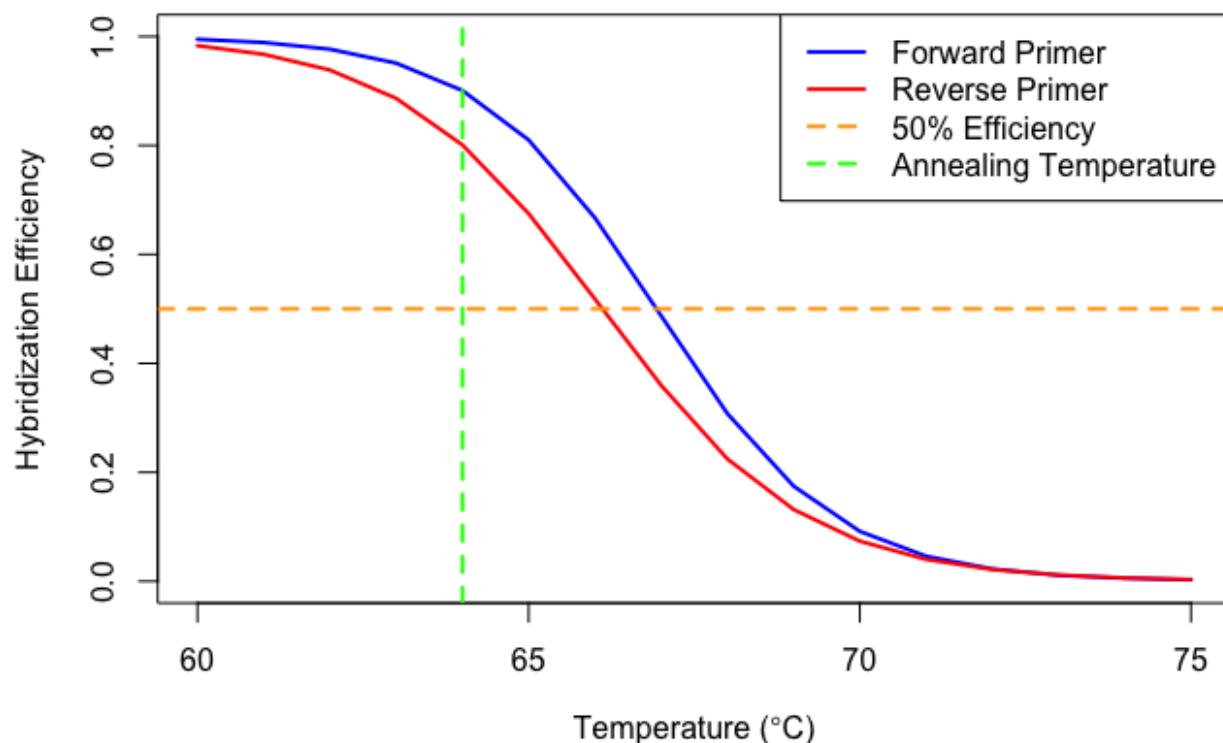
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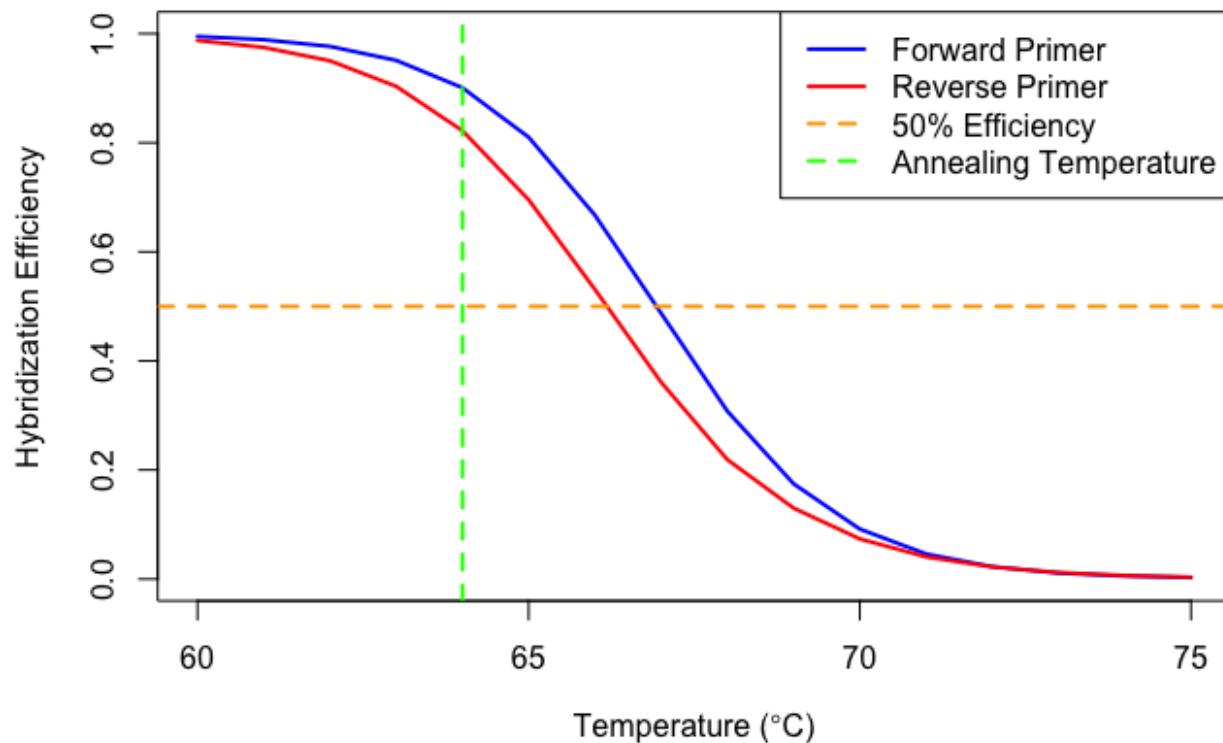
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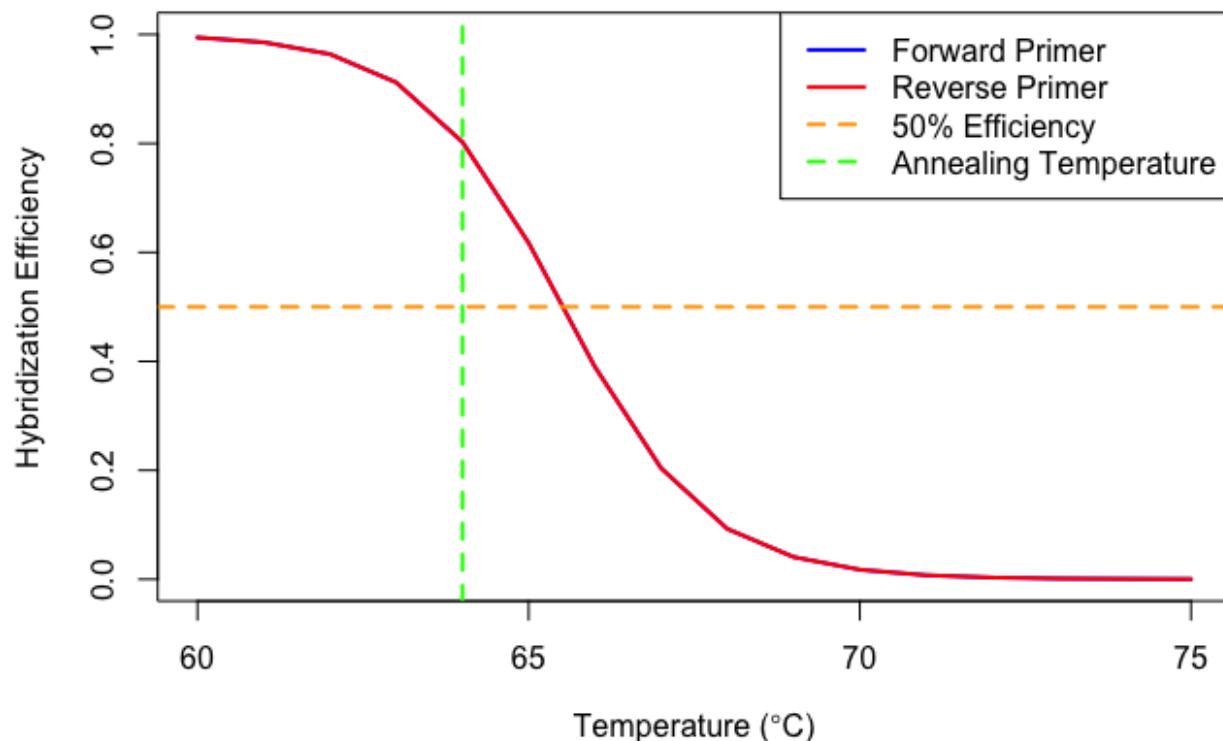
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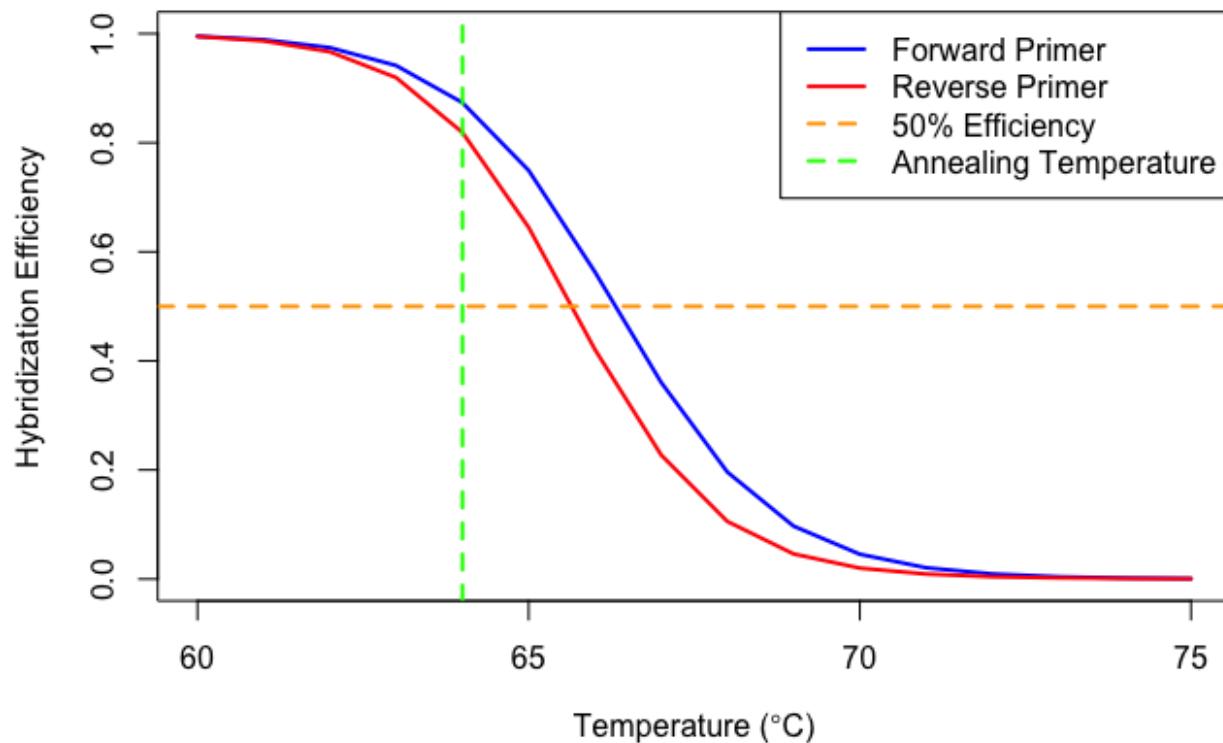
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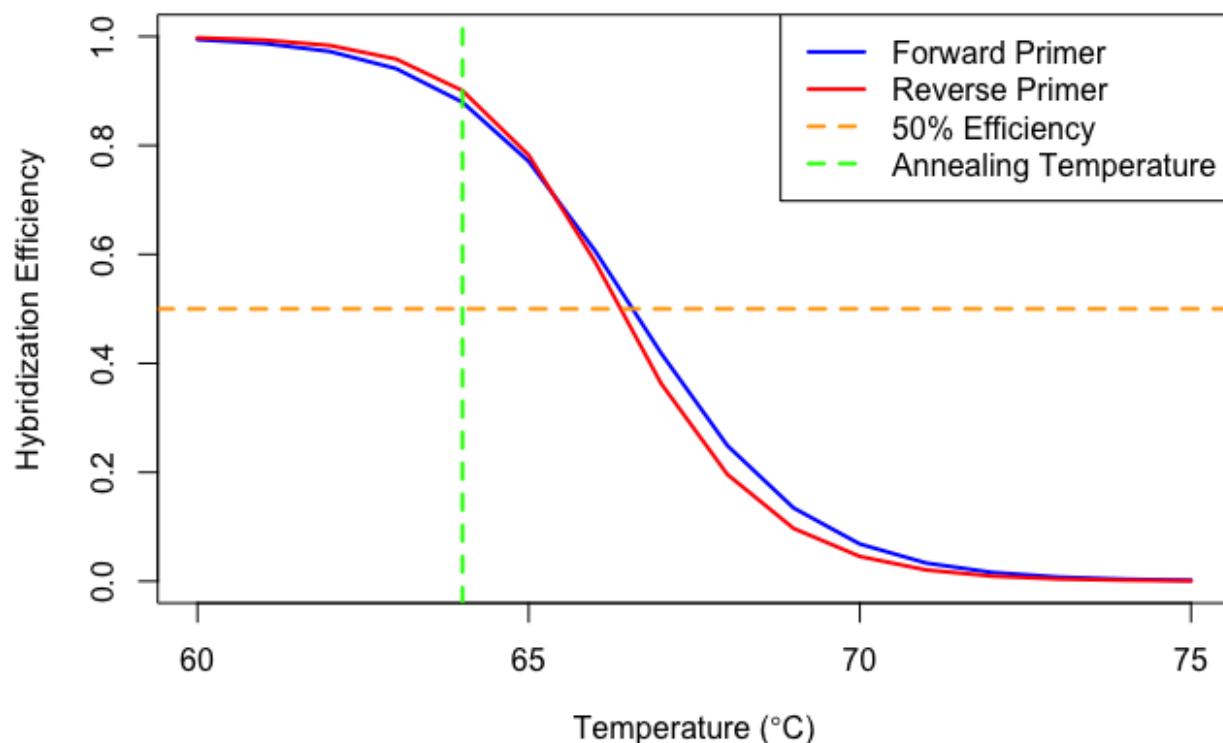
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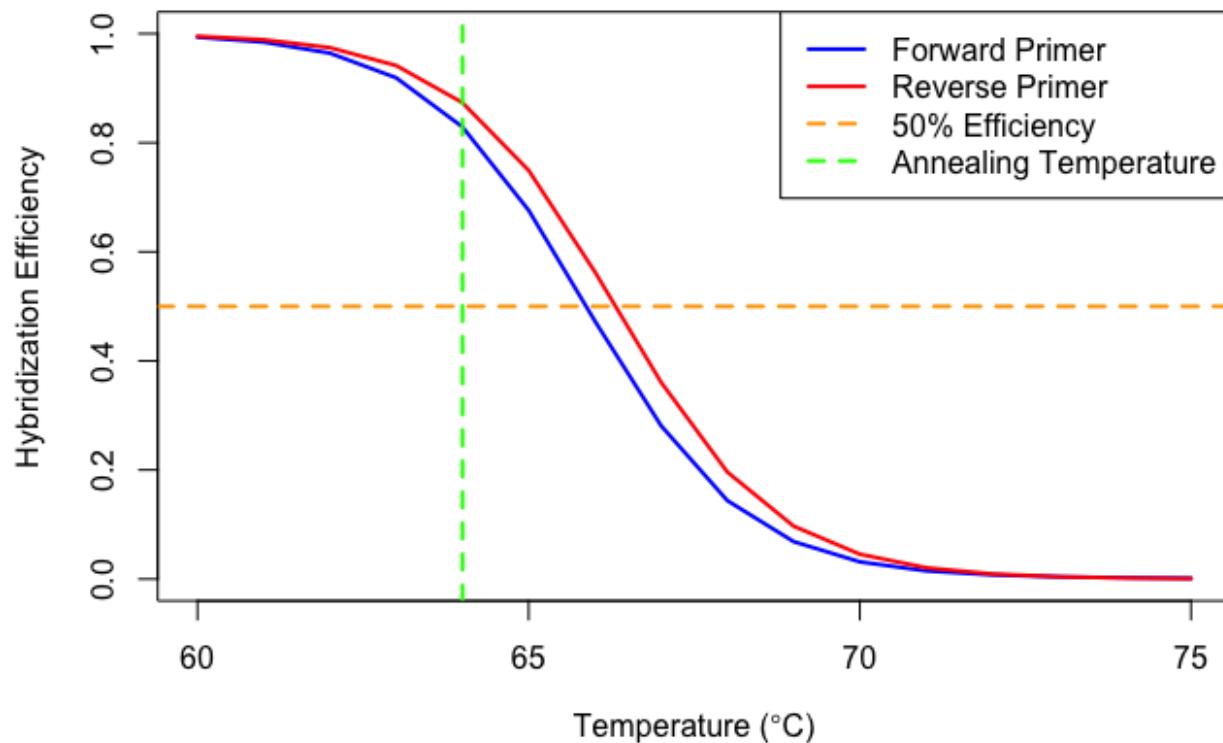
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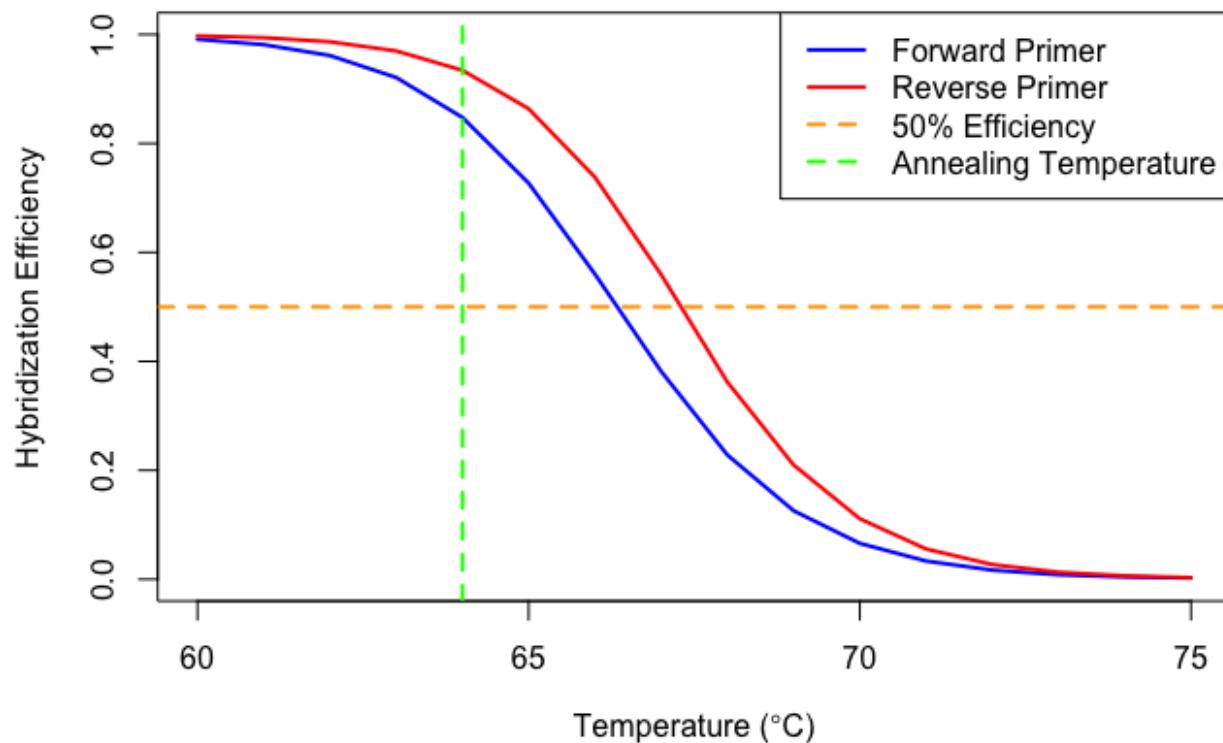
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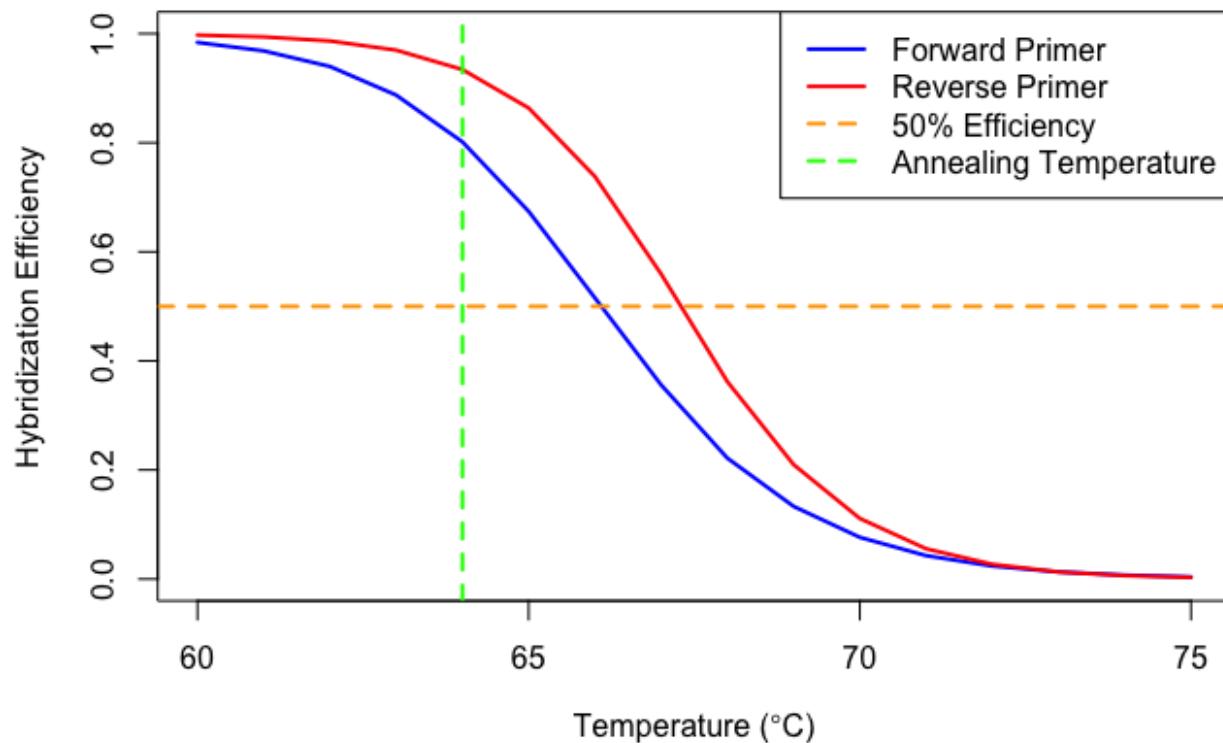
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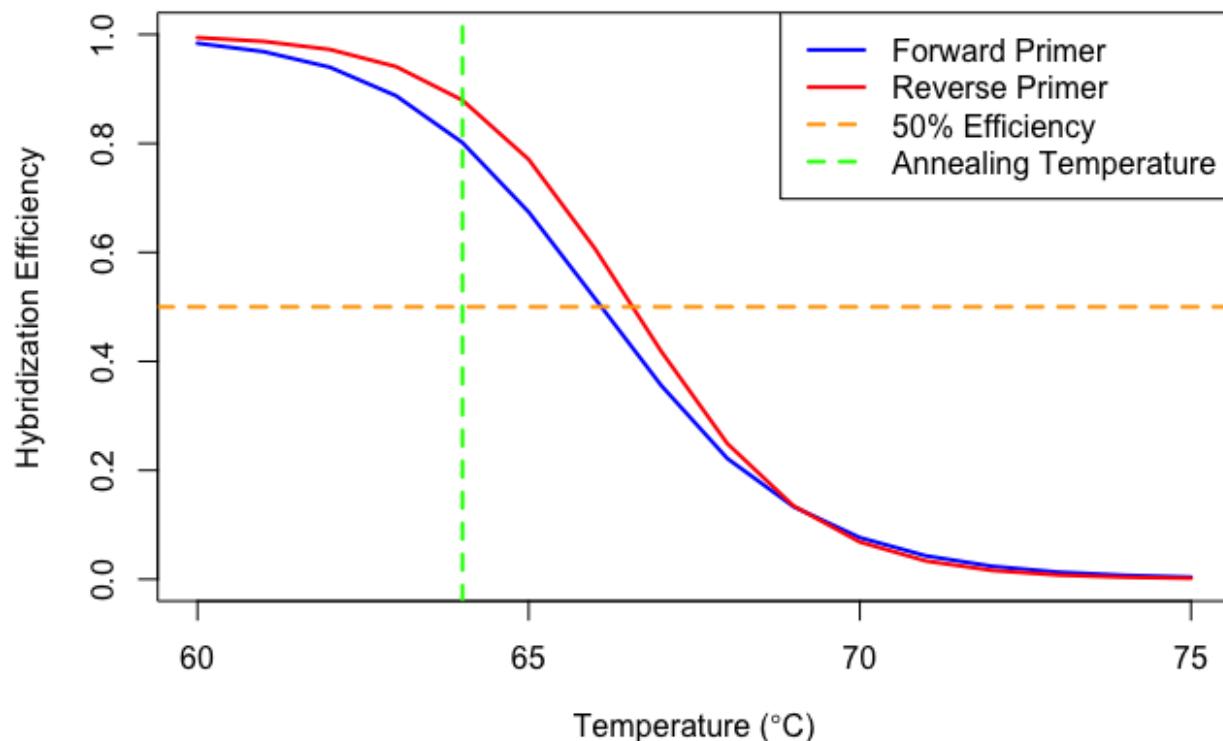
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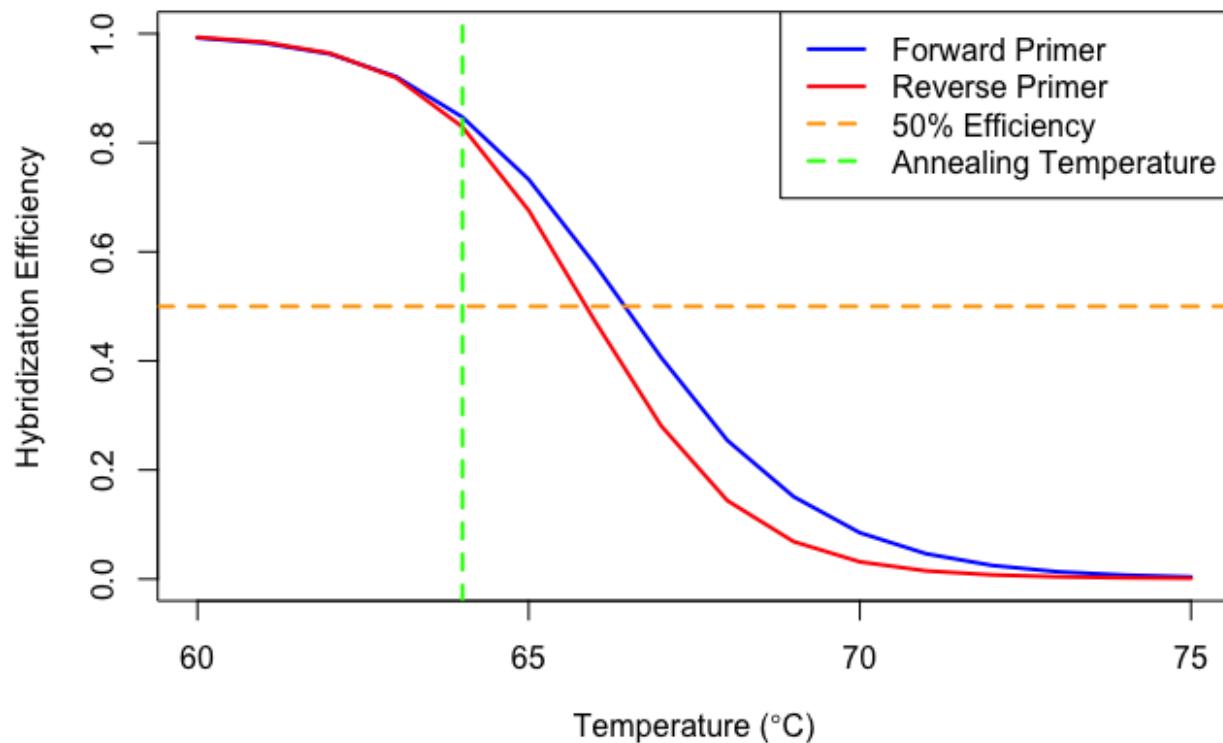
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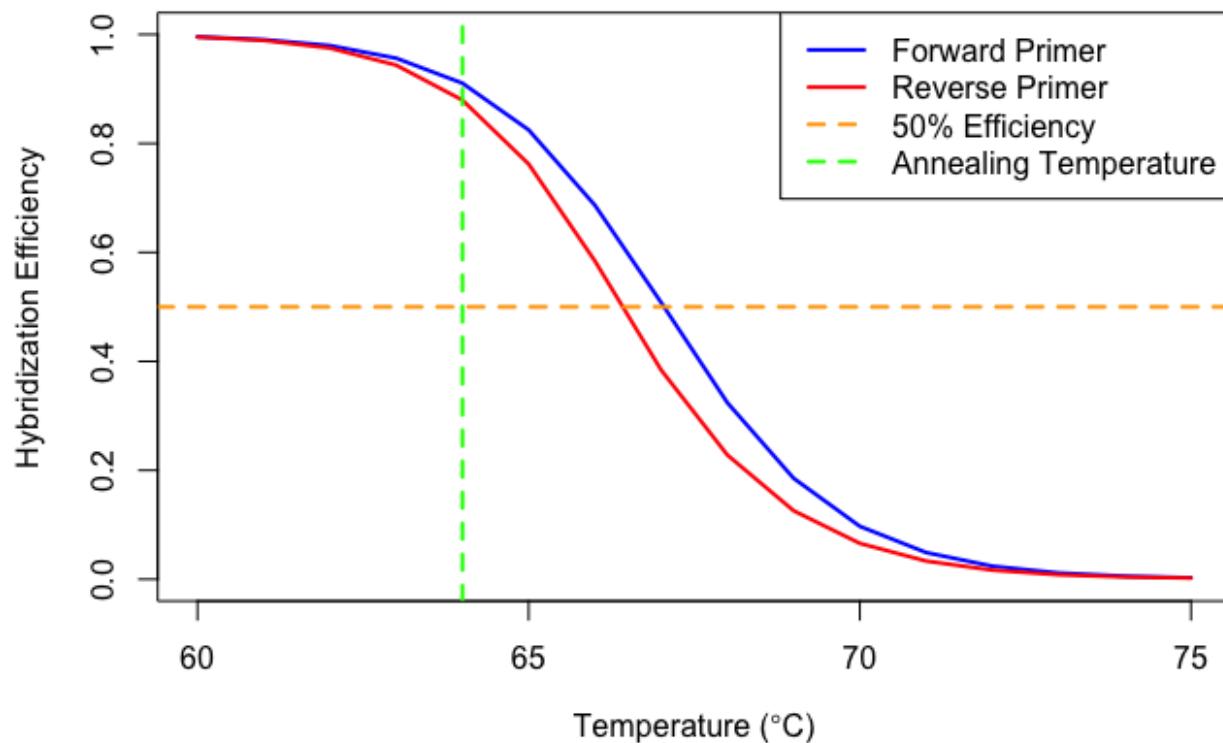
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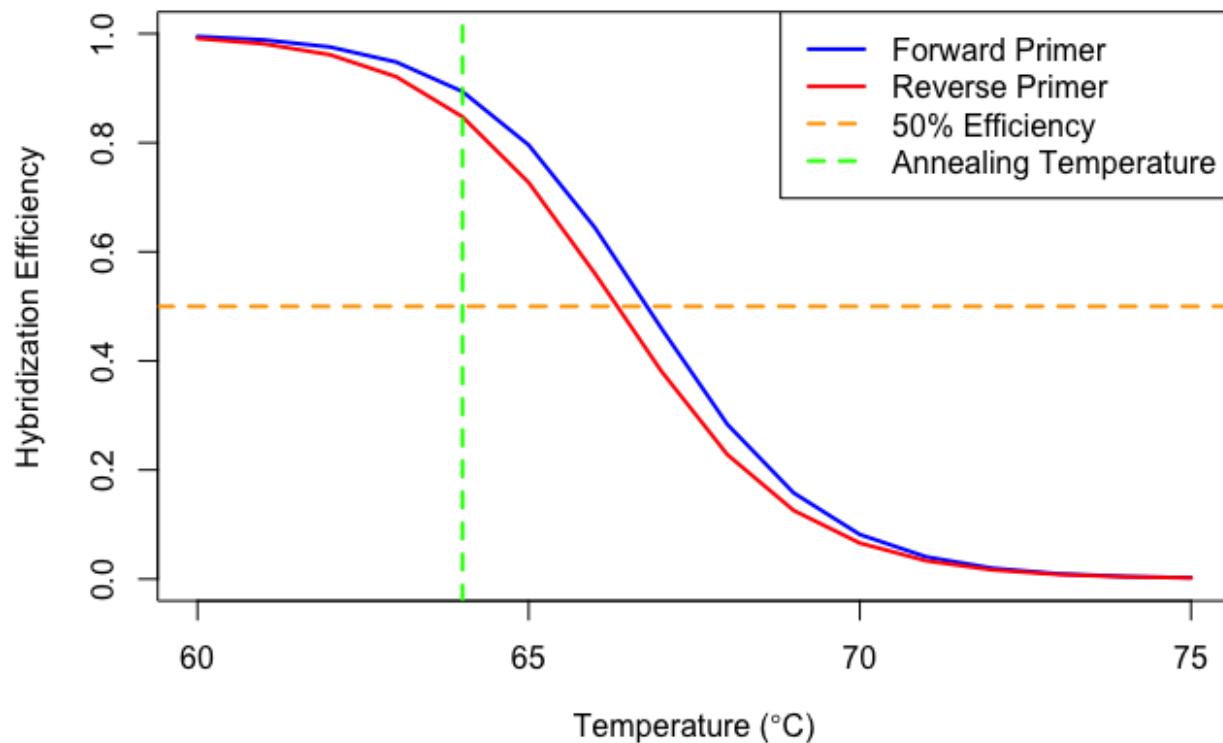
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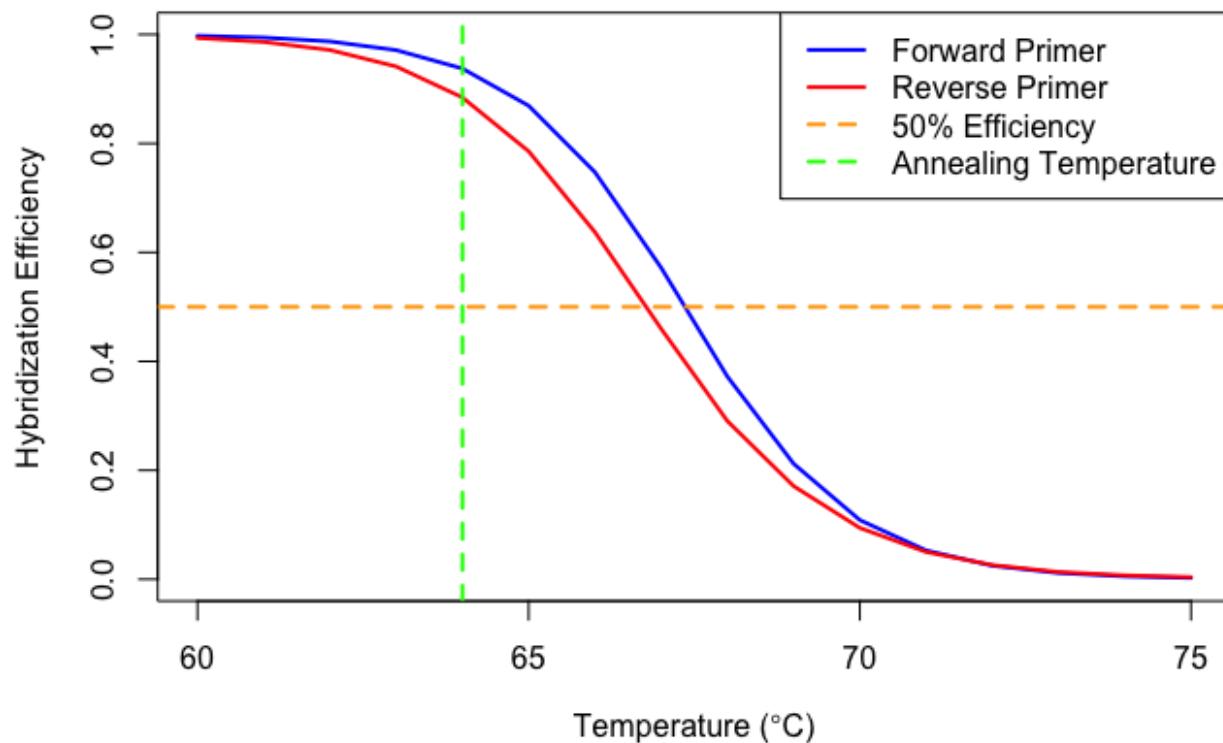
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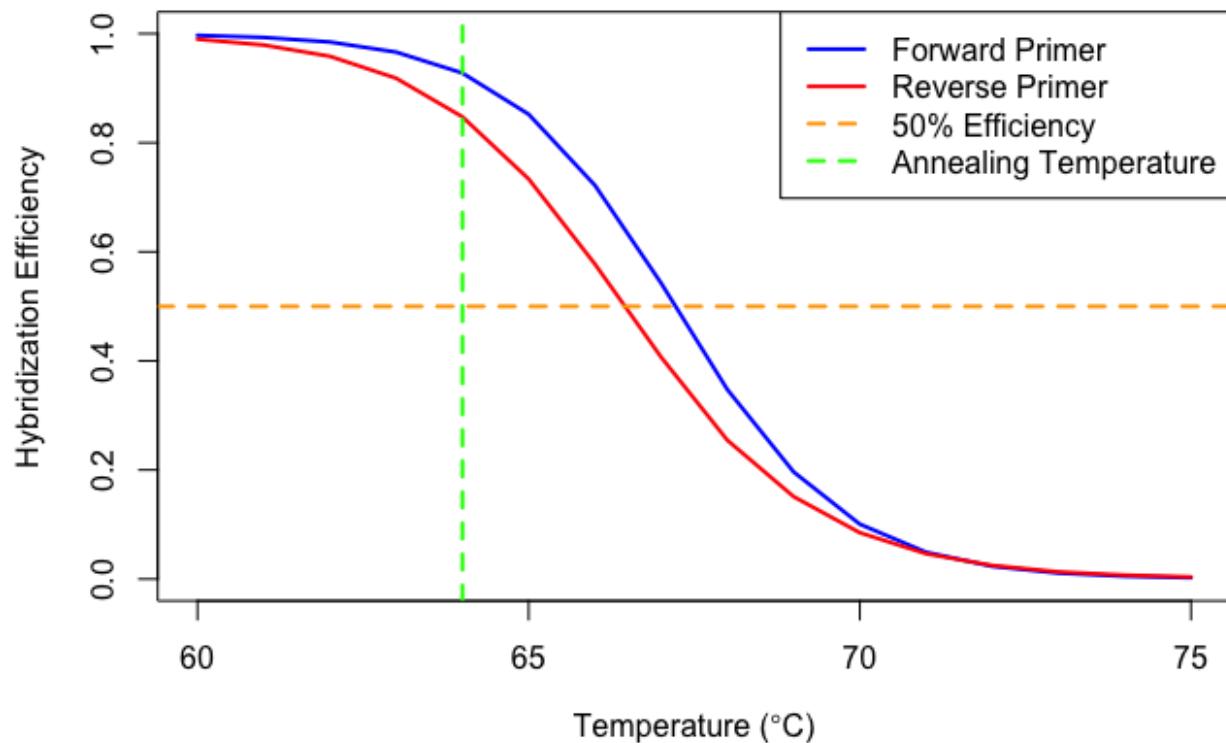
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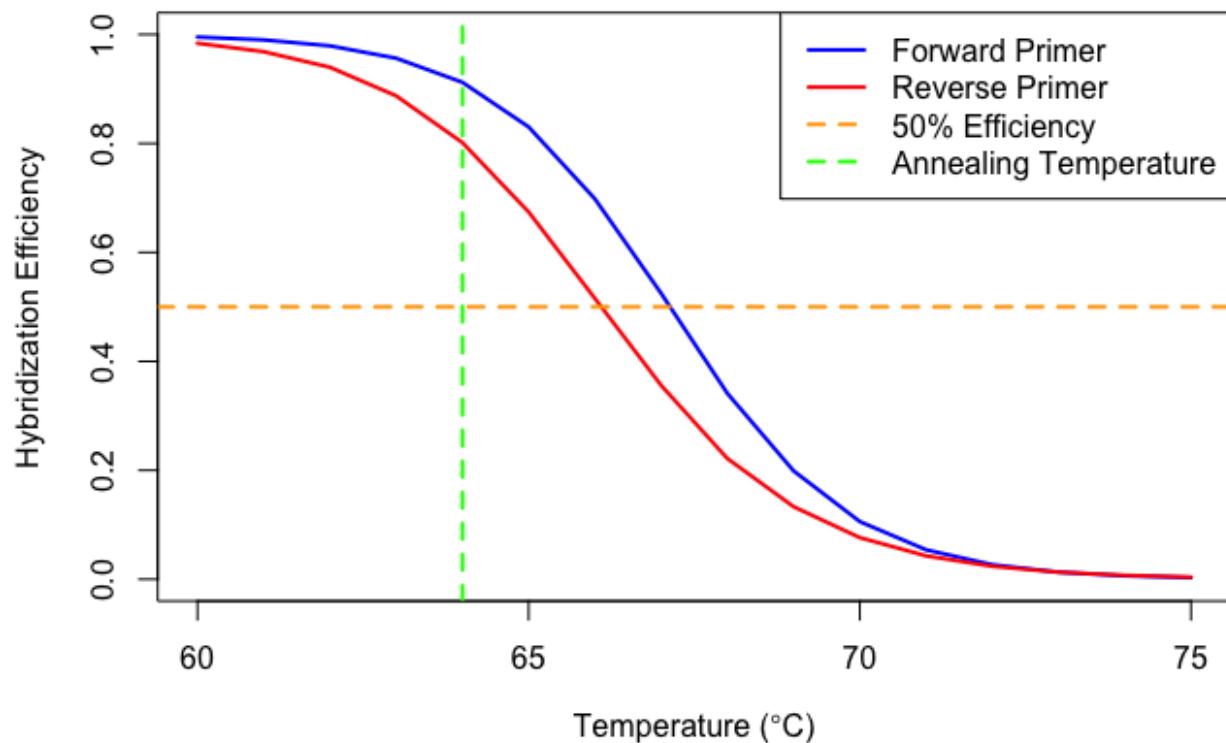
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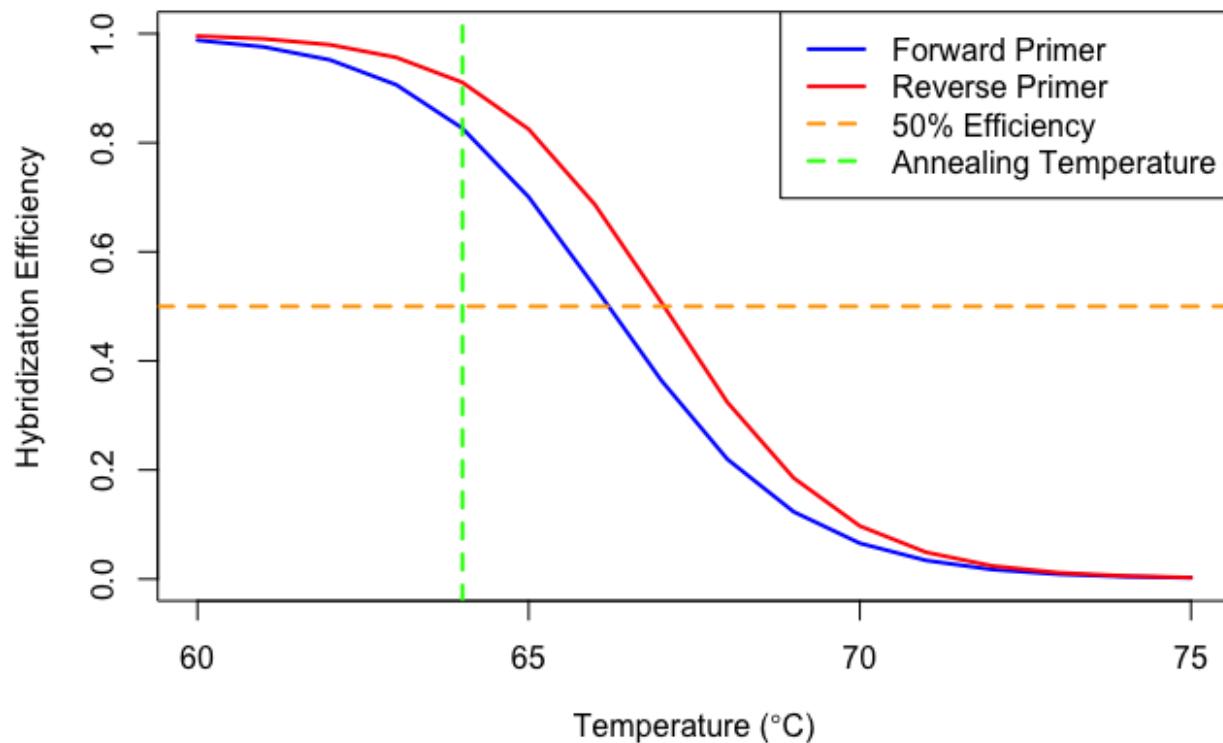
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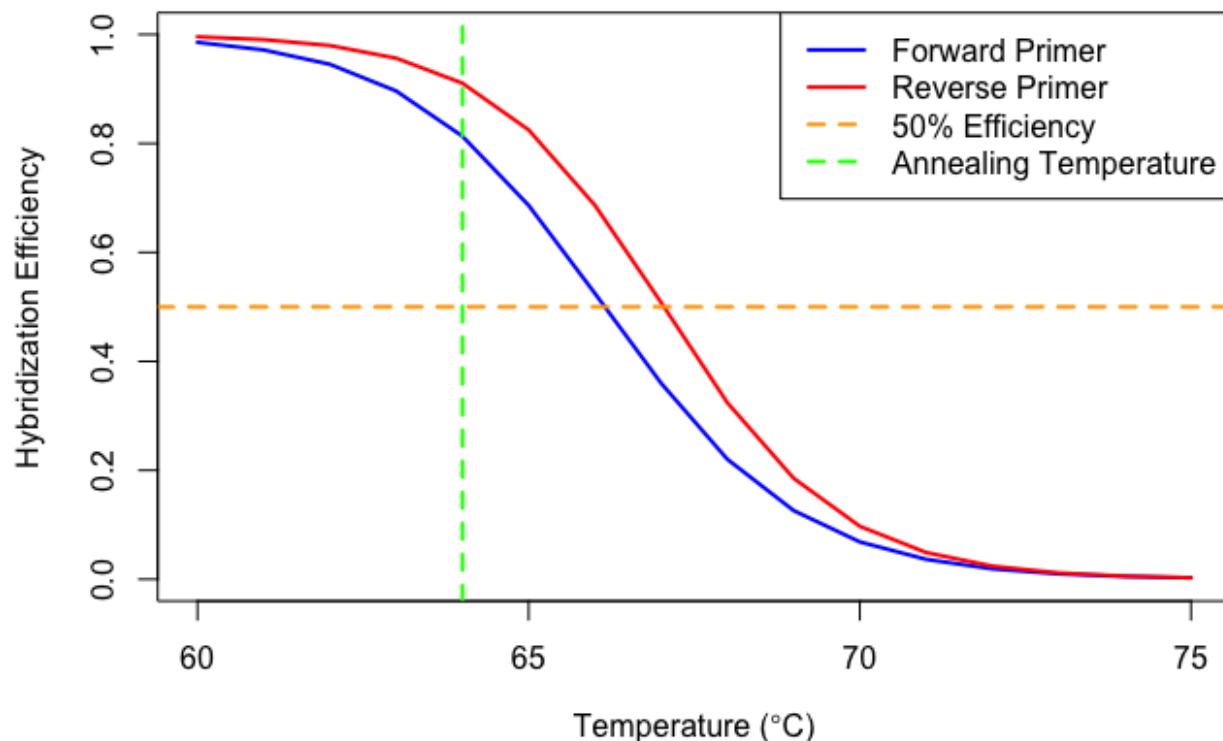
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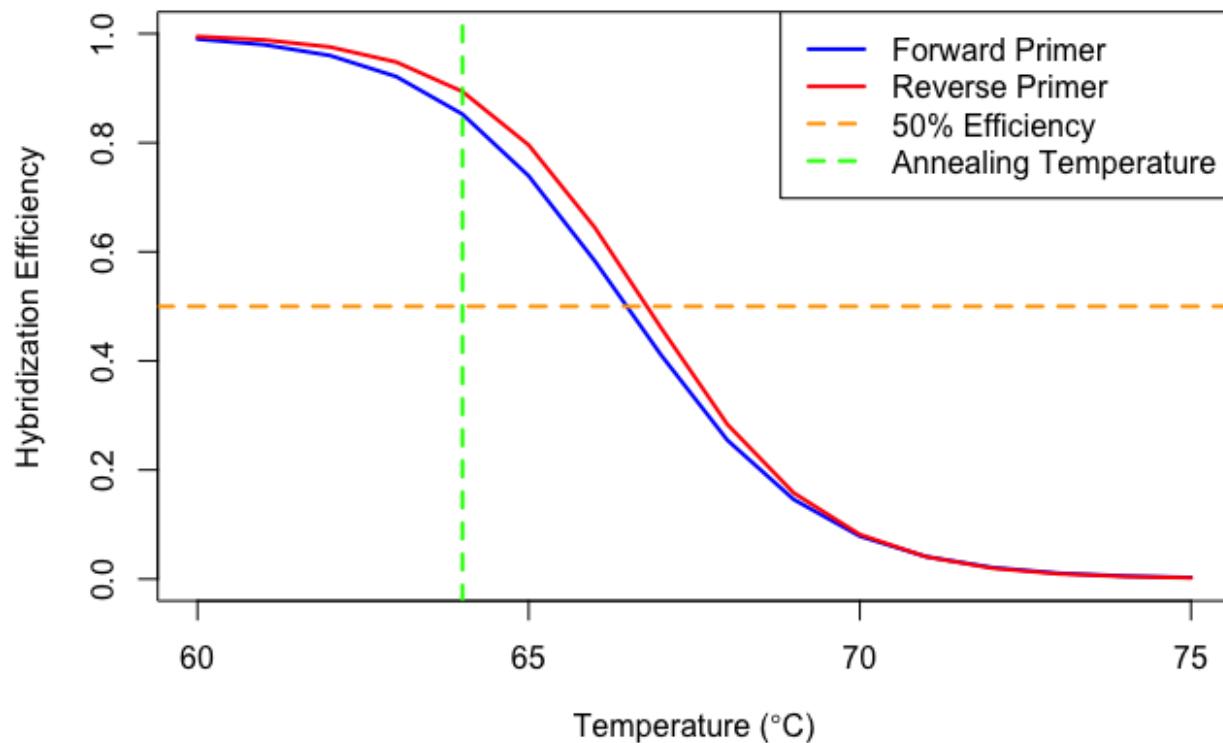
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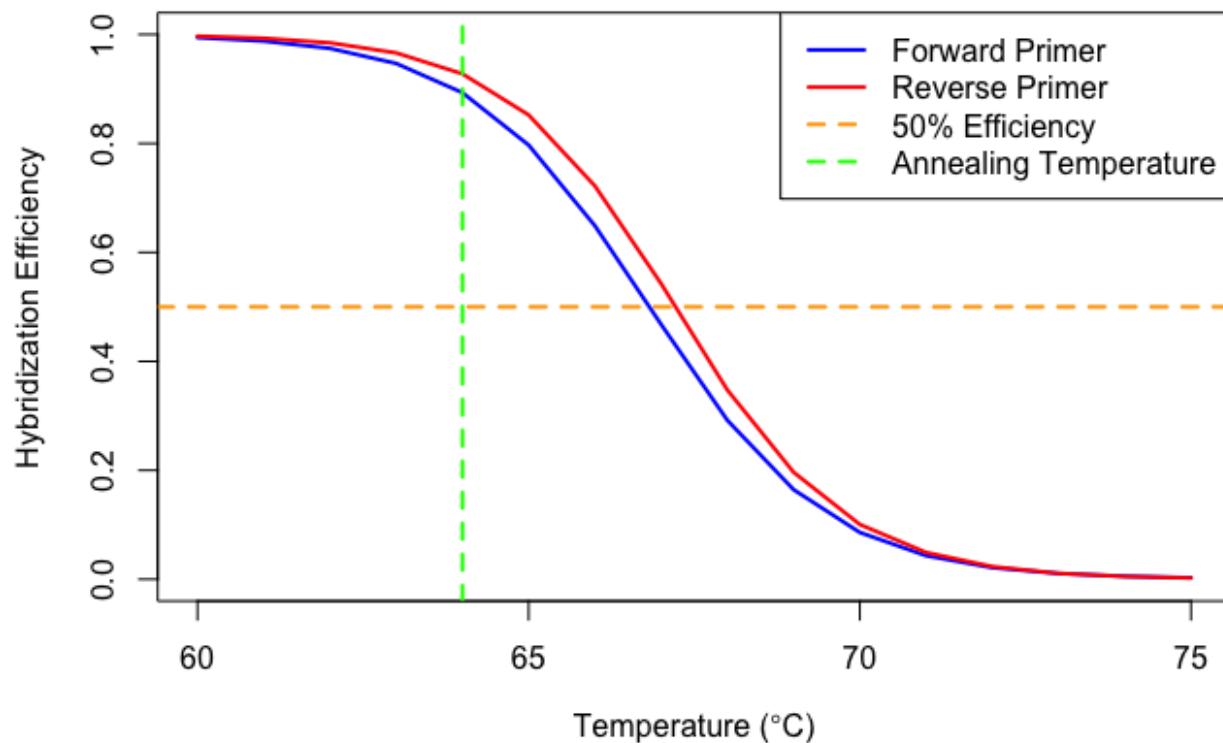
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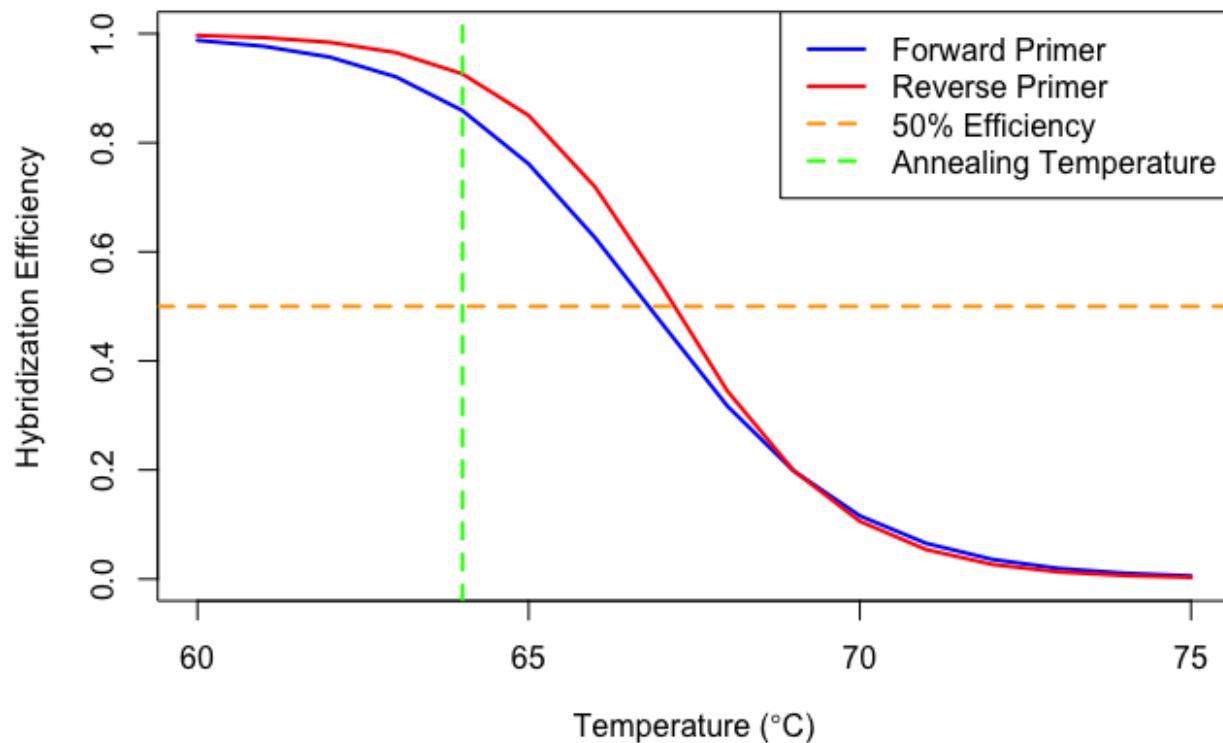
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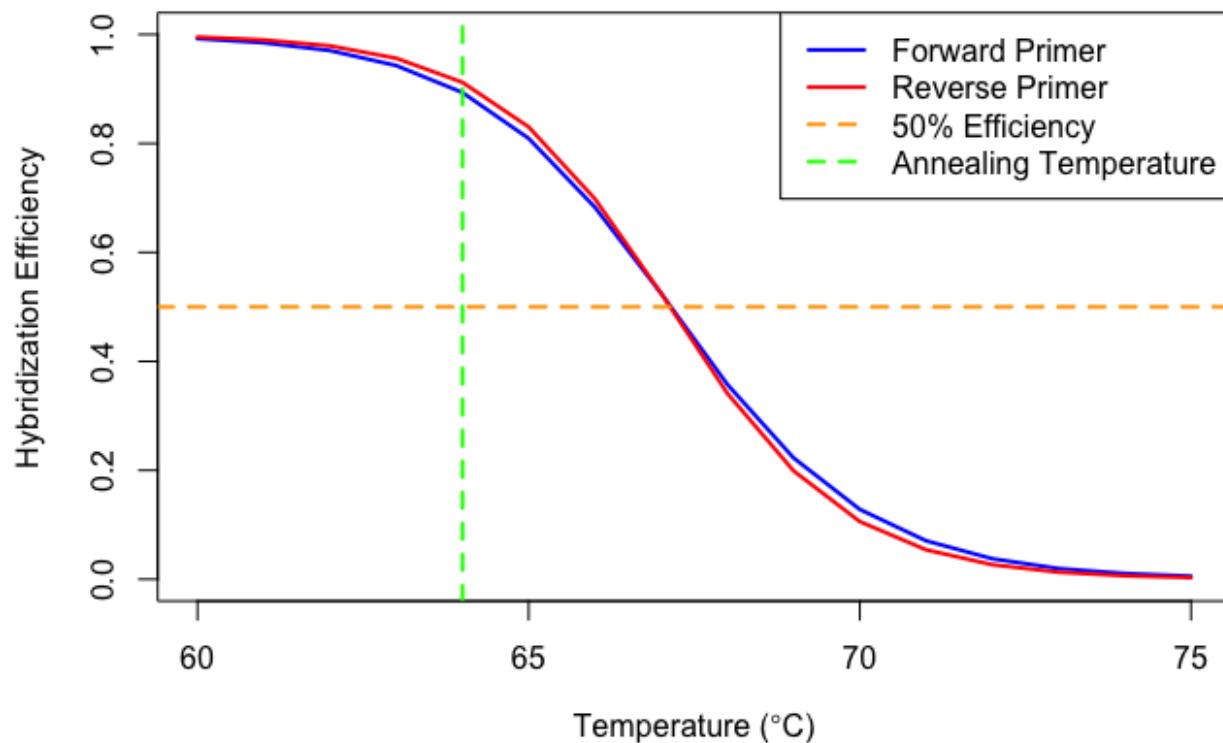
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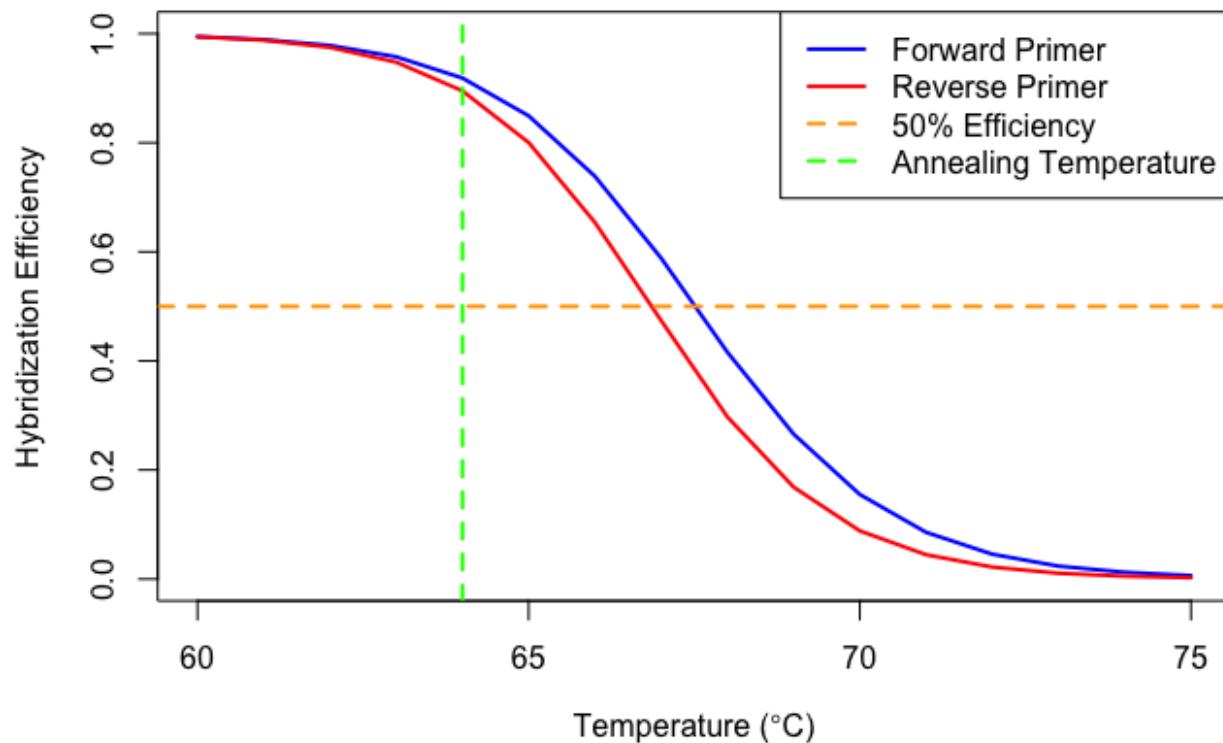
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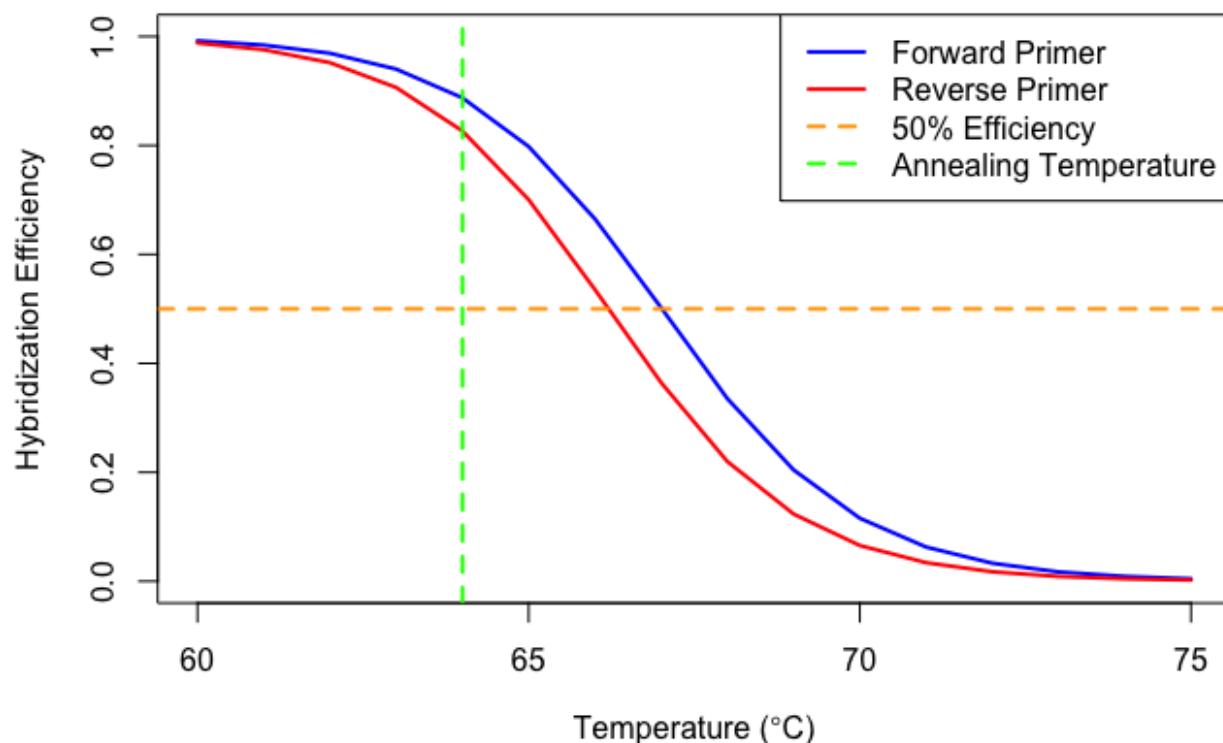
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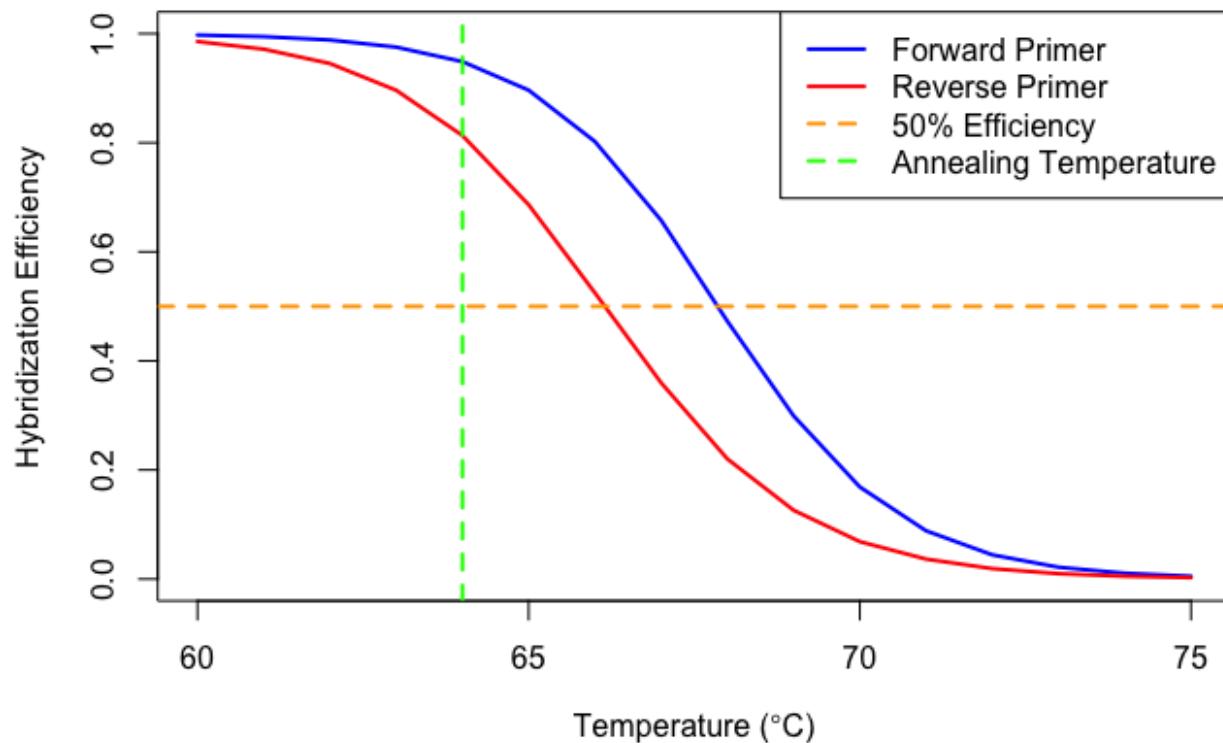
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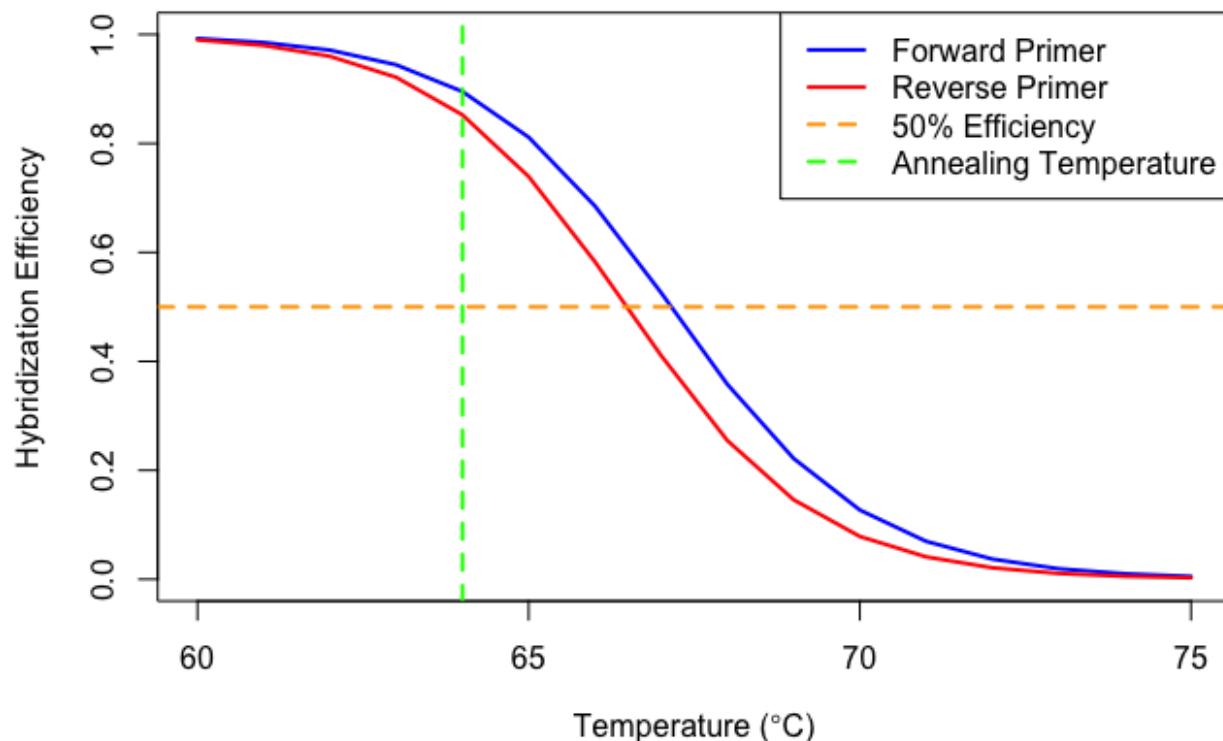
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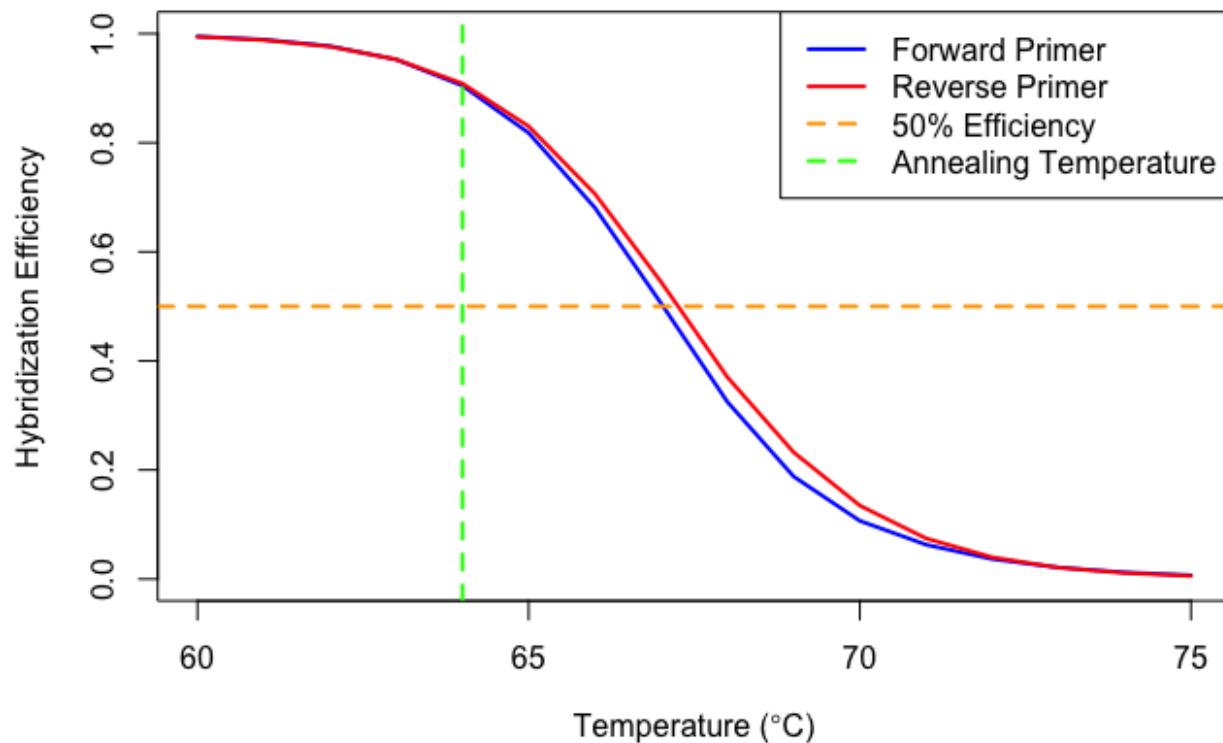
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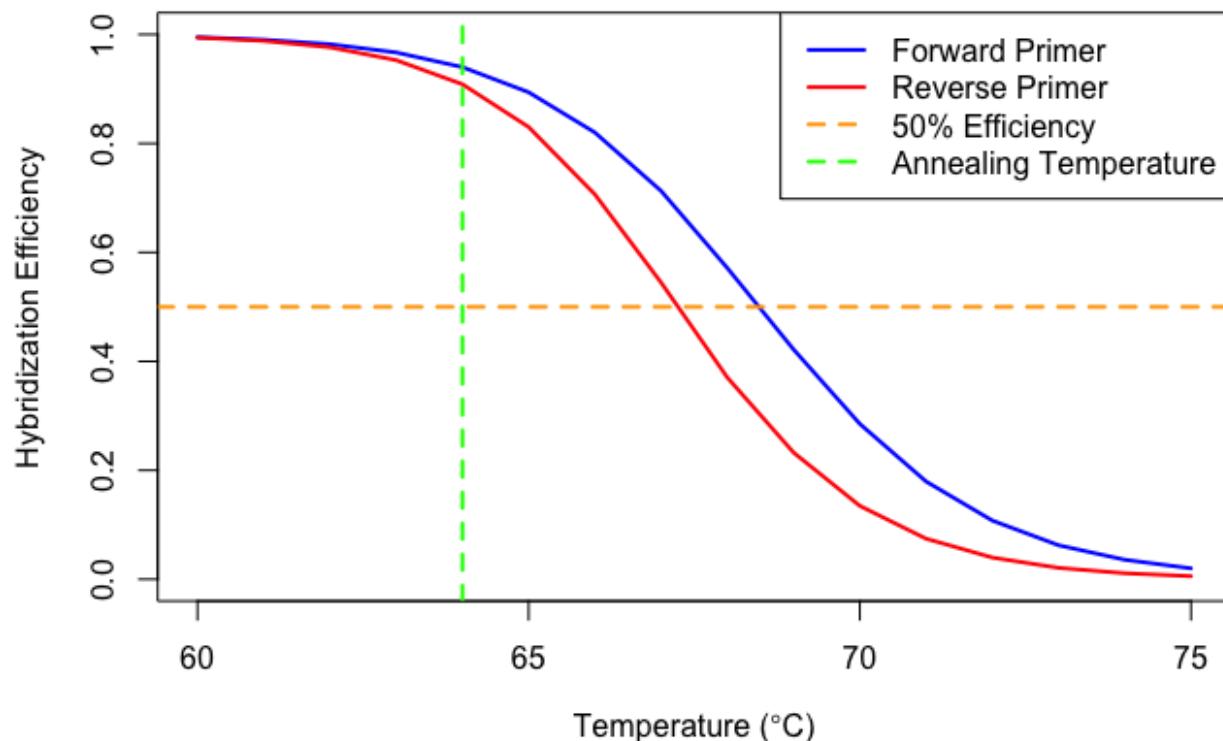
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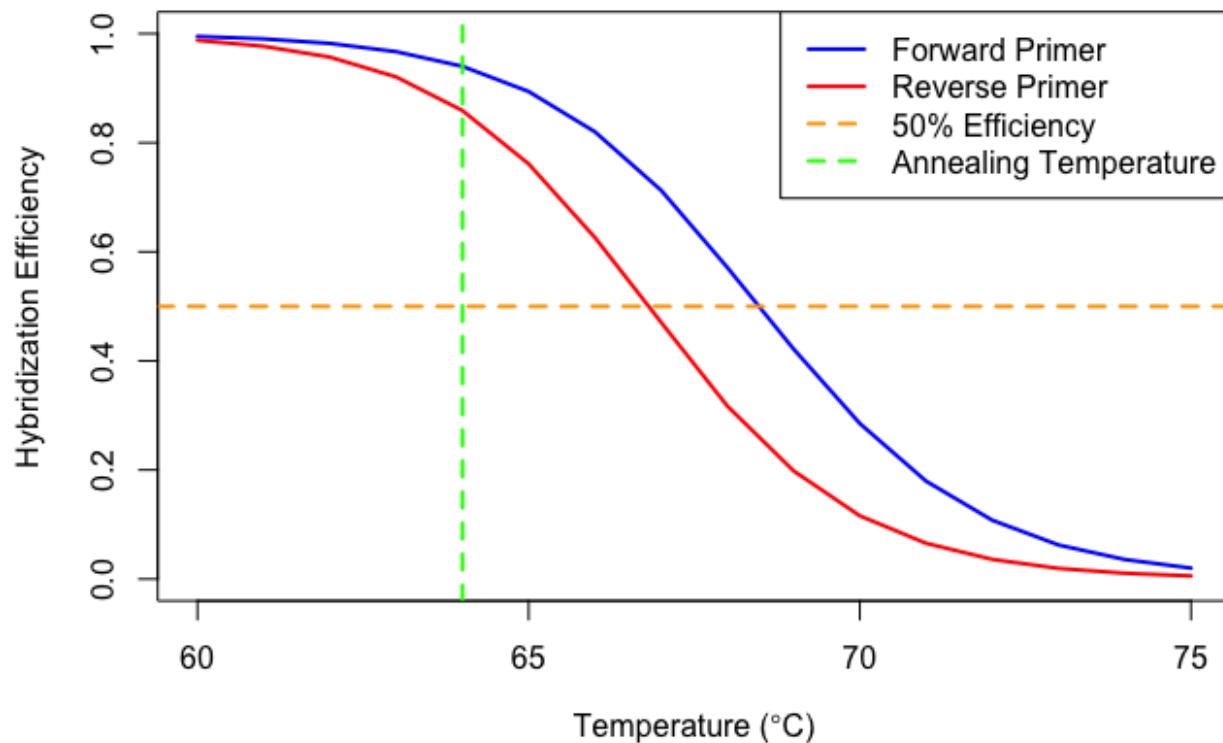
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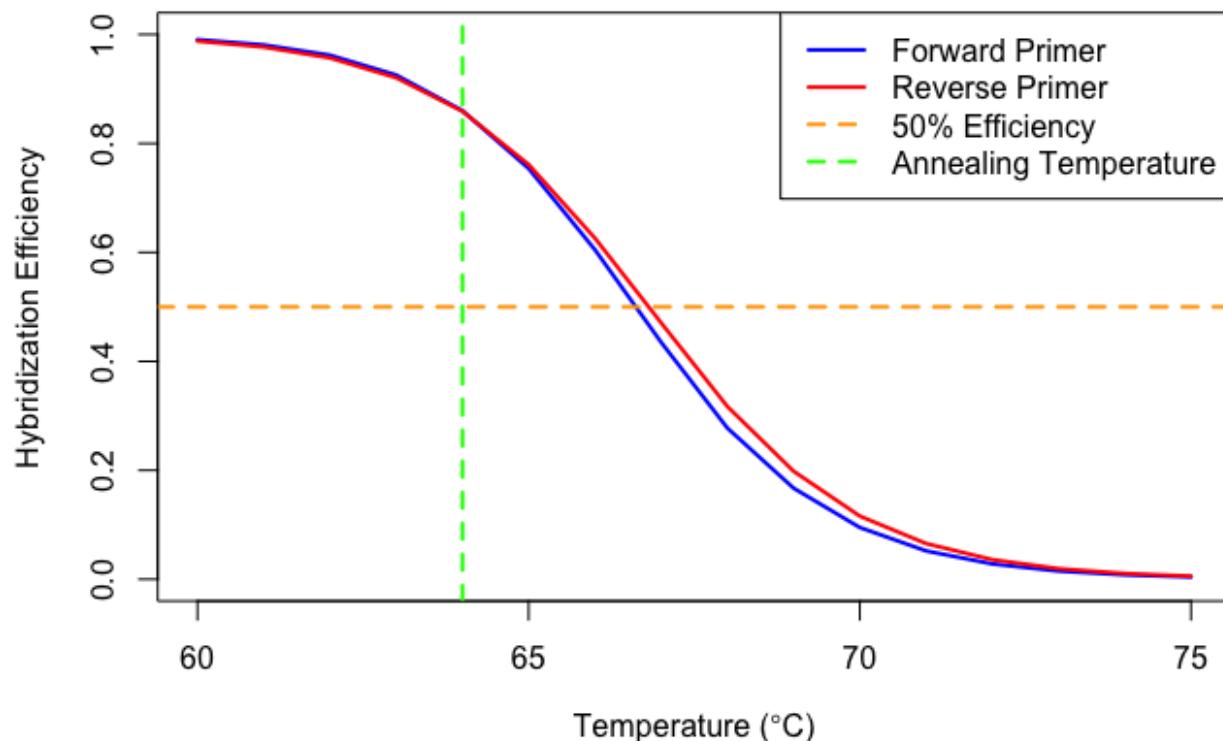
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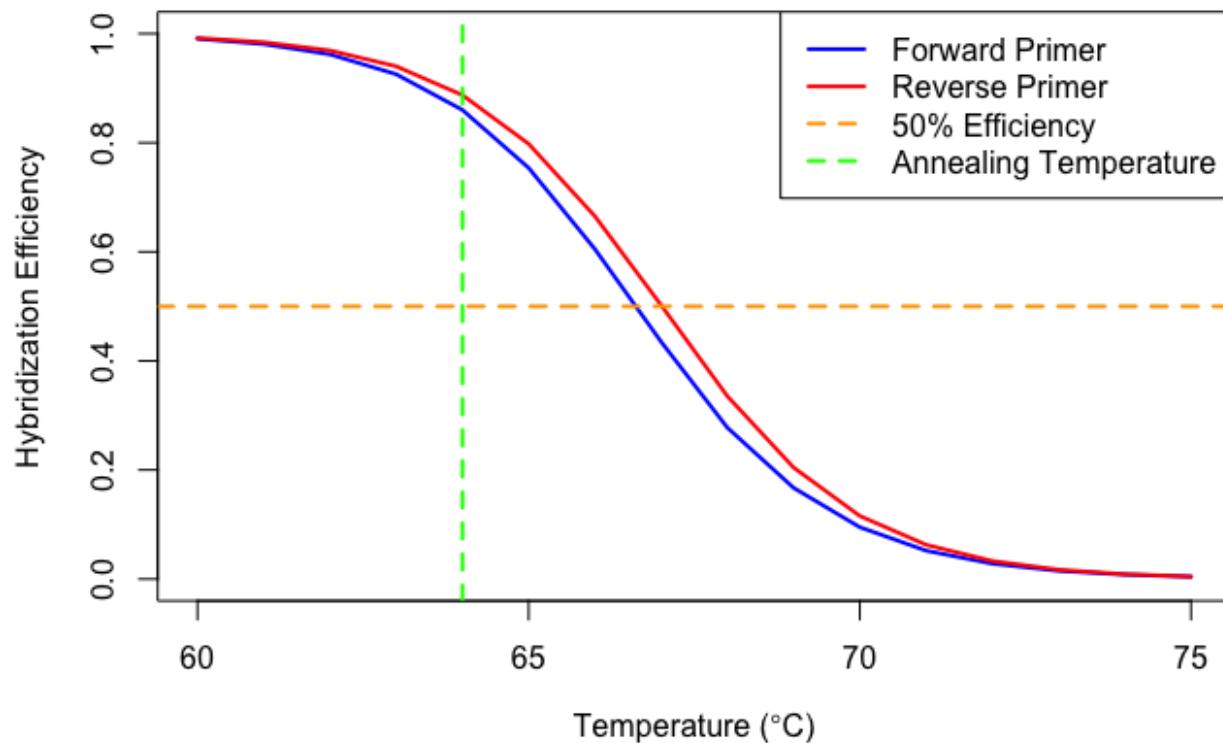
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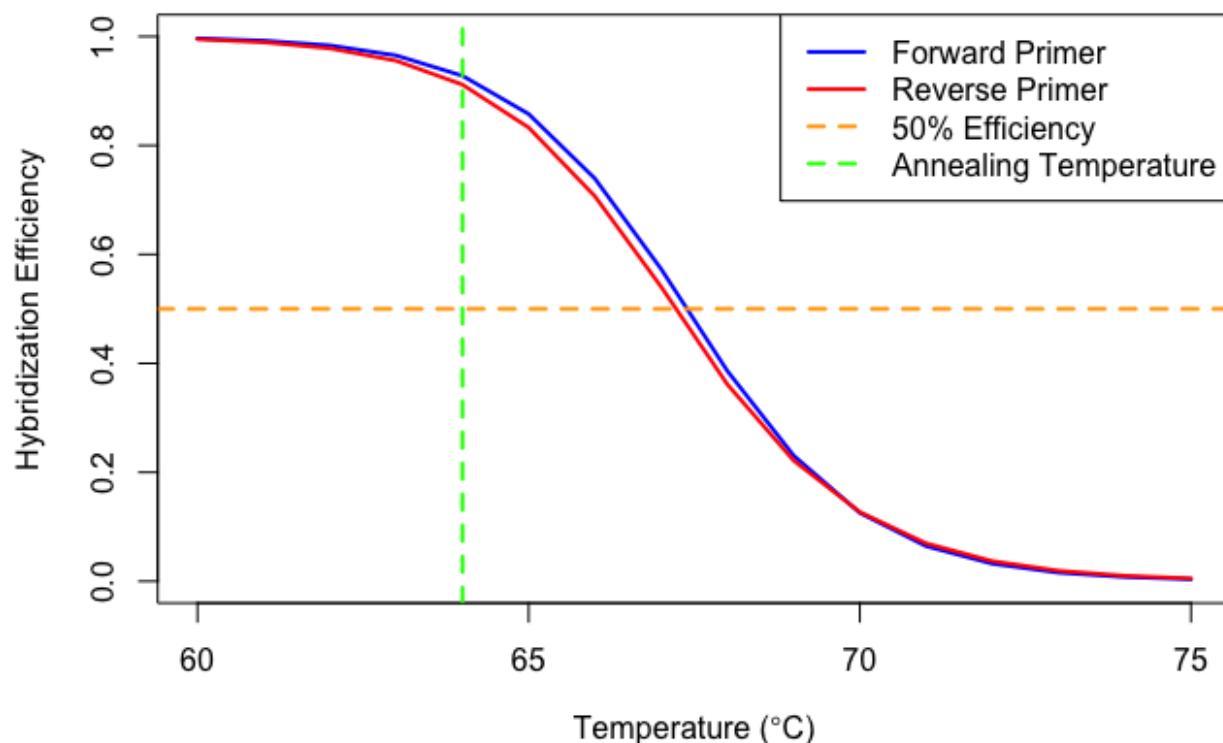
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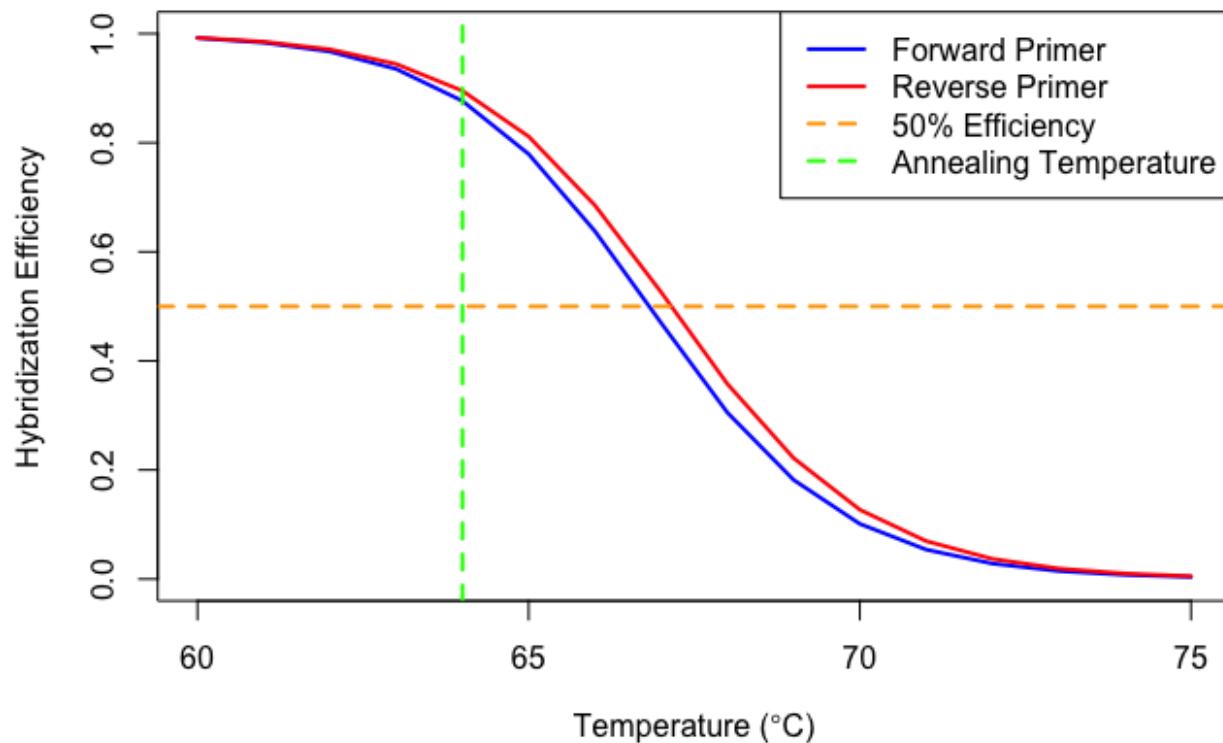
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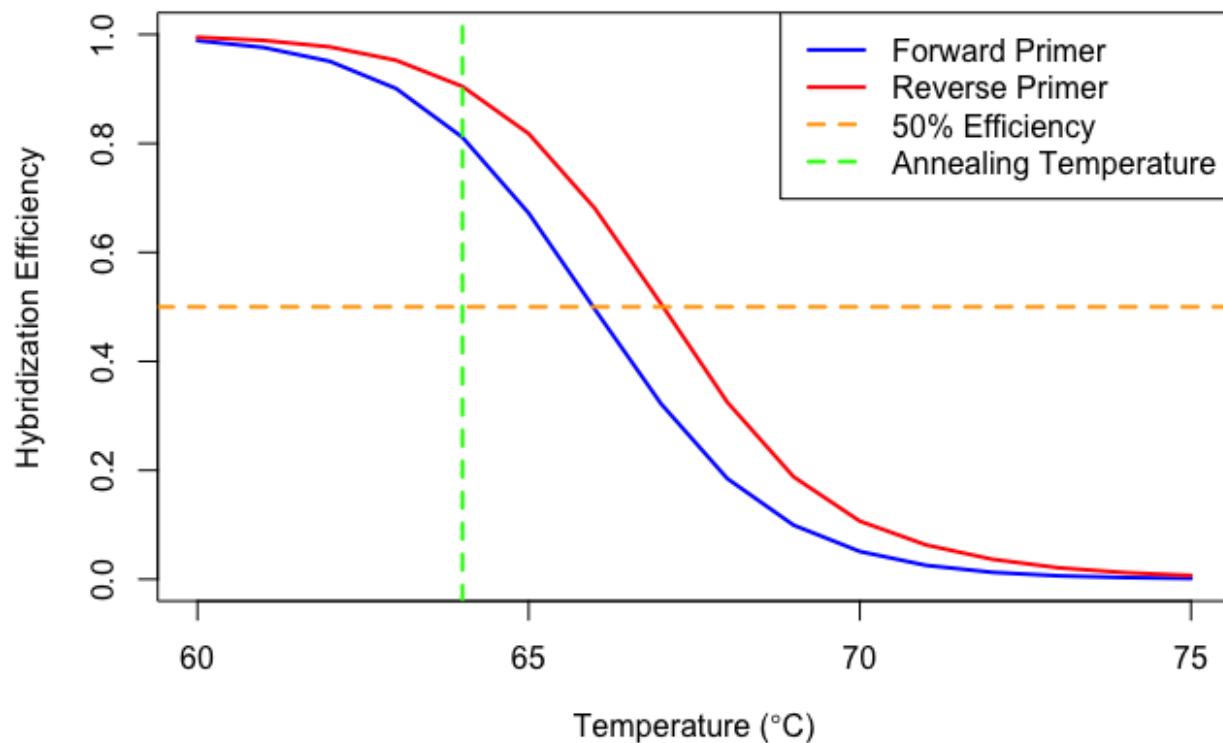
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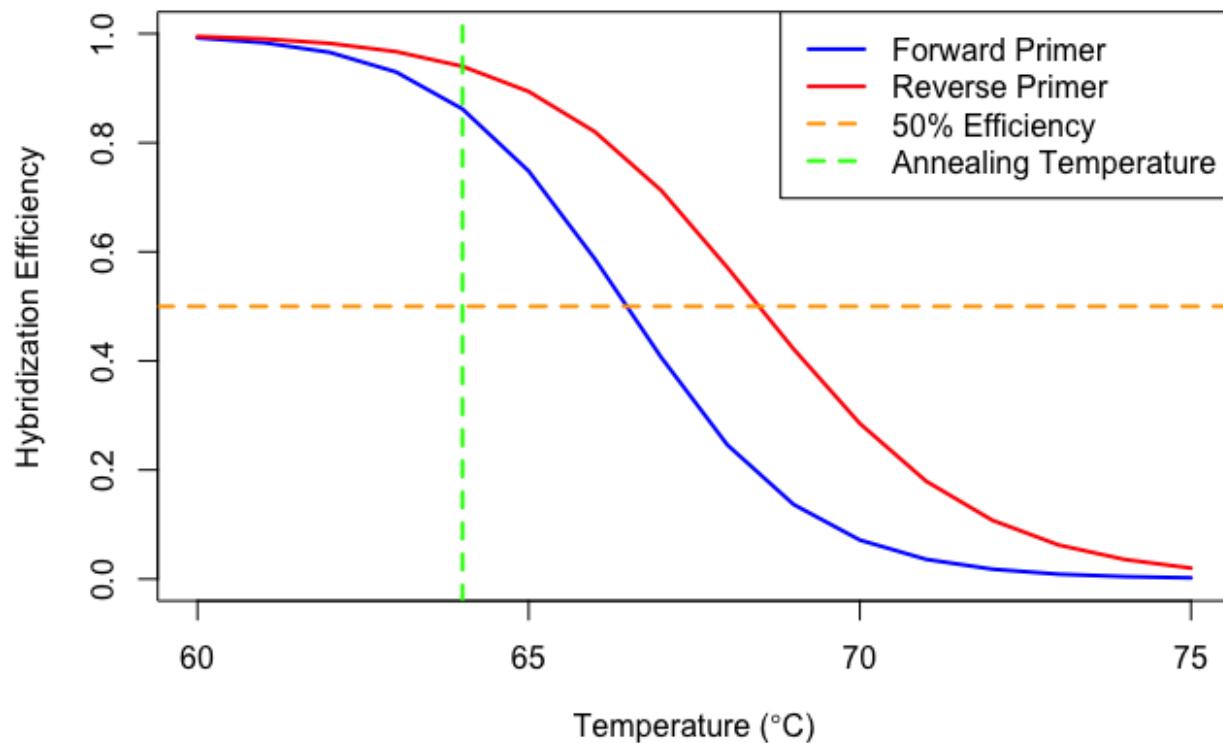
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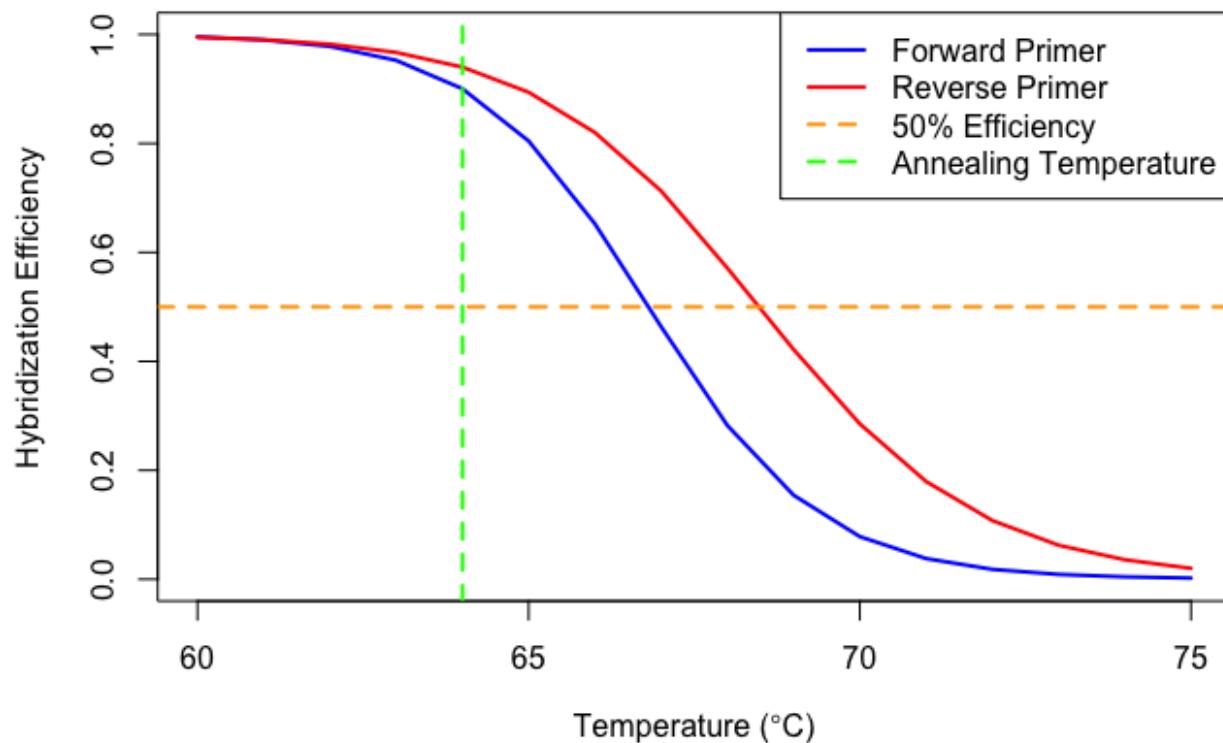
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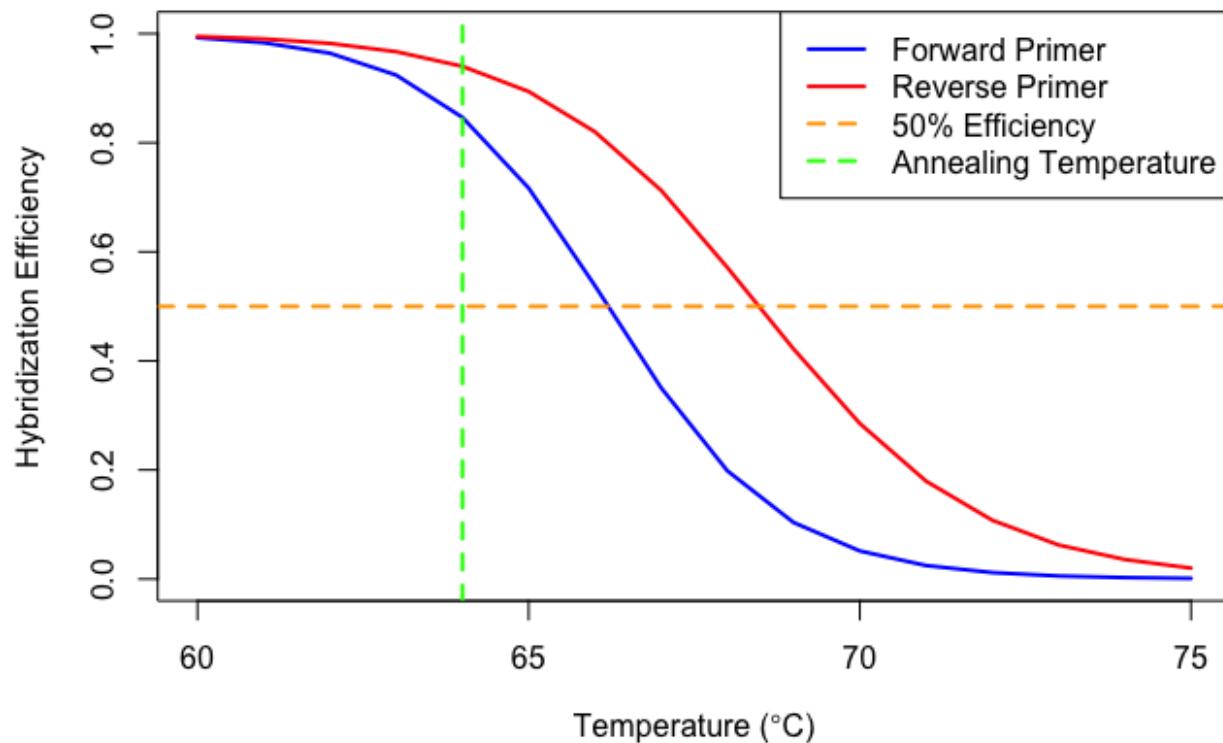
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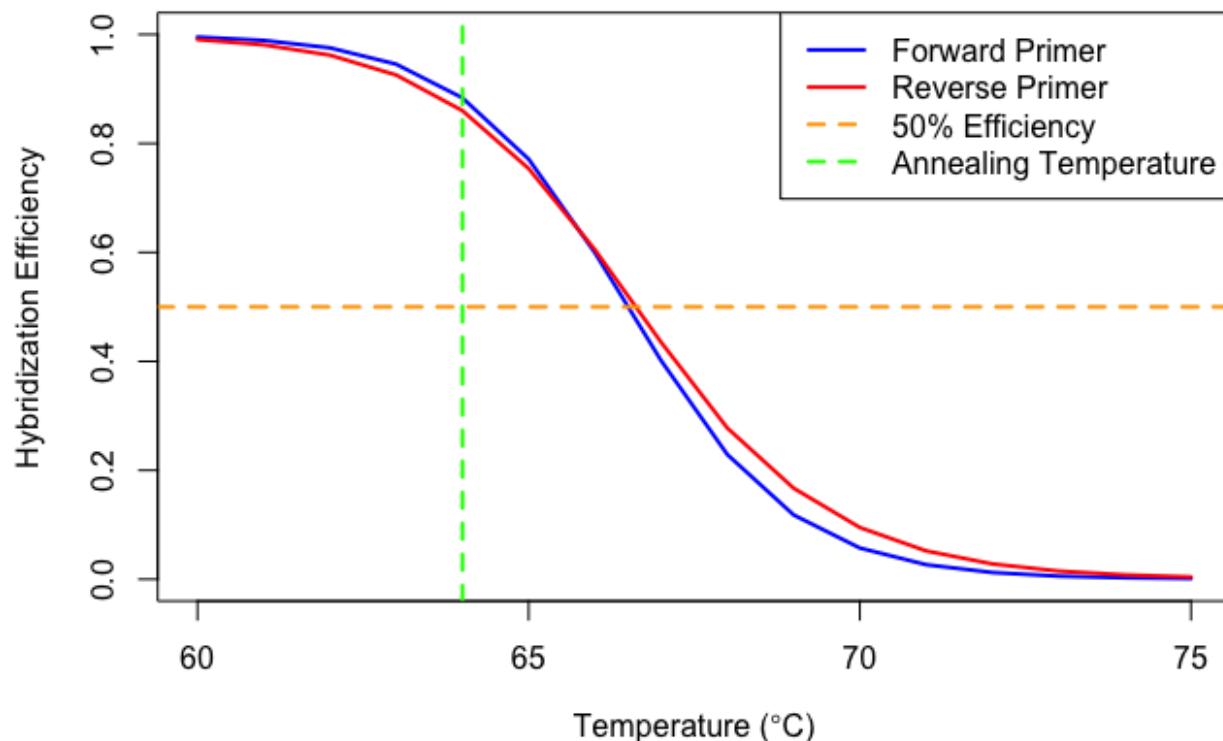
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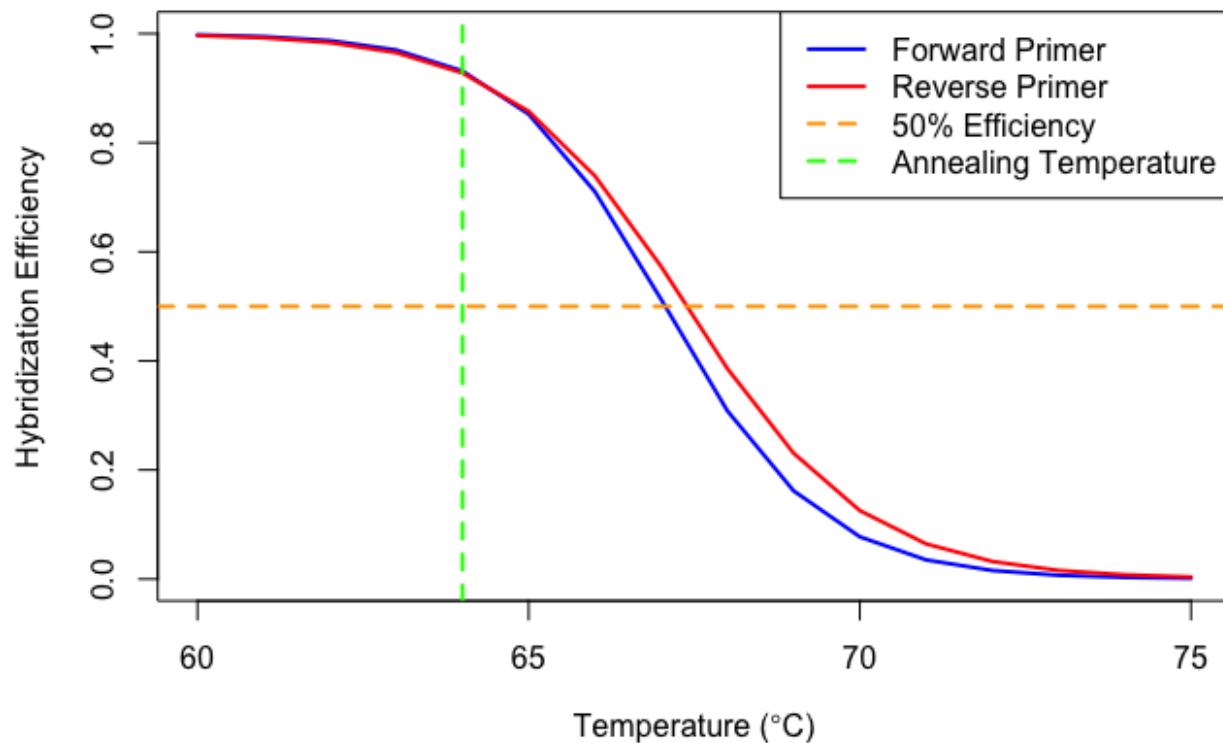
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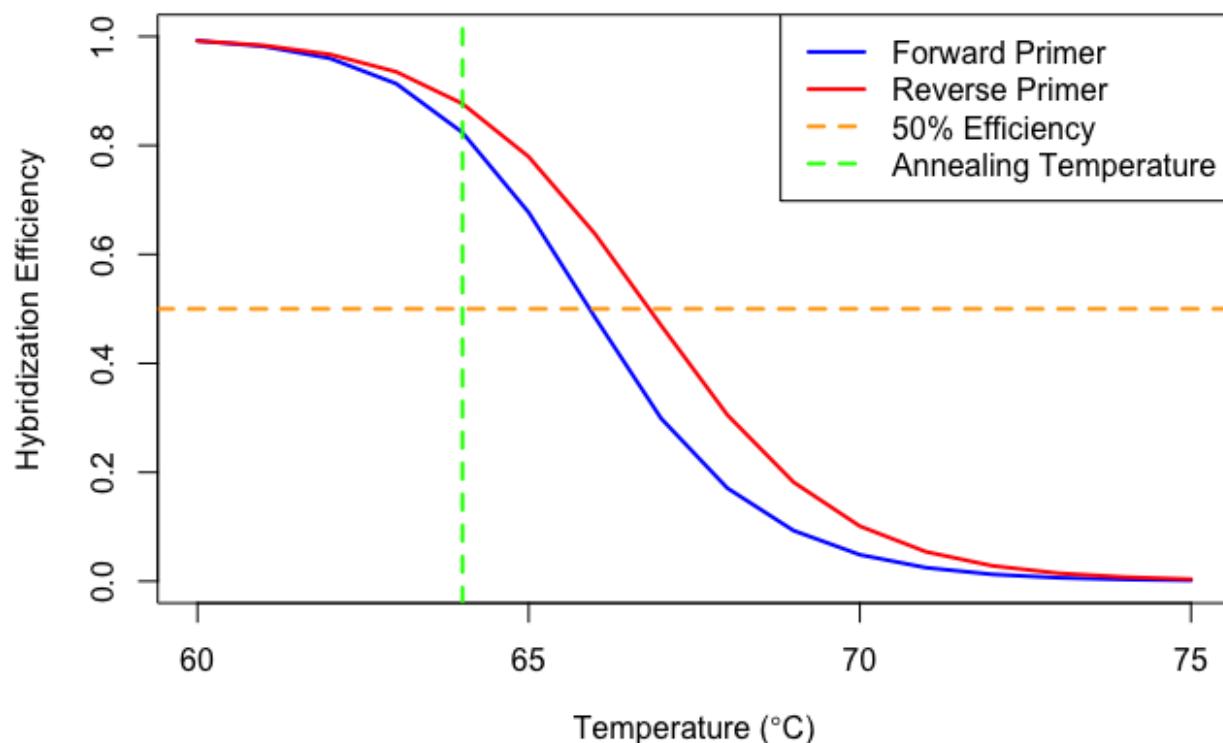
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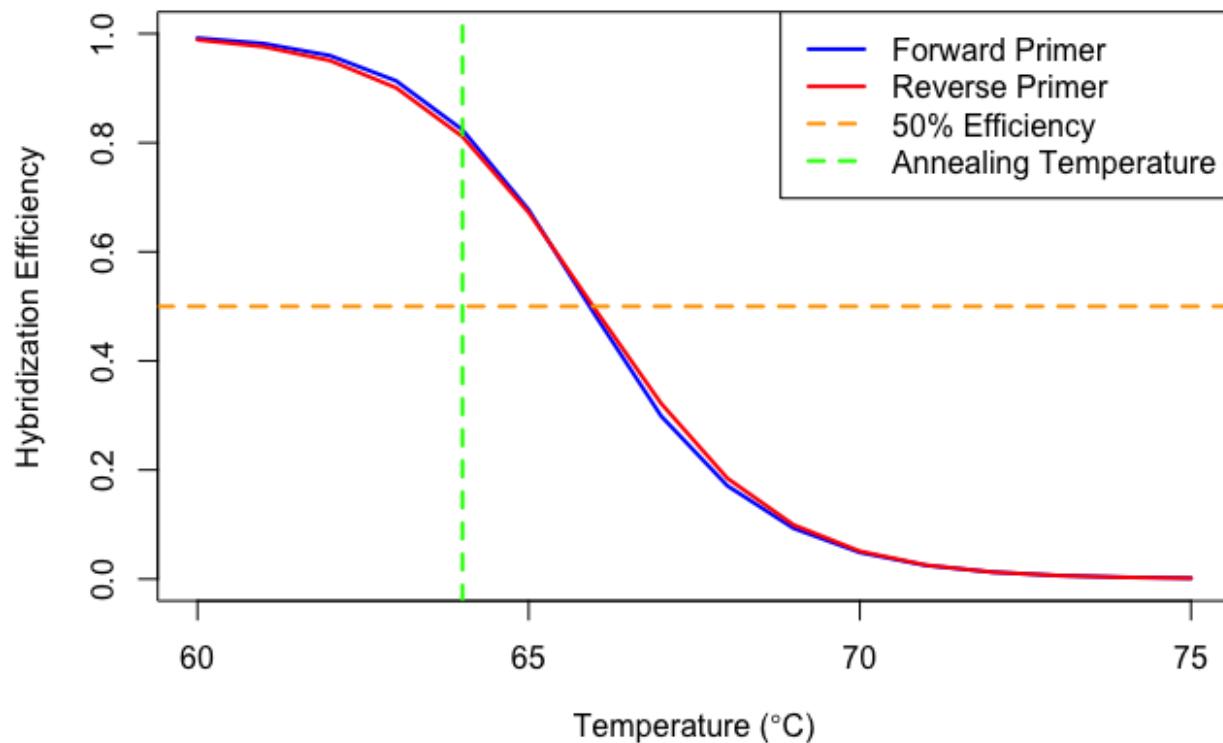
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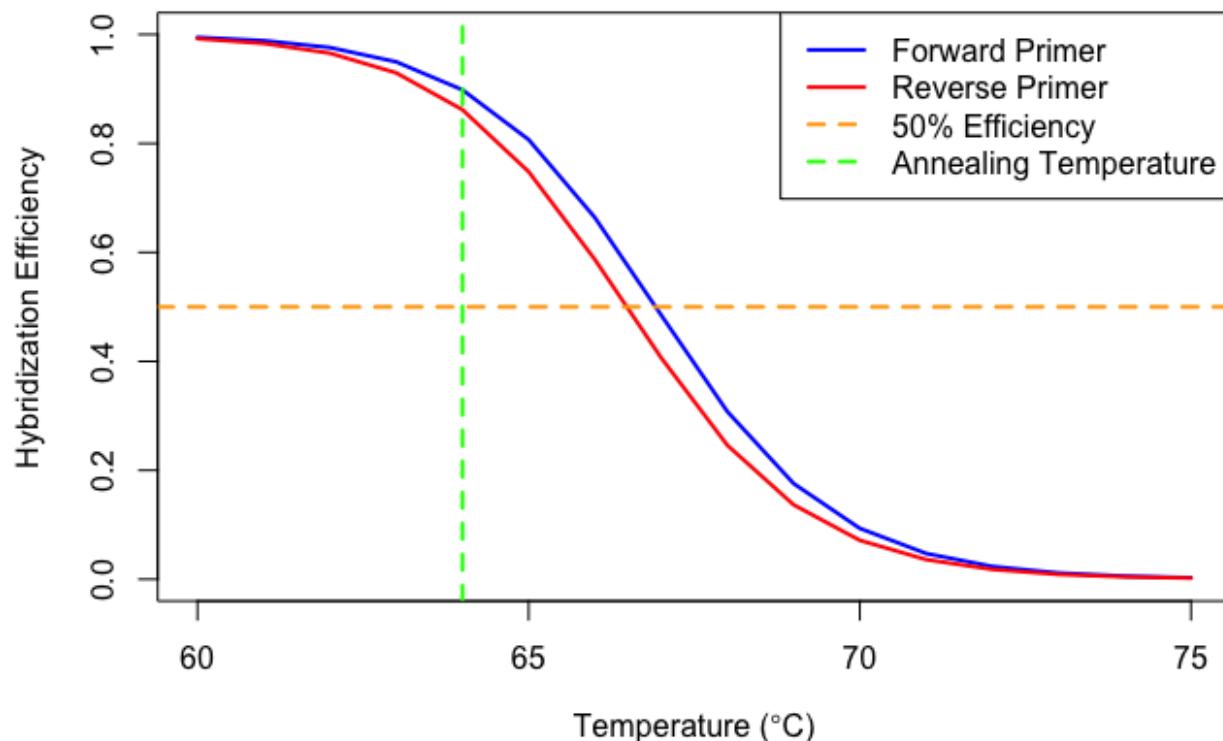
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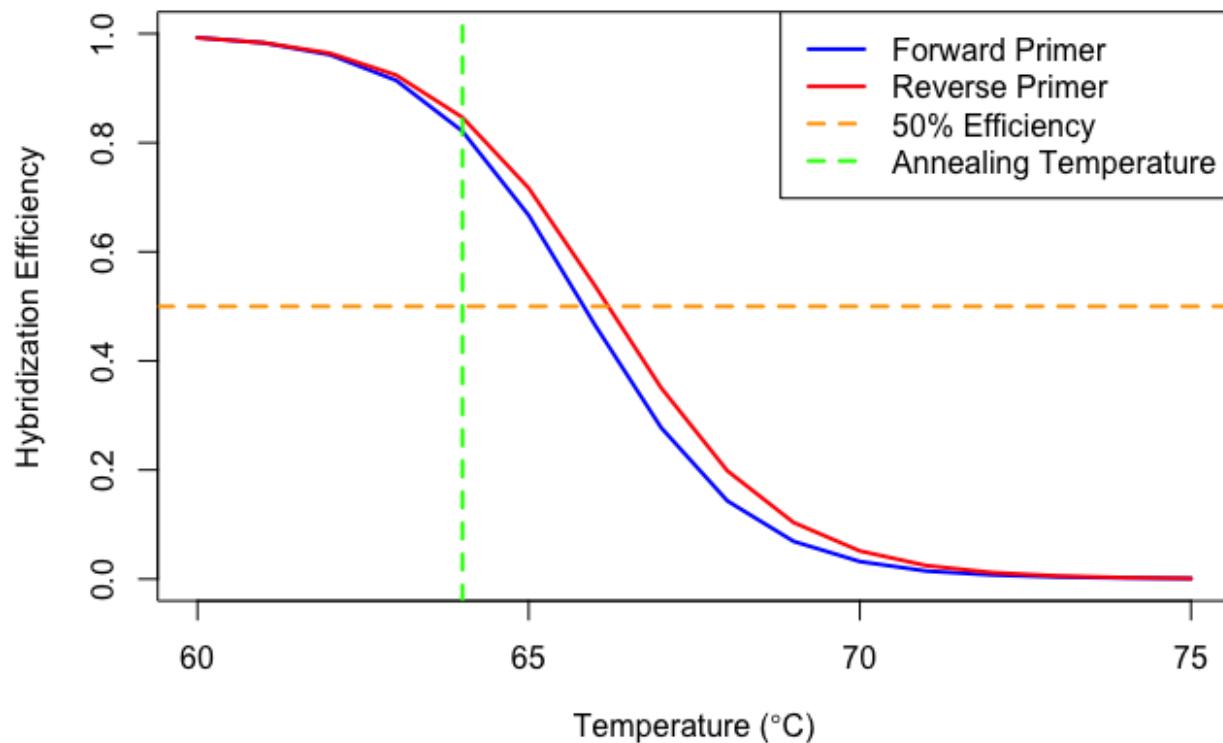
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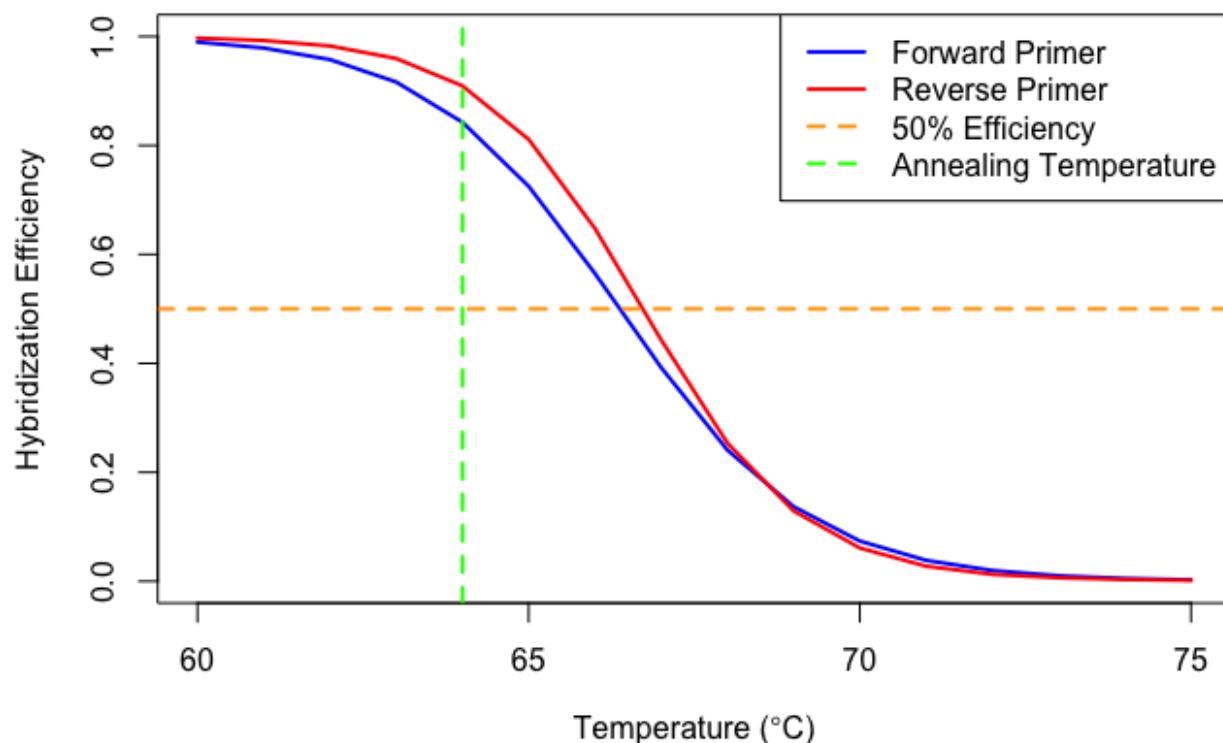
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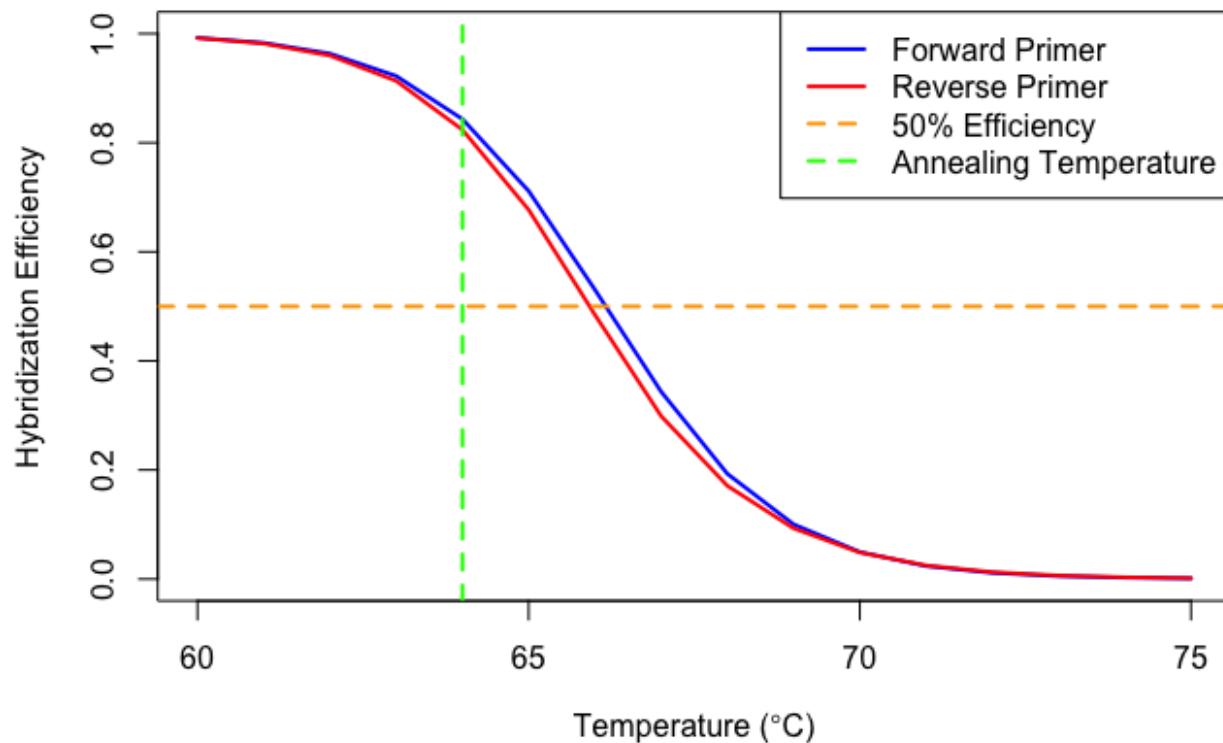
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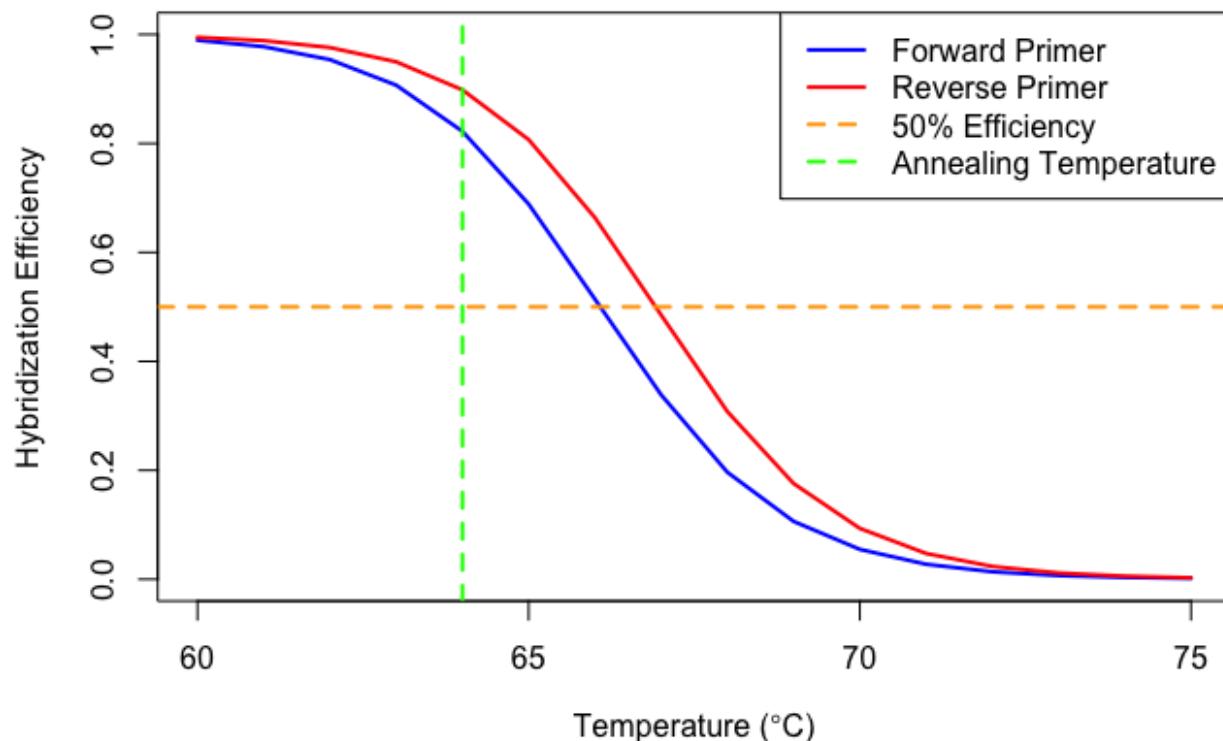
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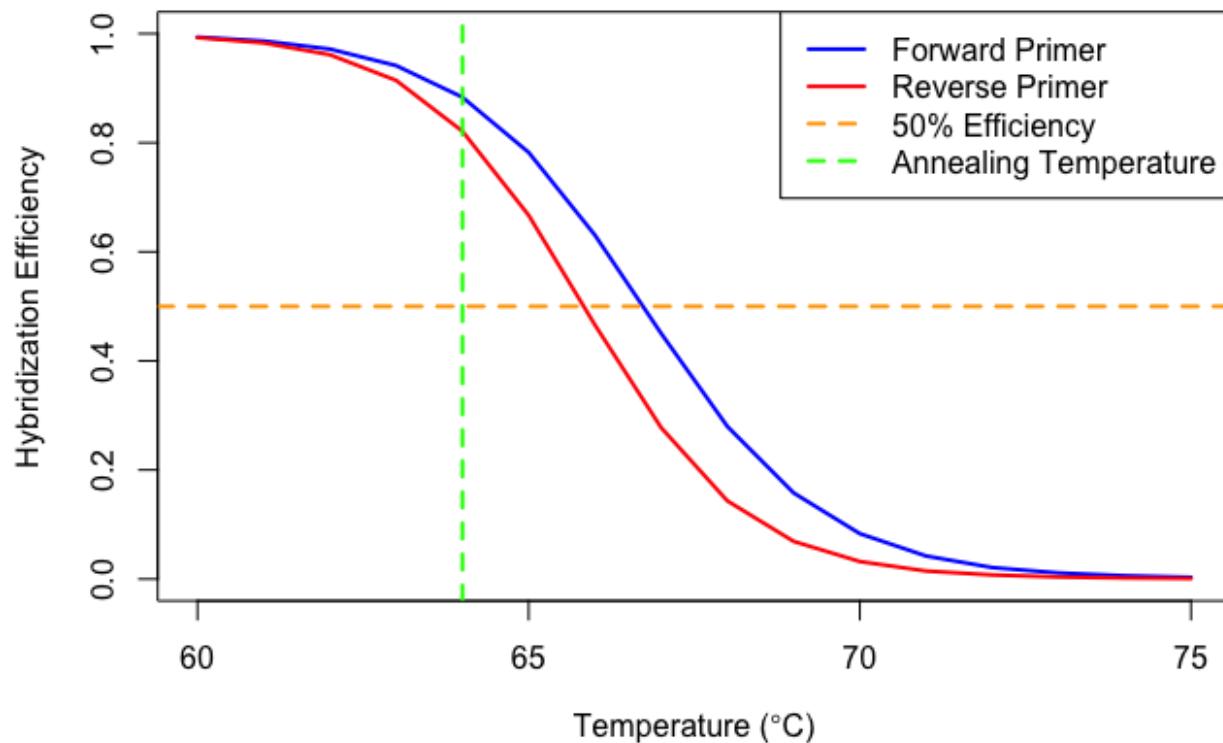
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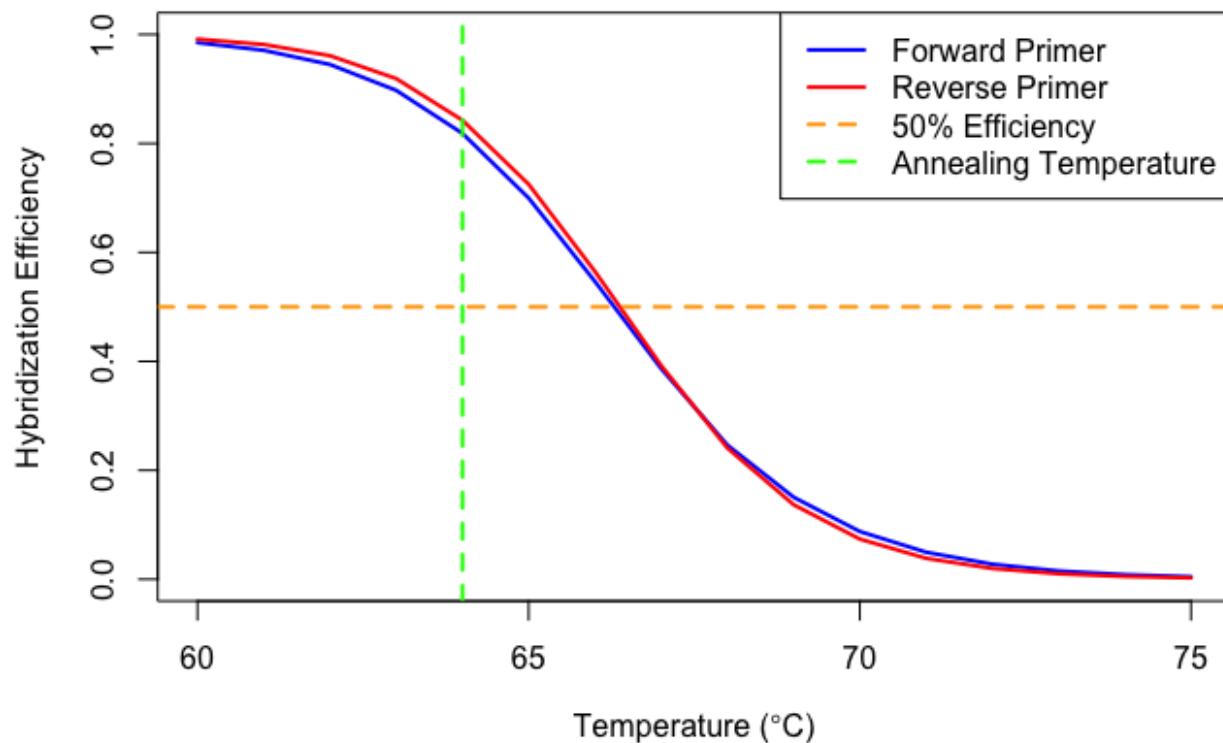
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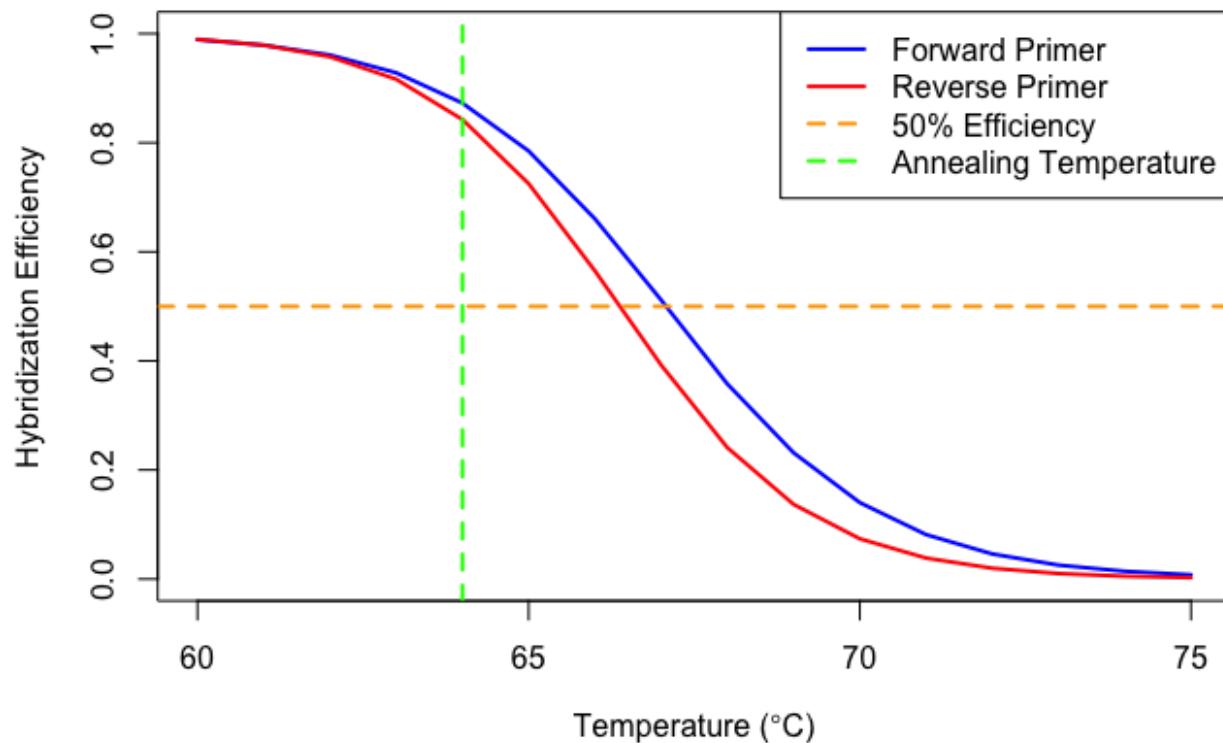
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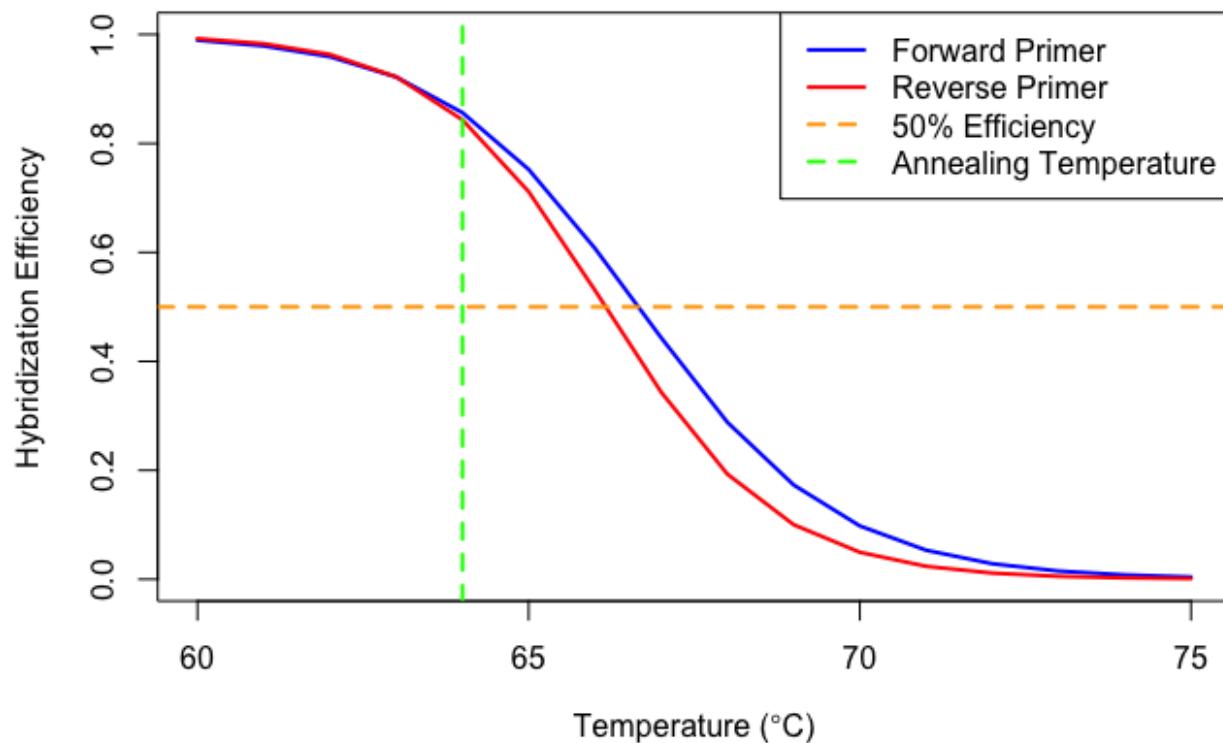
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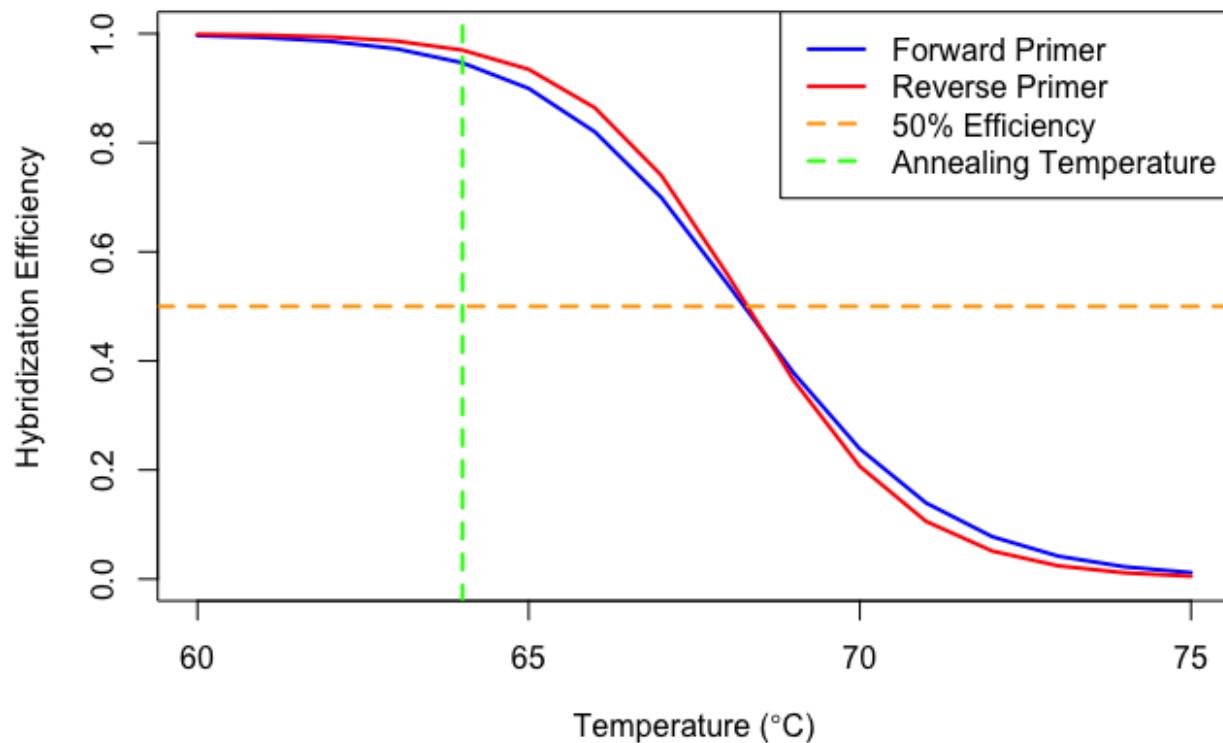
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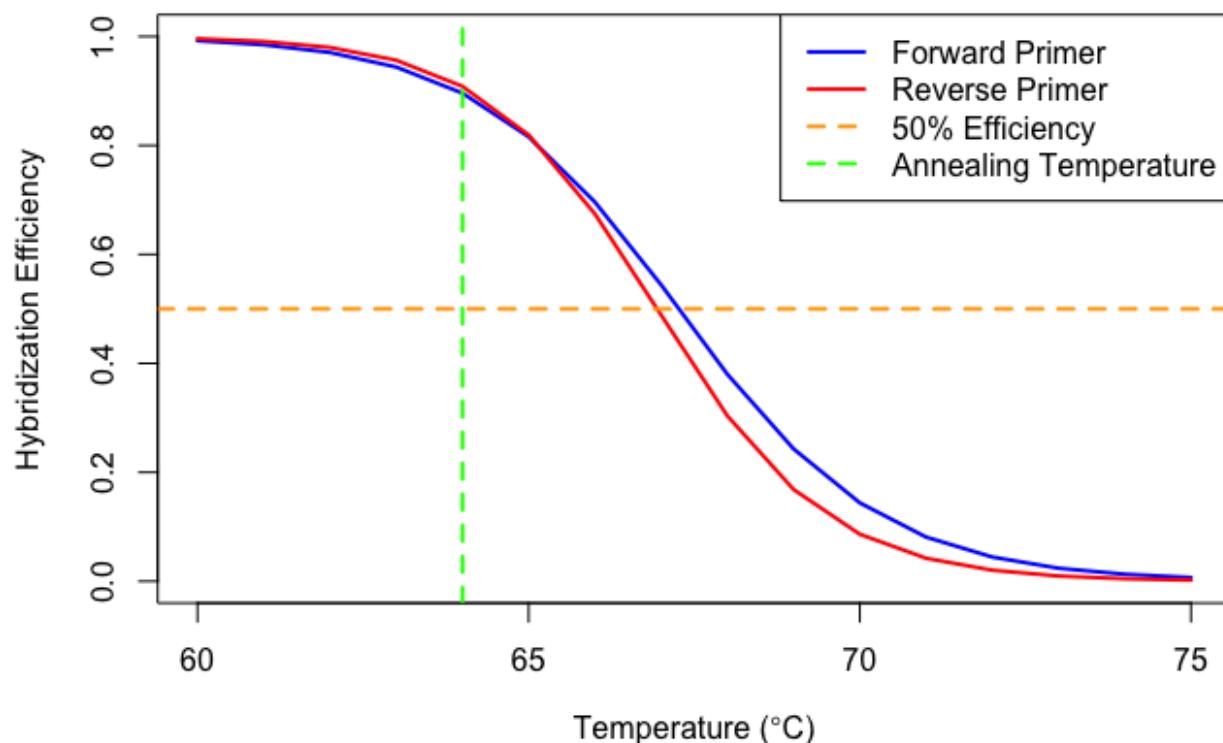
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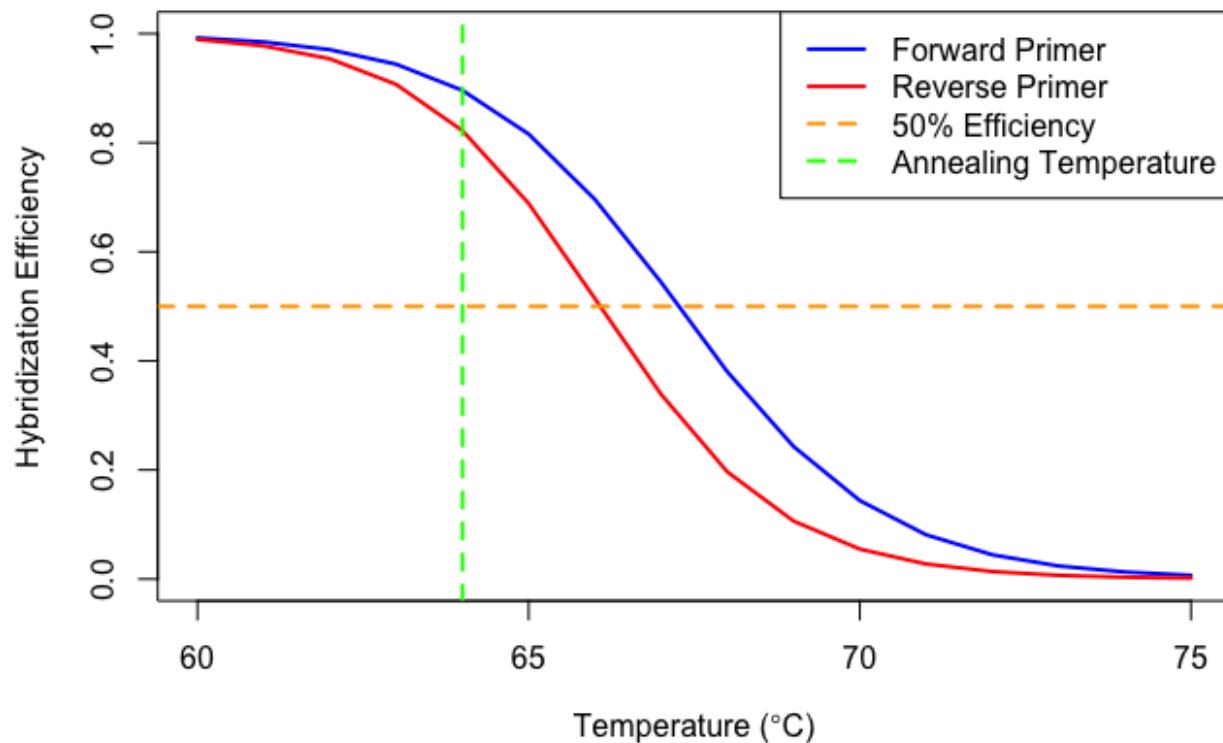
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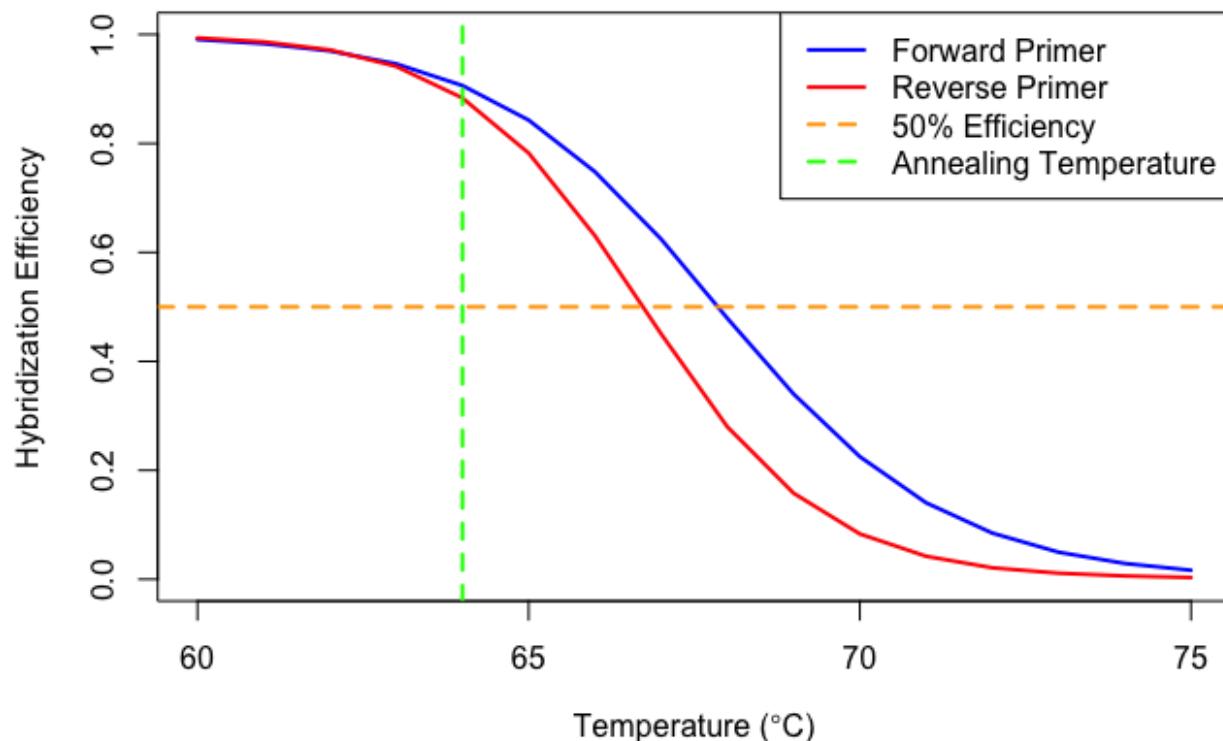
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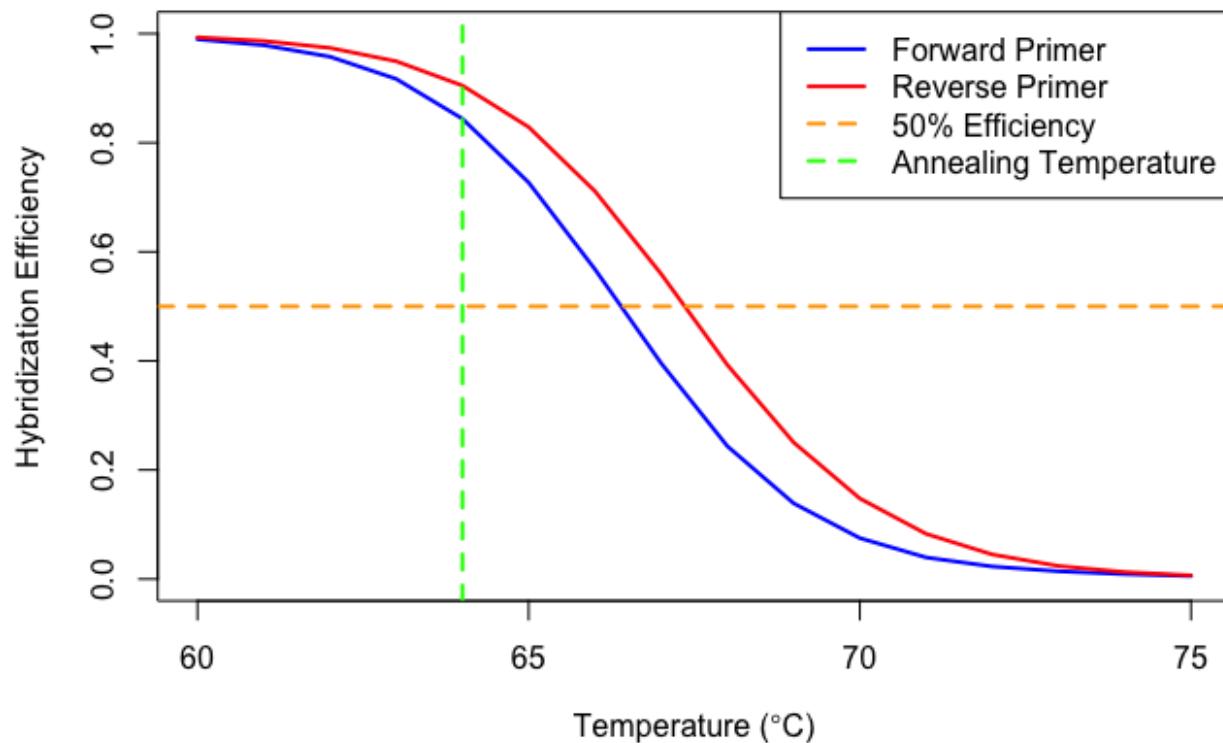
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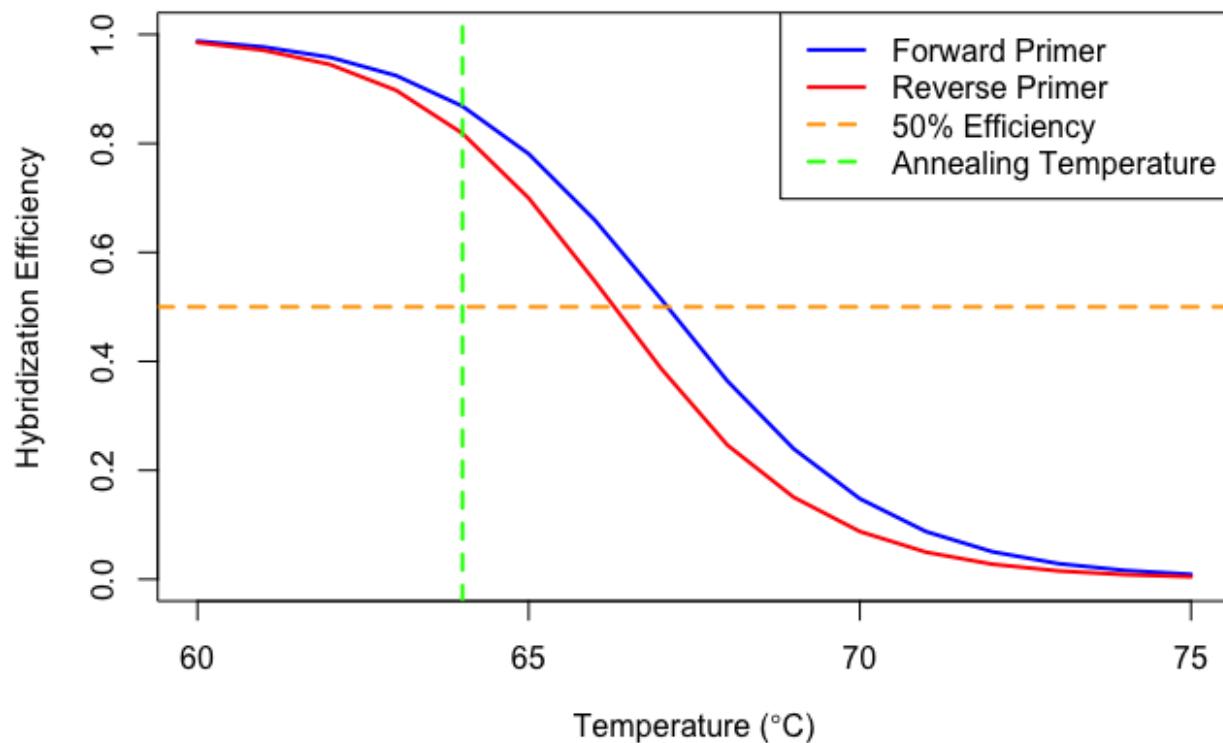
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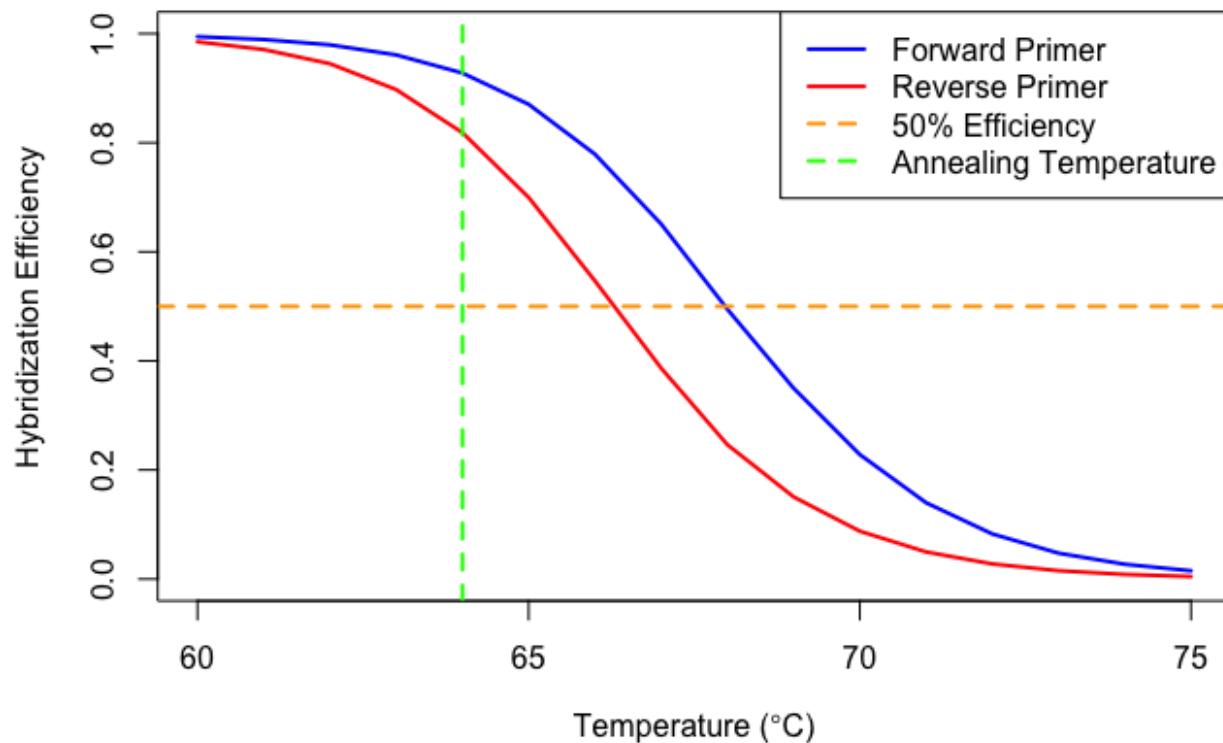
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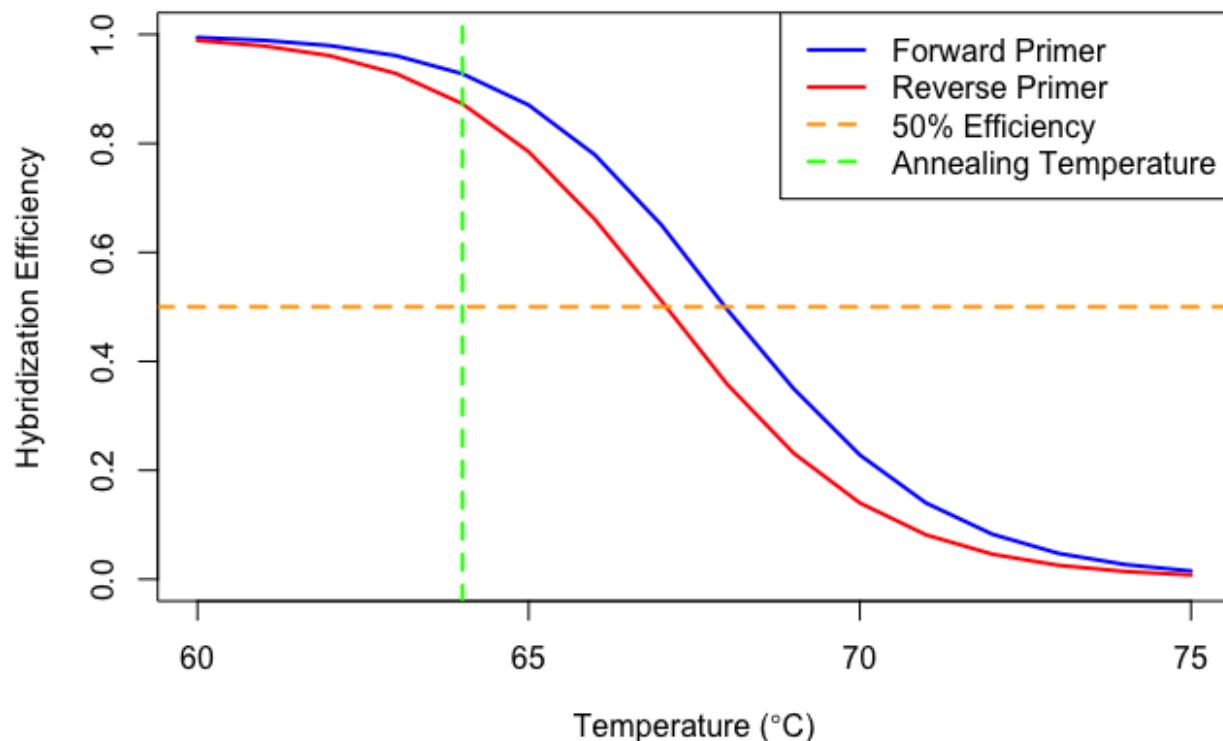
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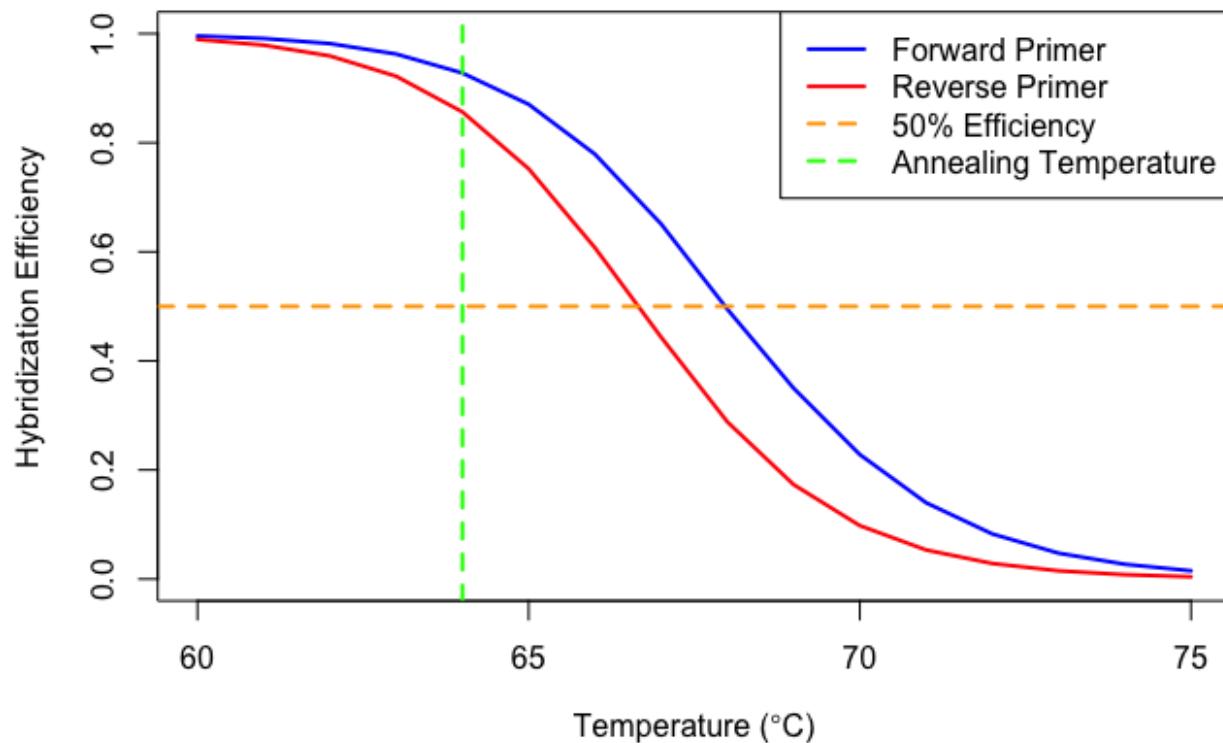
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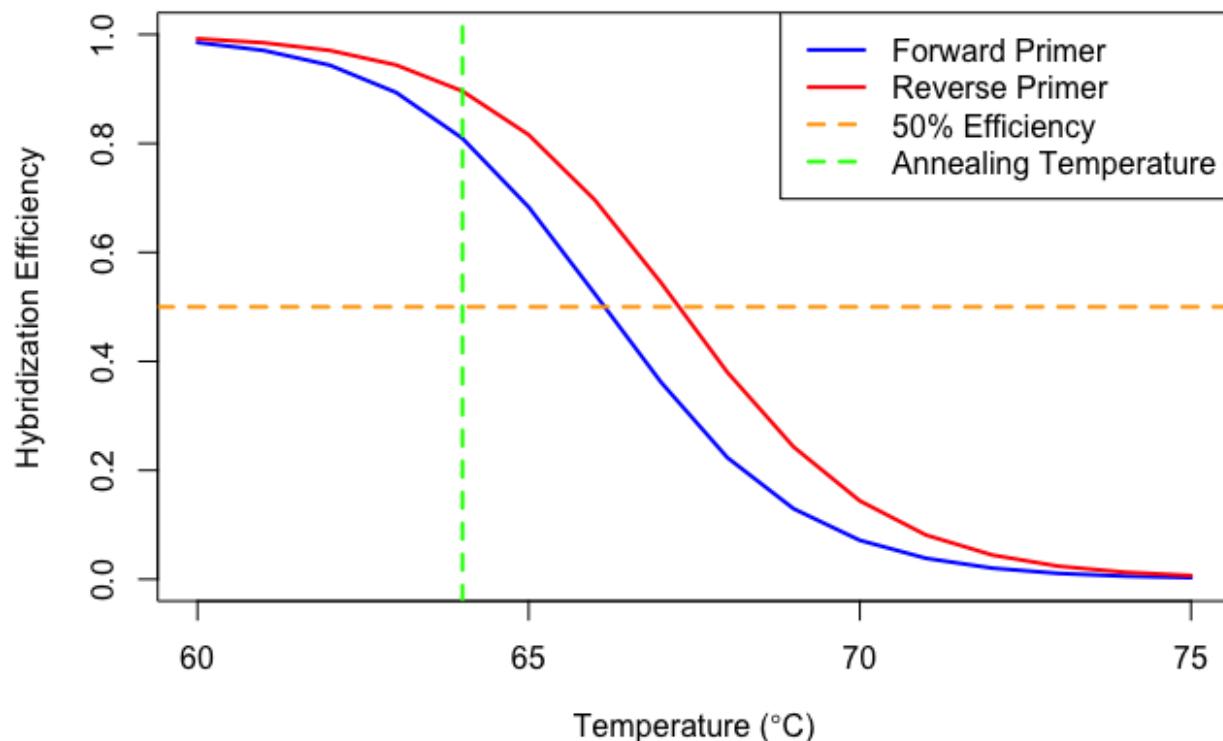
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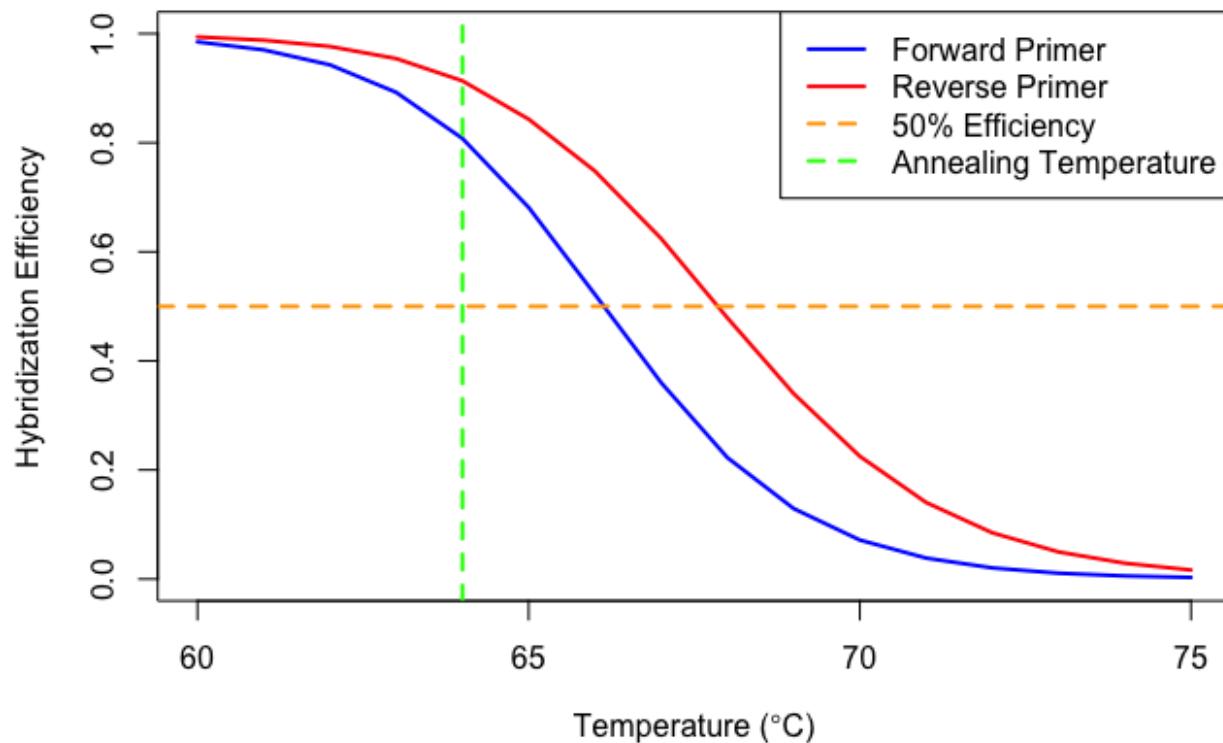
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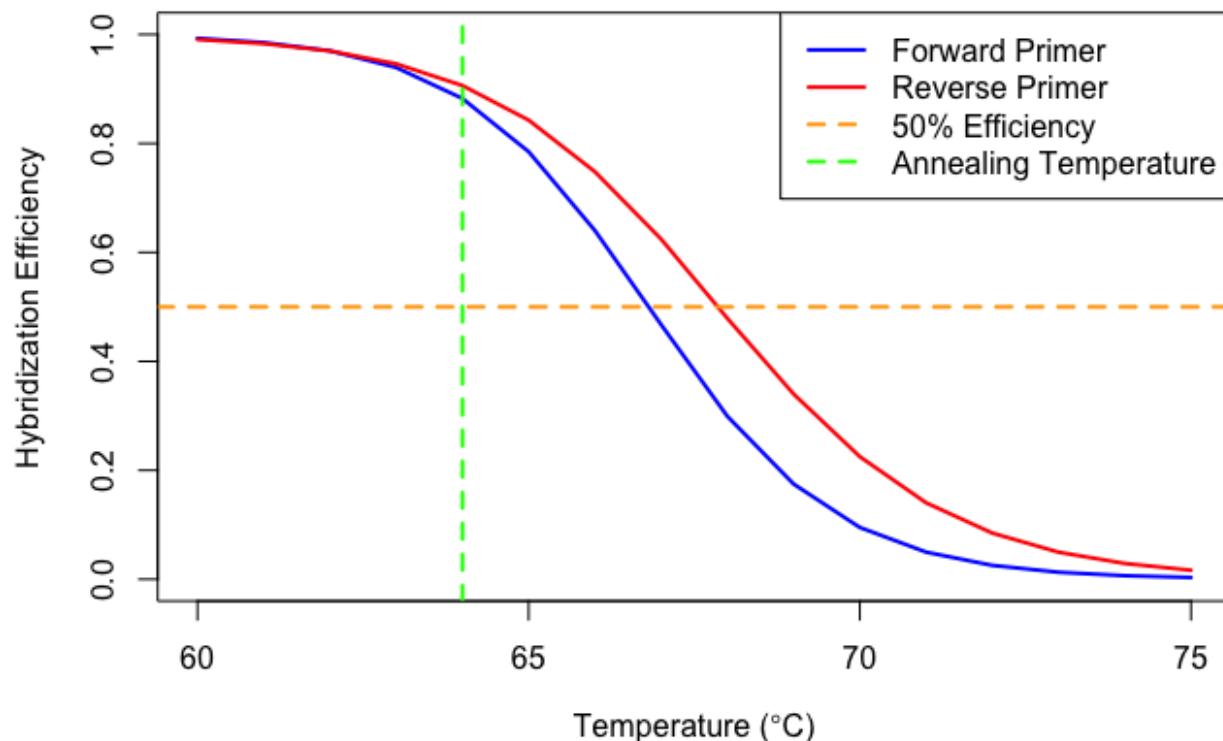
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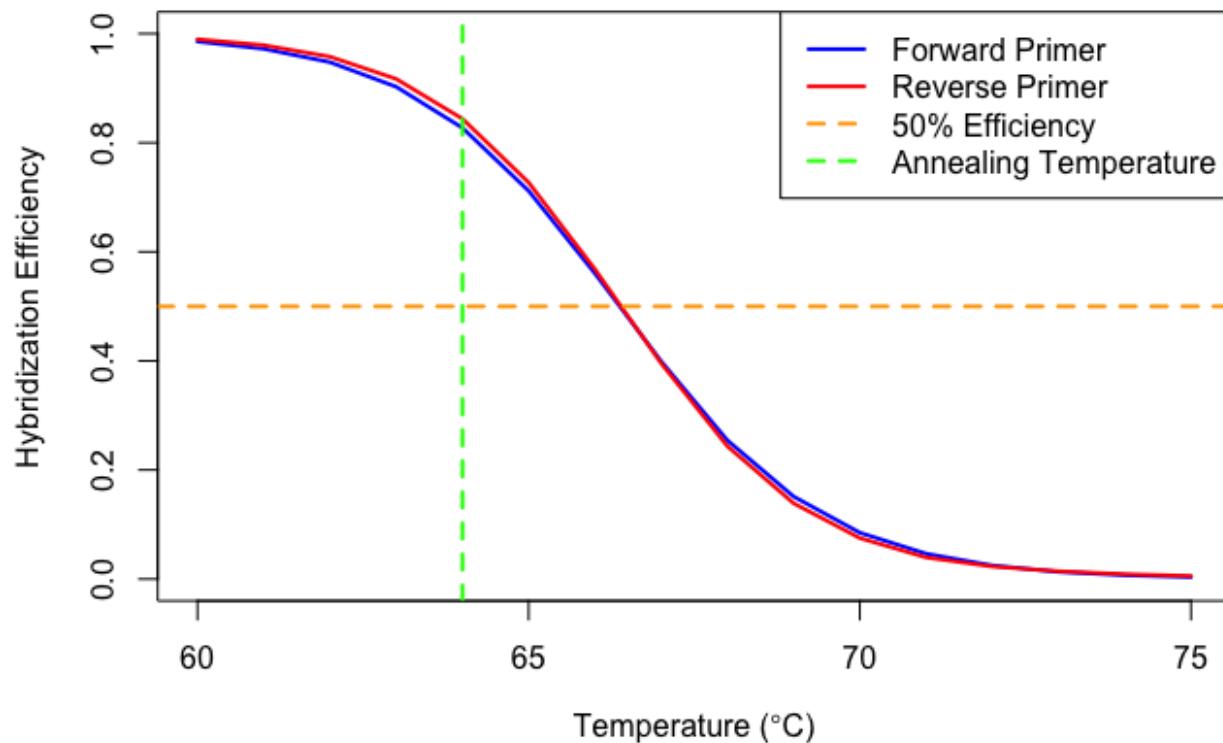
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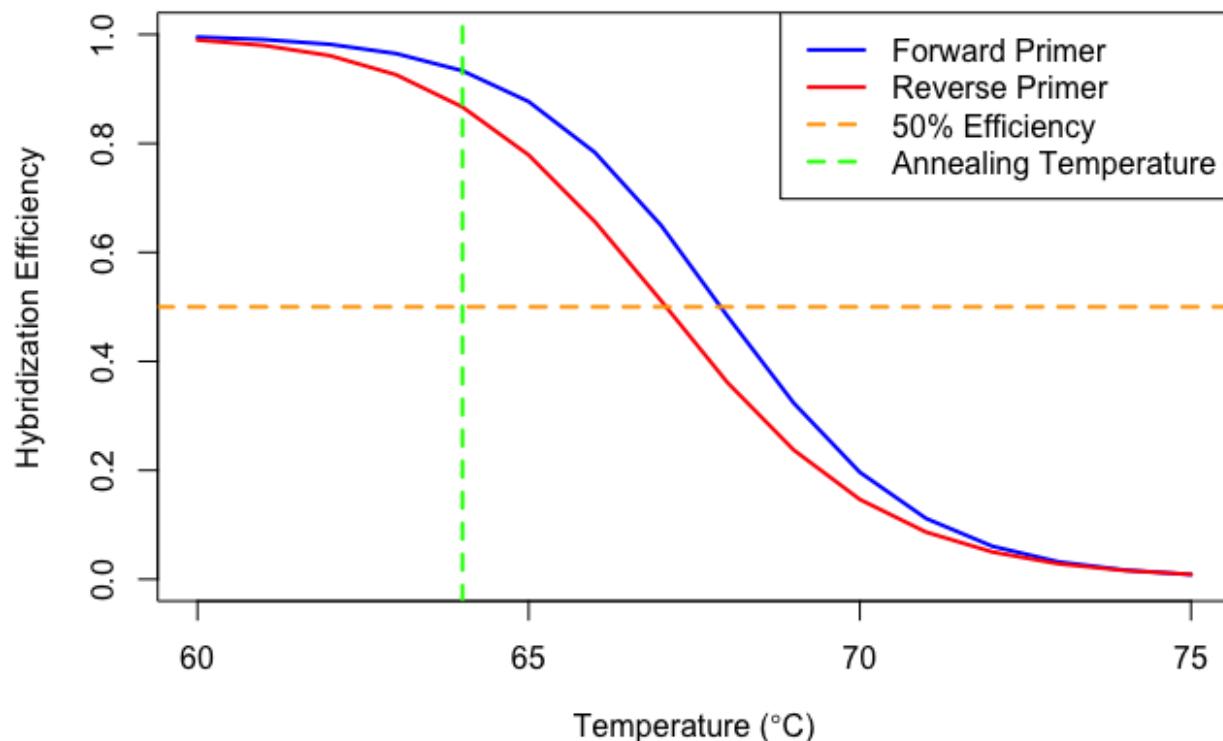
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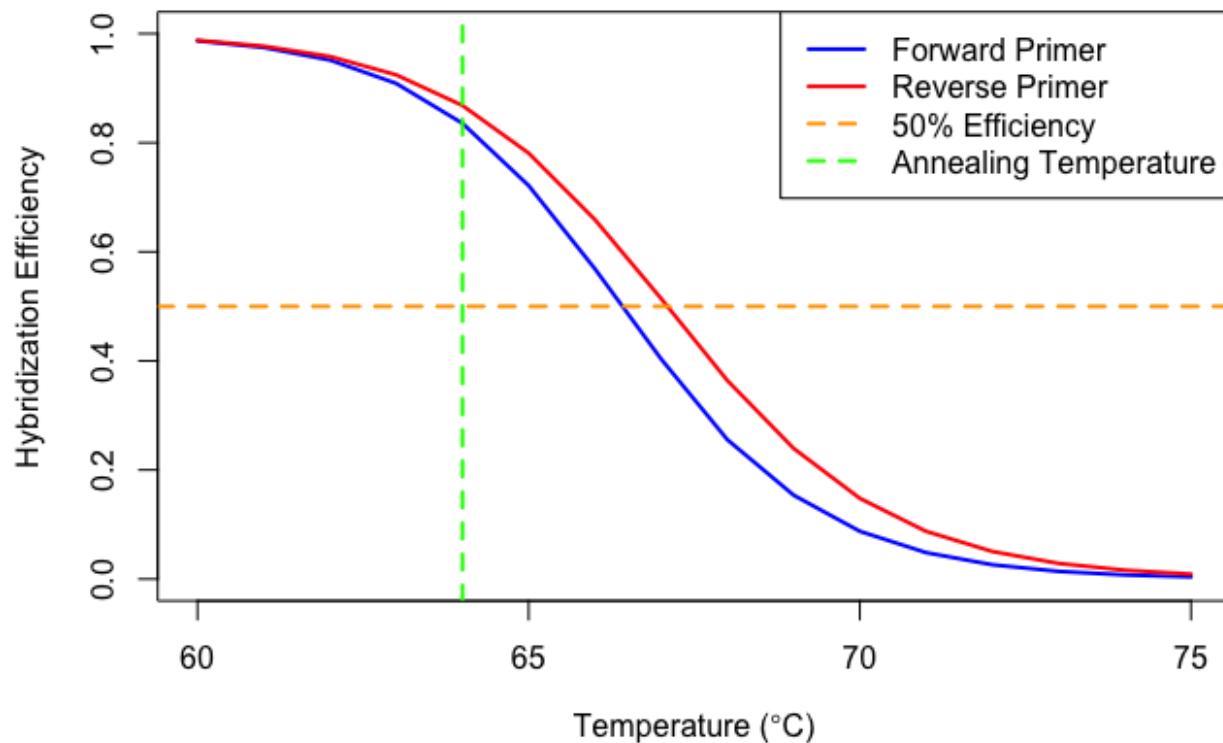
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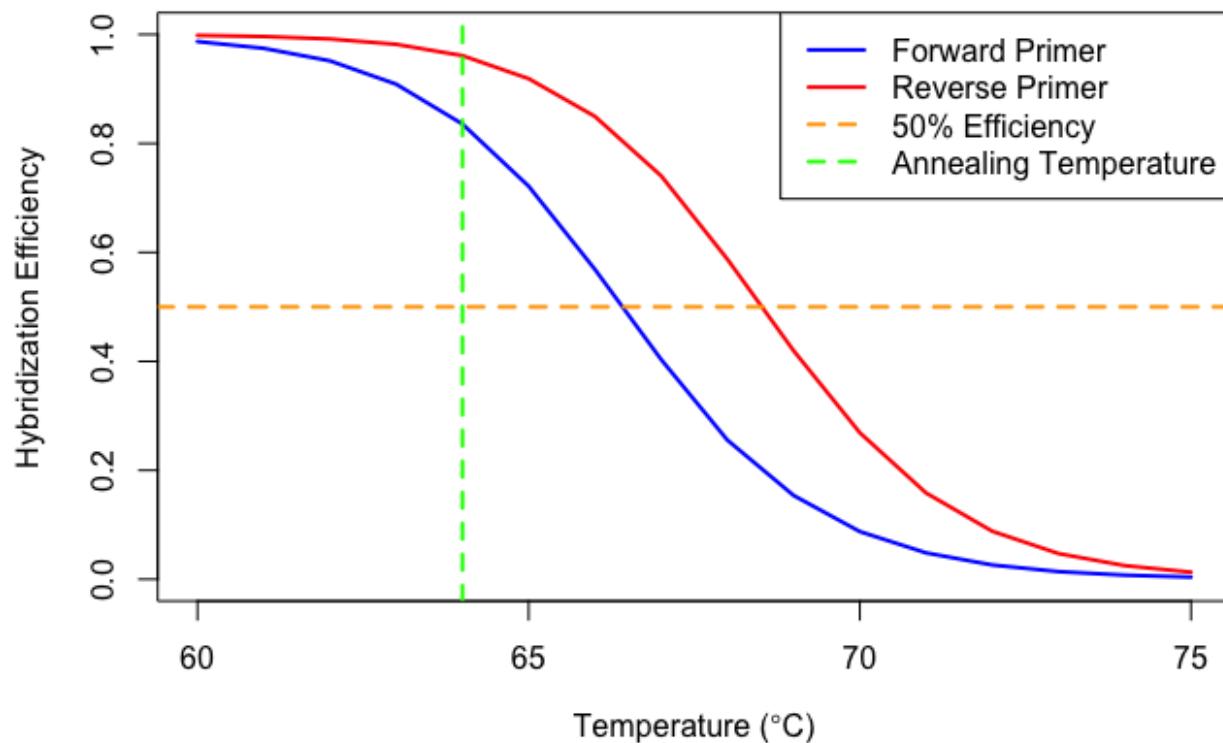
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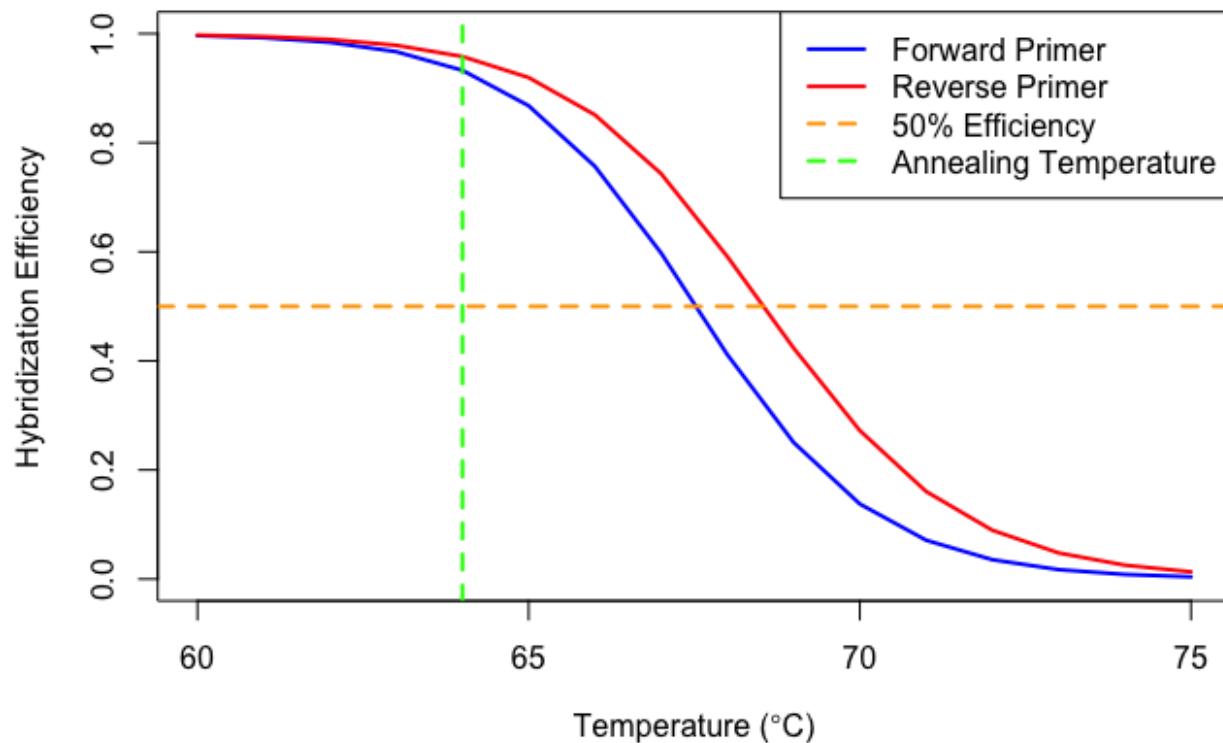
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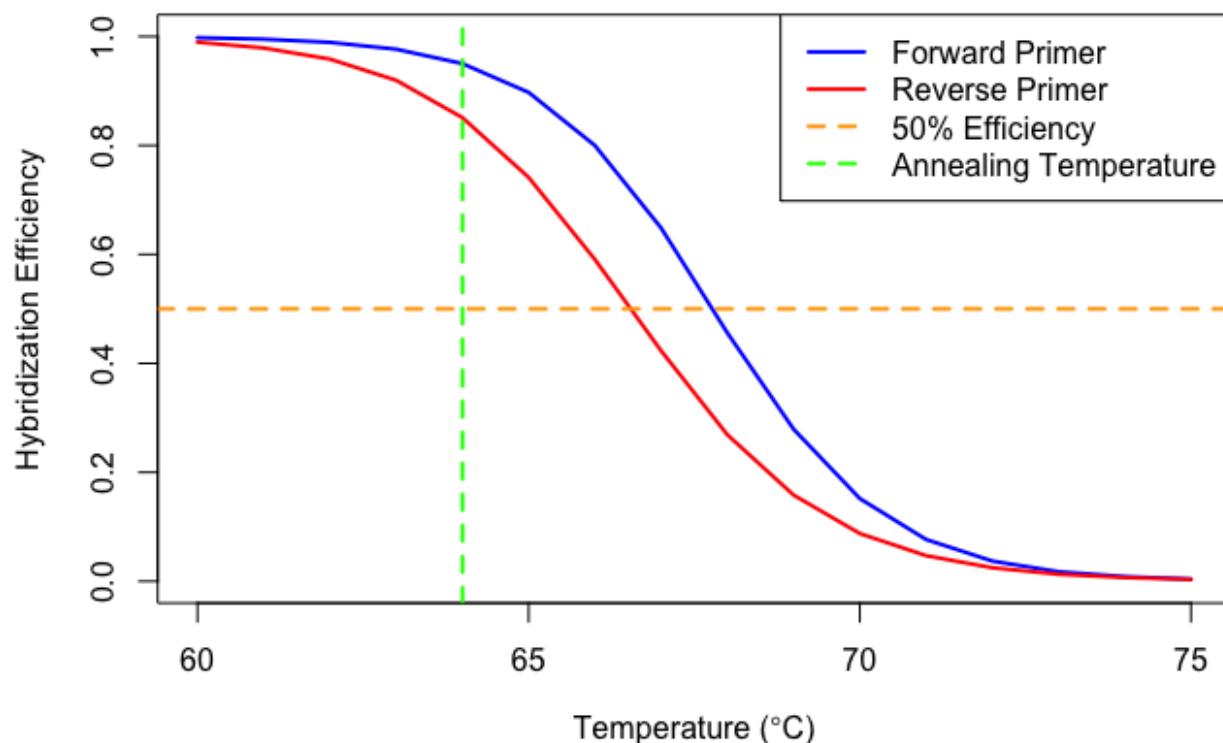
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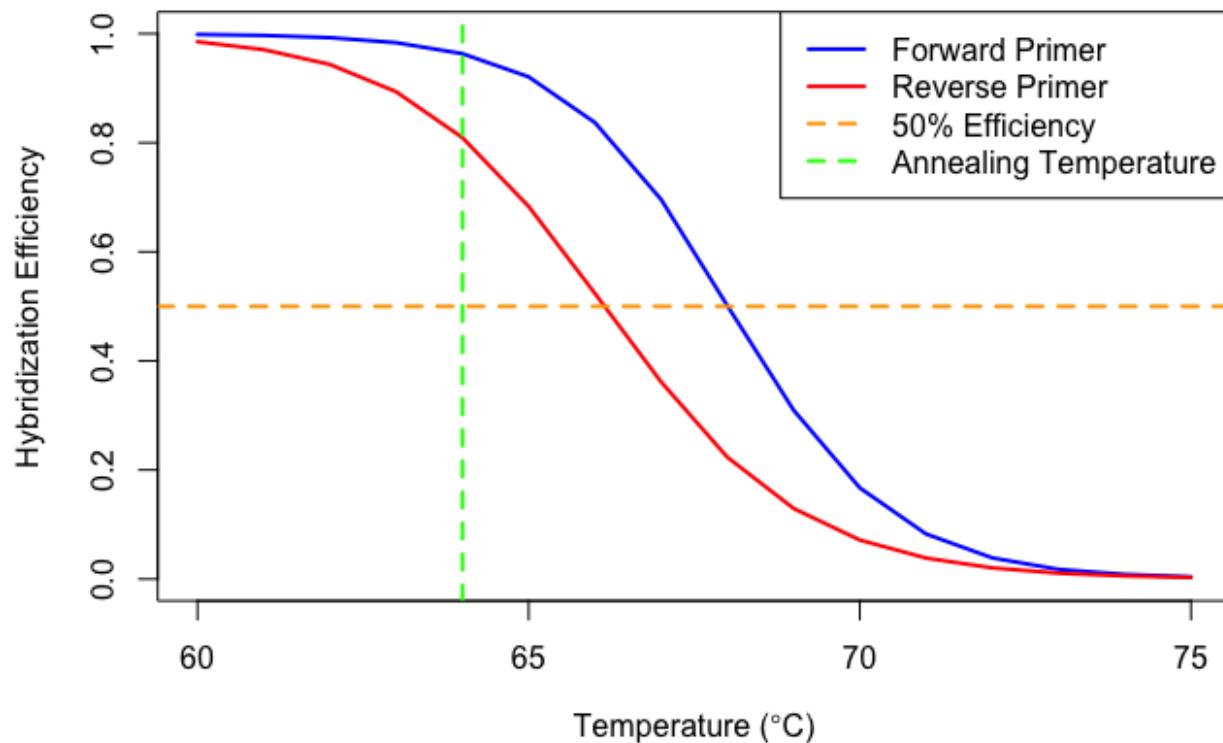
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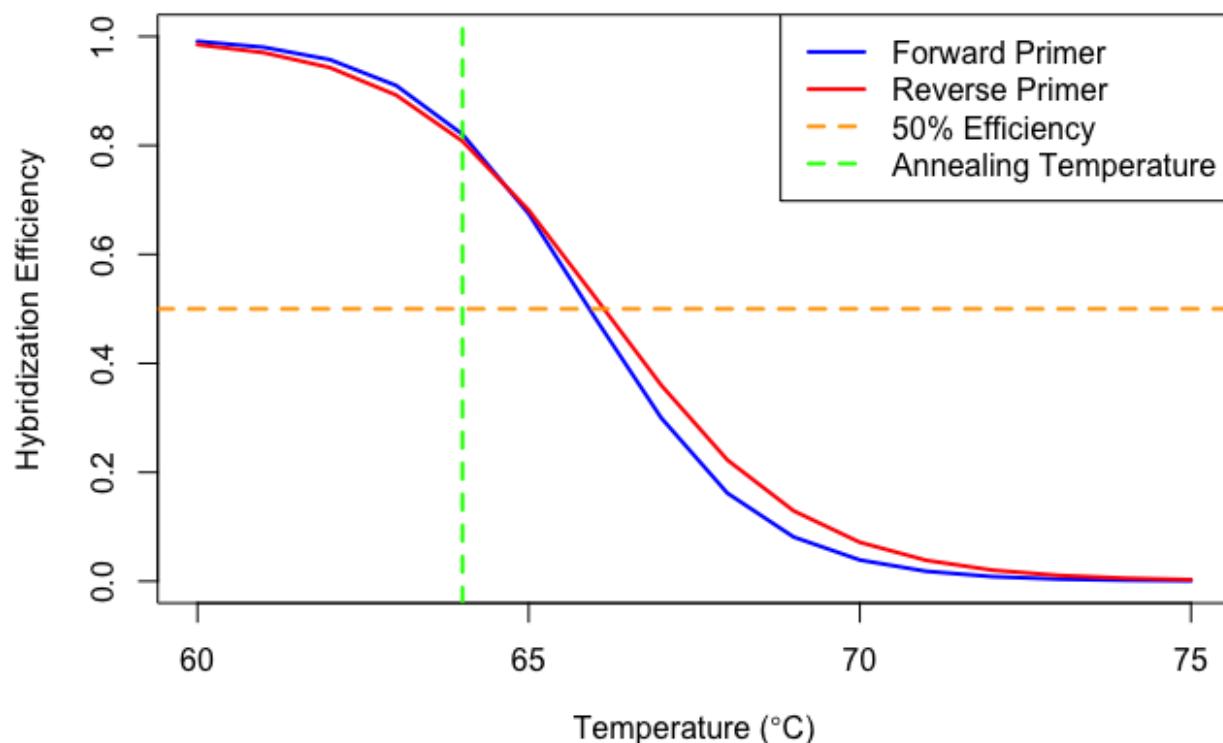
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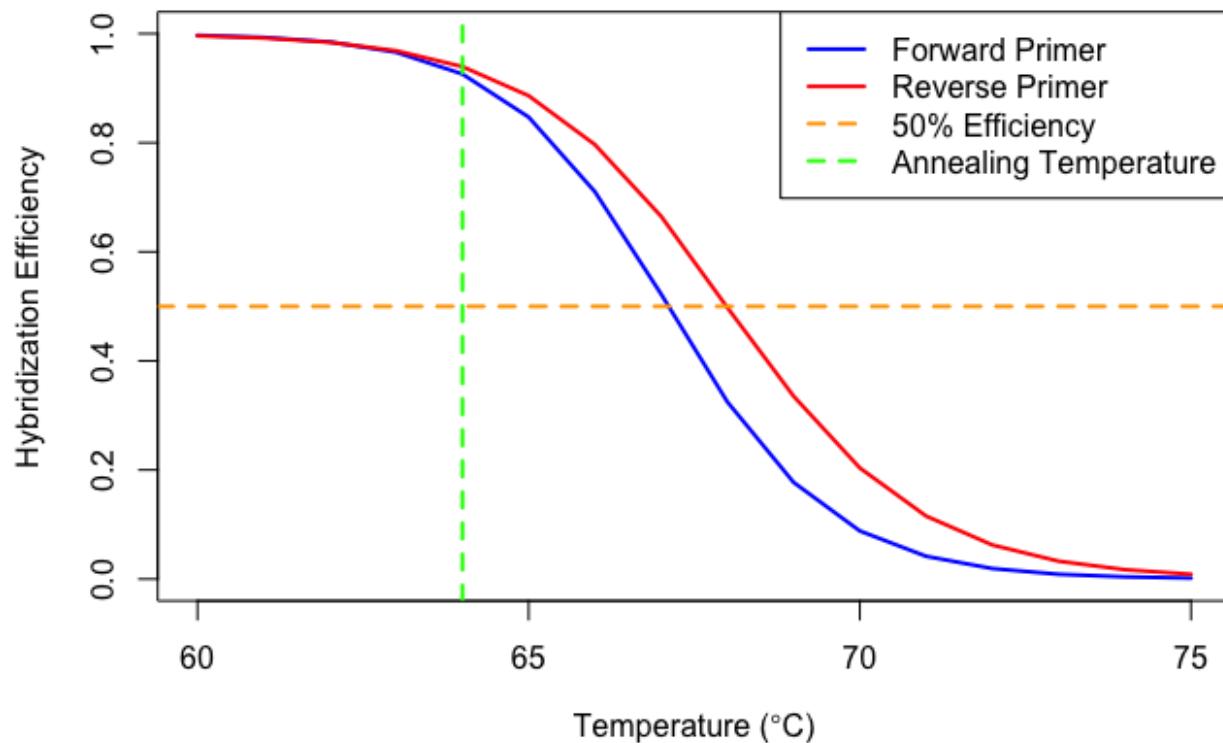
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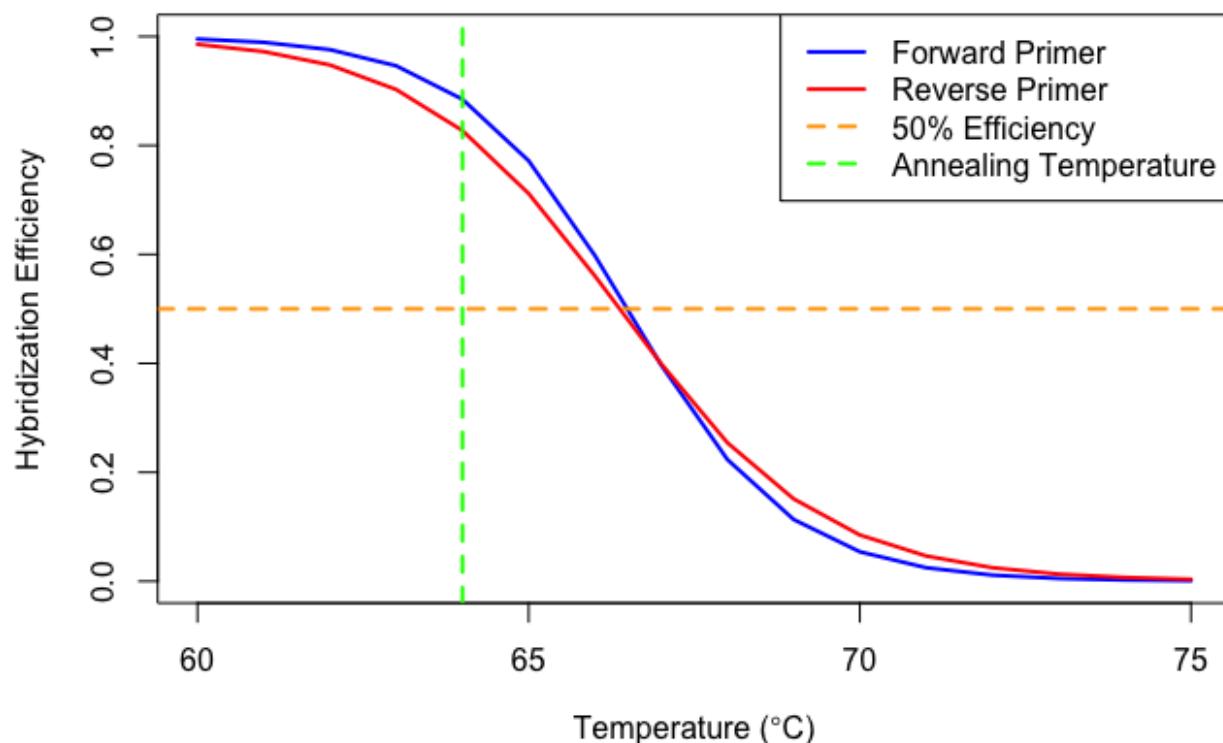
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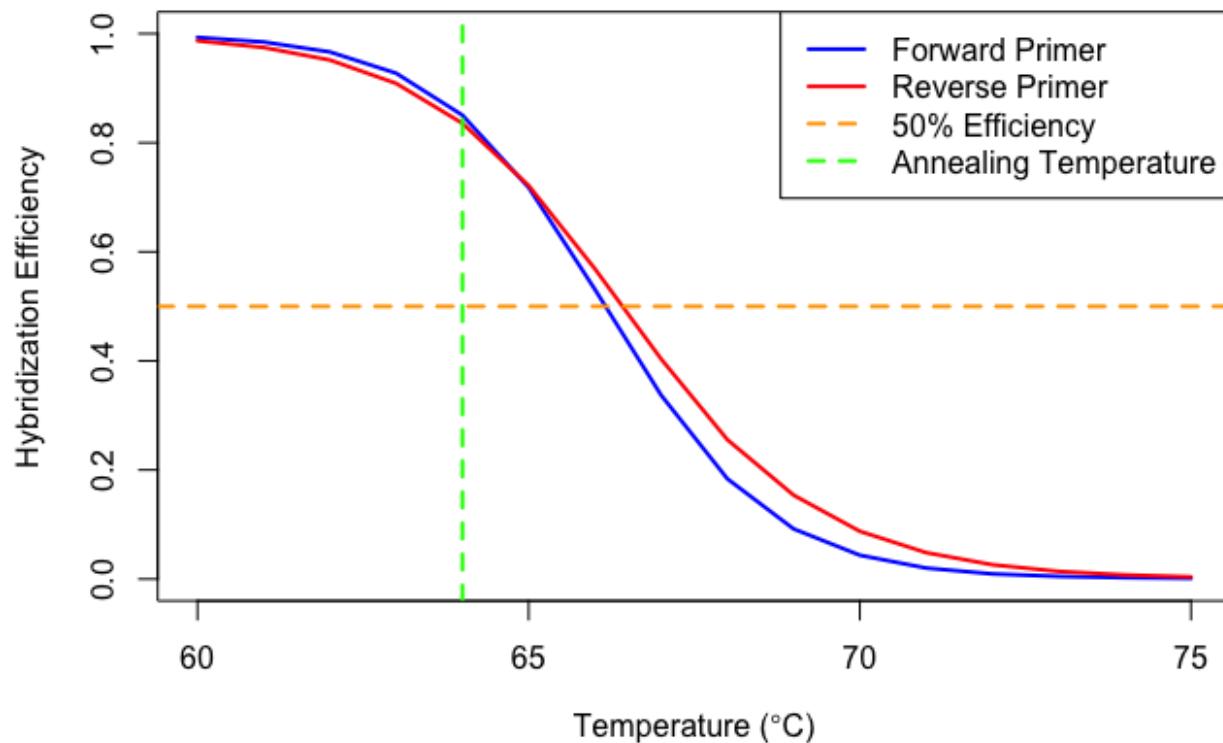
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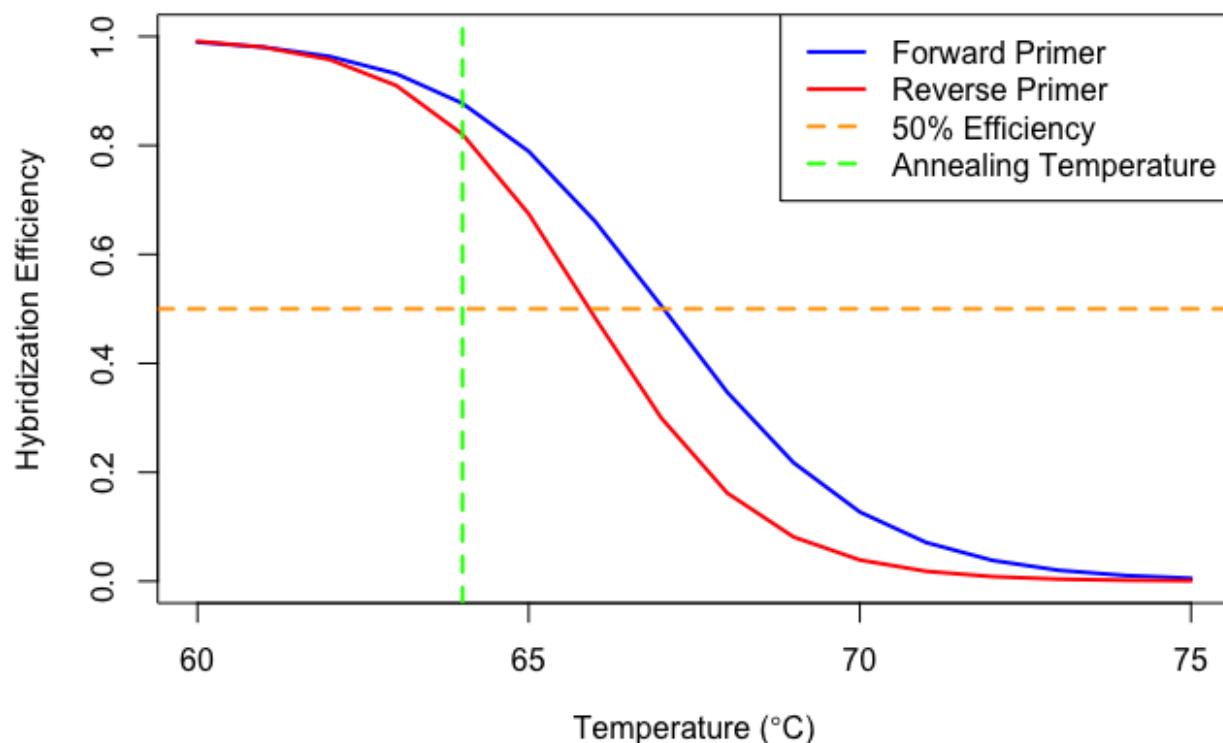
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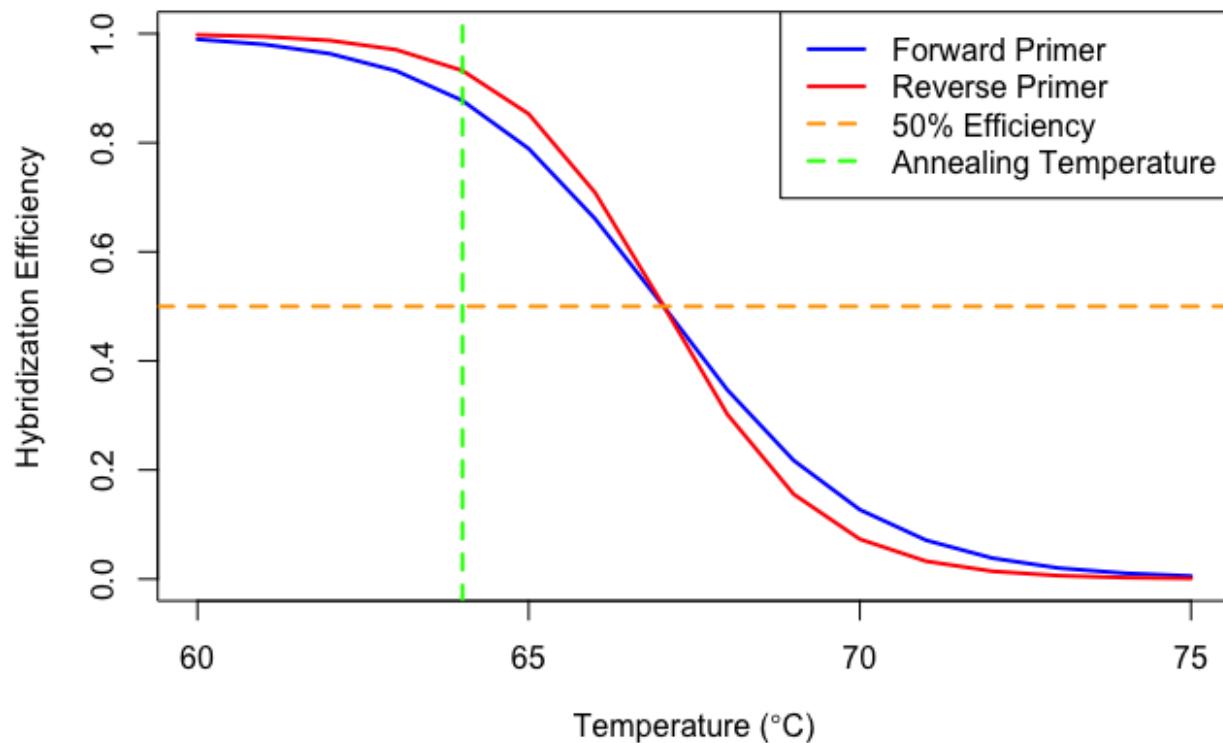
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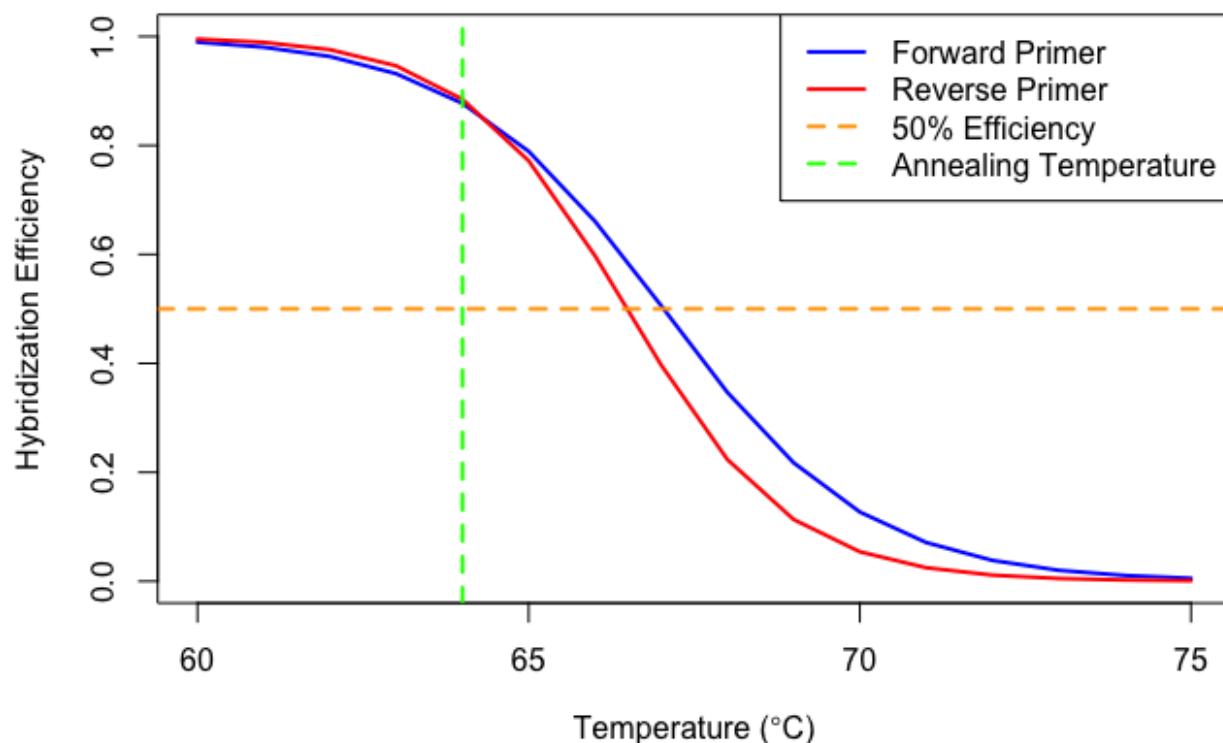
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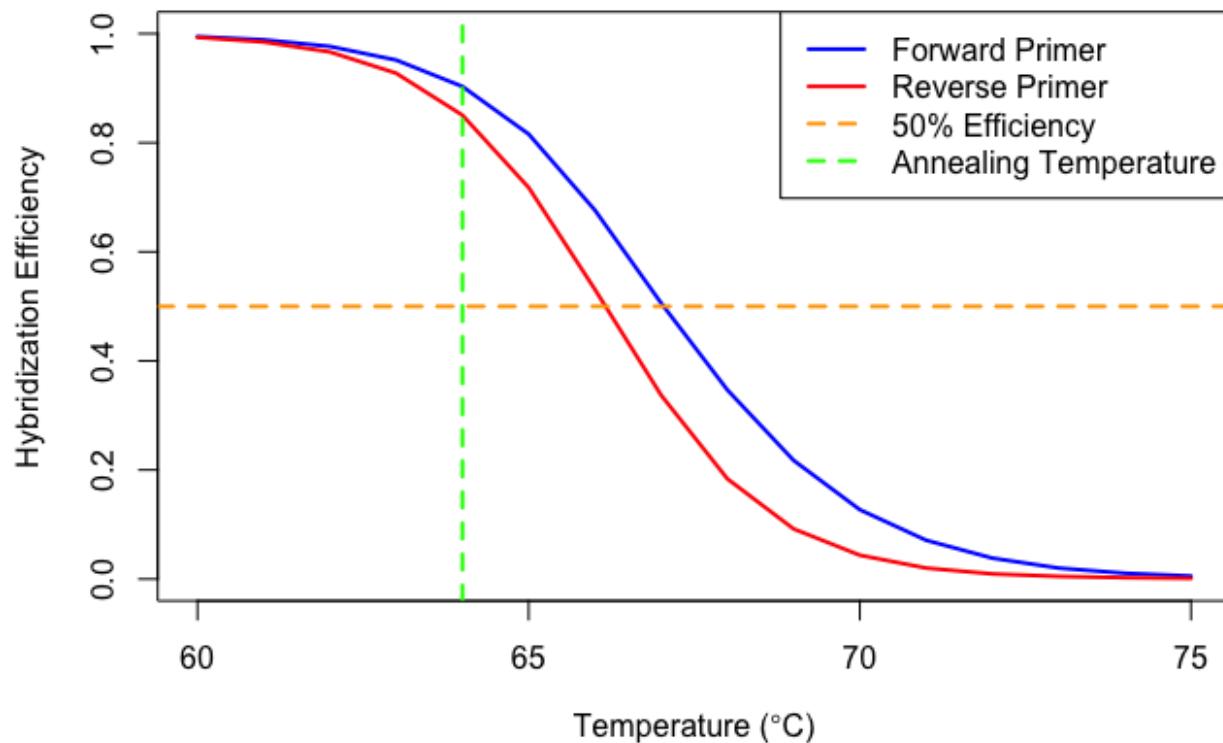
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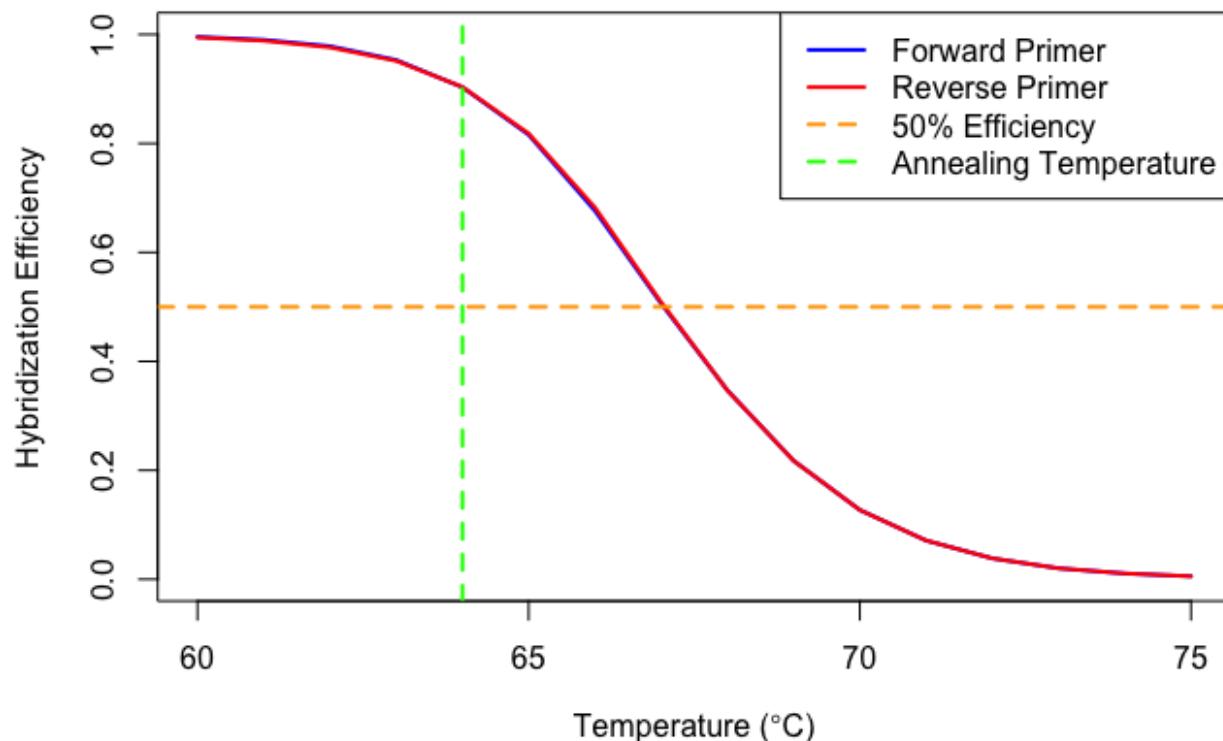
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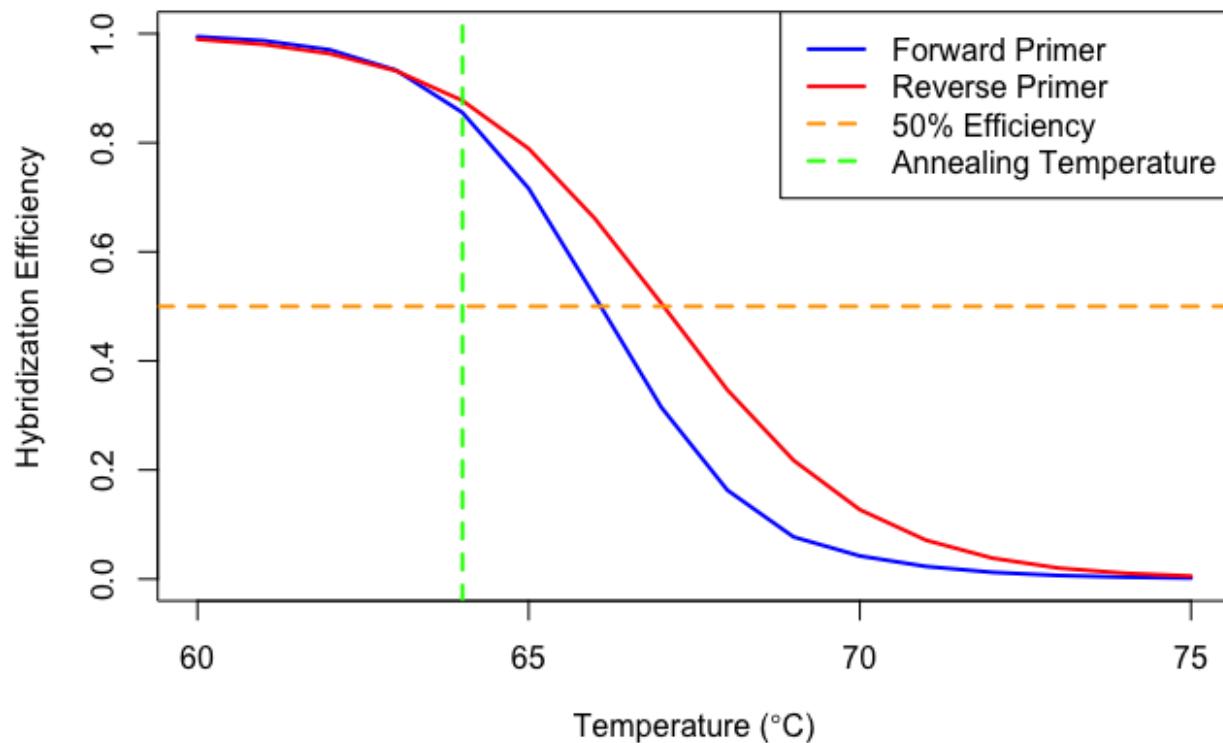
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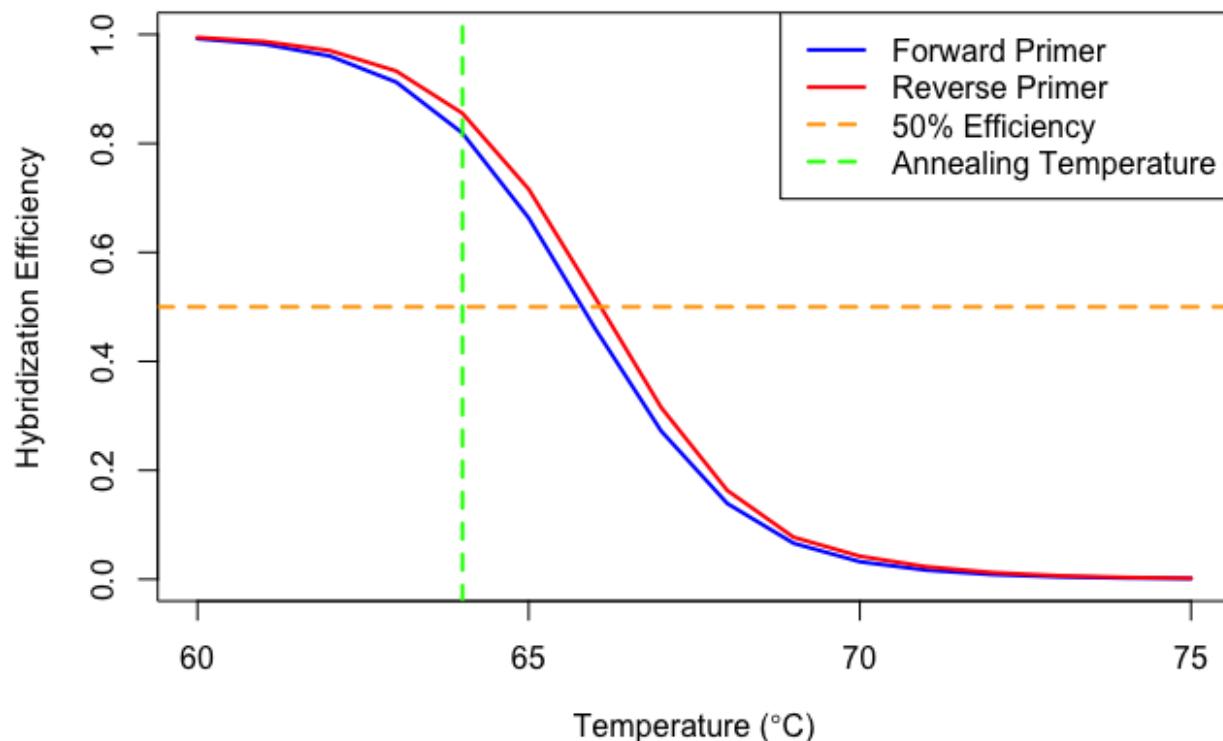
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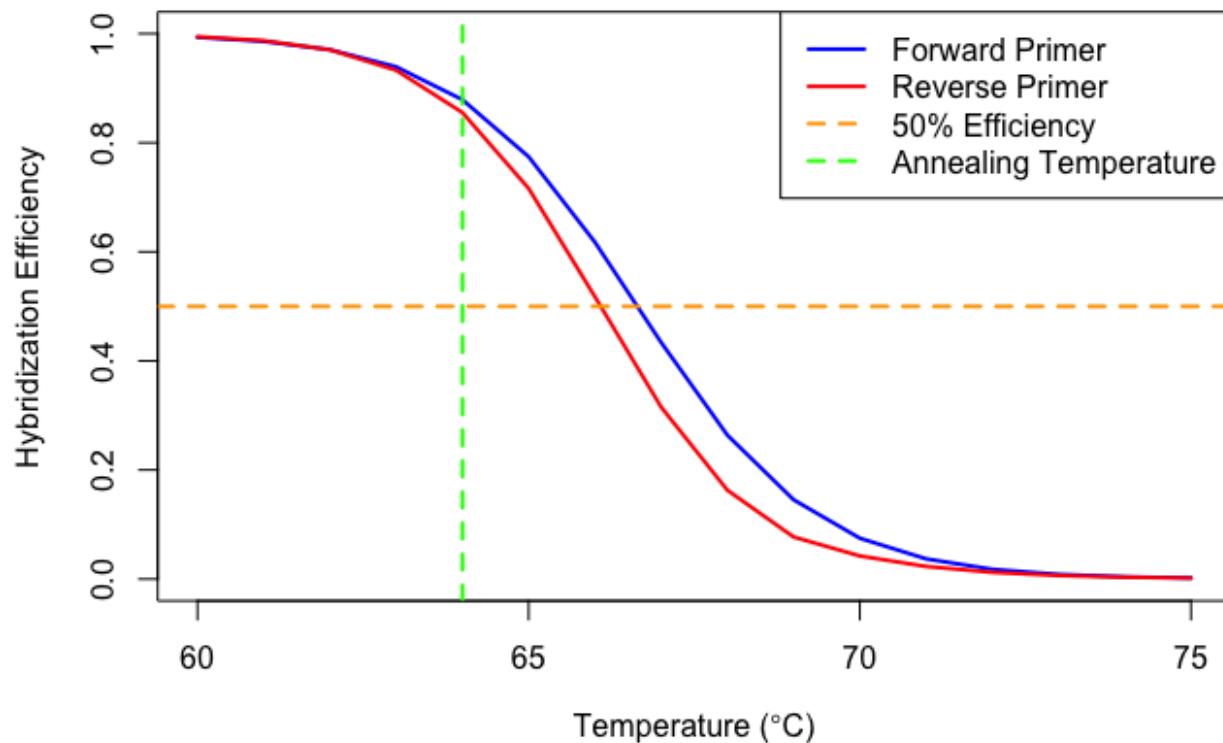
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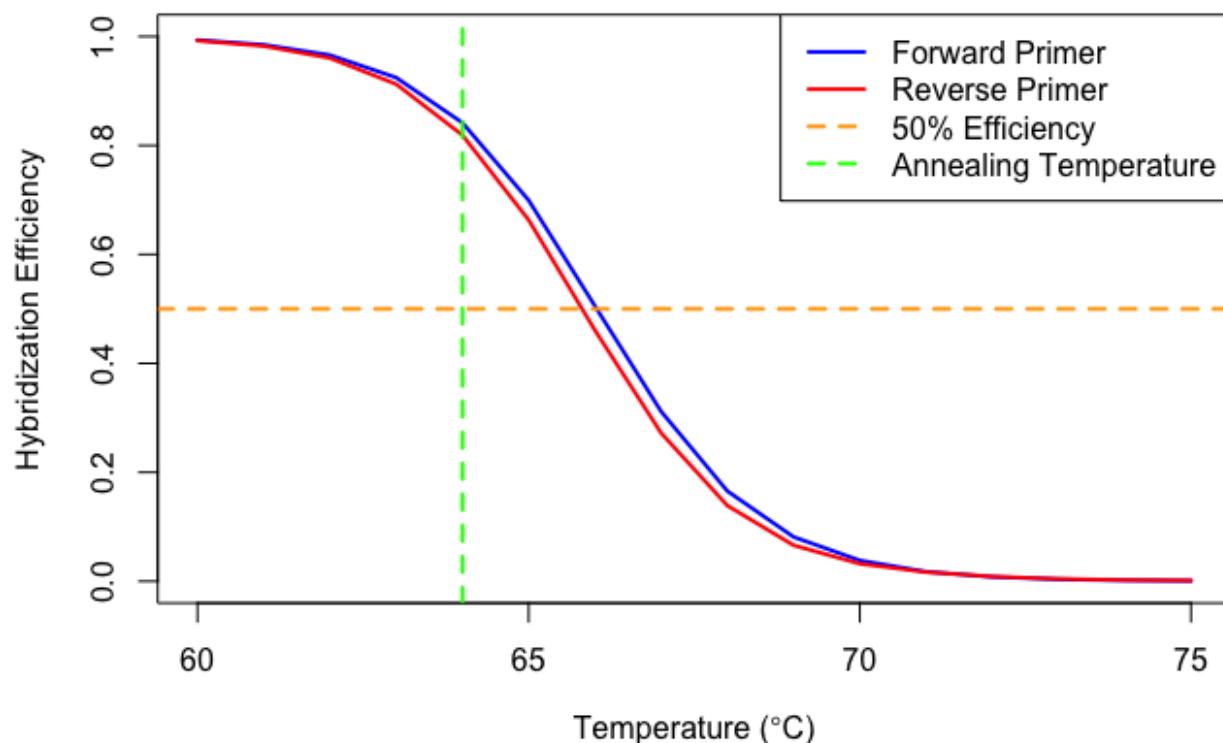
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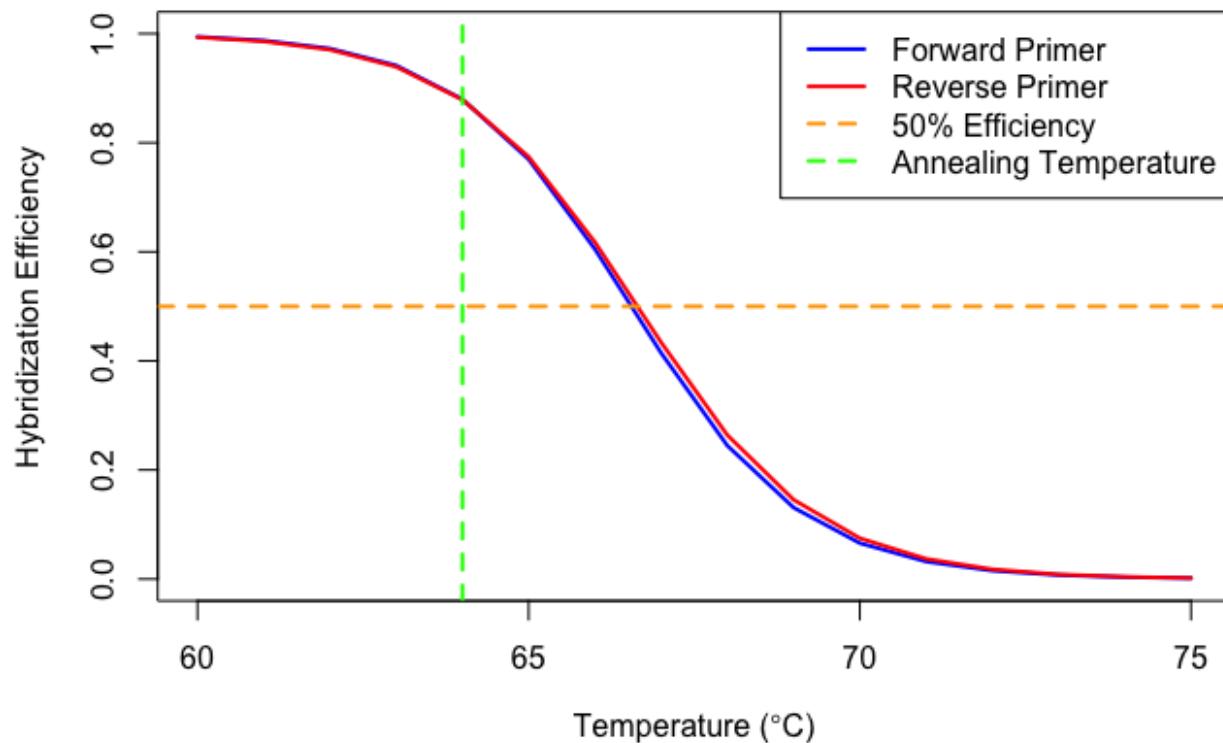
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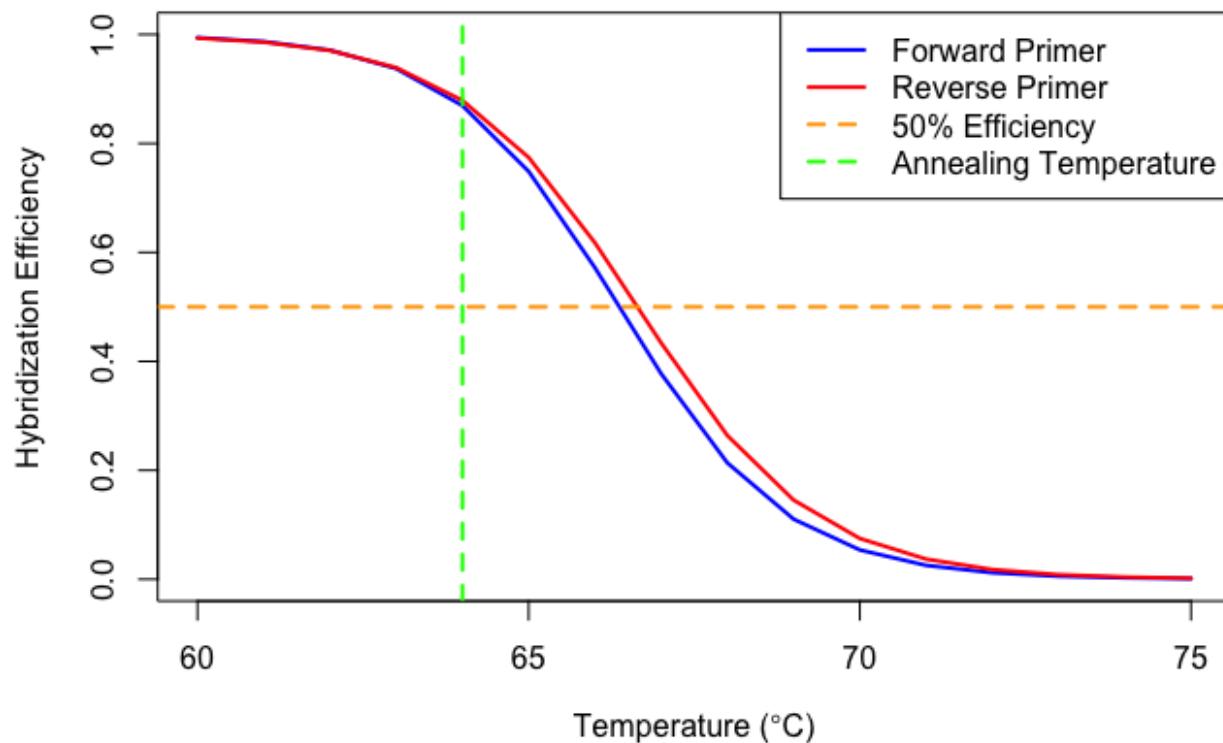
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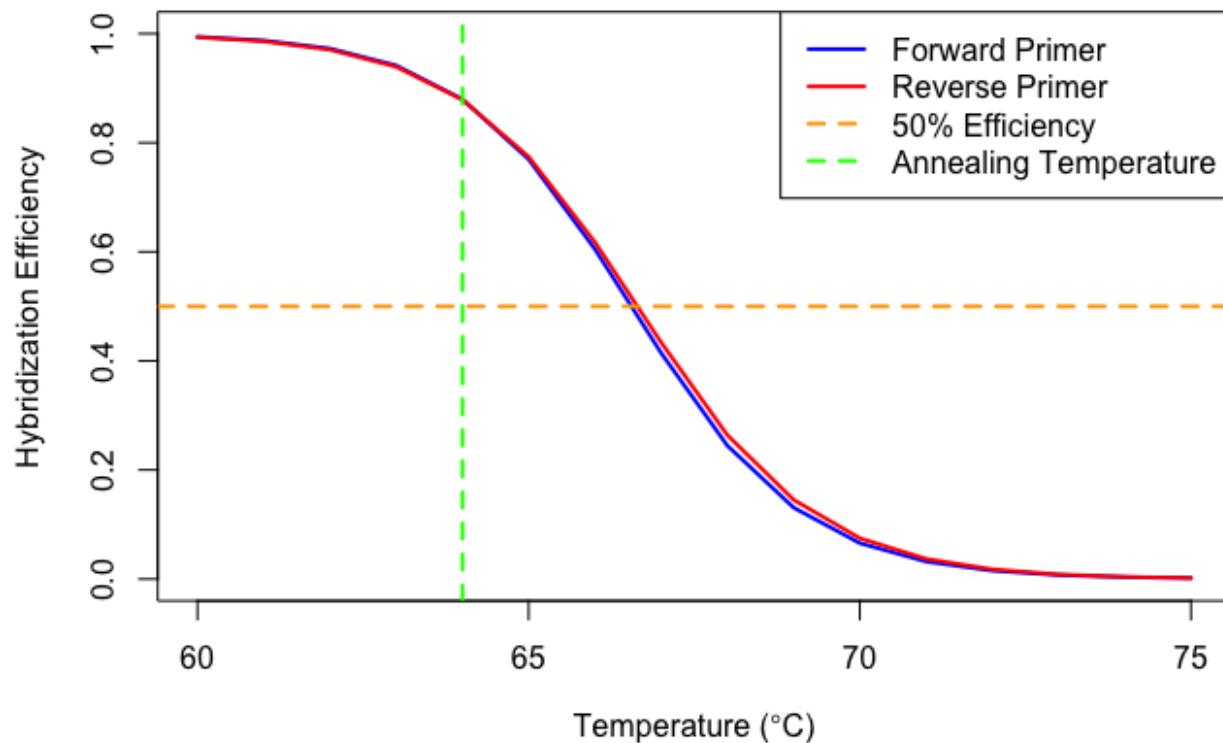
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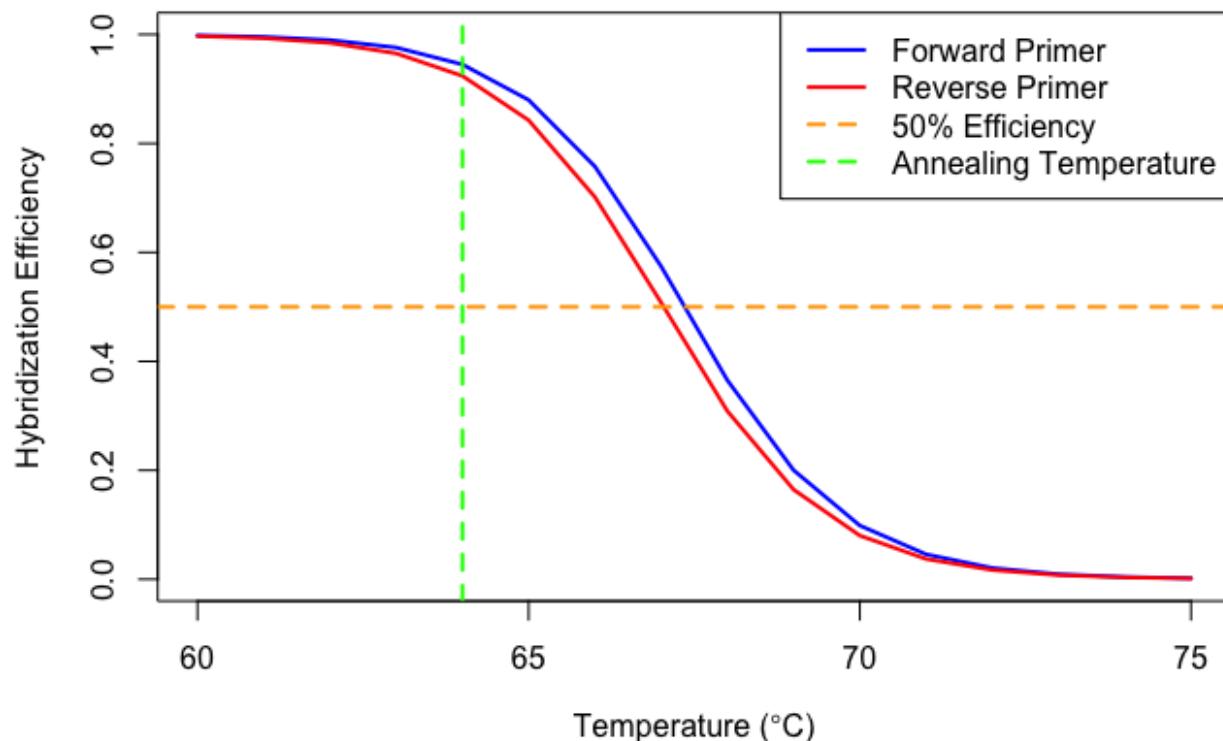
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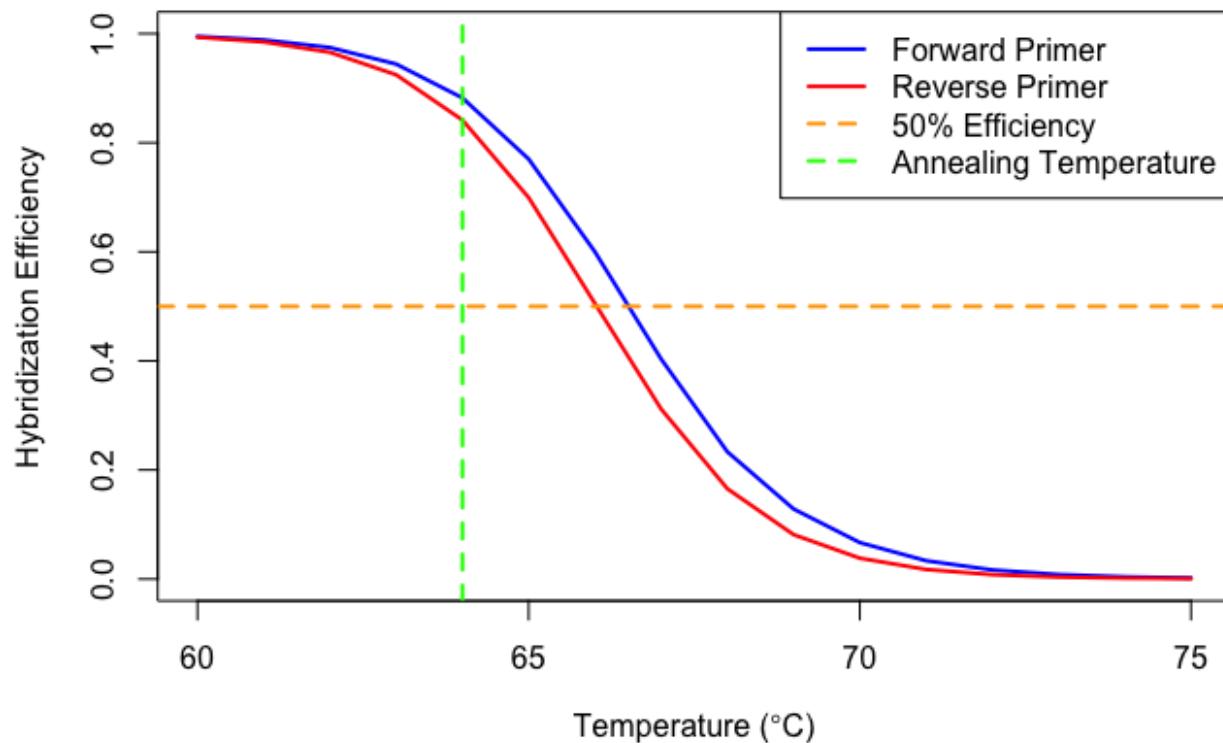
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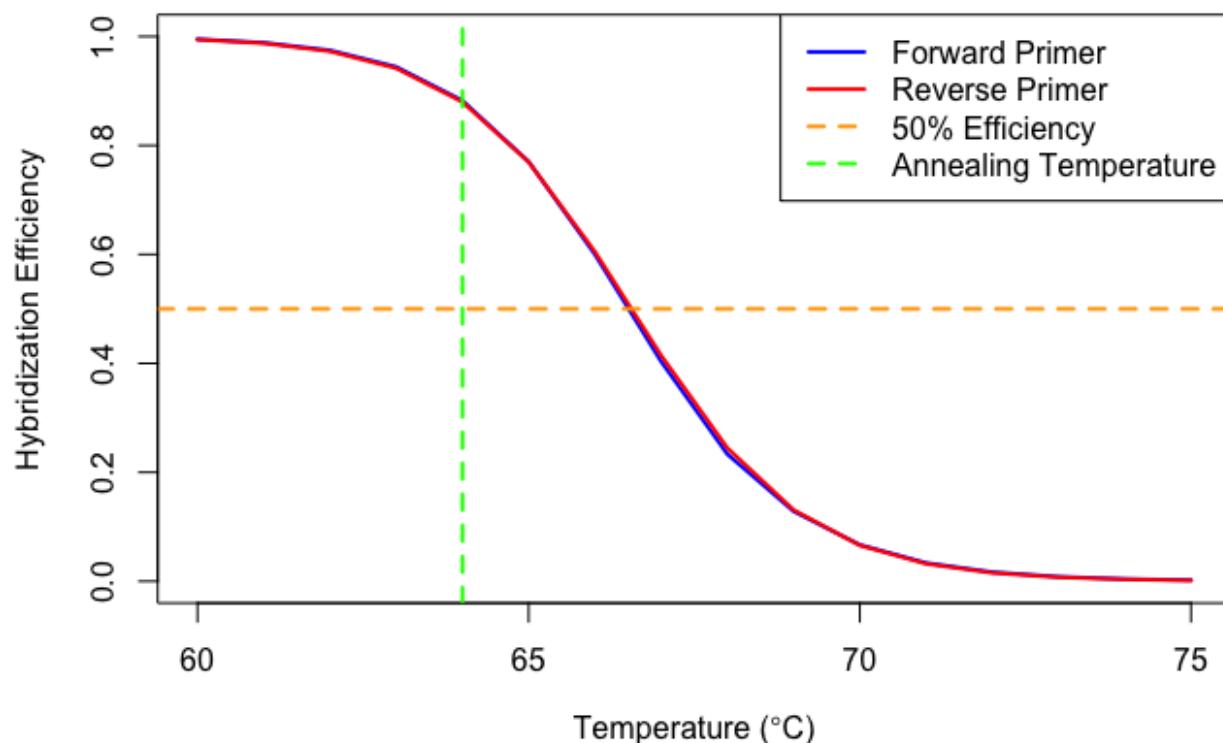
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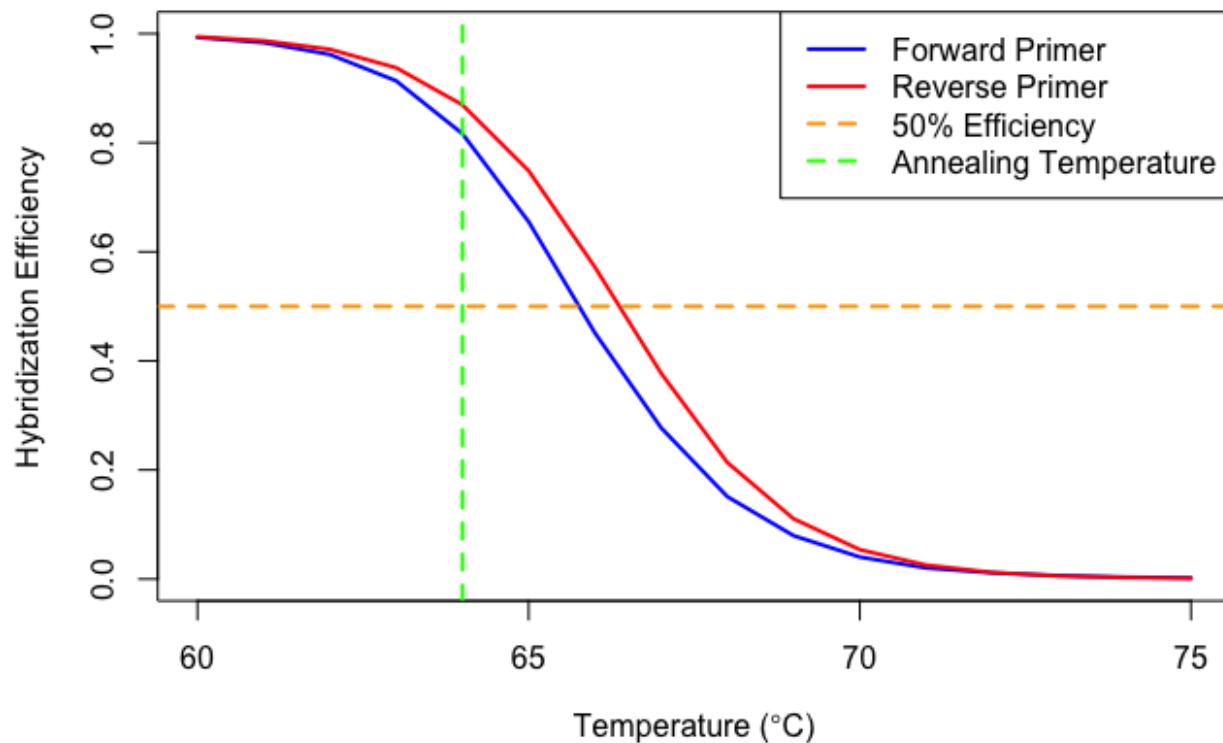
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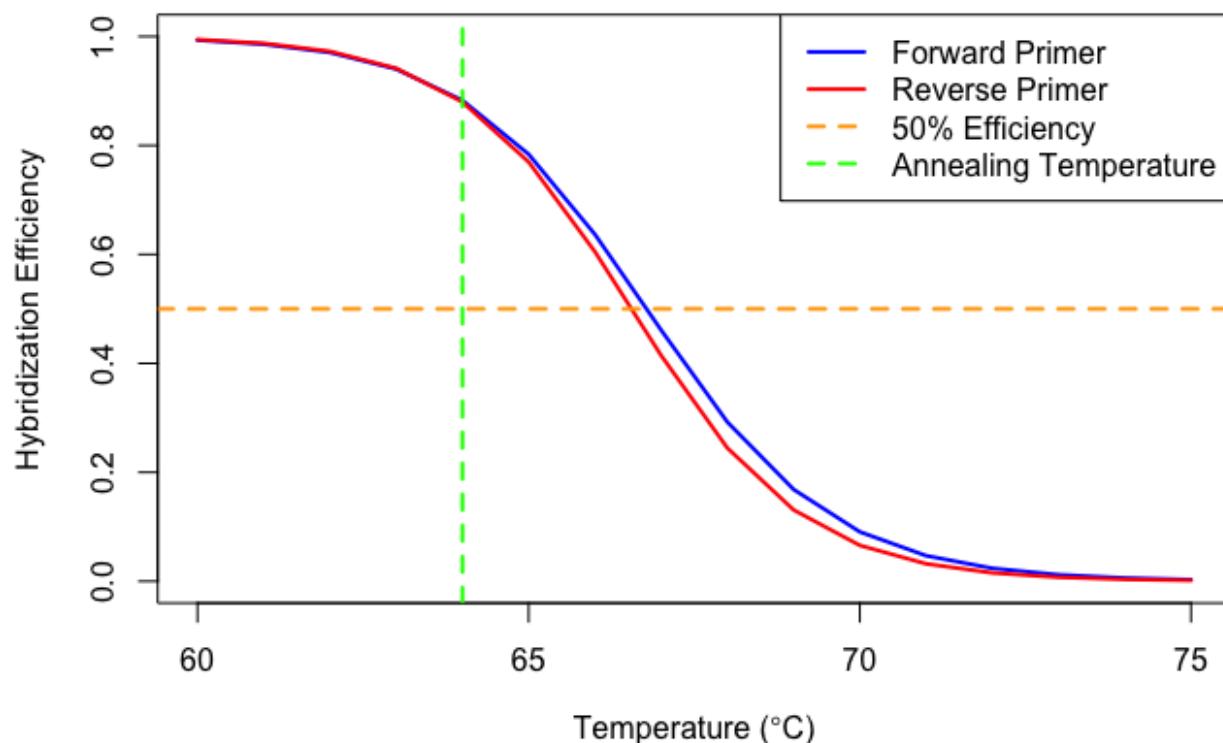
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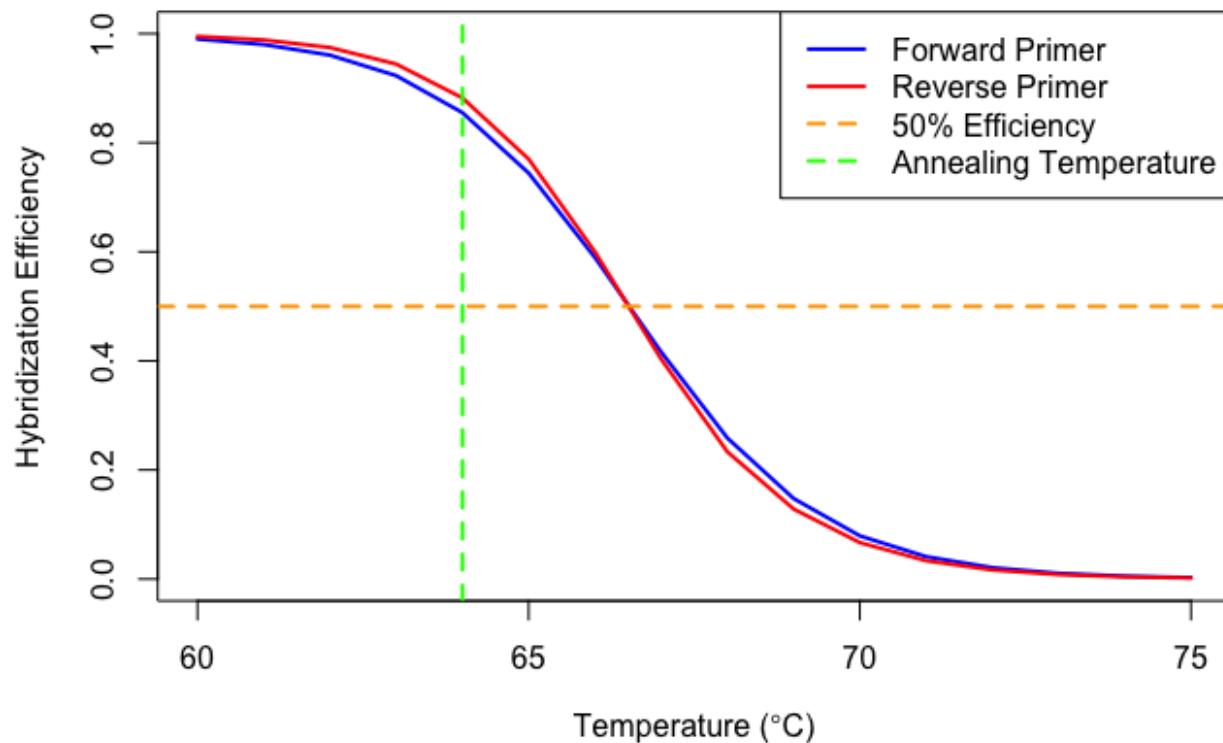
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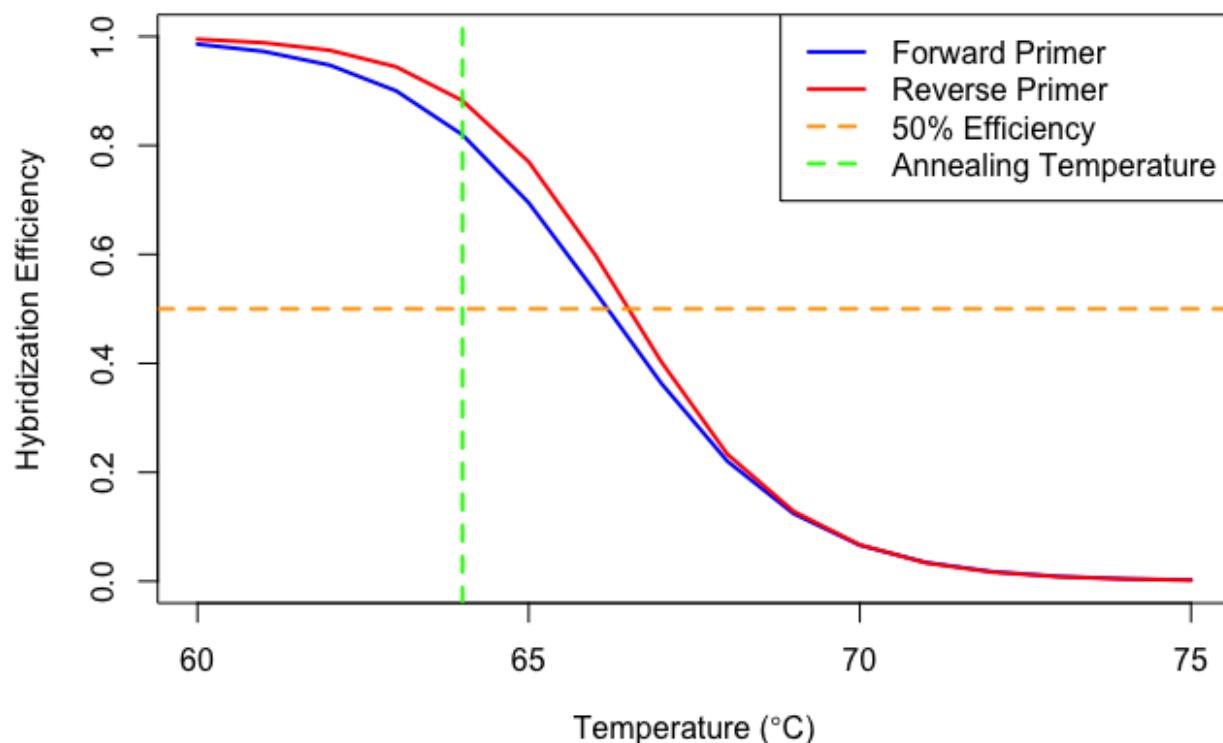
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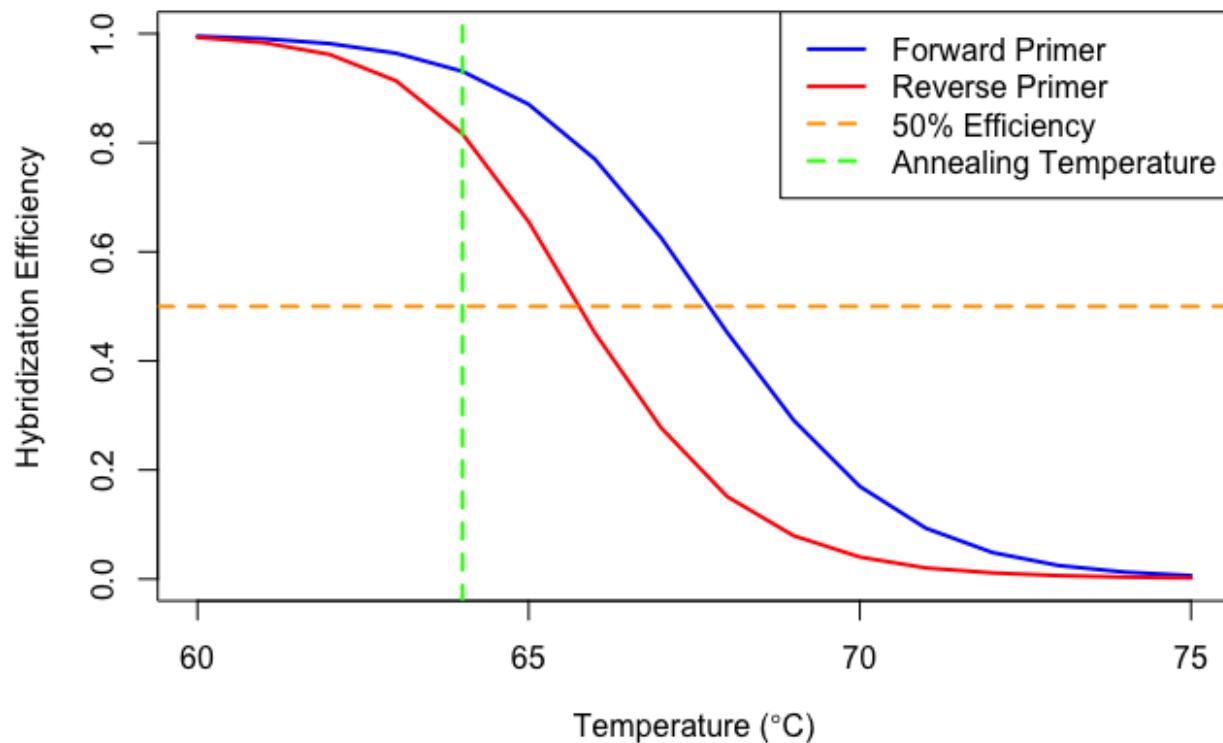
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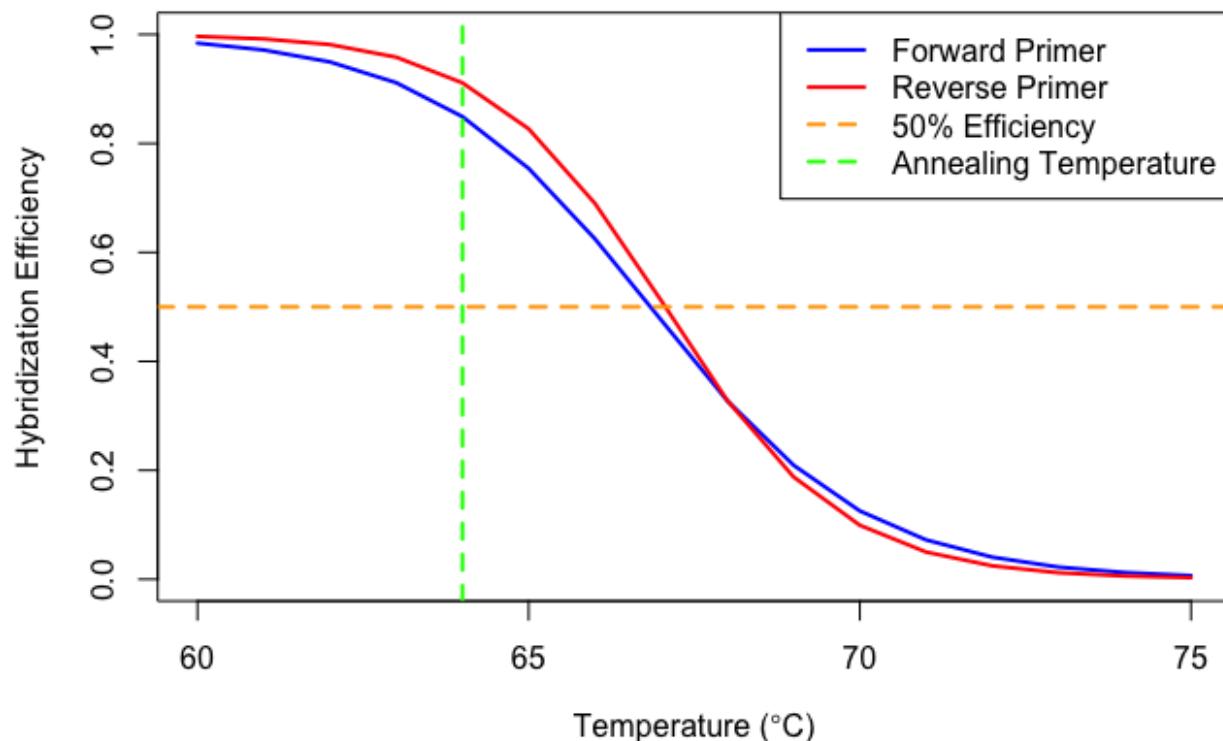
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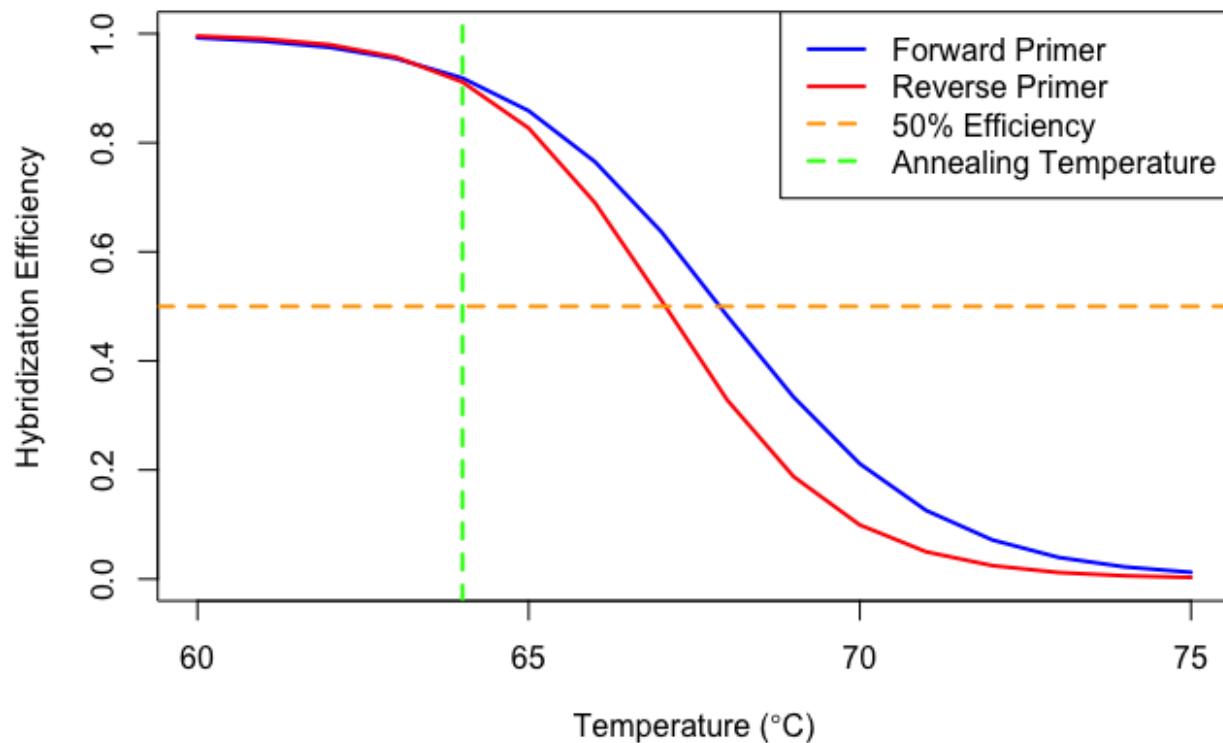
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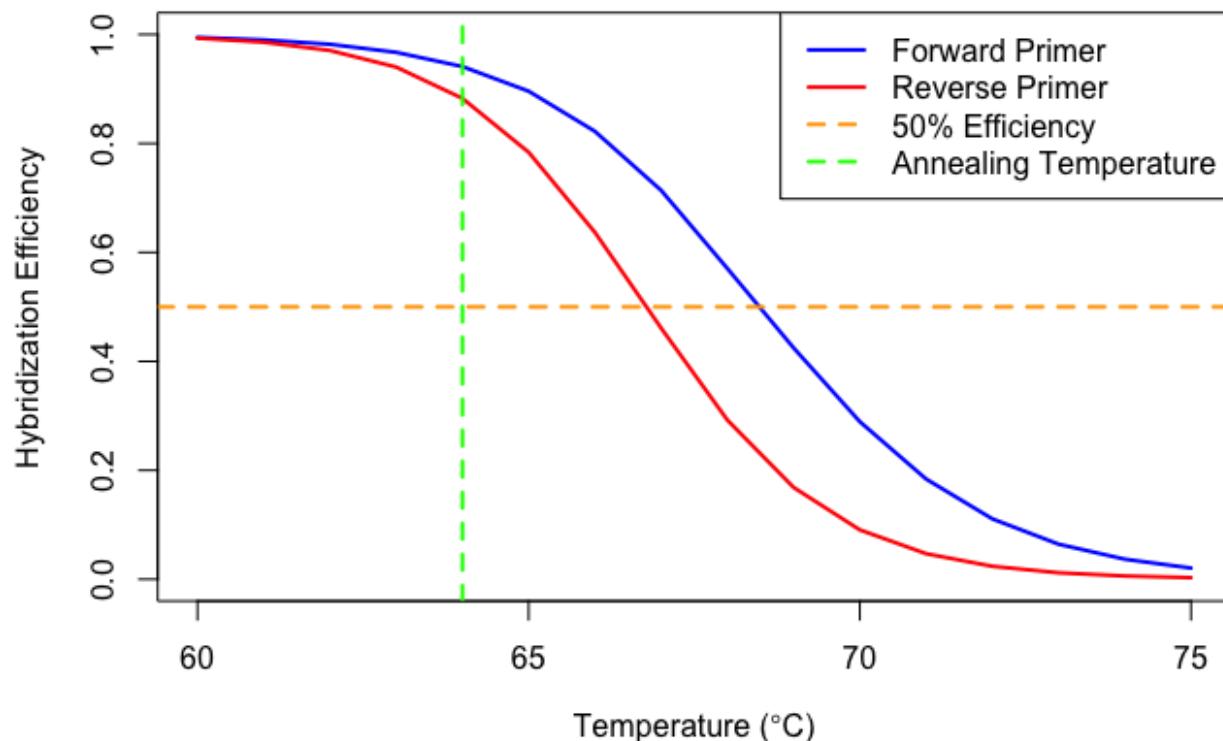
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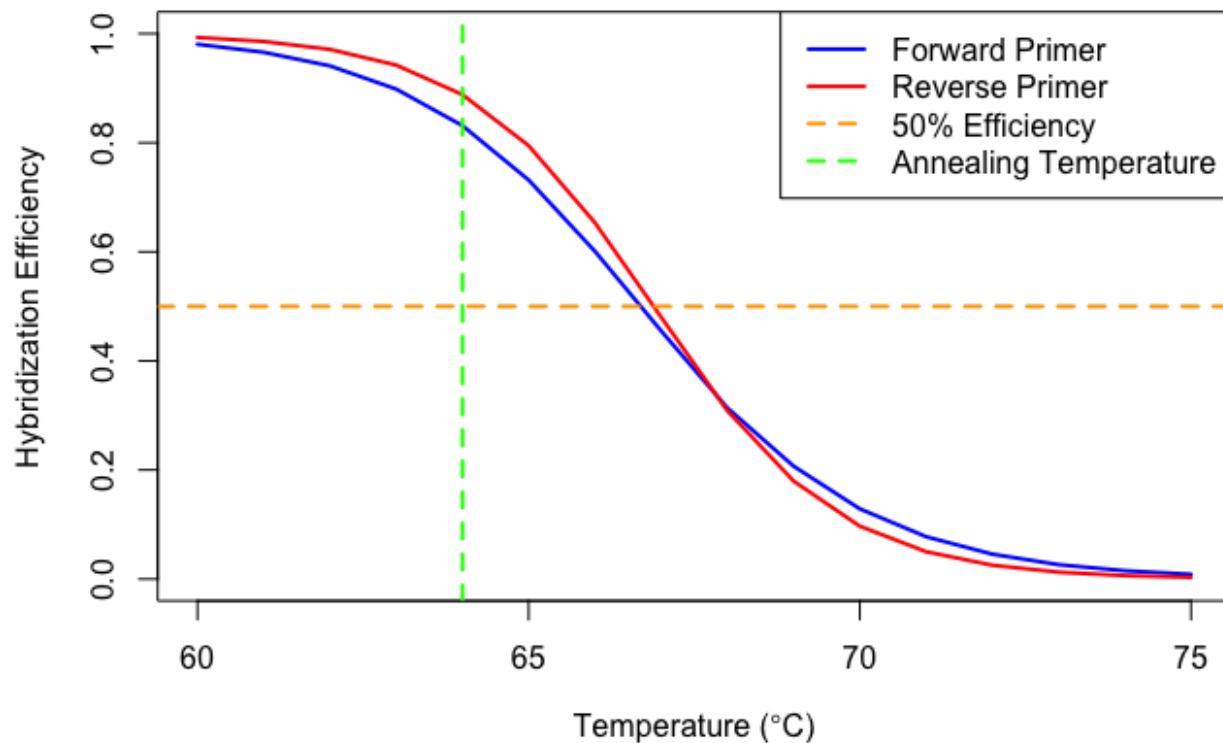
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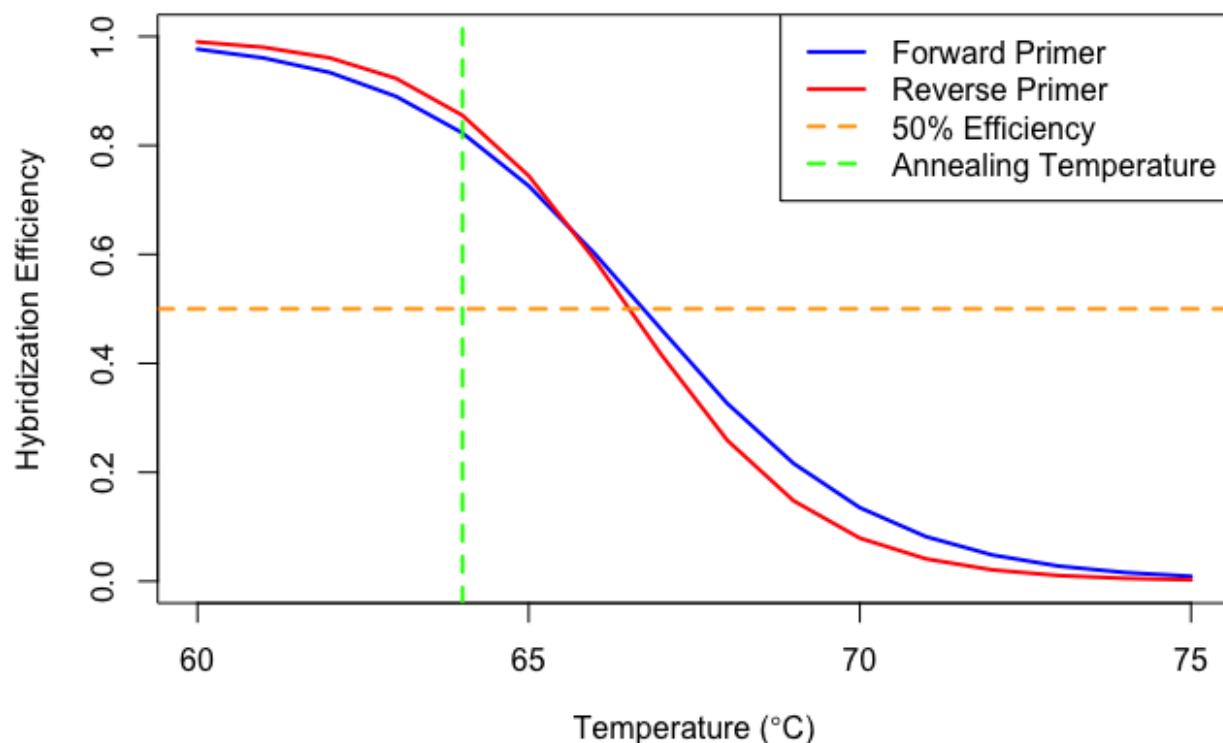
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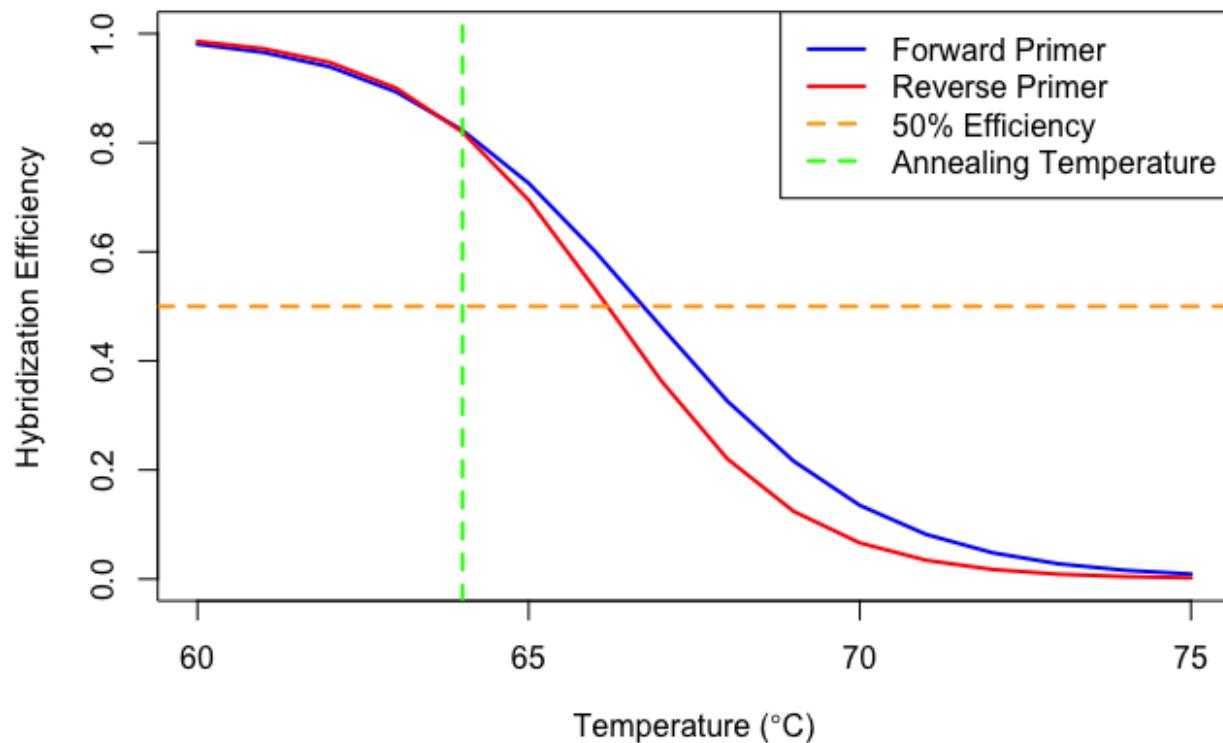
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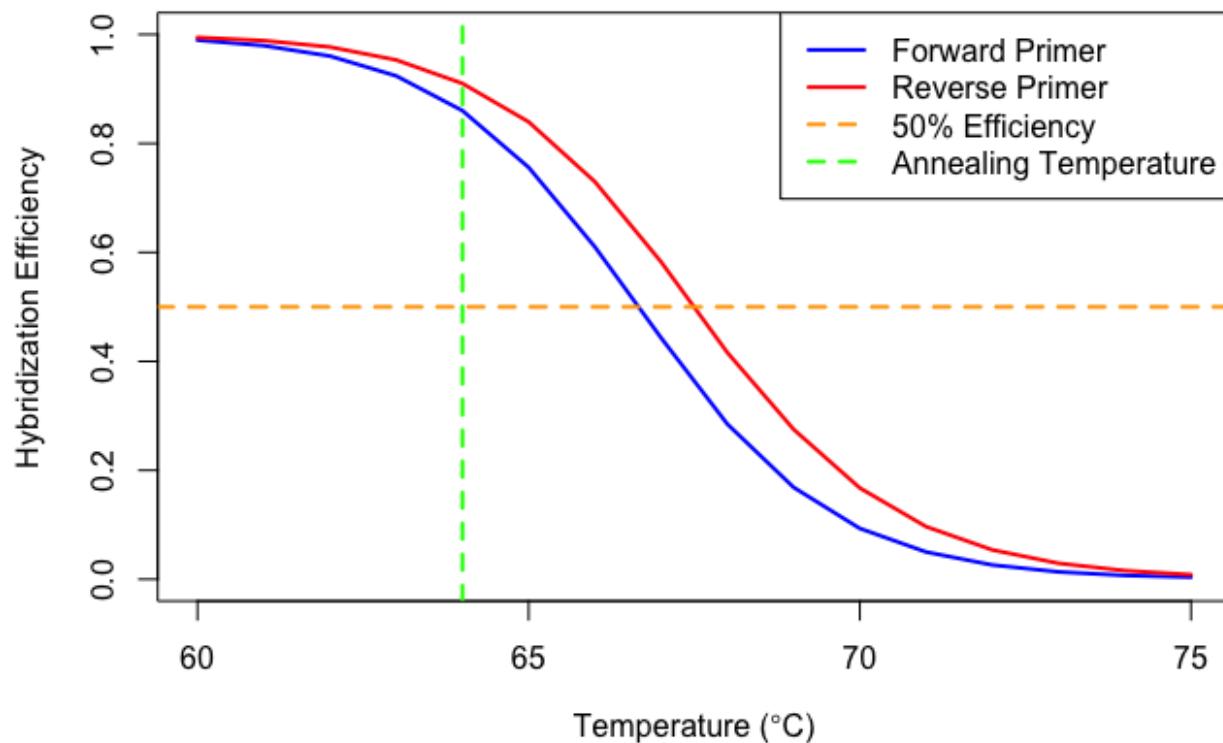
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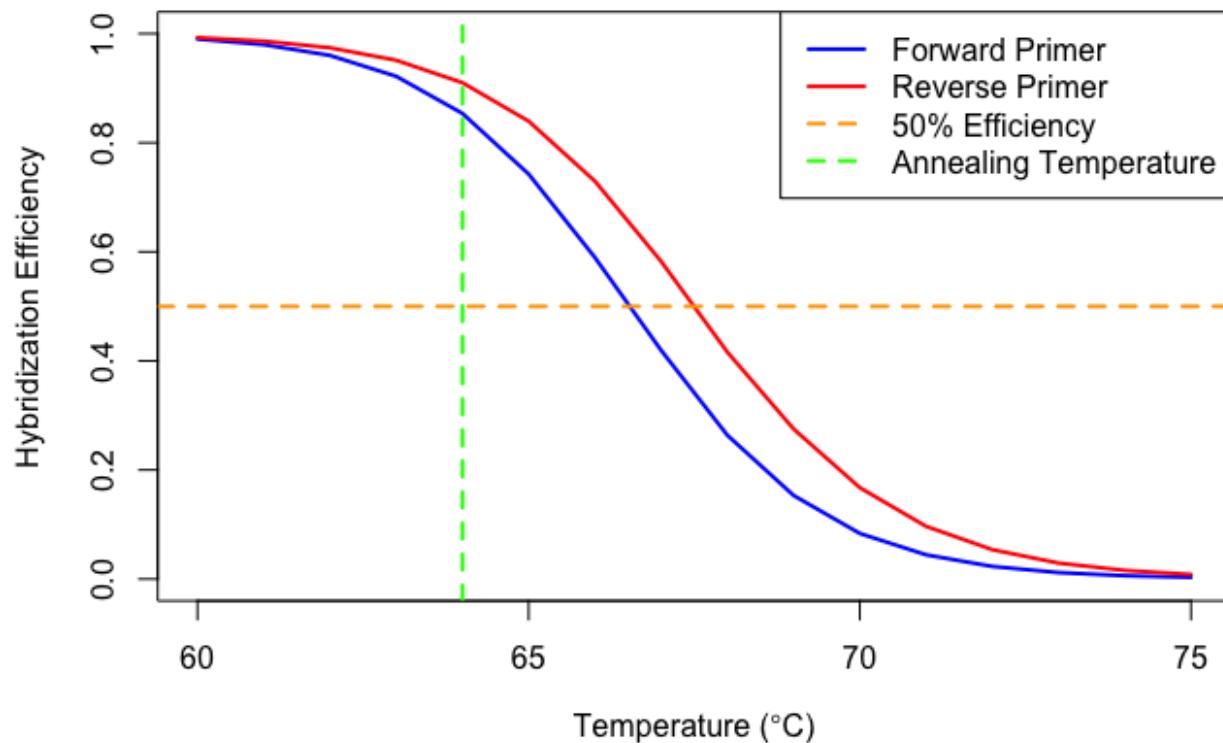
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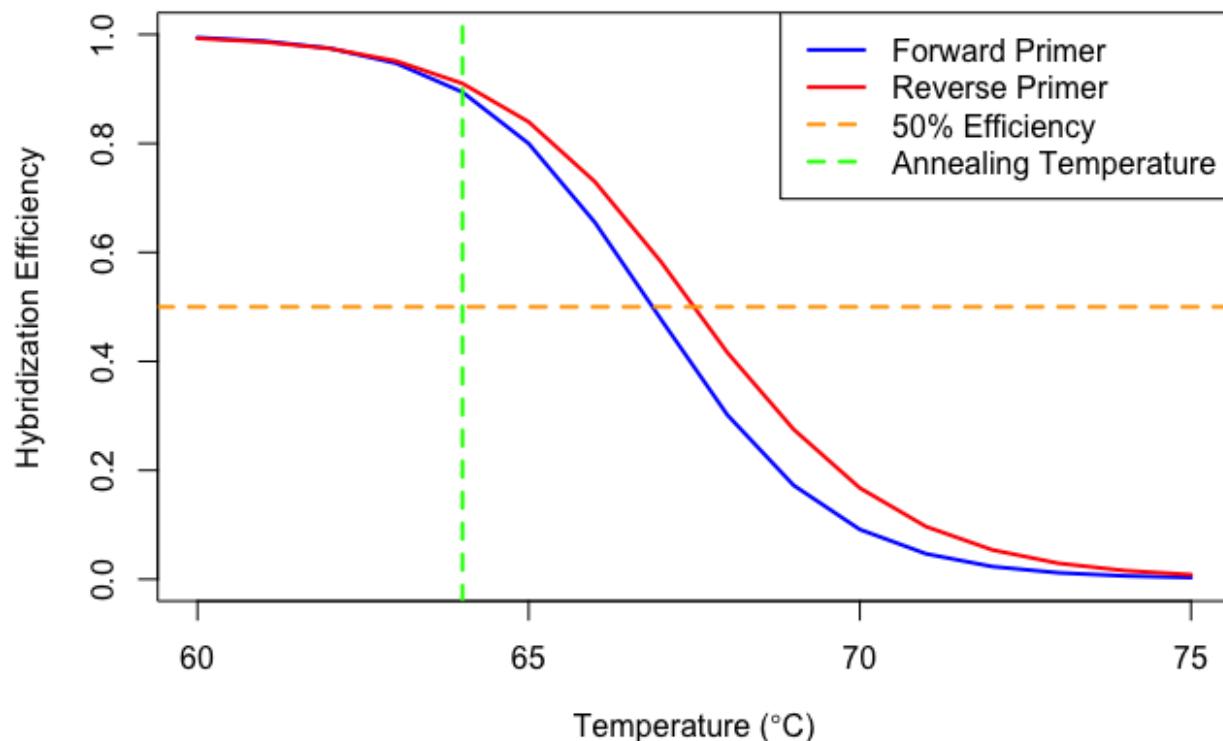
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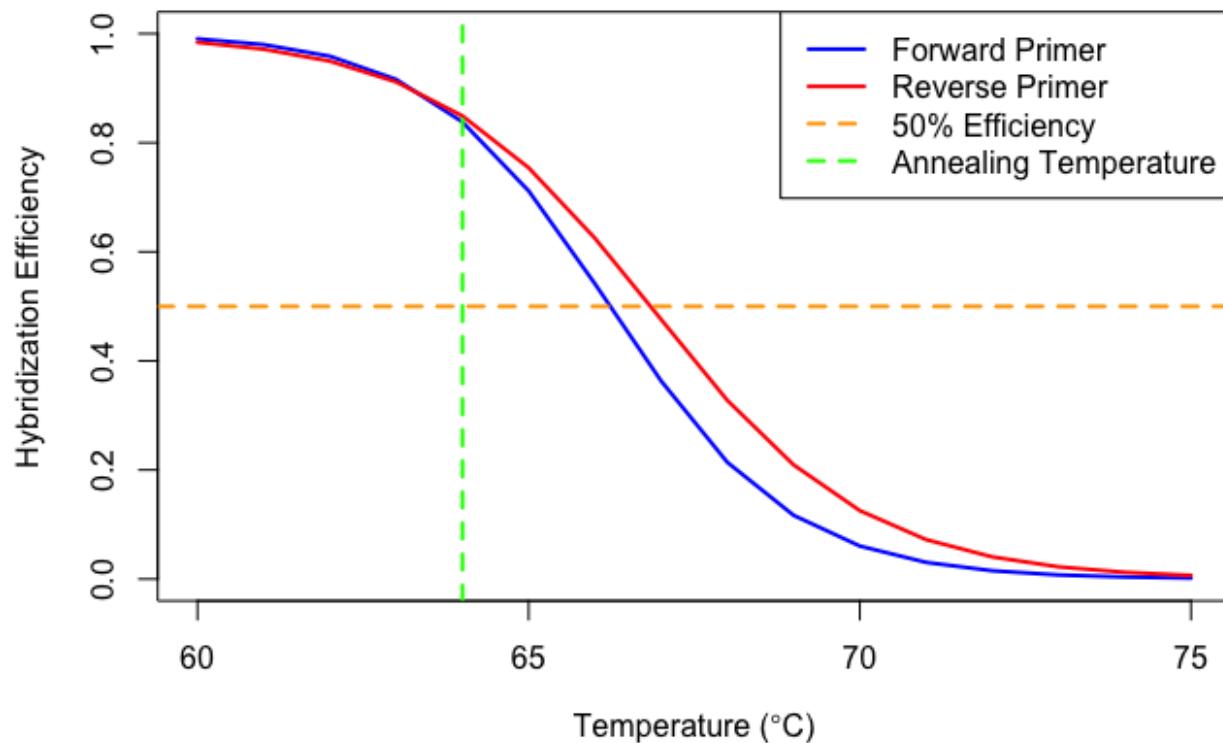
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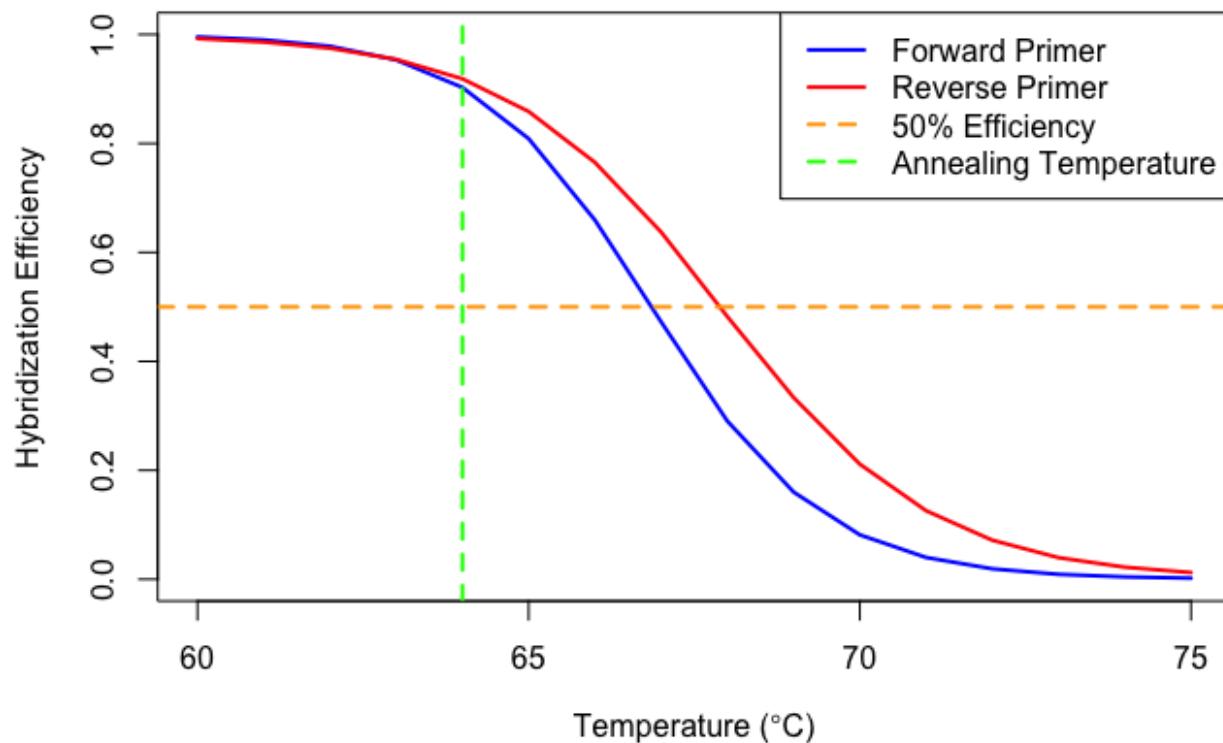
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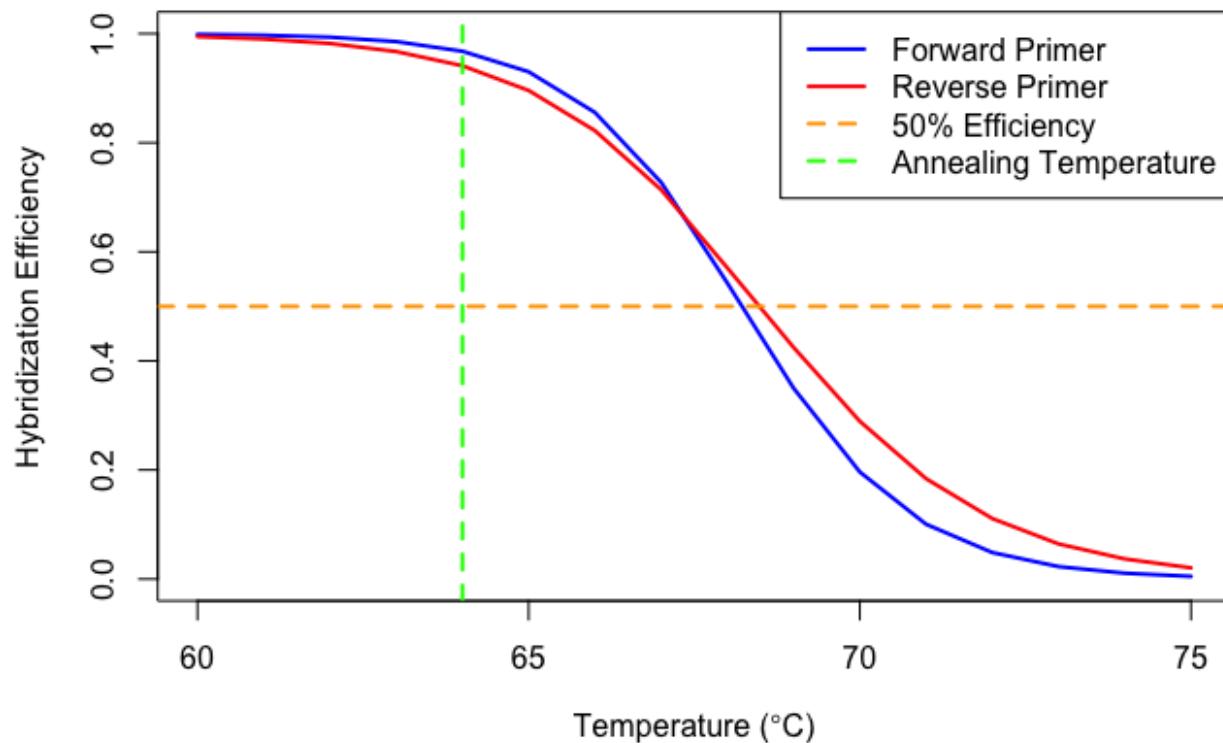
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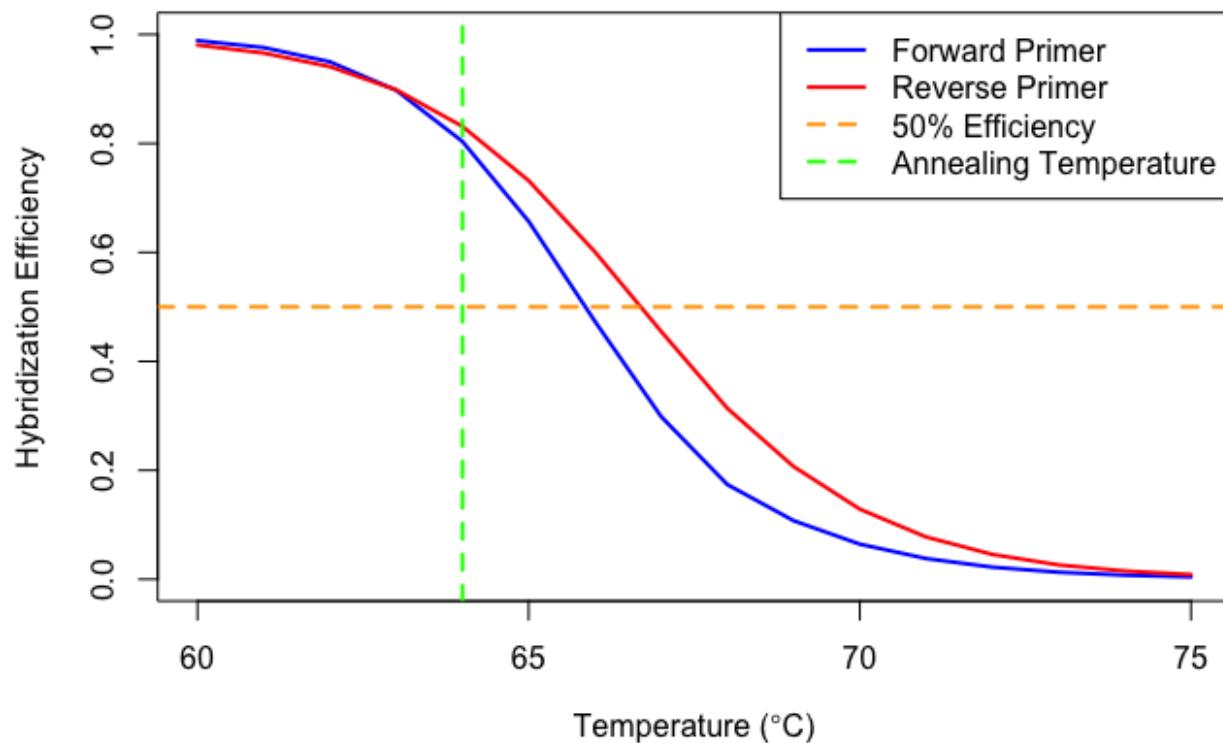
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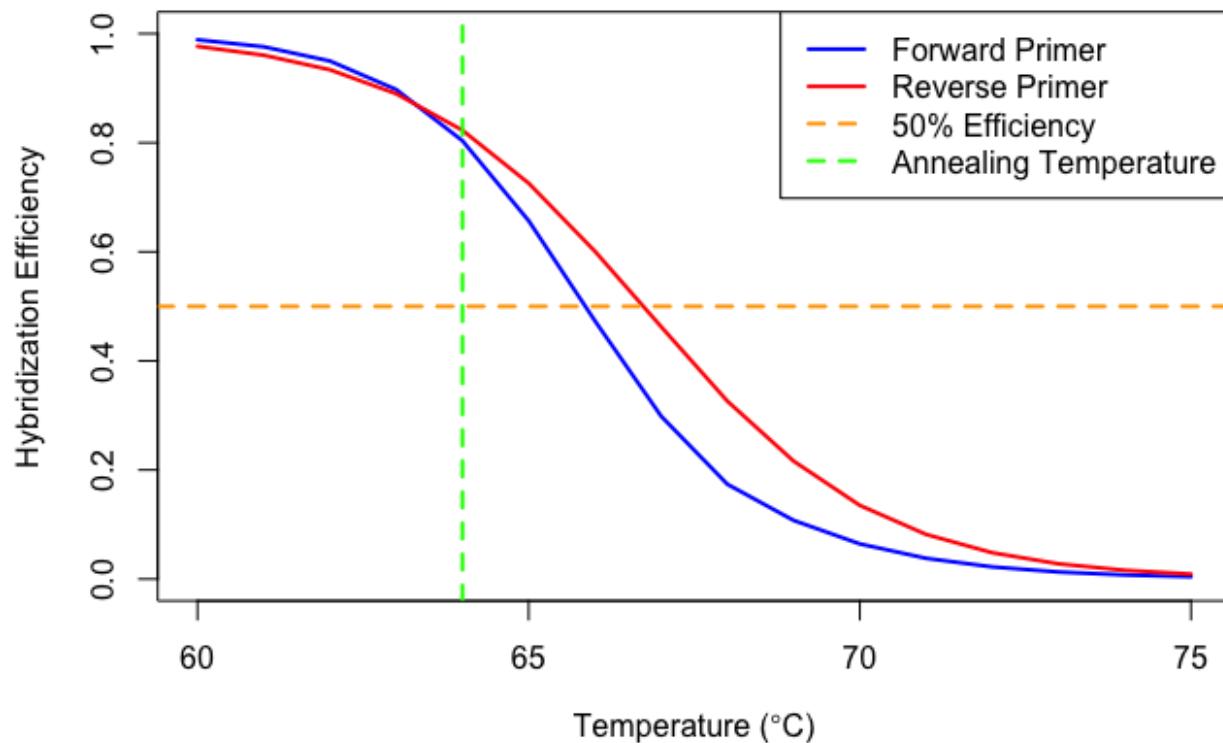
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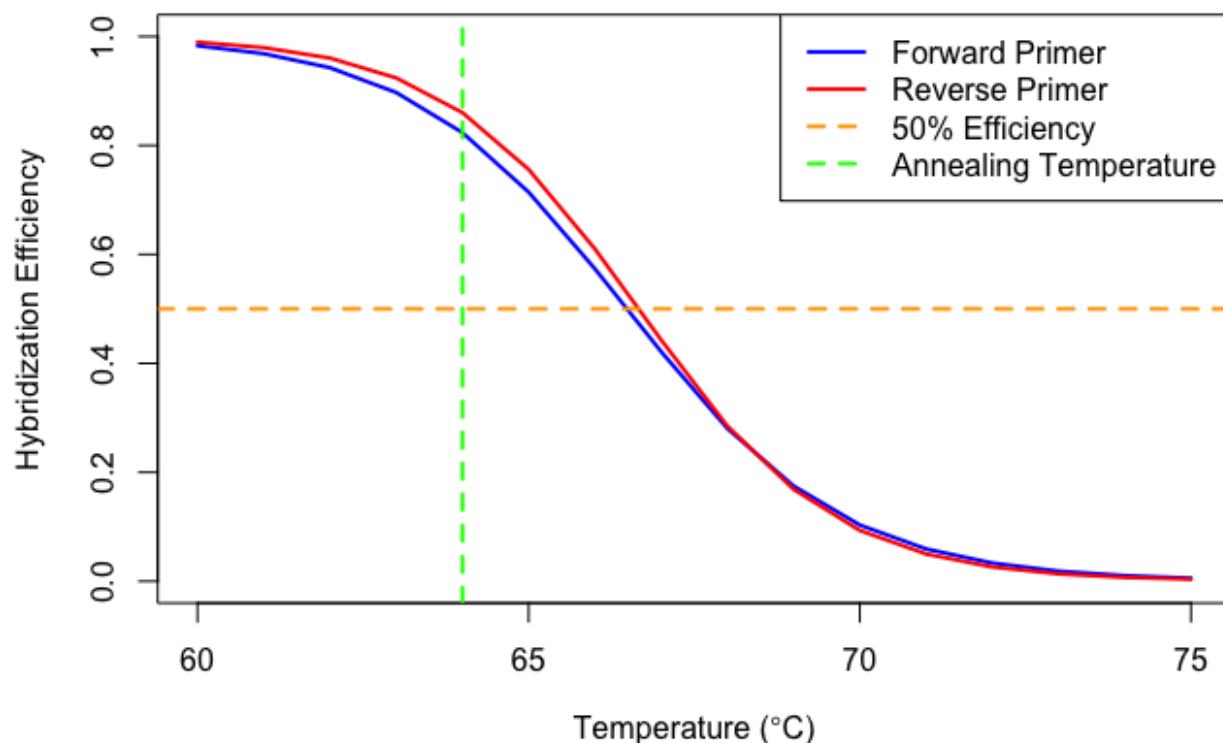
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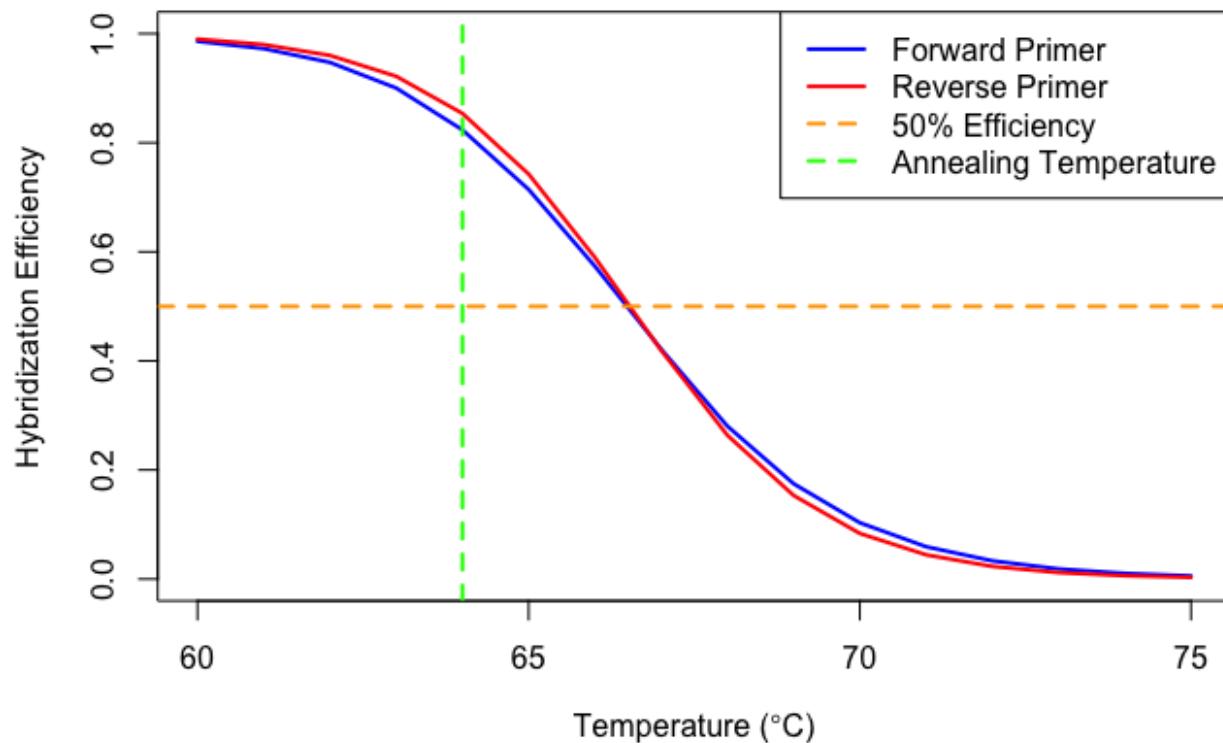
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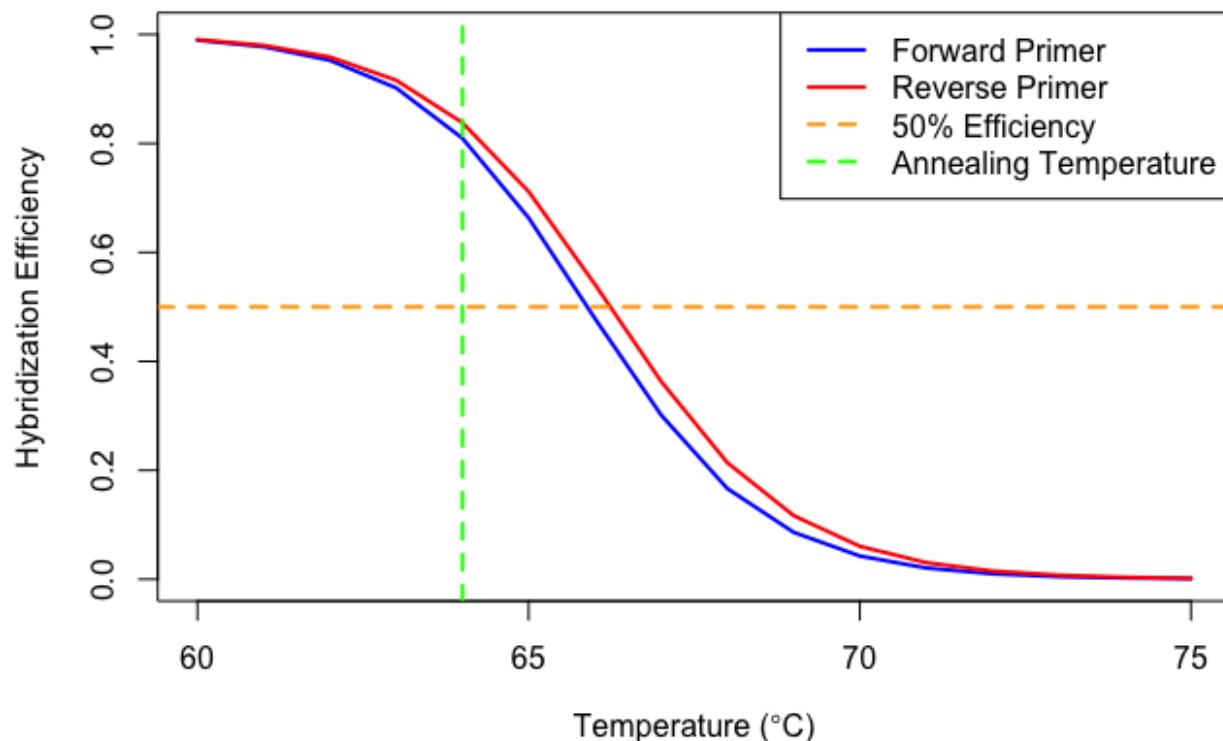
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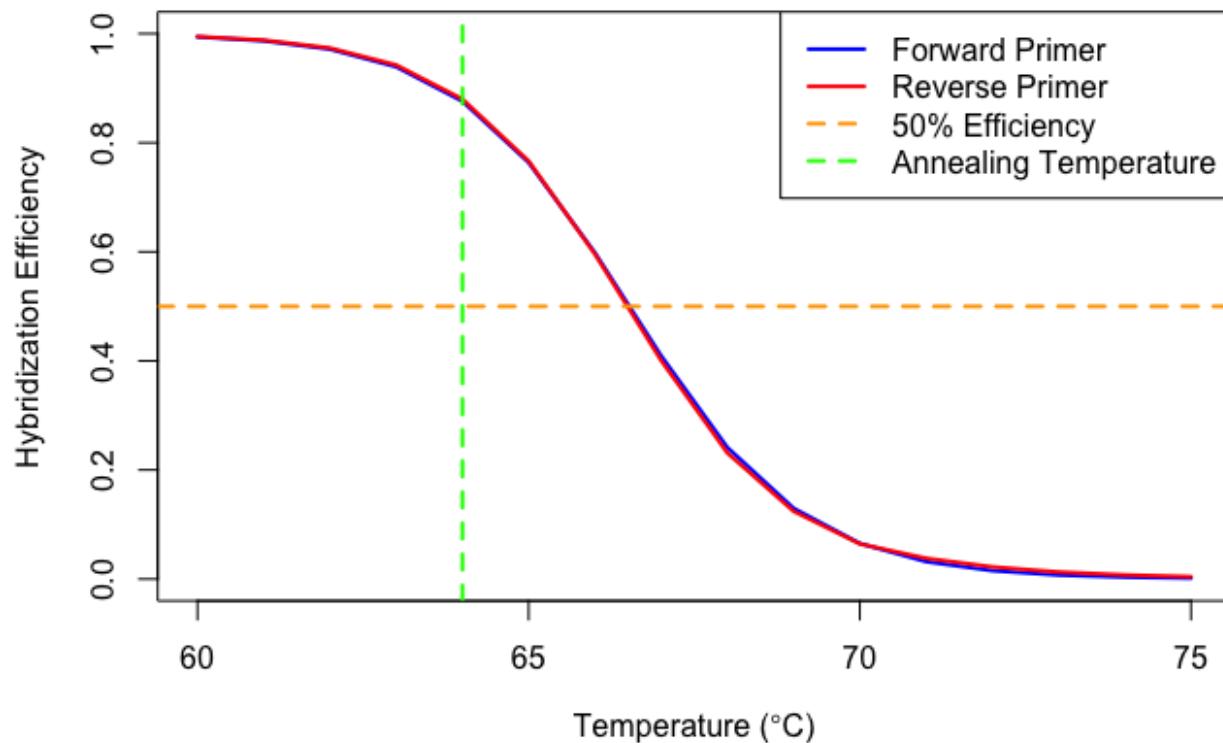
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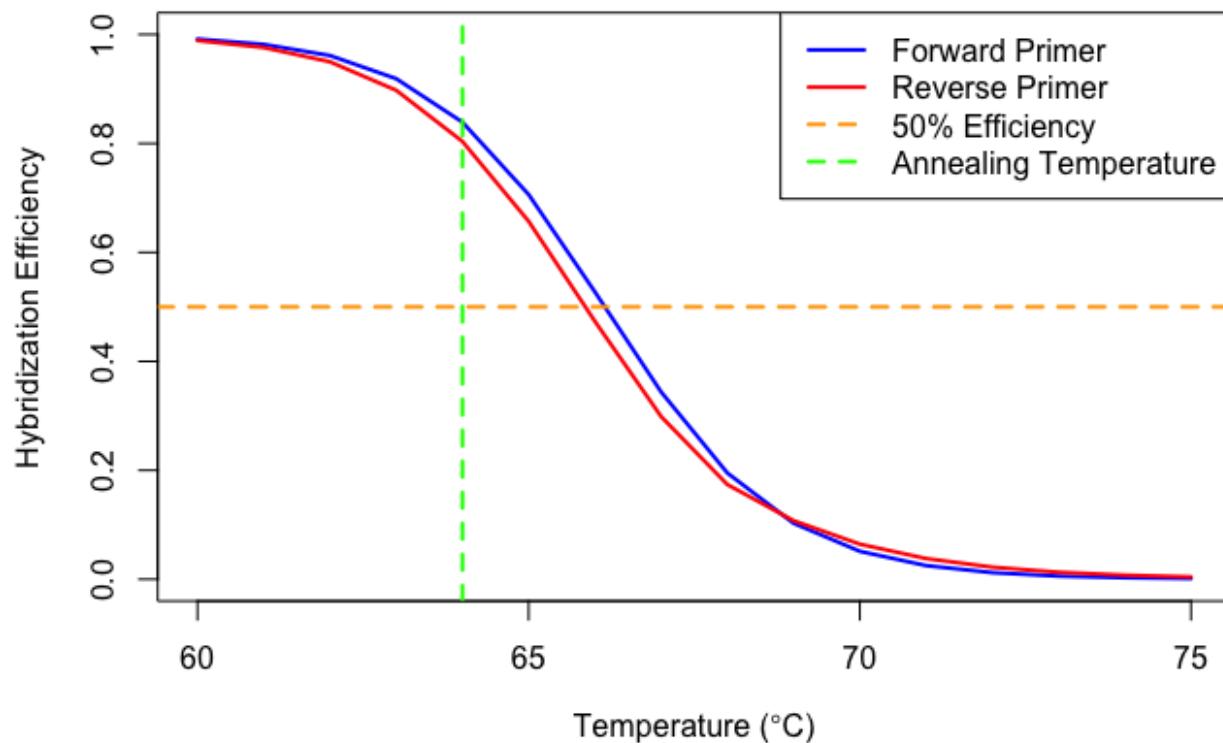
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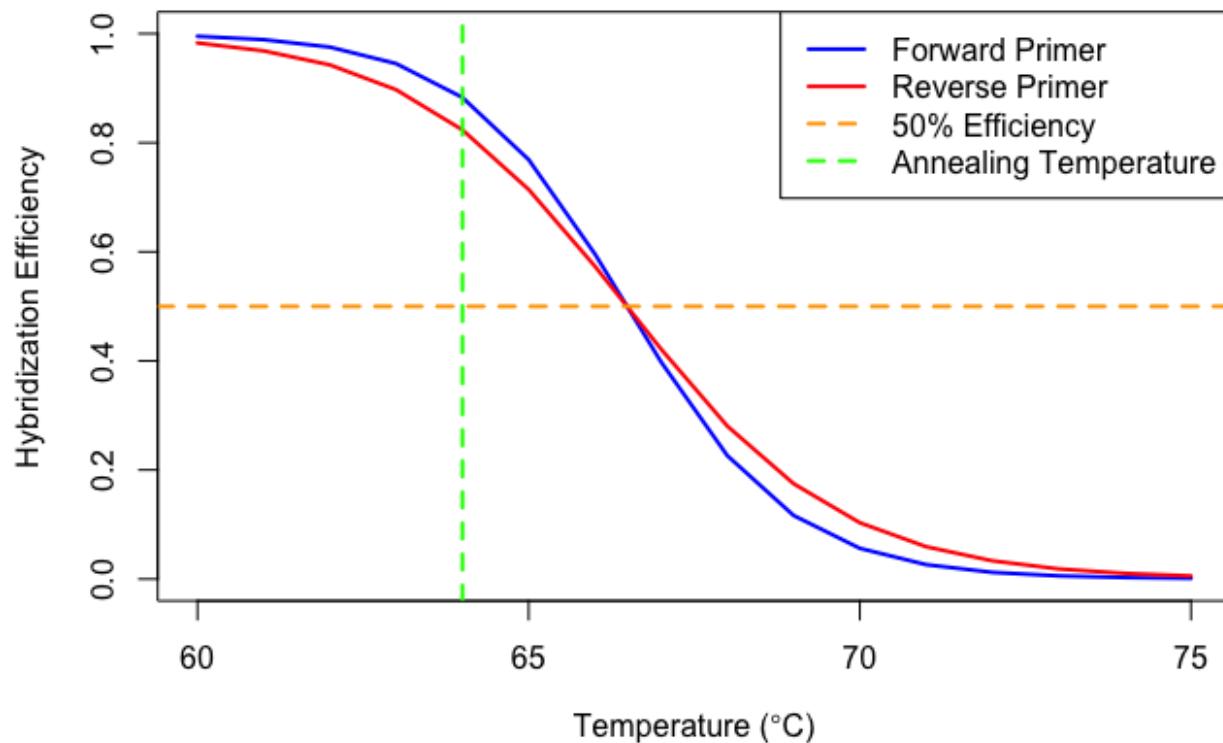
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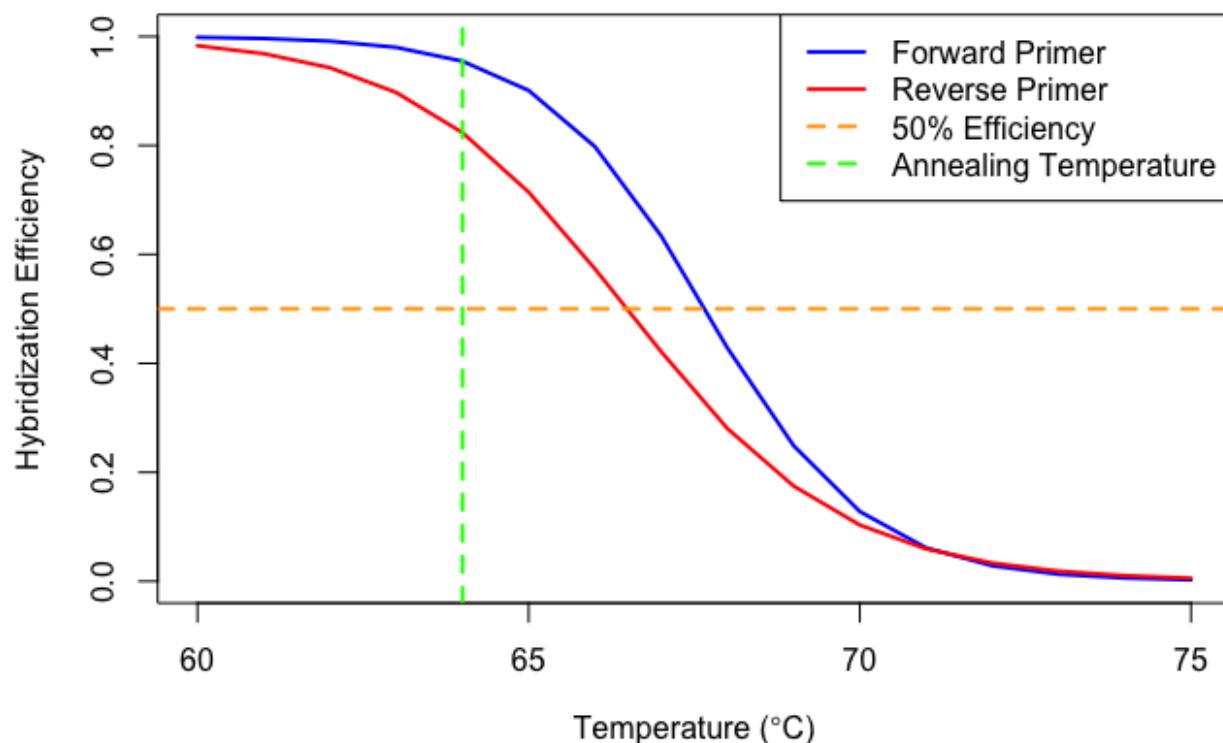
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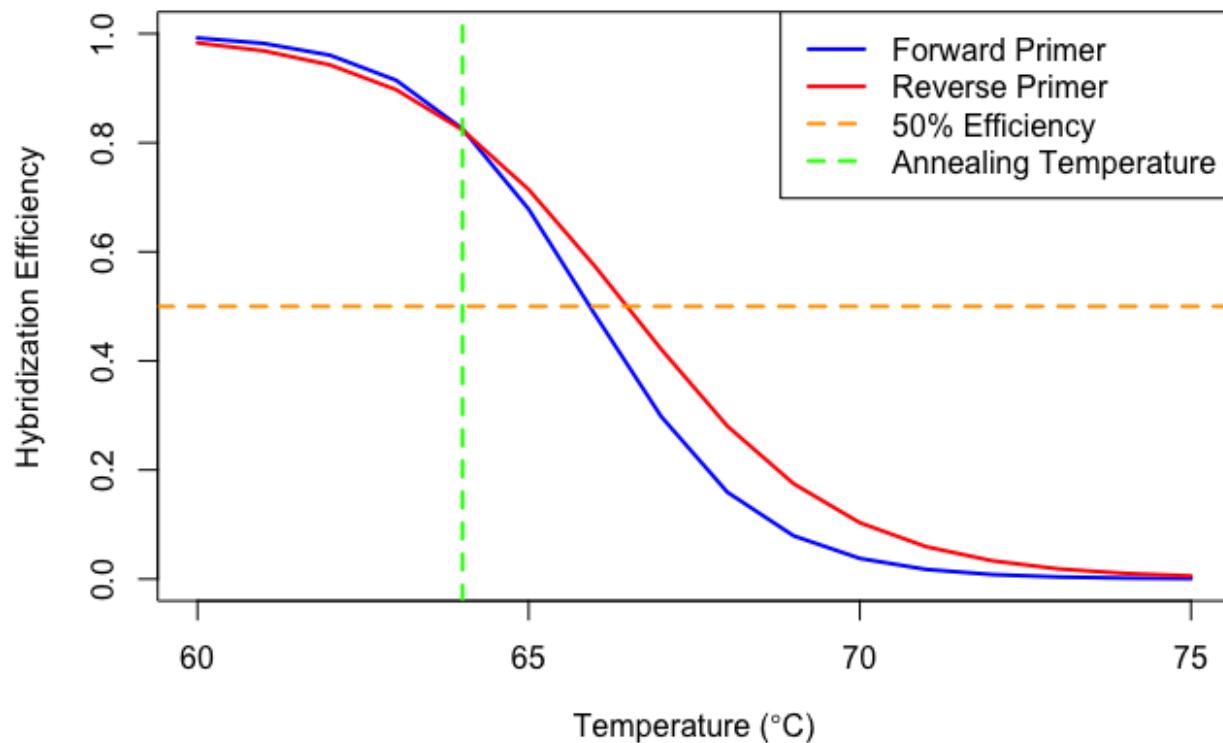
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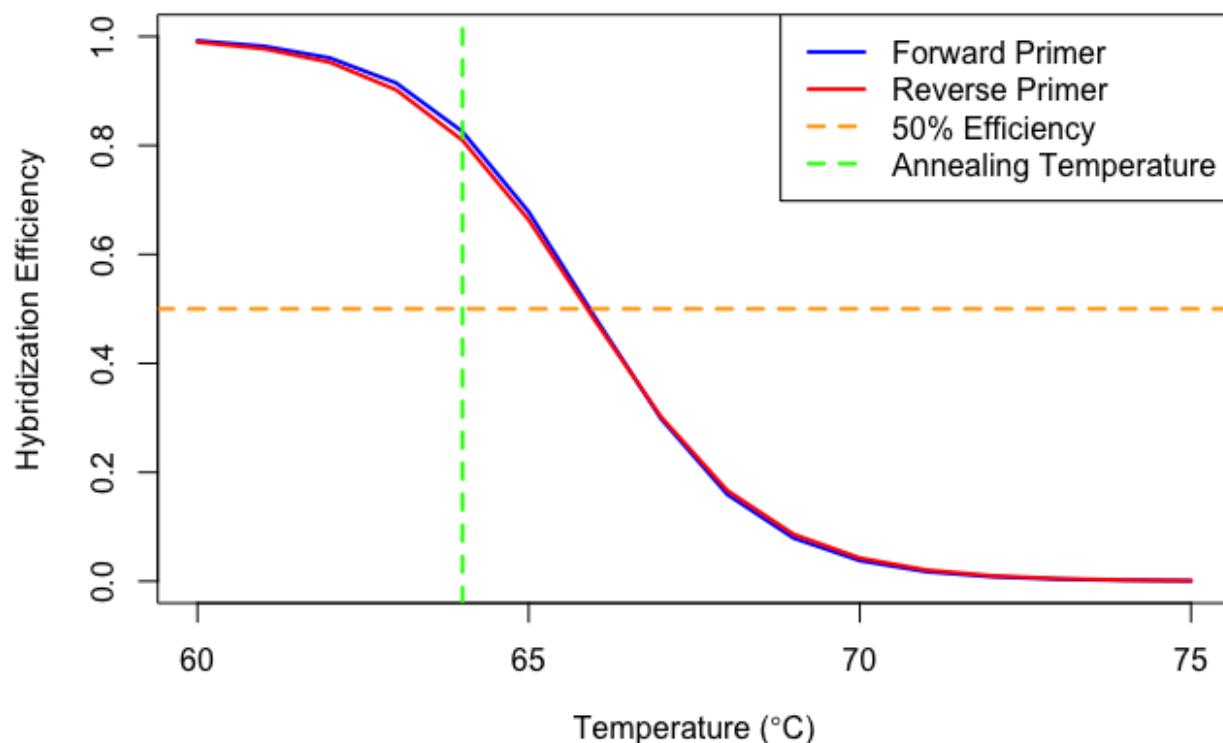
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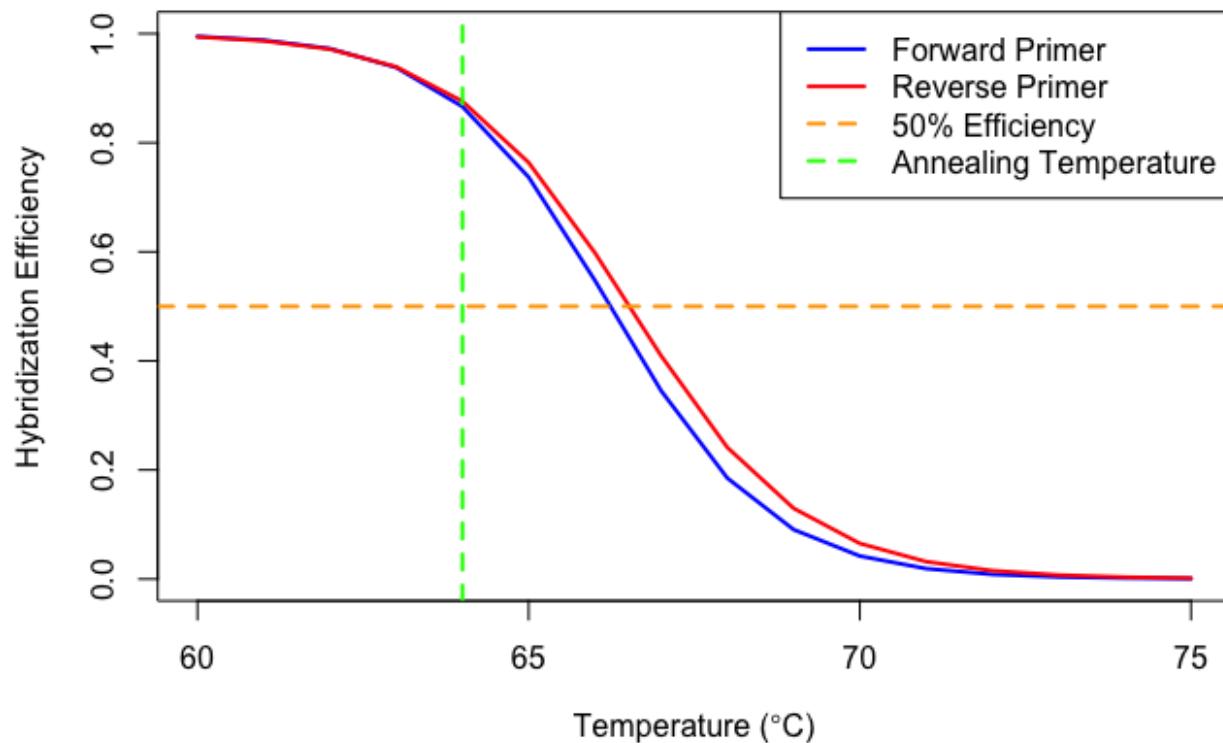
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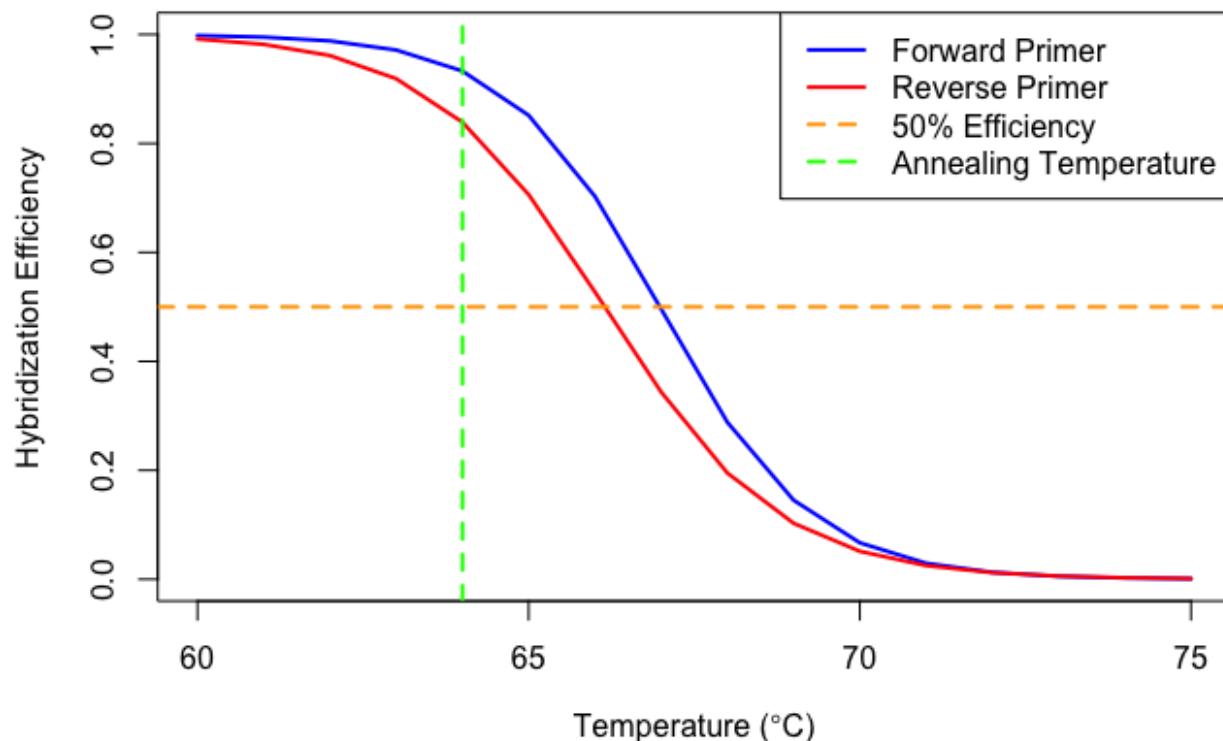
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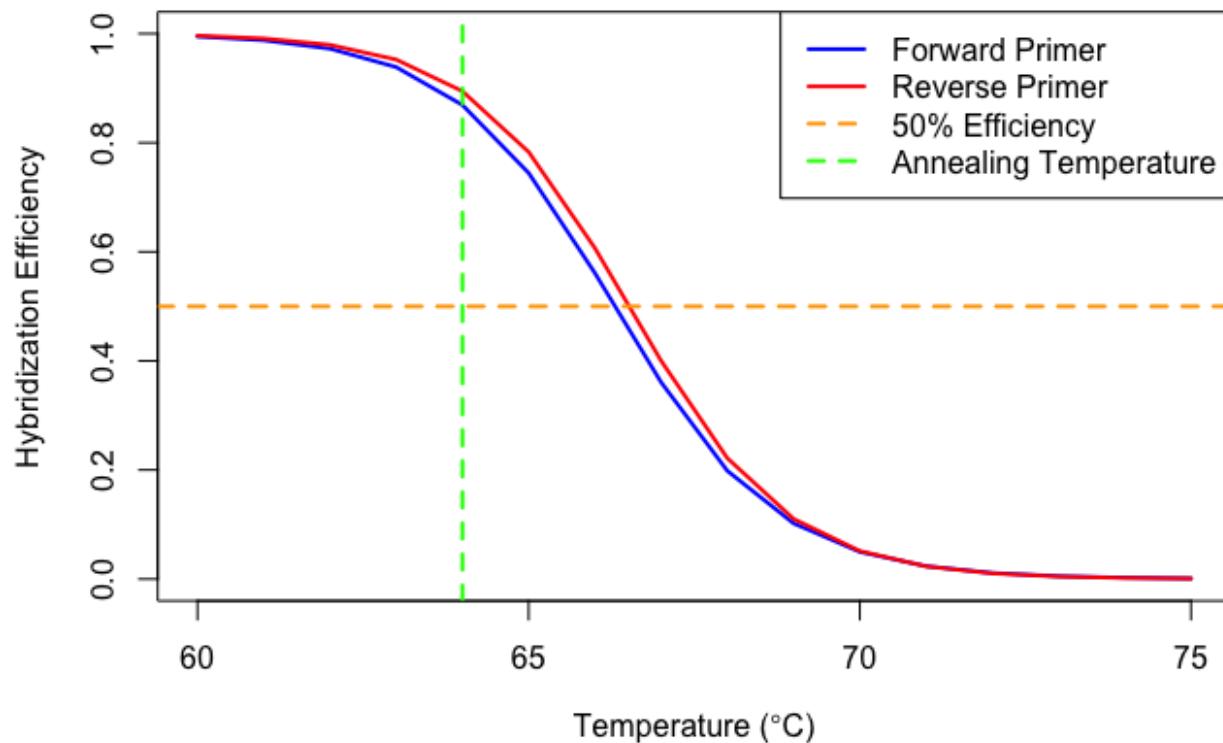
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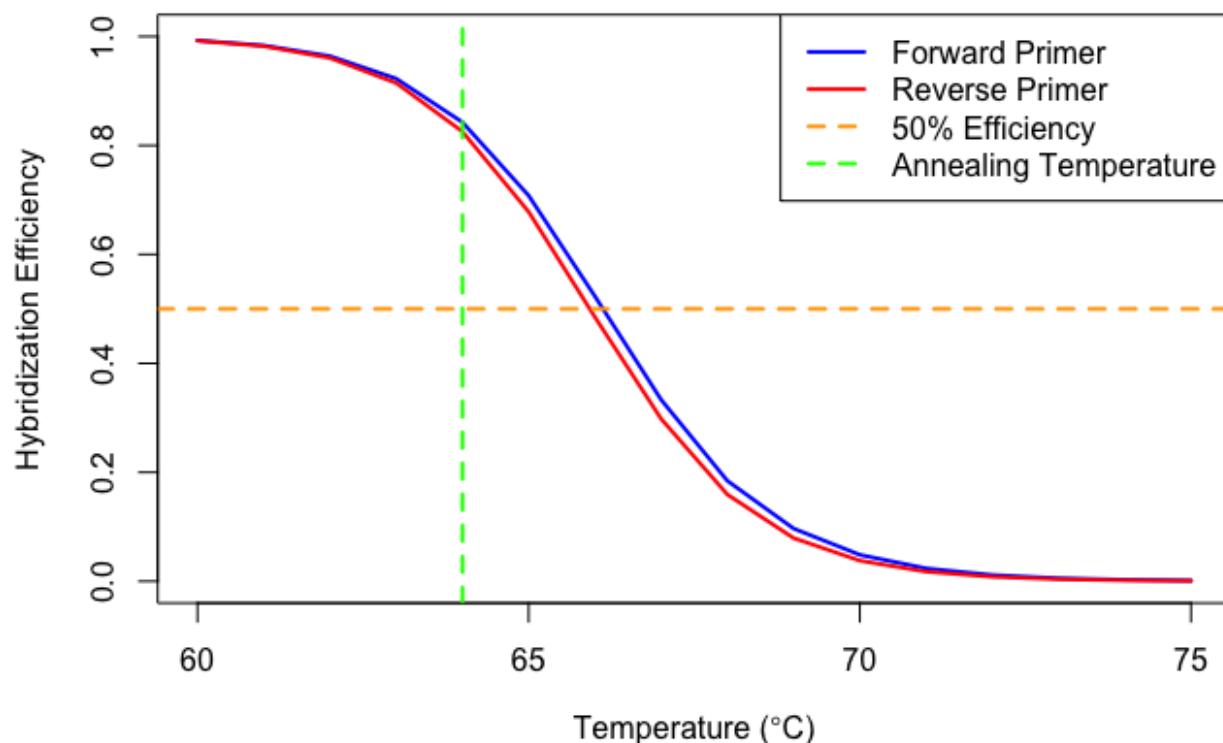
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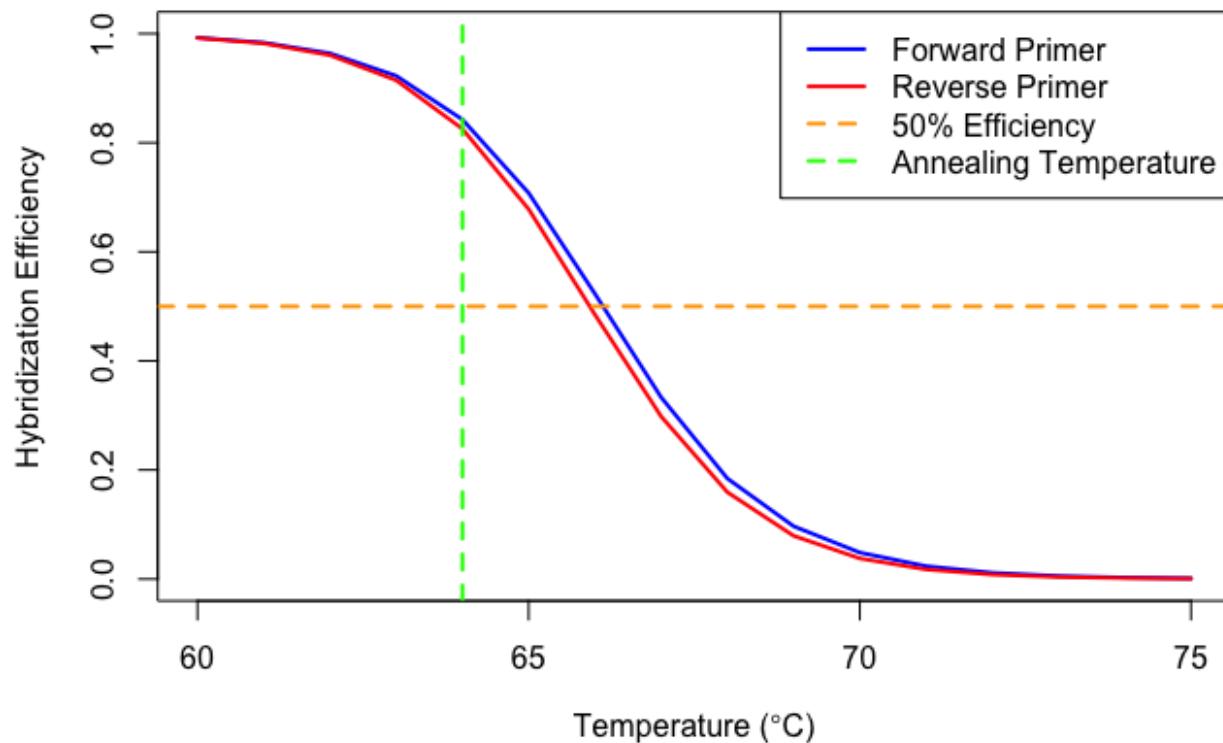
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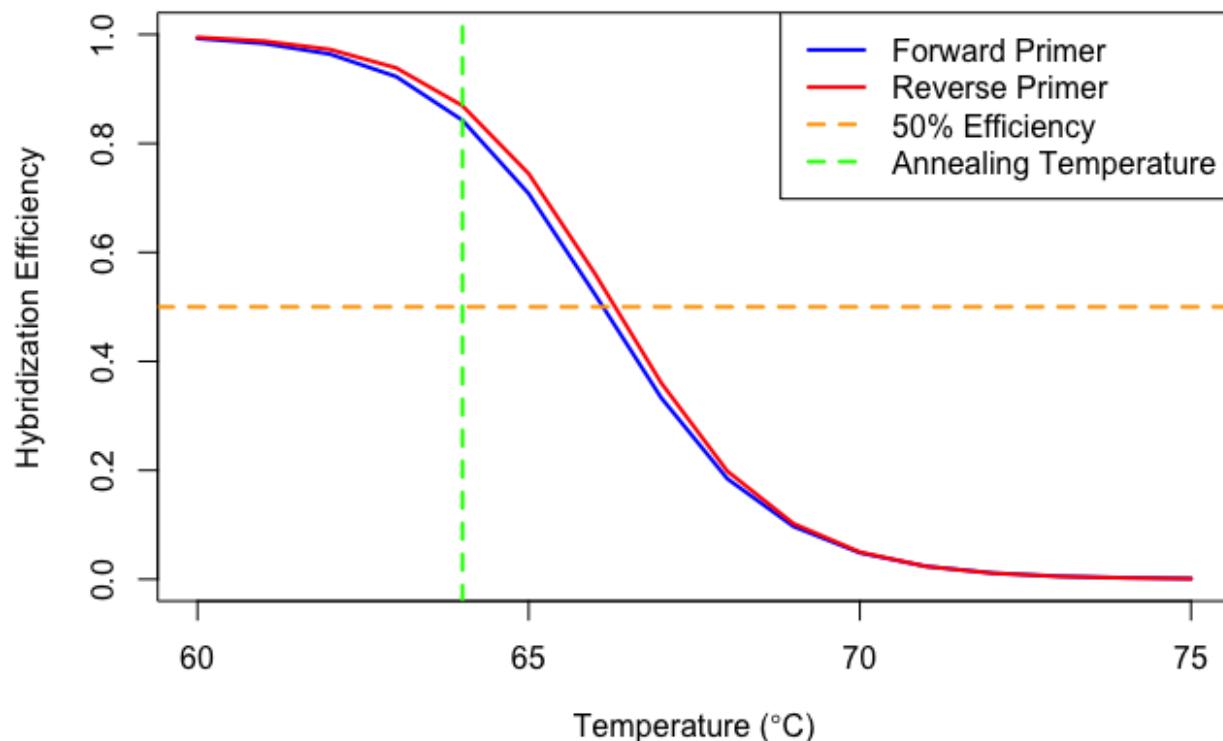
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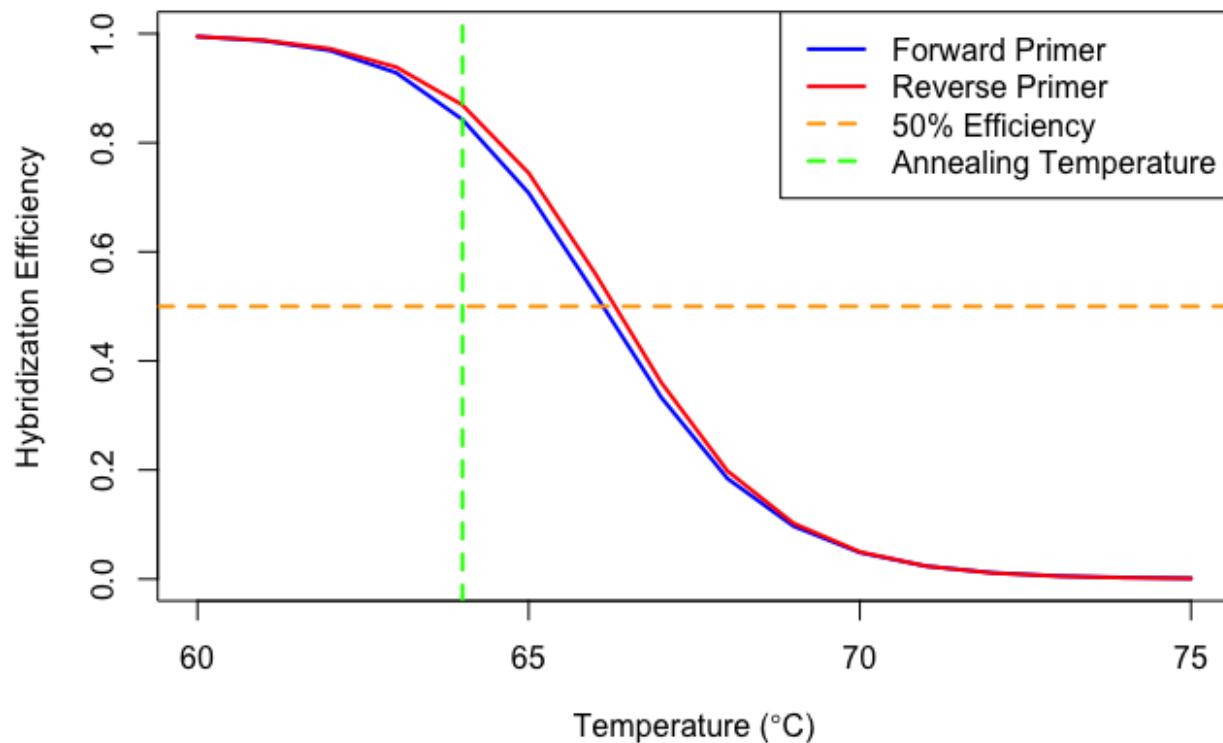
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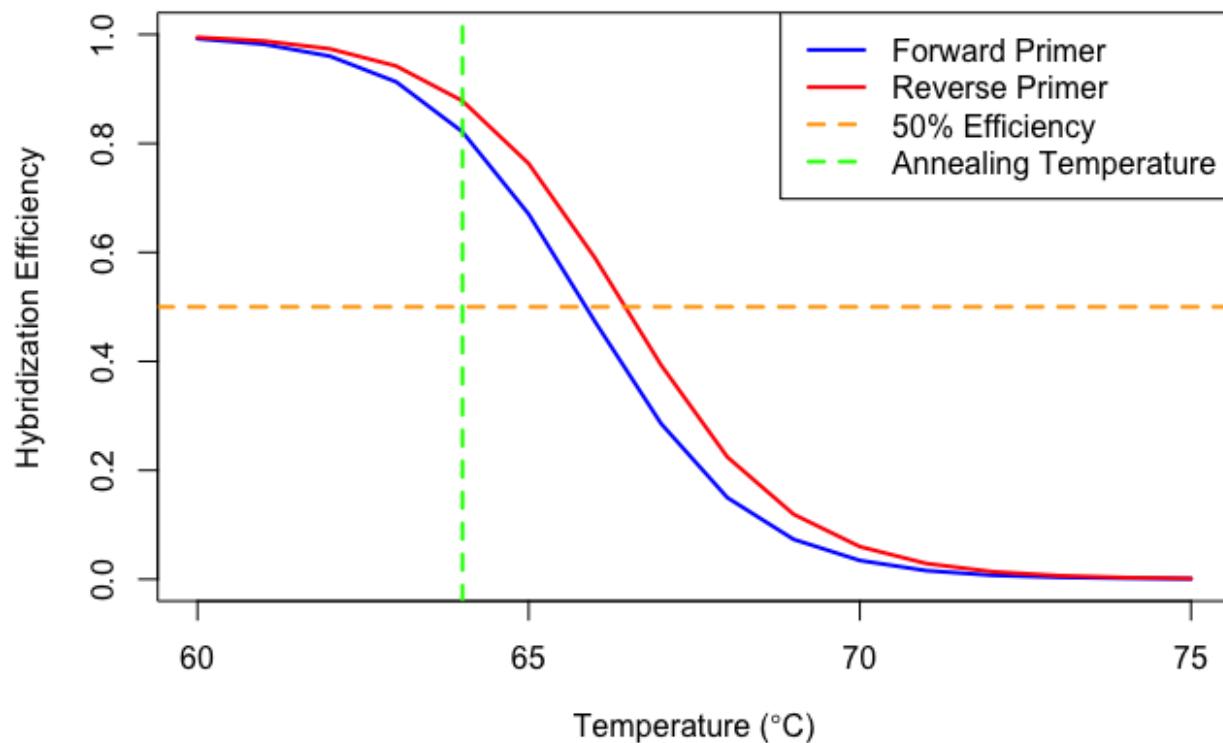
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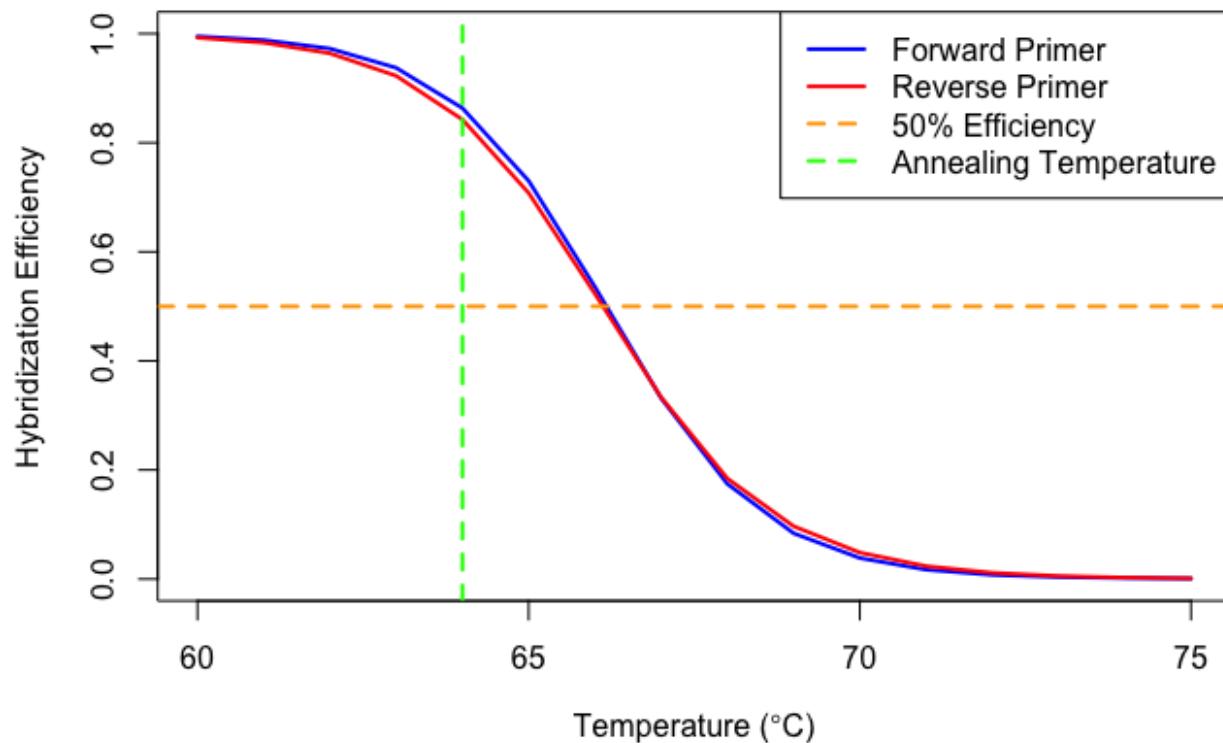
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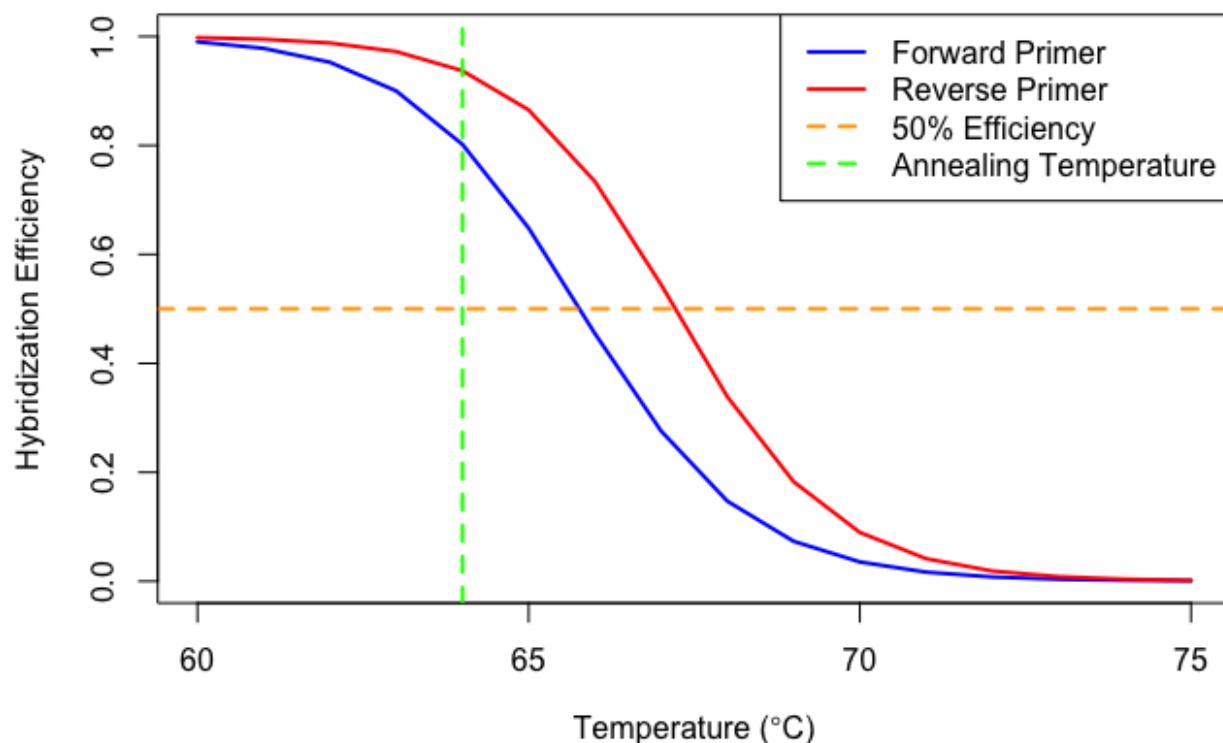
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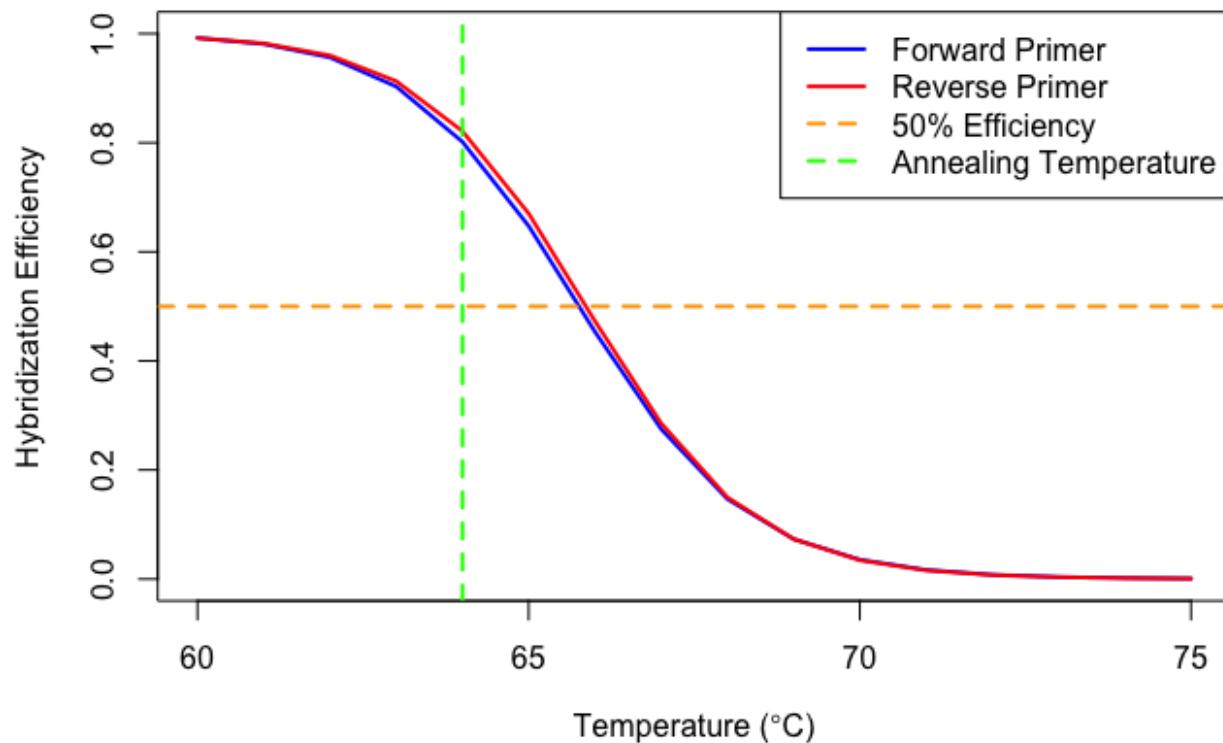
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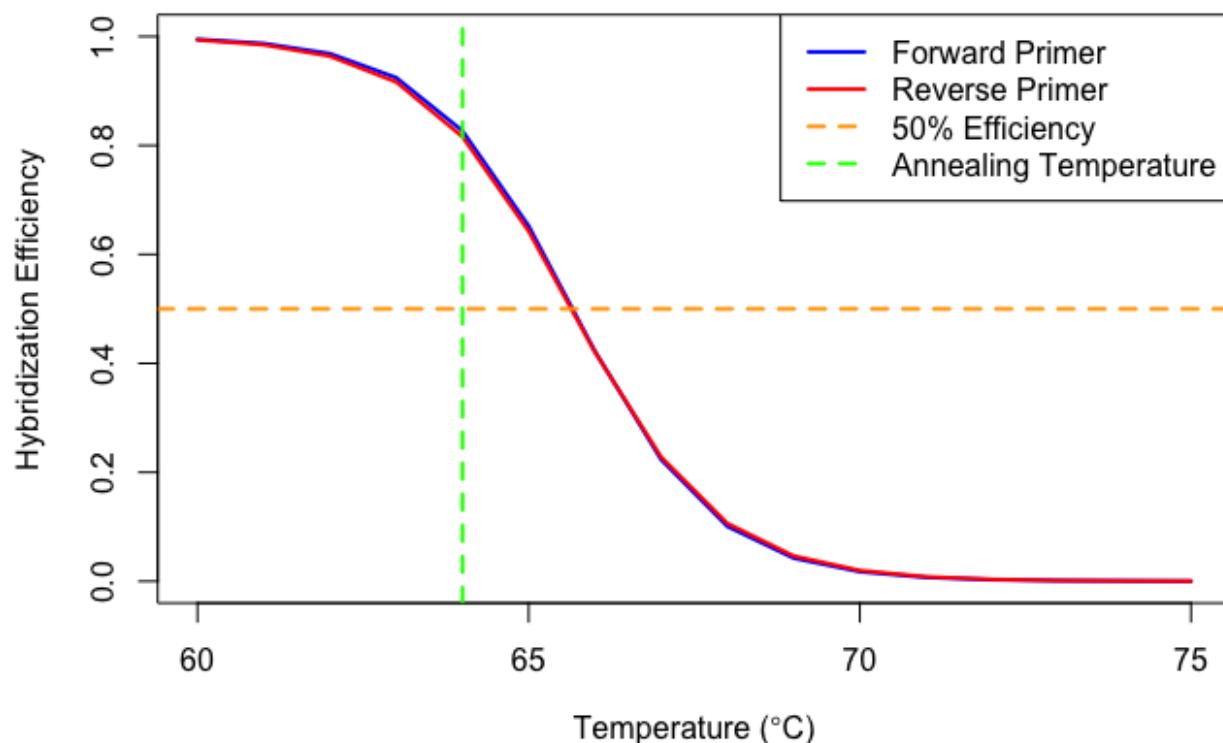
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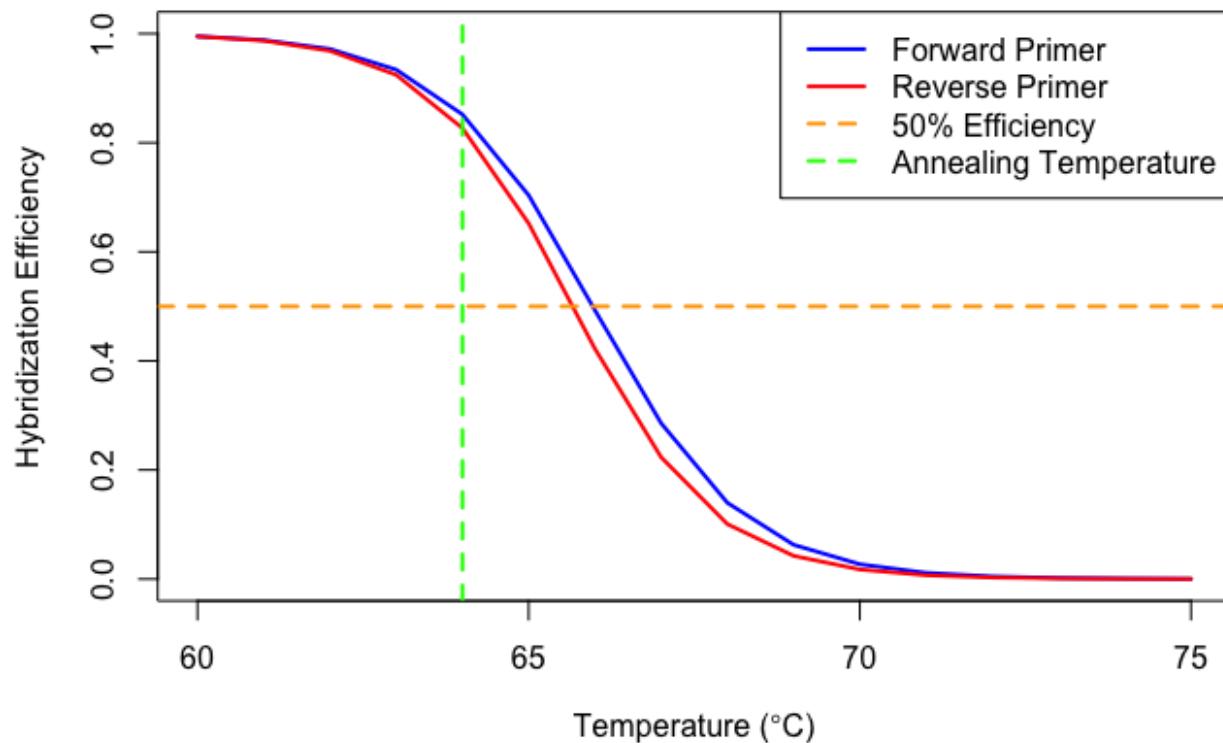
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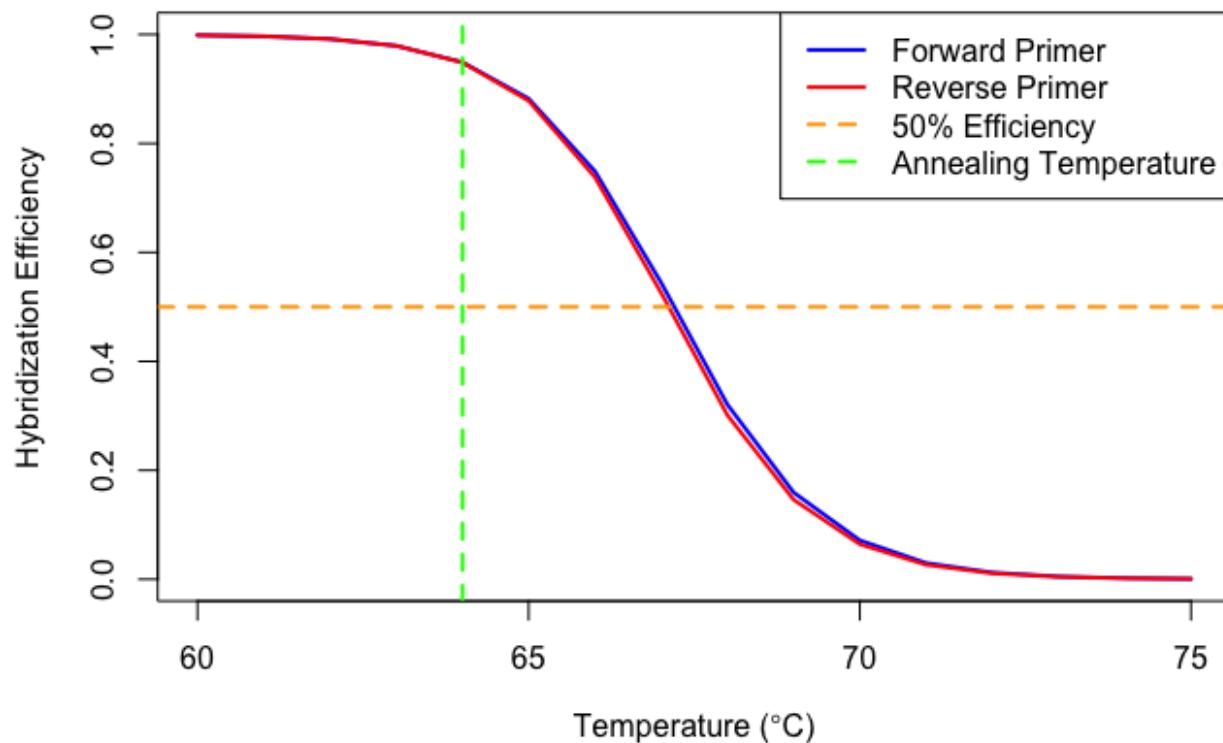
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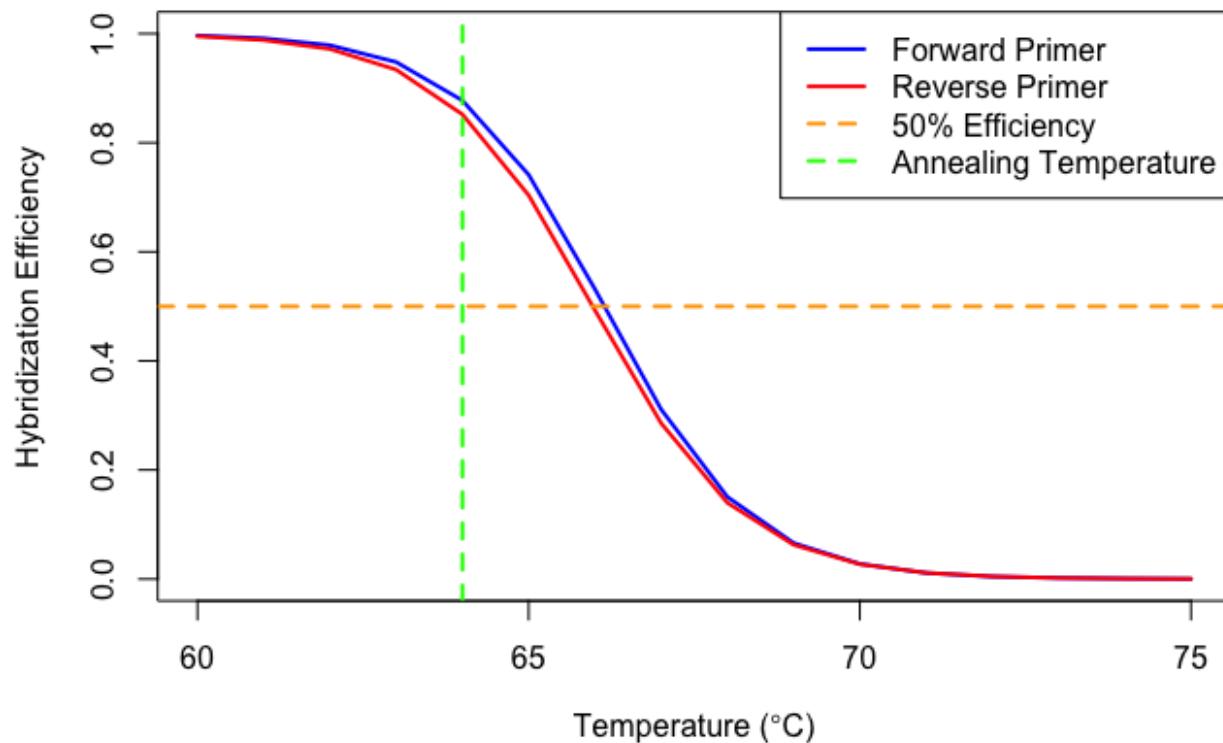
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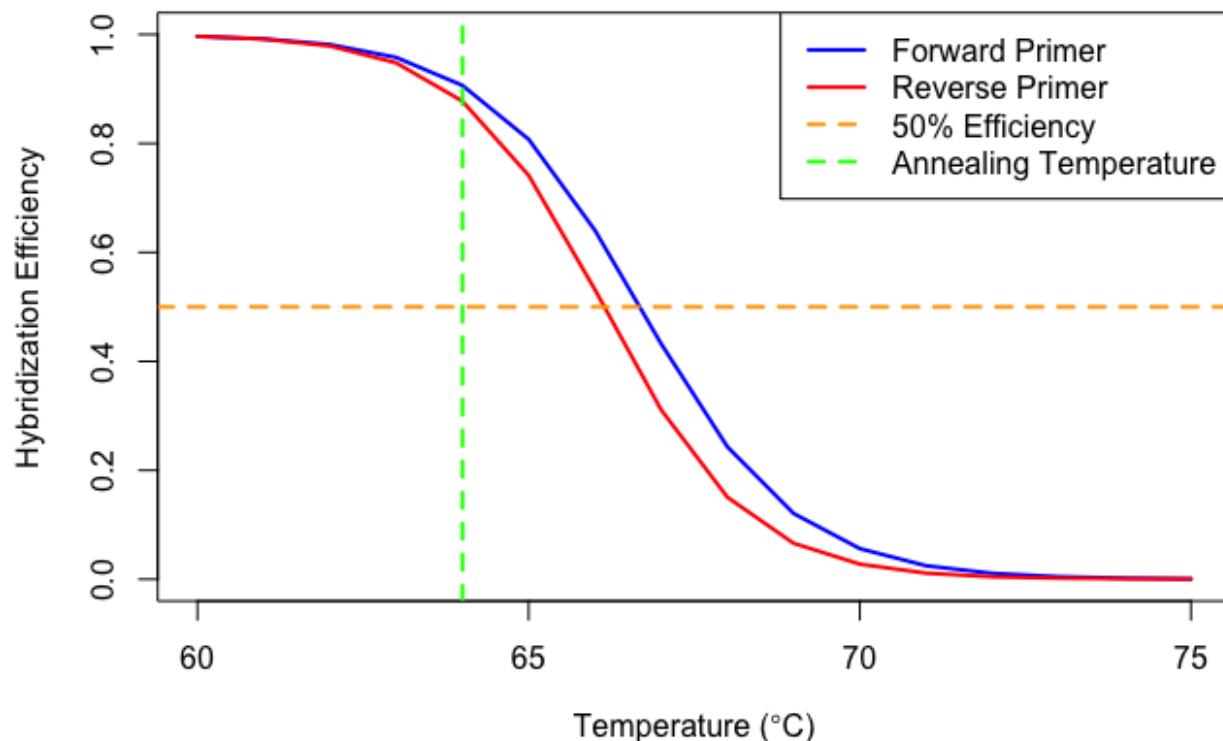
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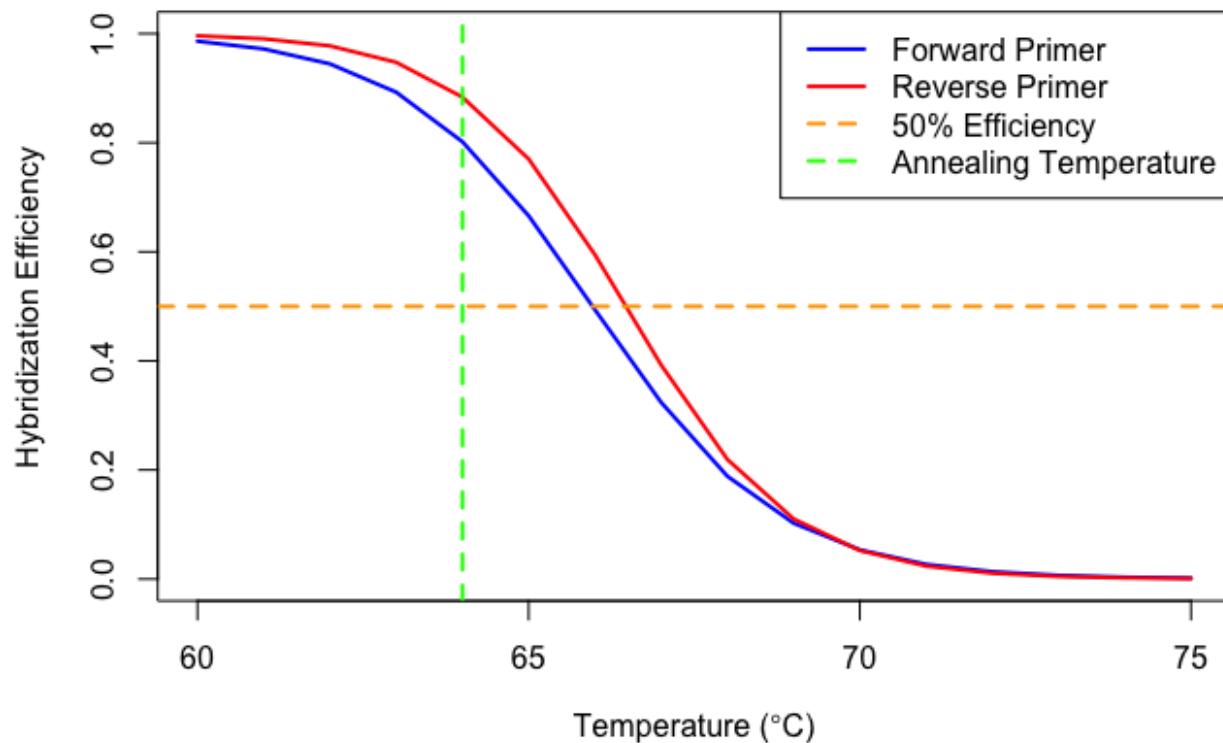
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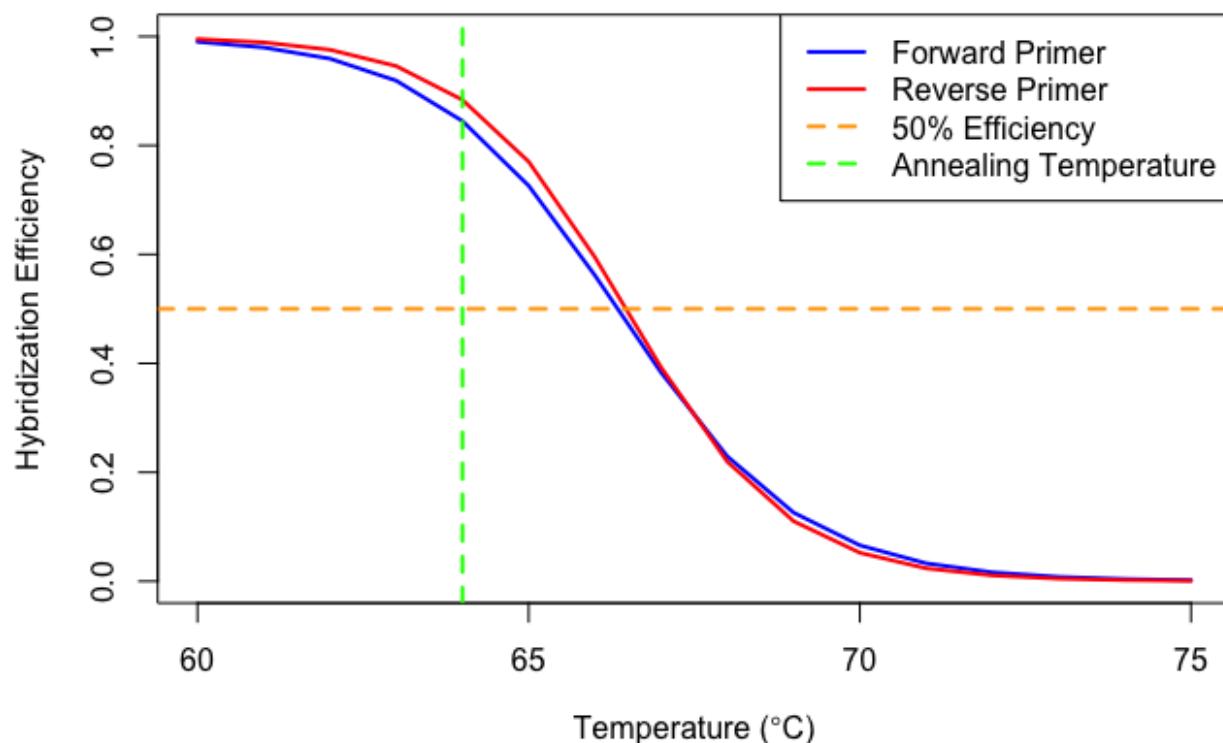
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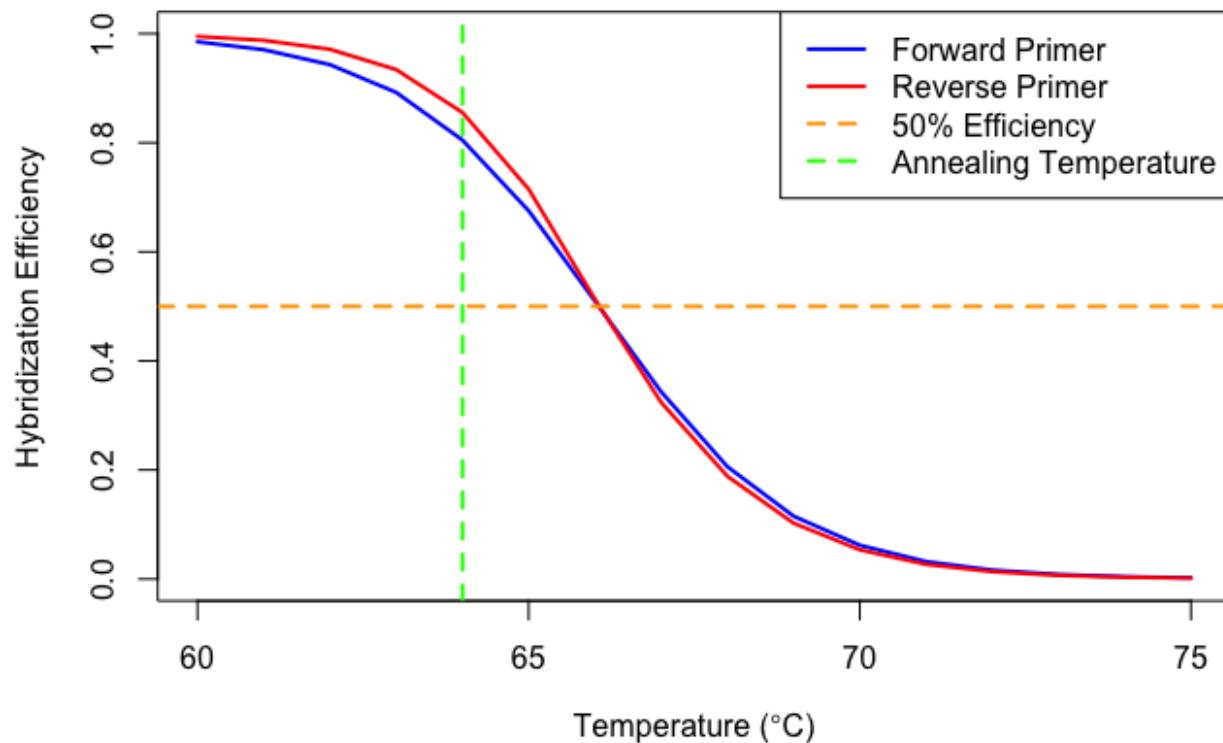
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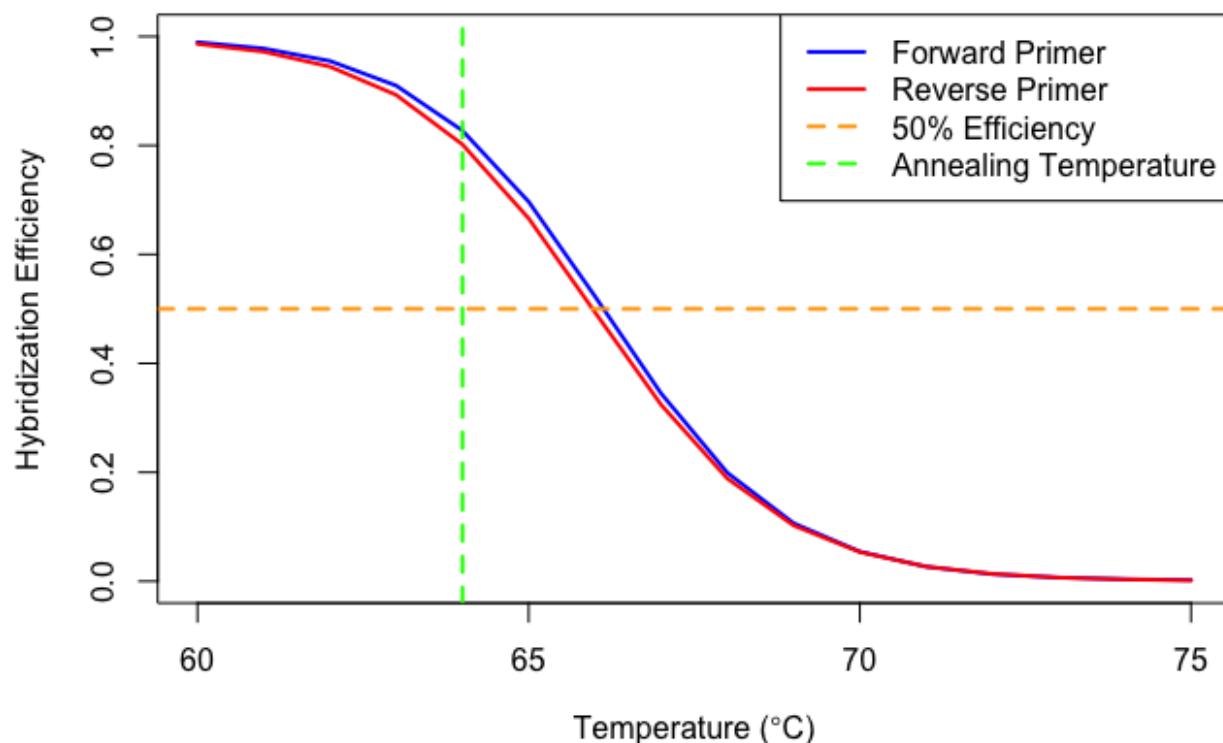
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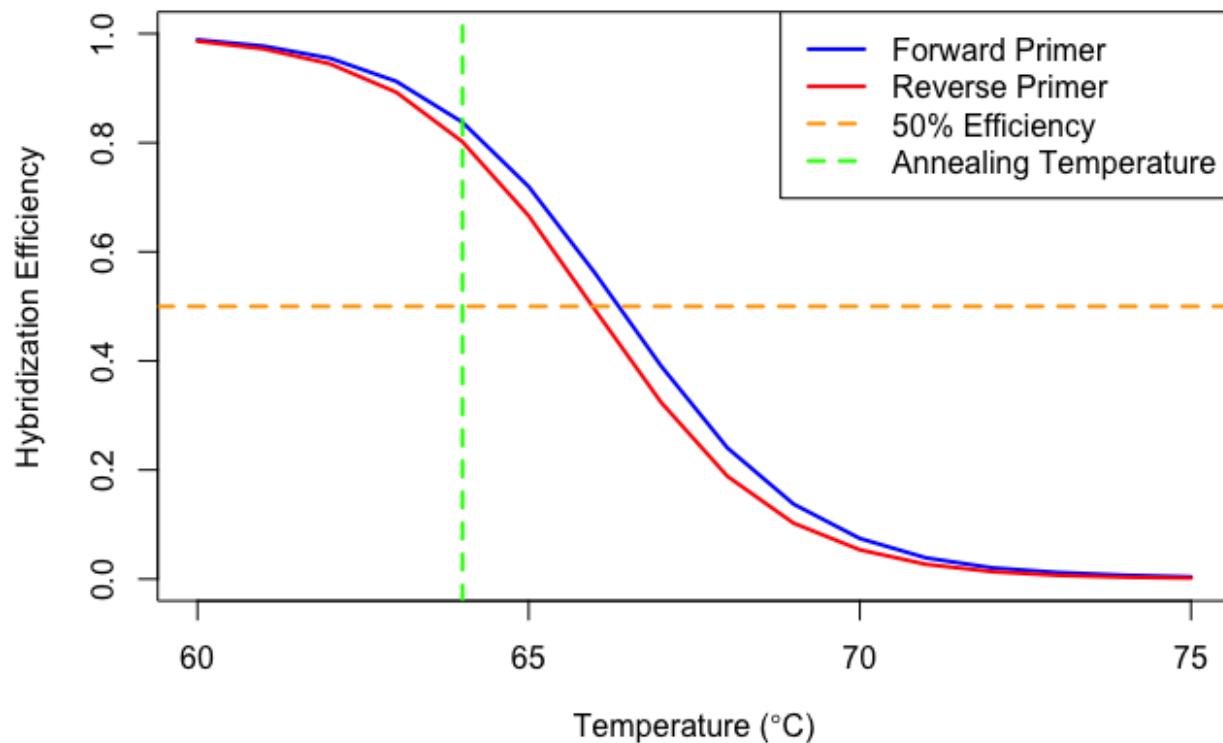
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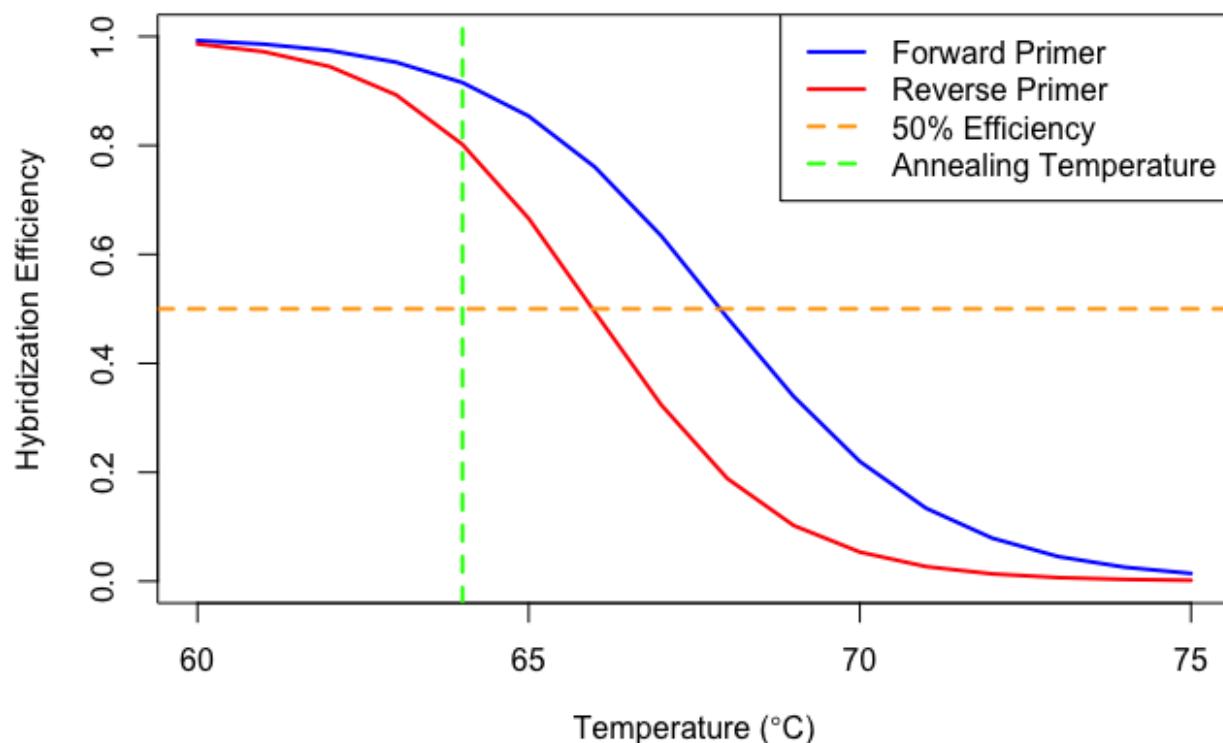
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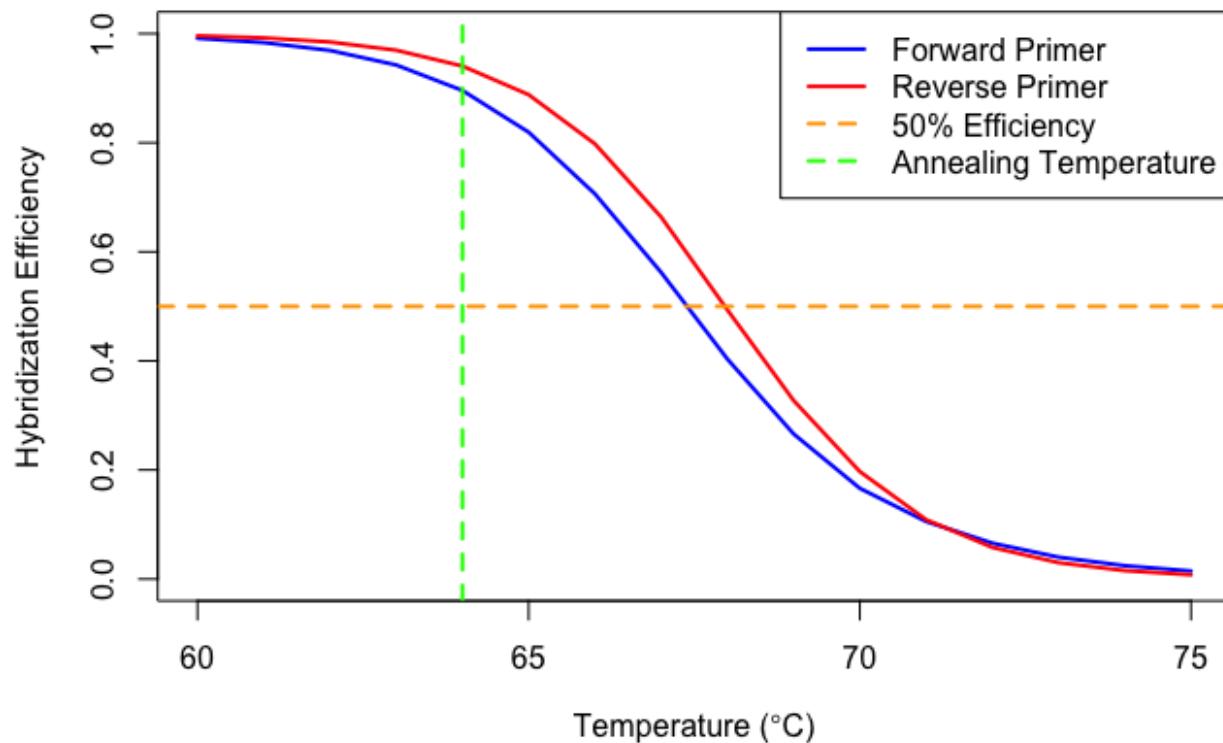
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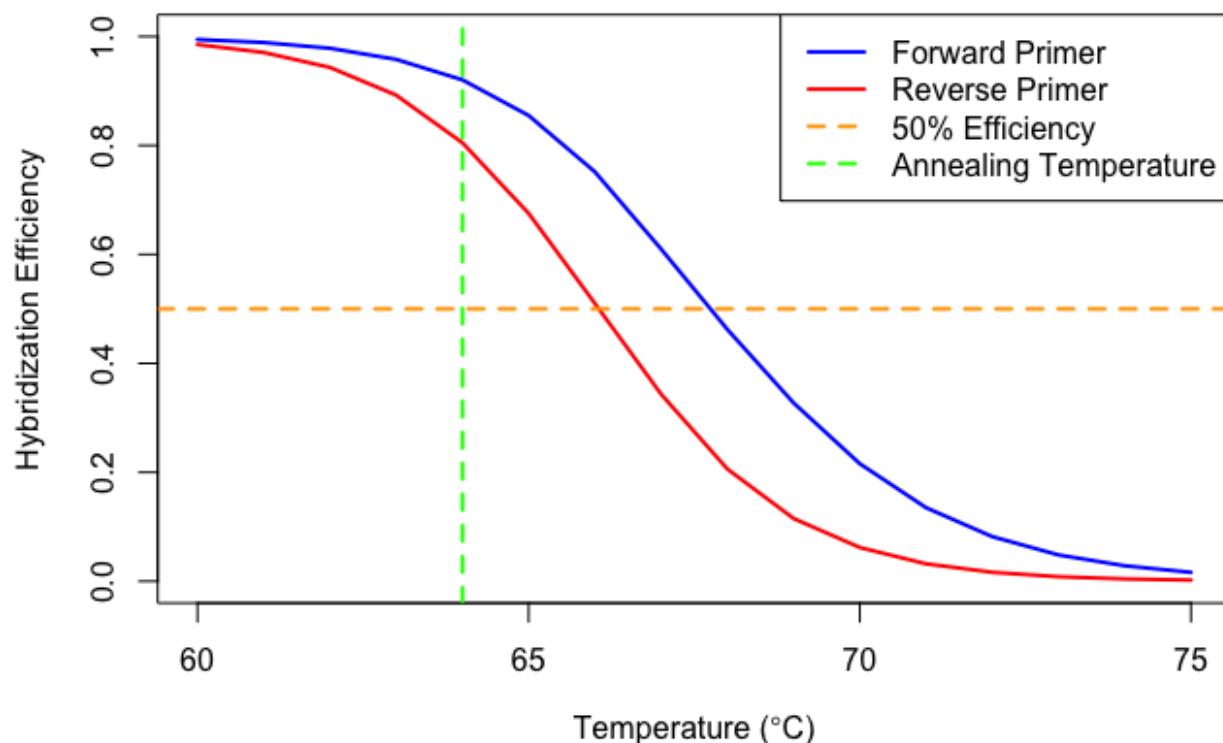
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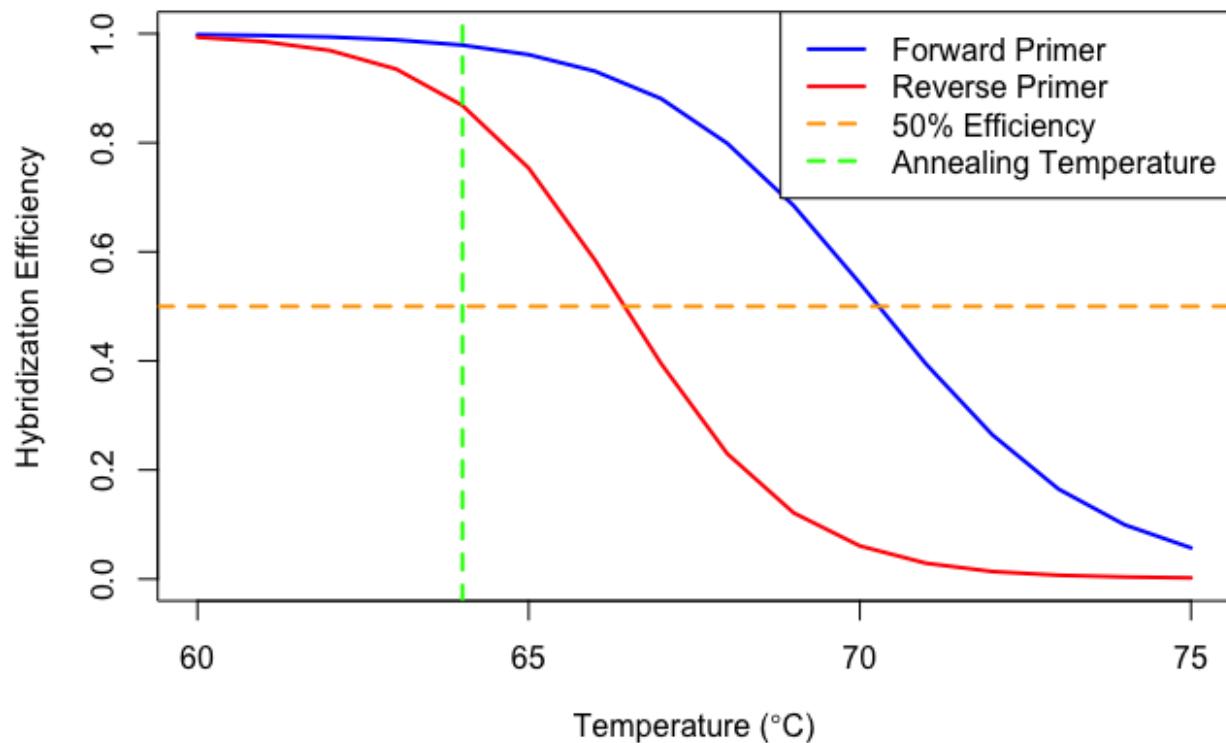
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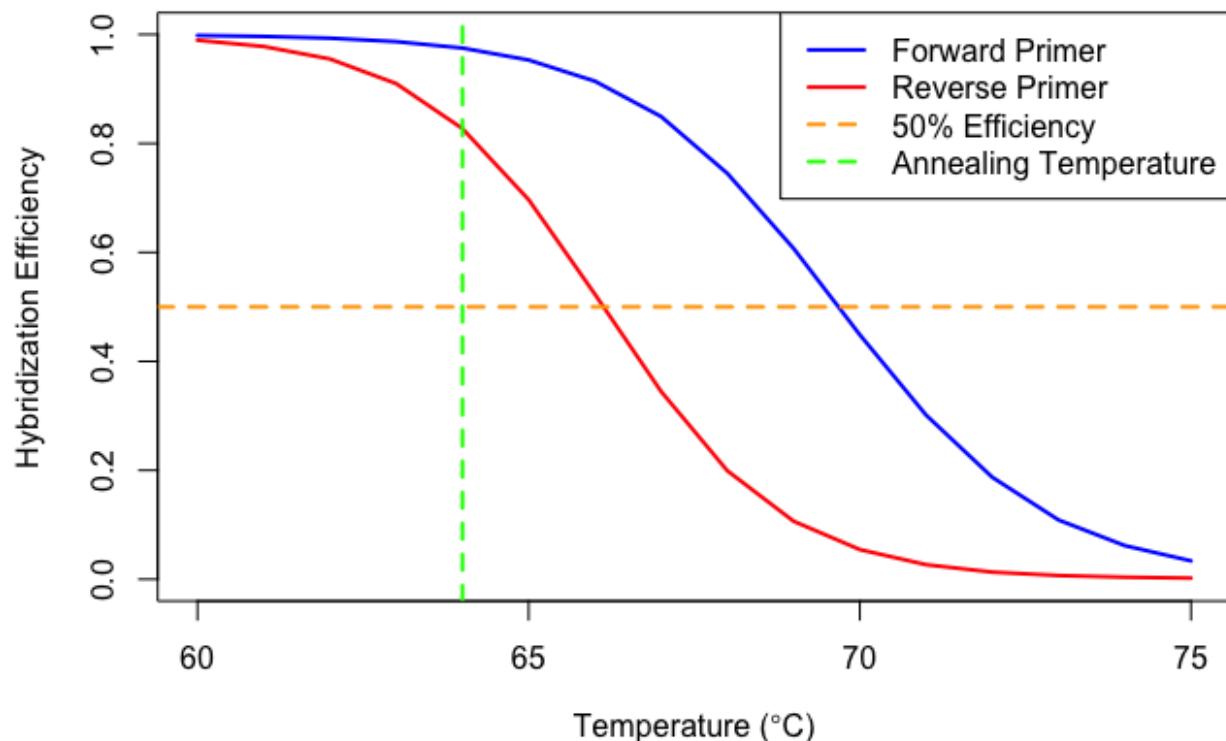
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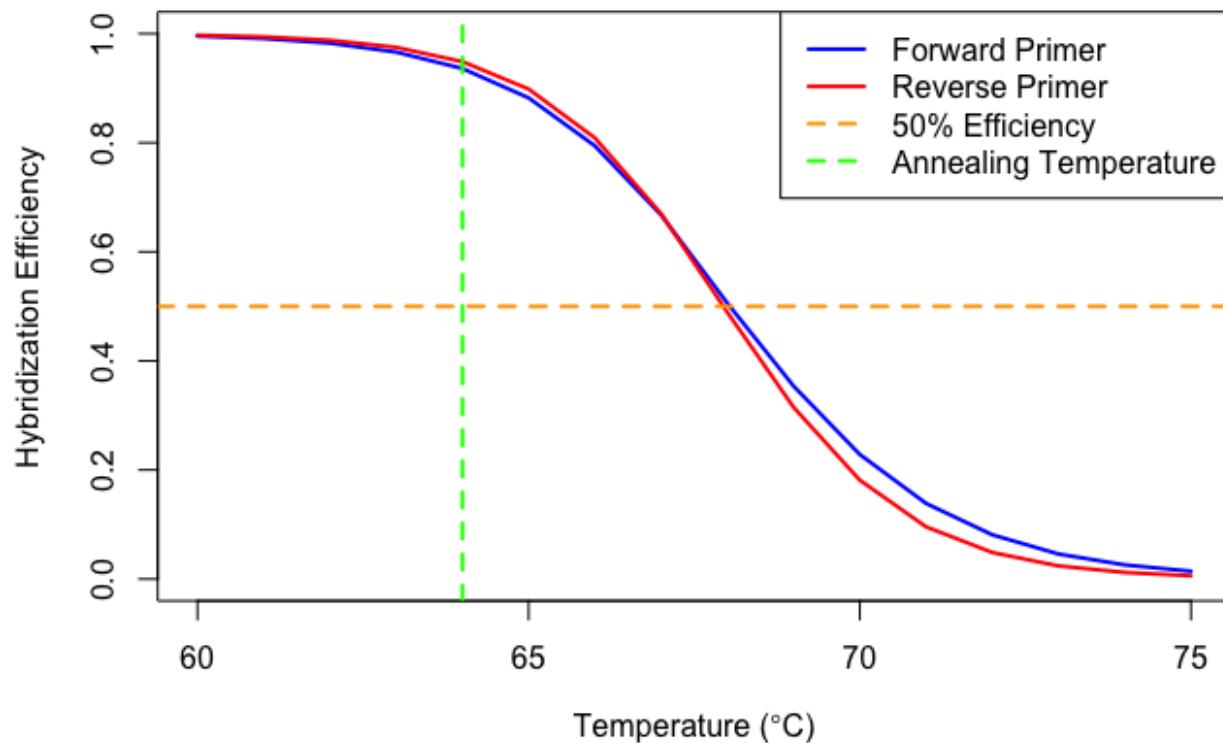
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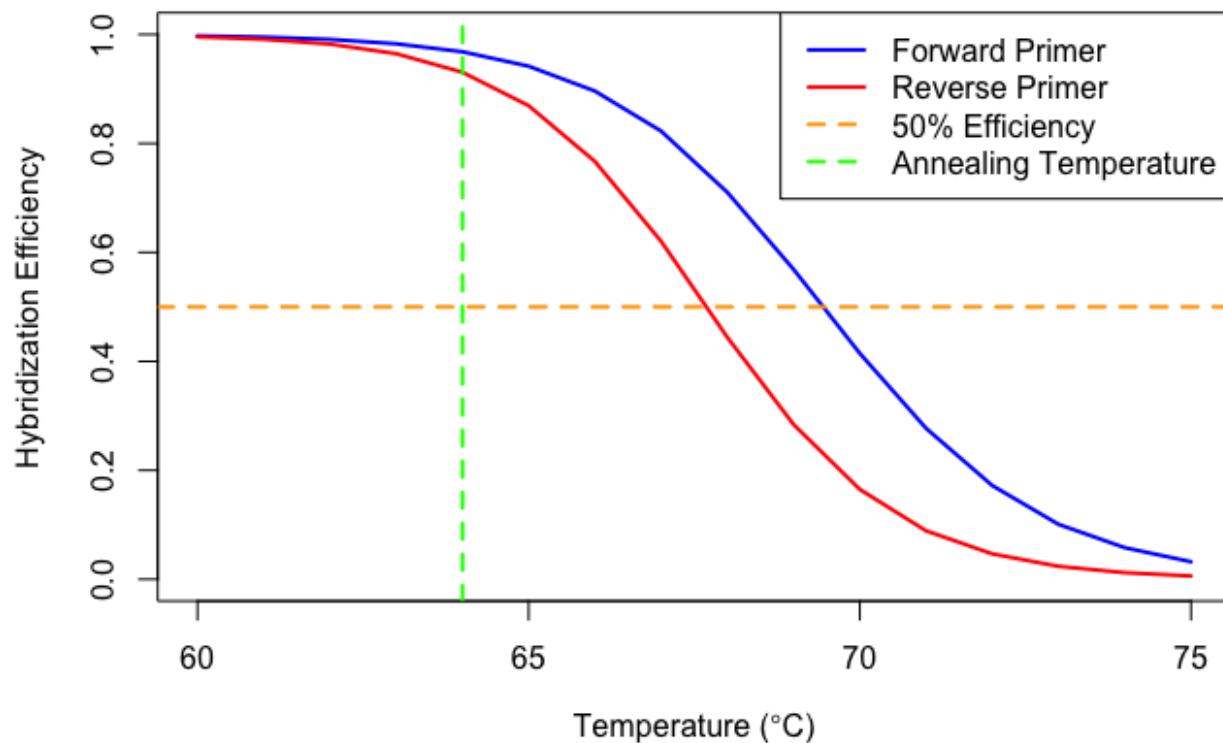
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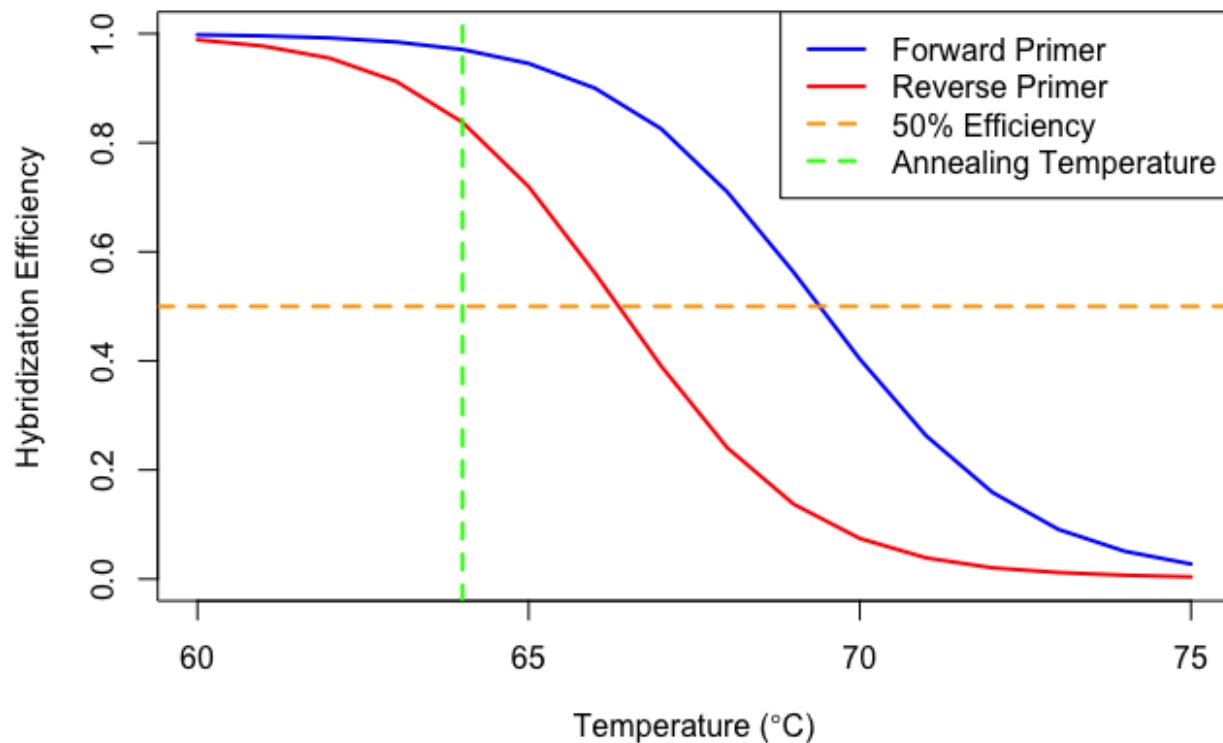
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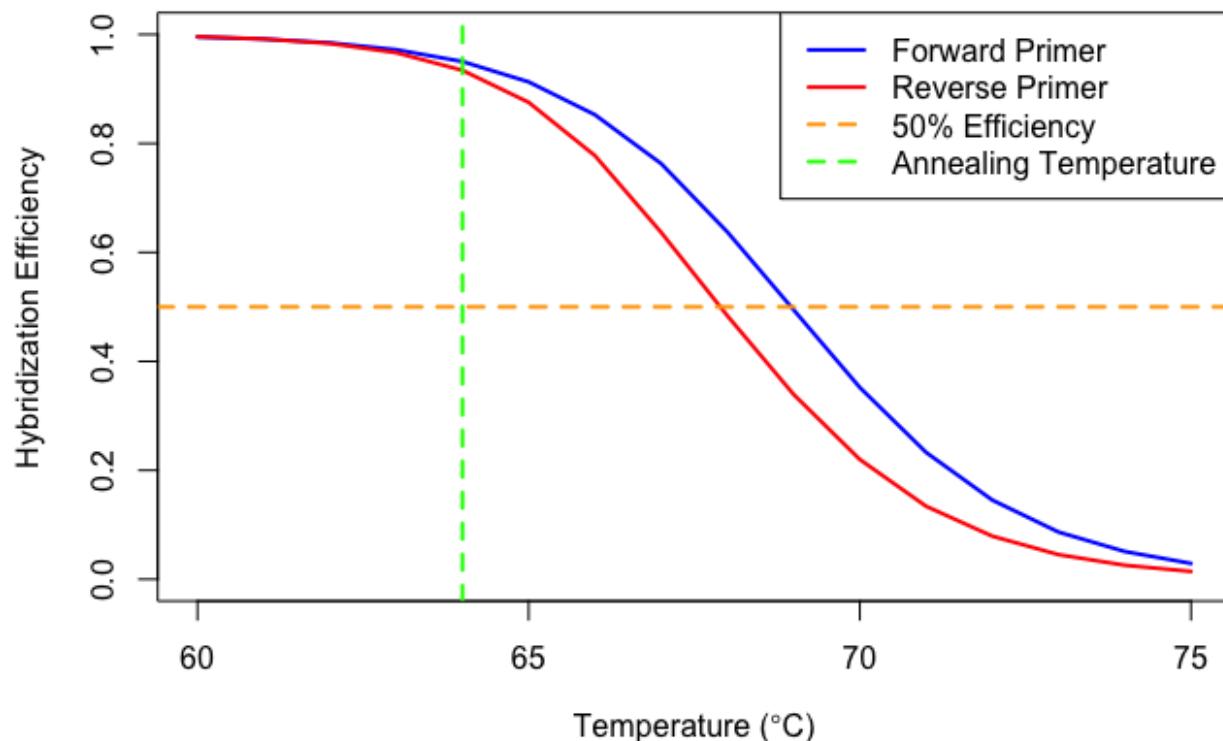
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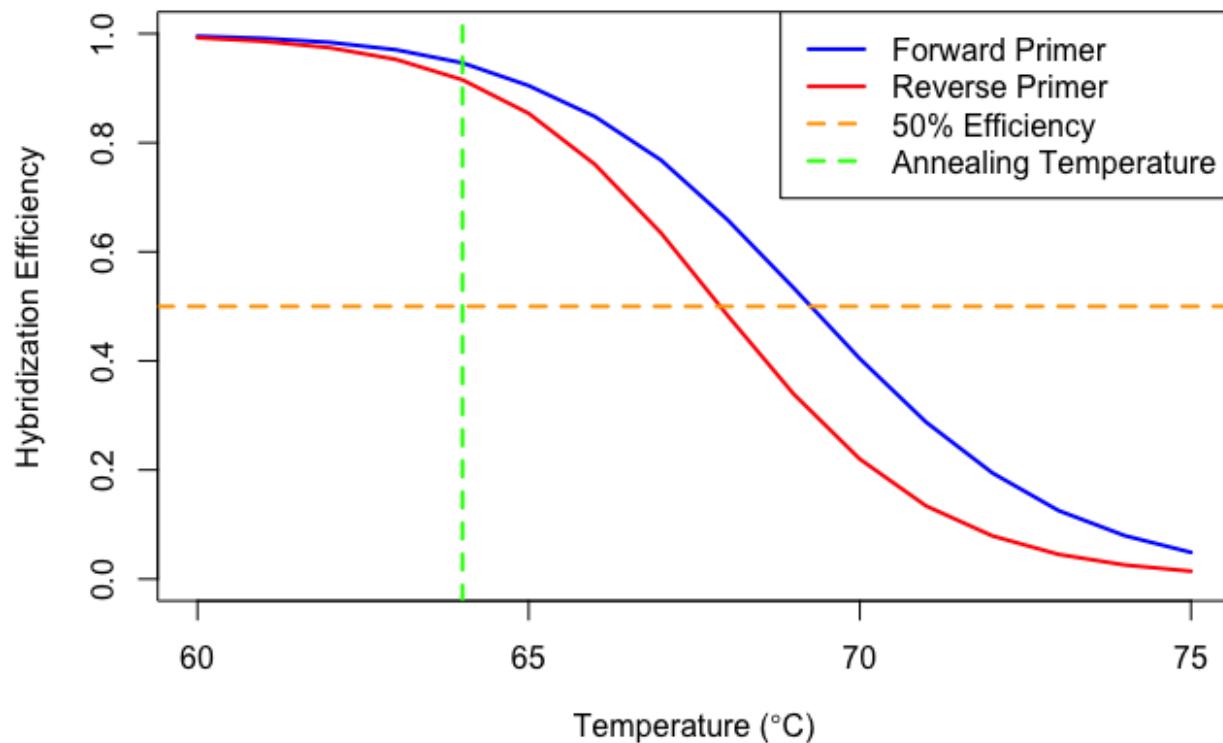
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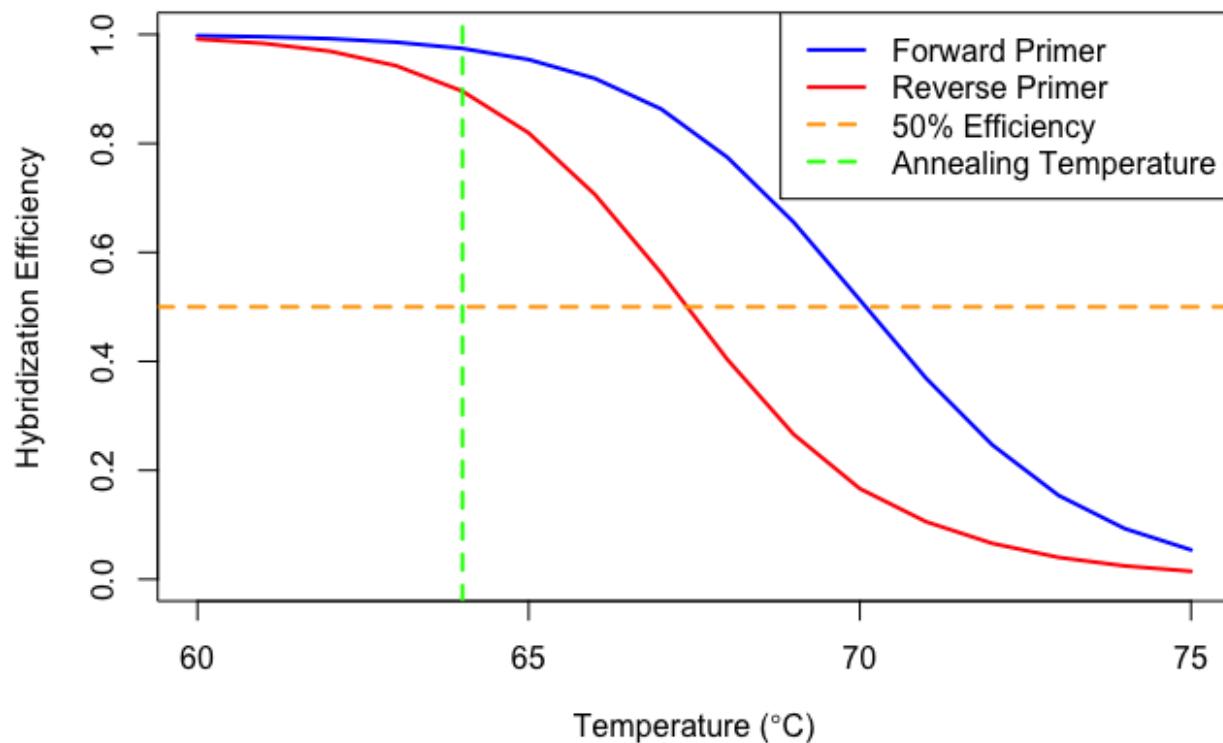
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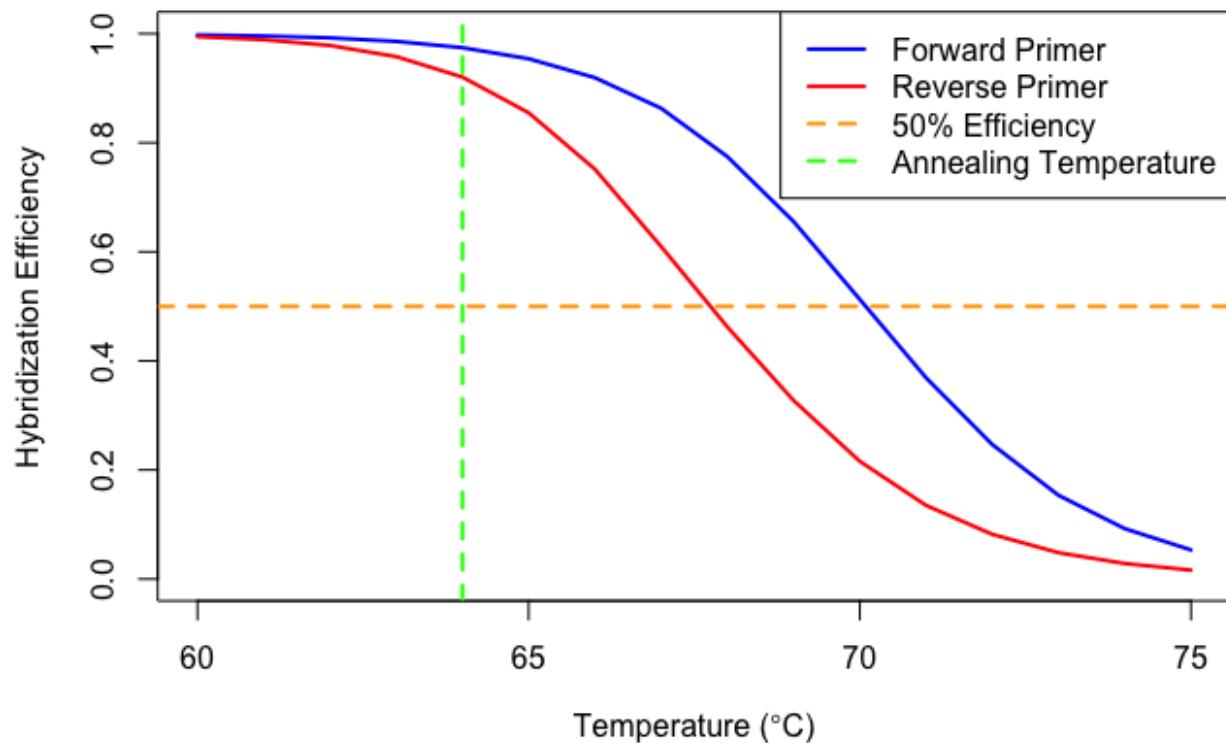
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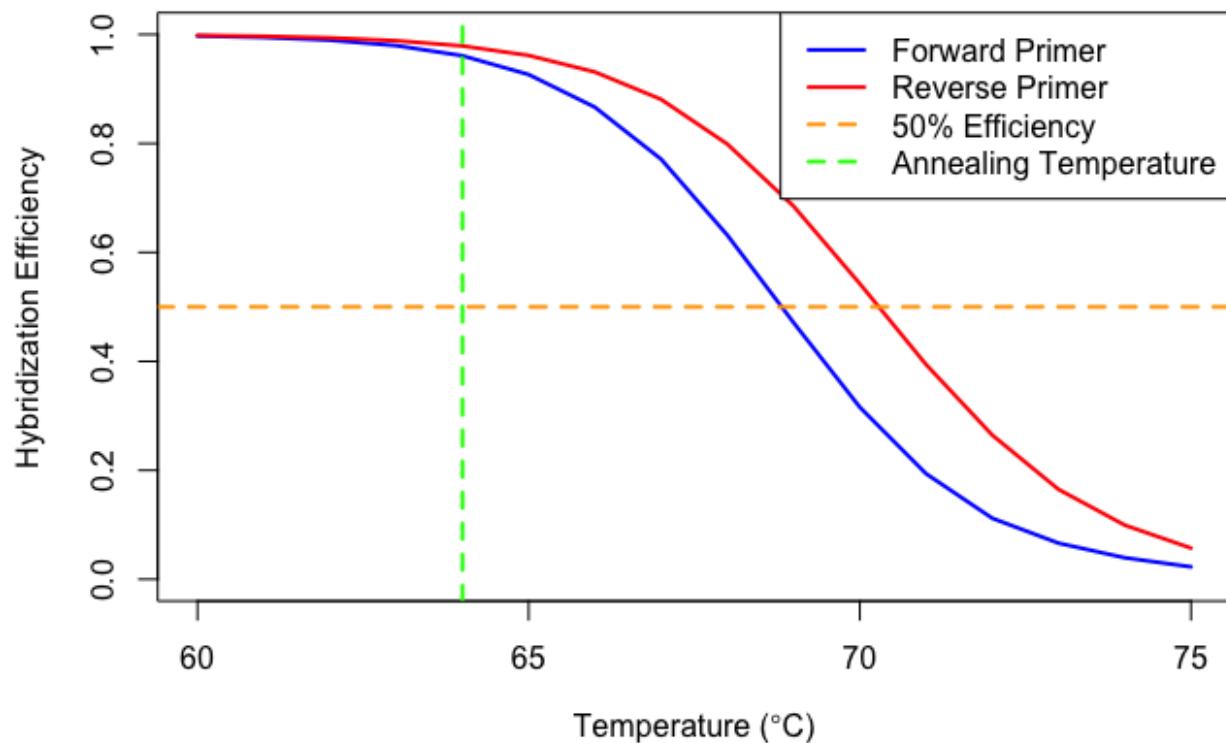
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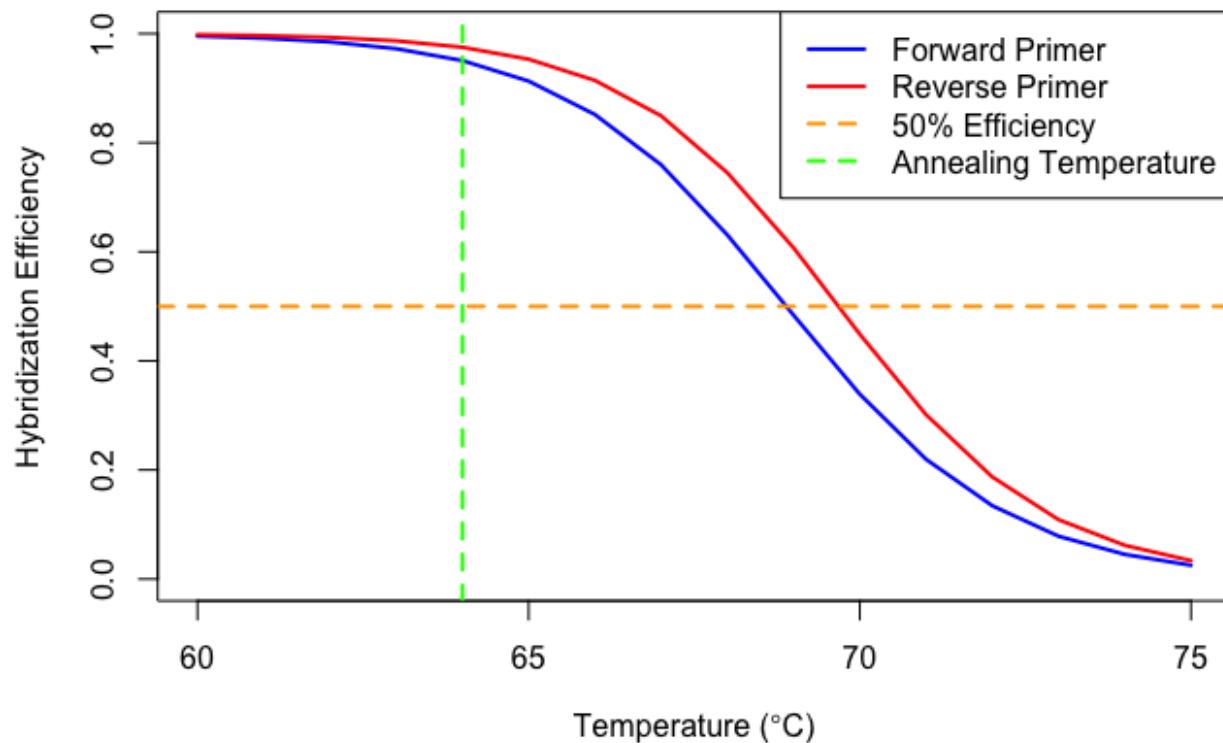
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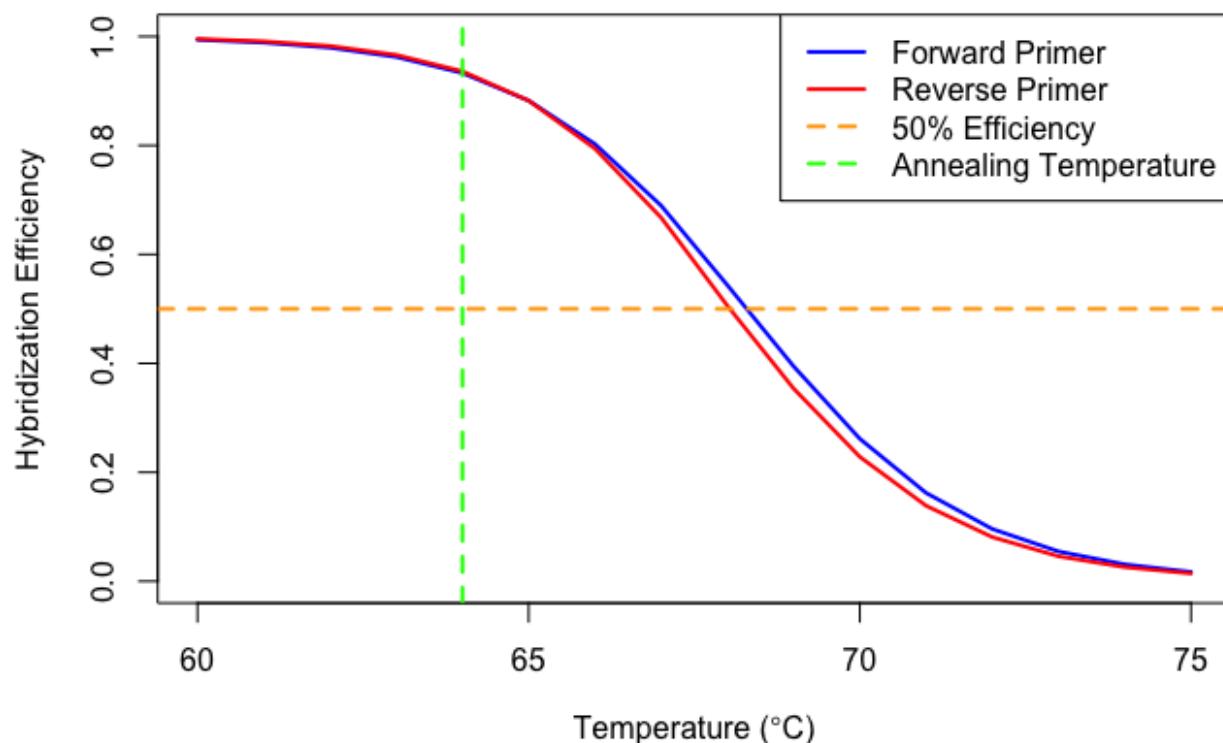
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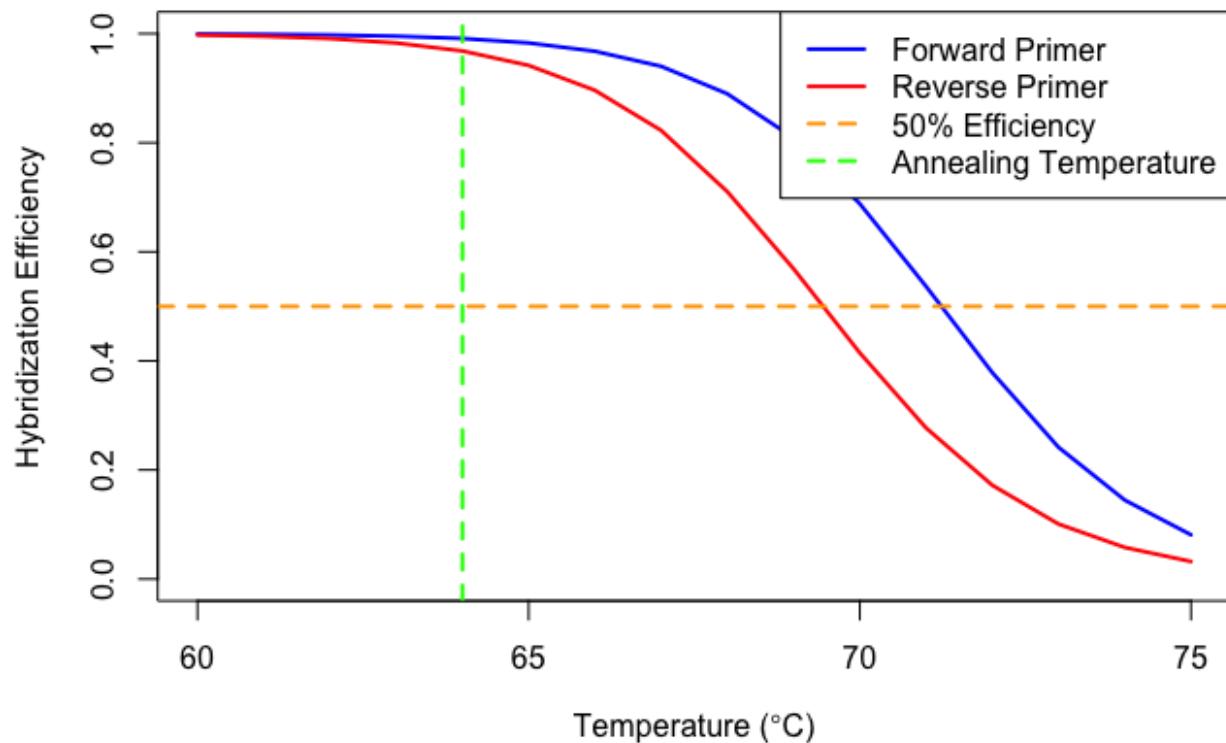
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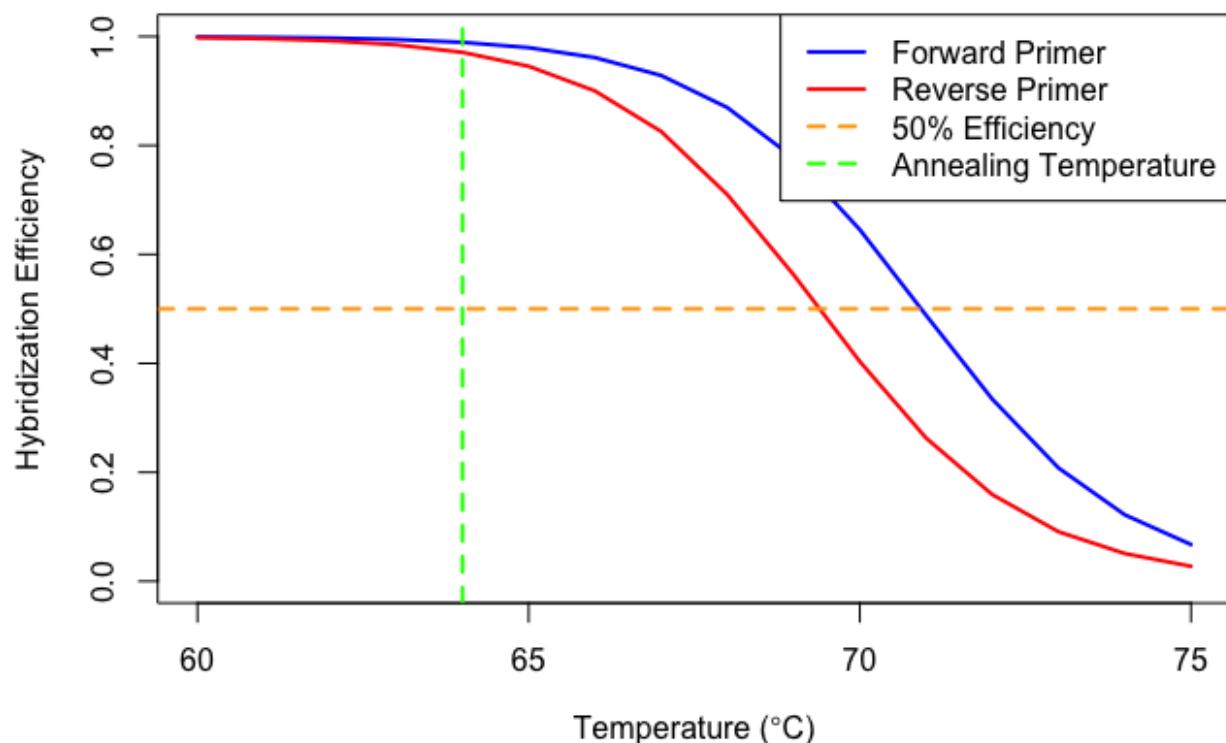
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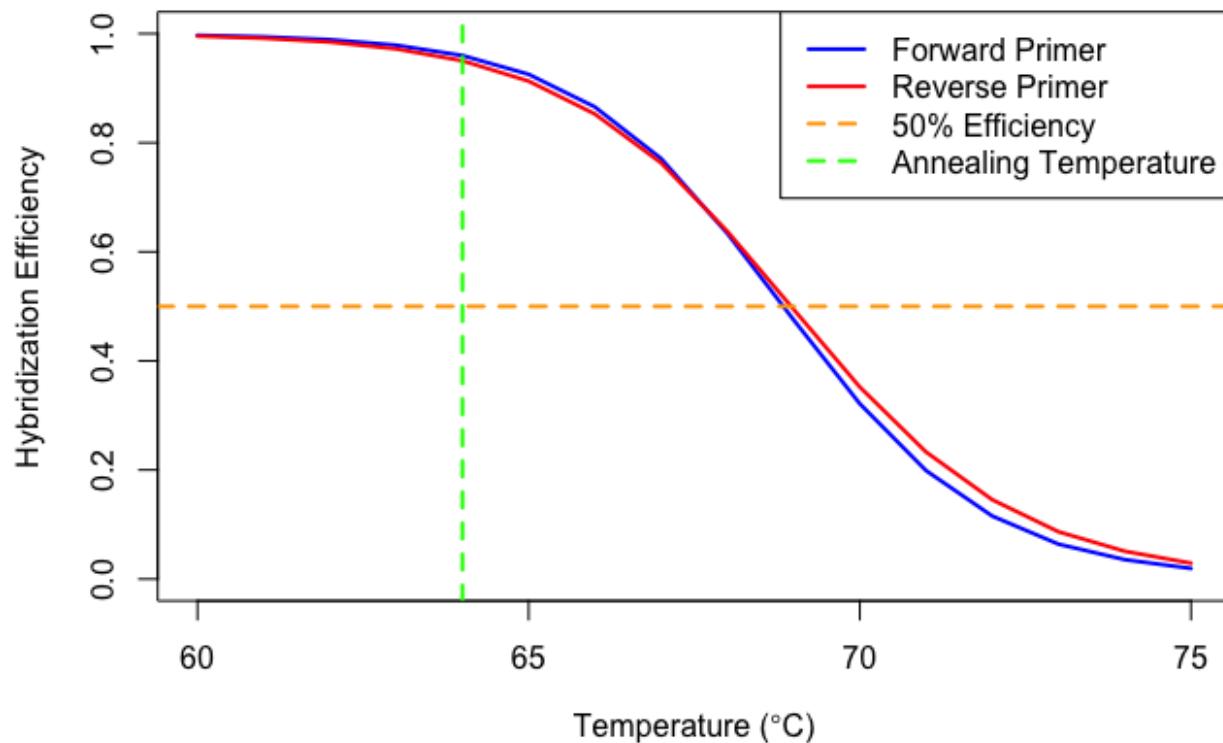
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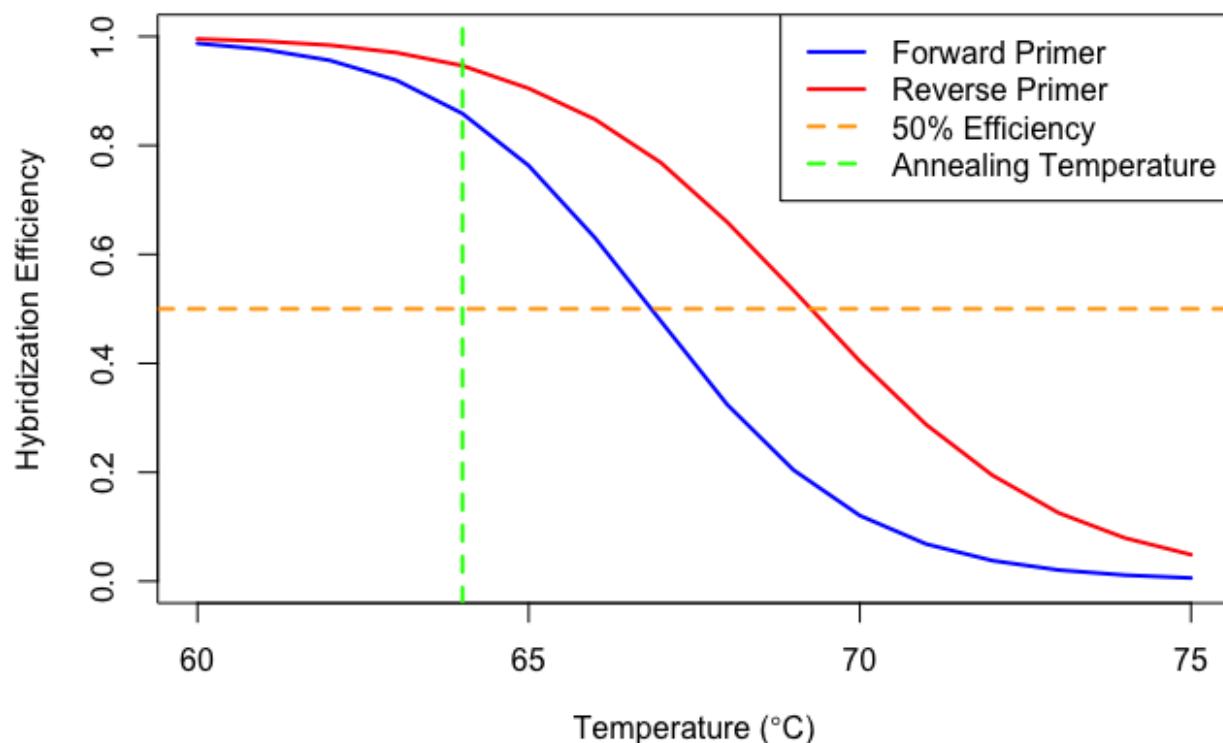
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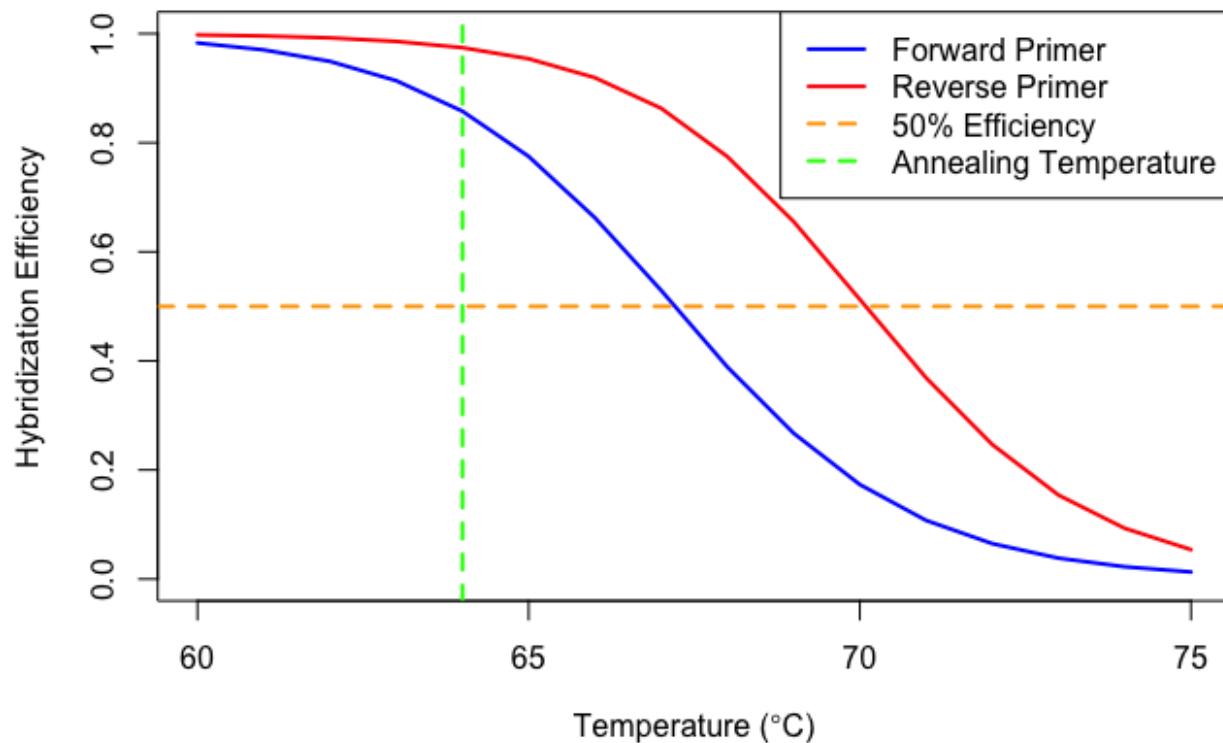
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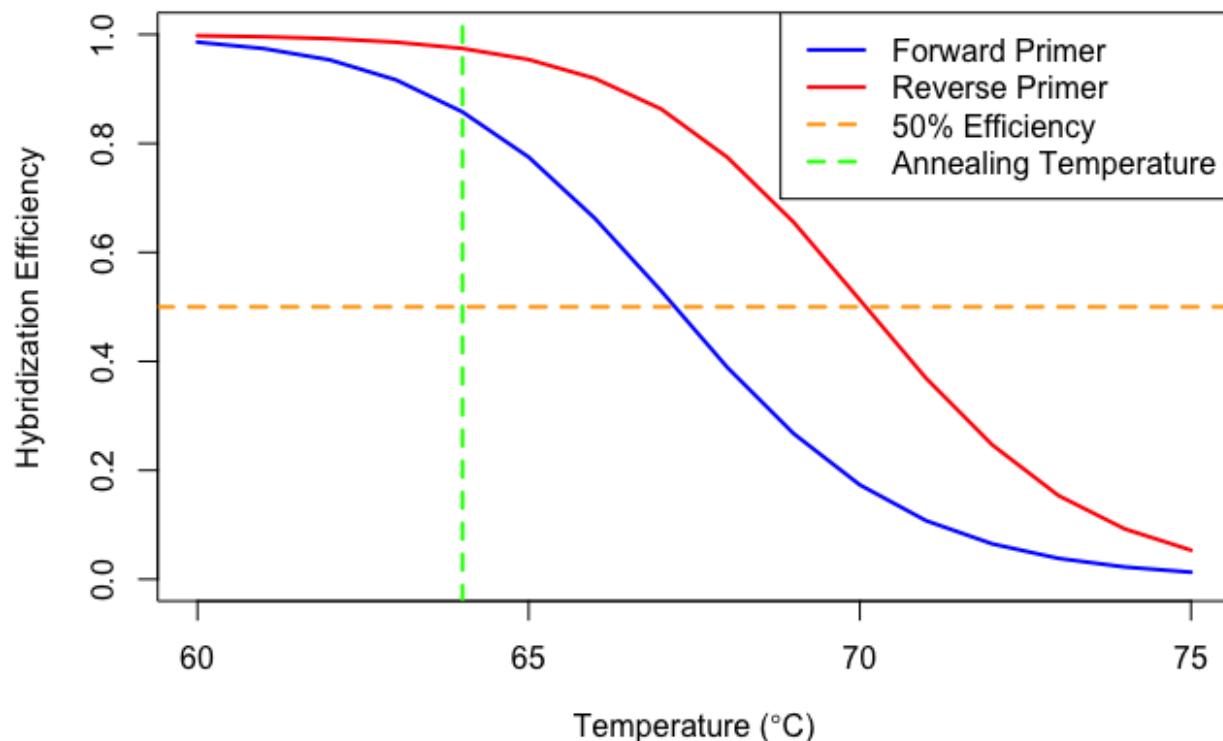
Denaturation Plot



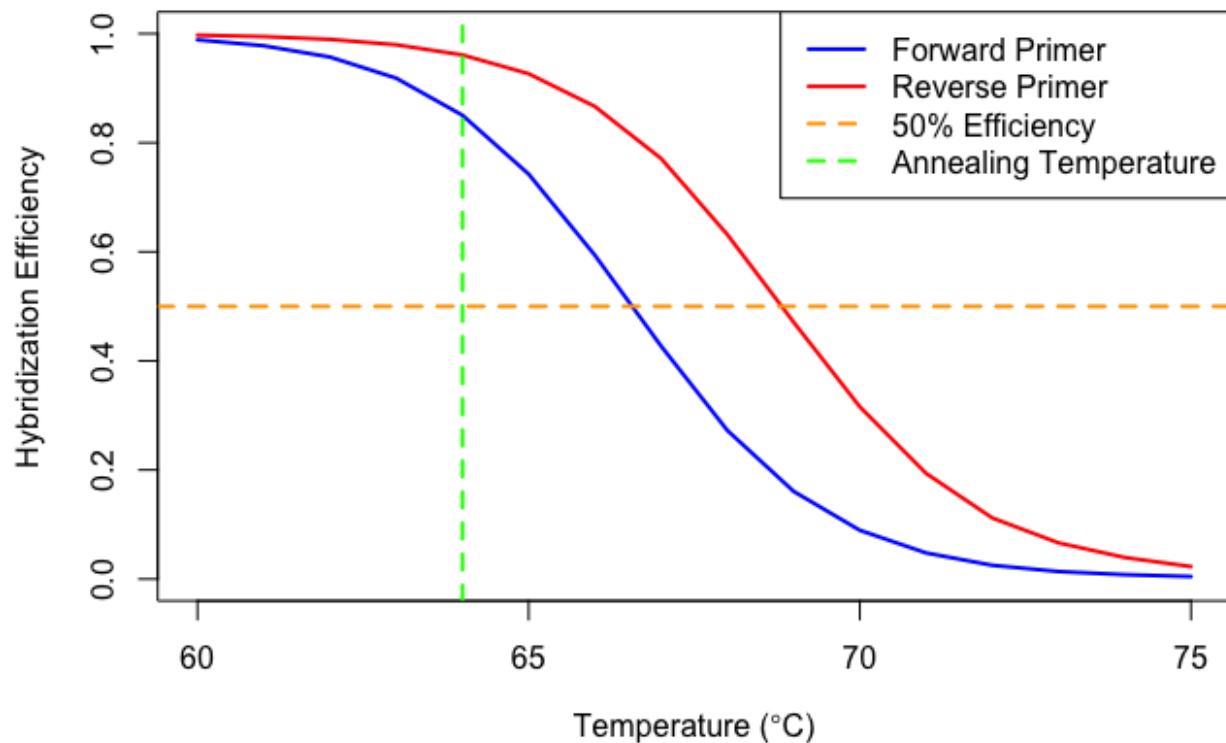
Denaturation Plot



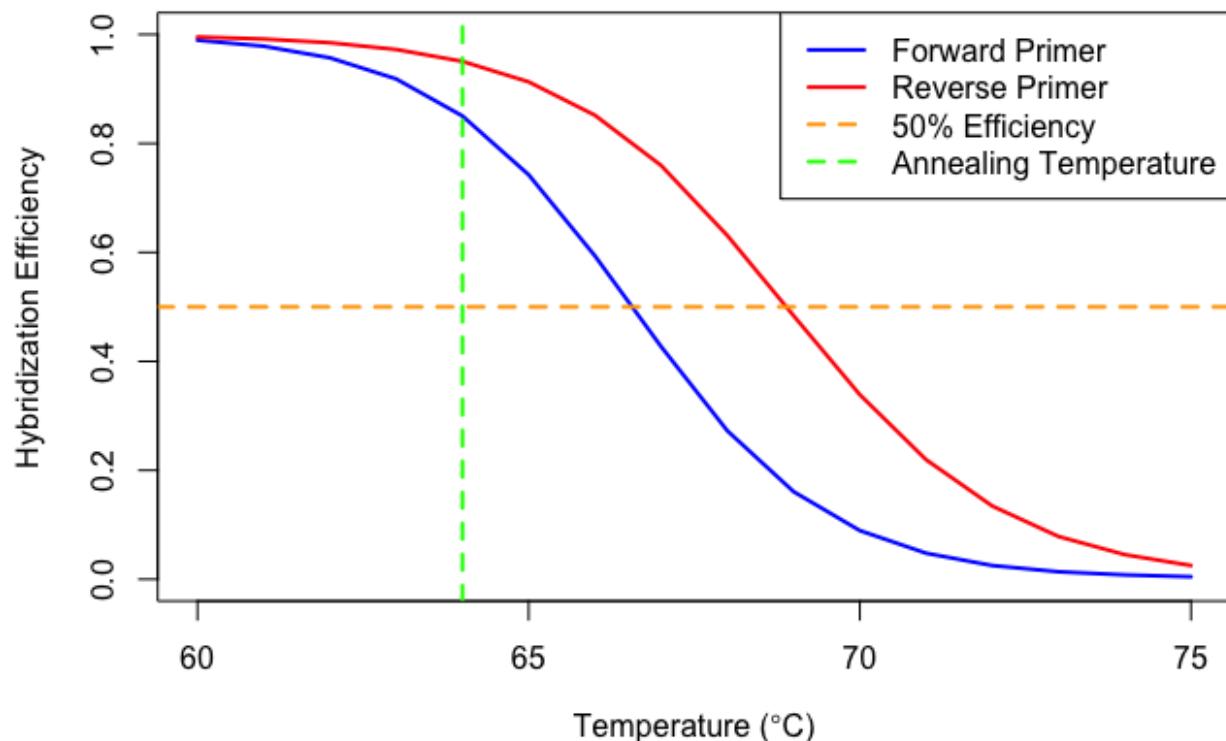
Denaturation Plot



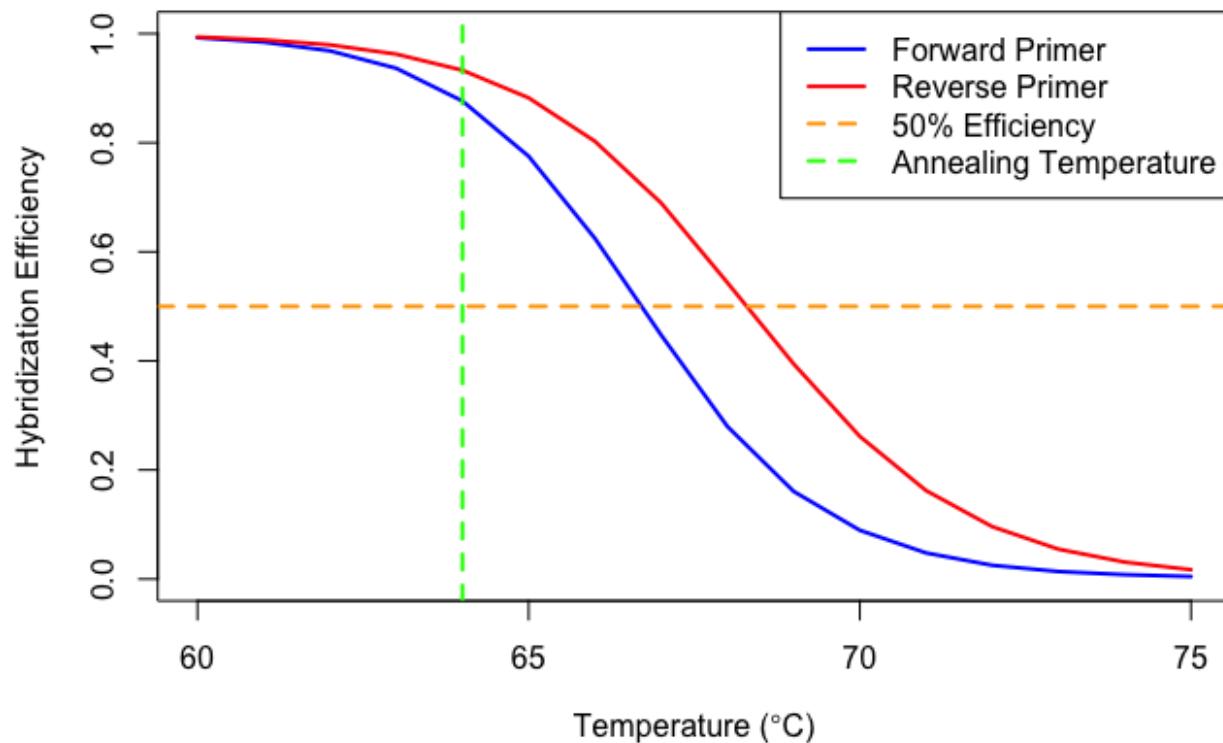
Denaturation Plot



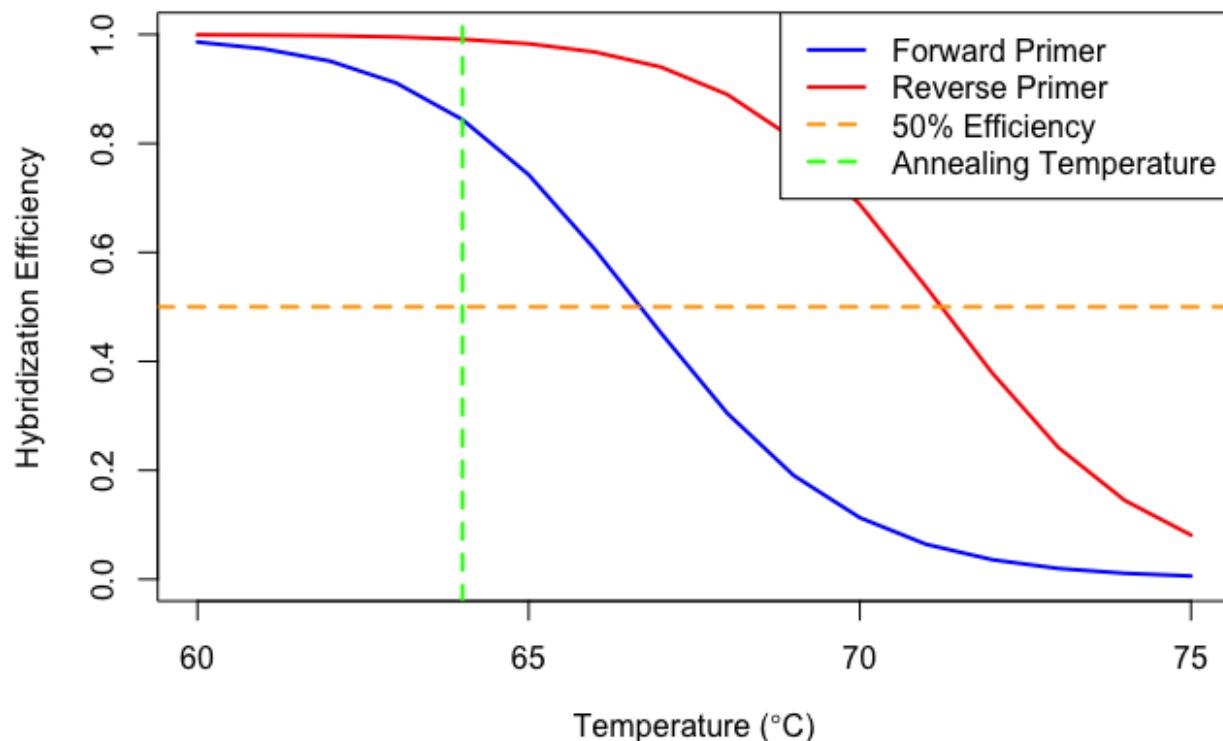
Denaturation Plot



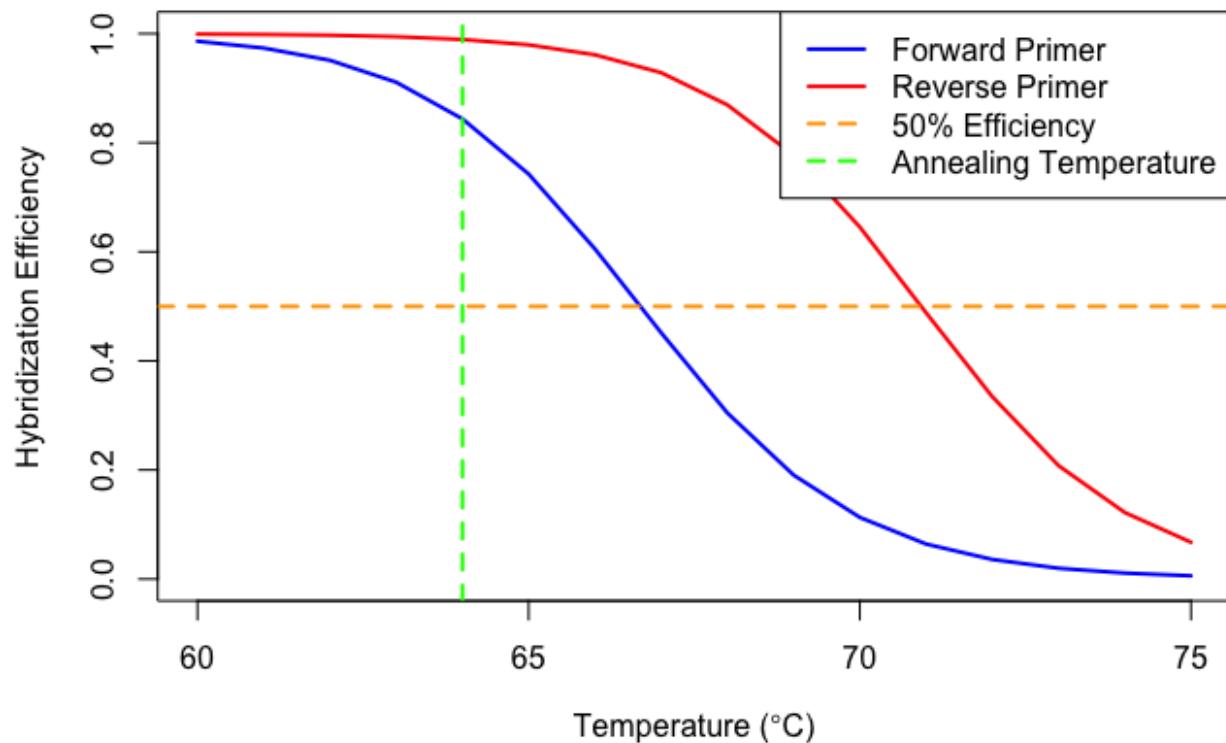
Denaturation Plot



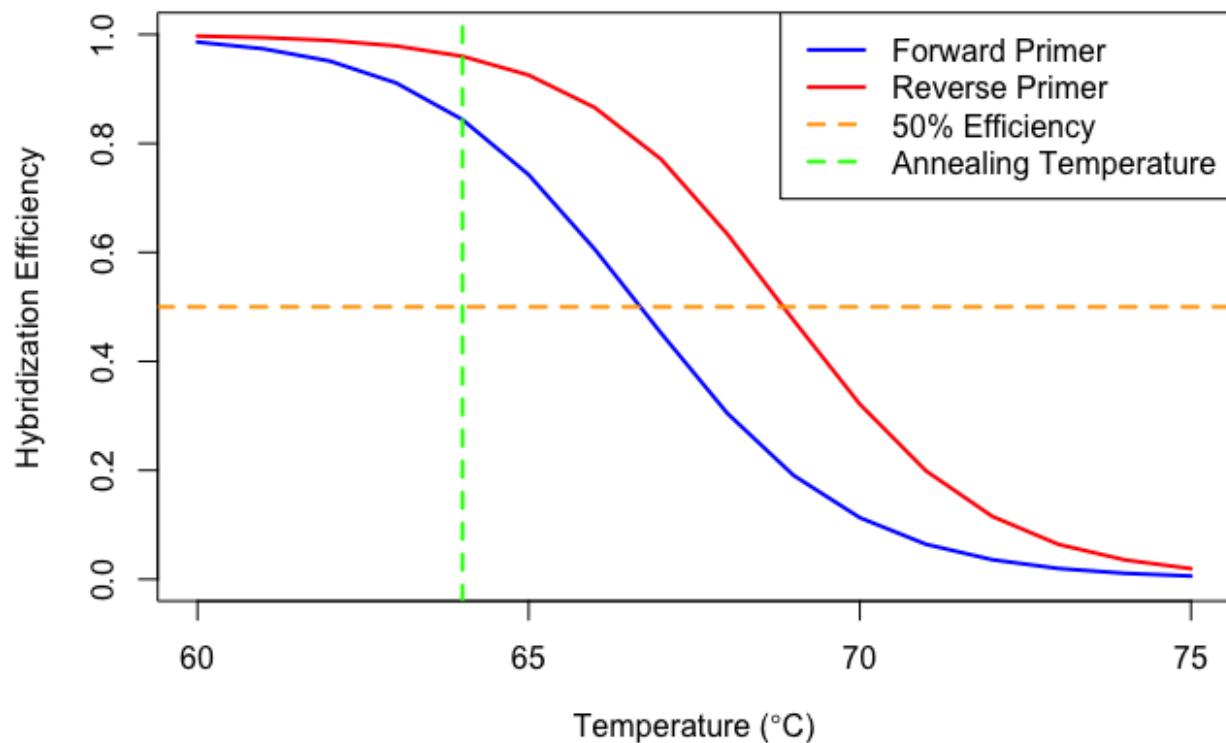
Denaturation Plot



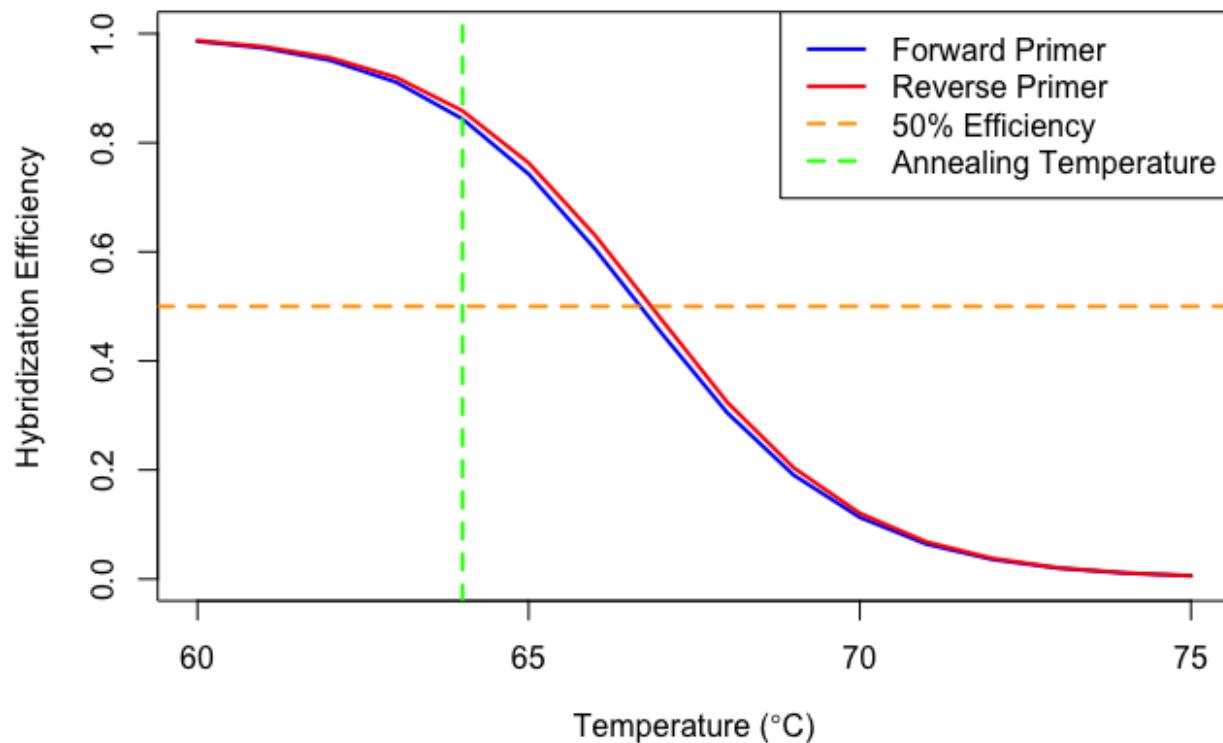
Denaturation Plot



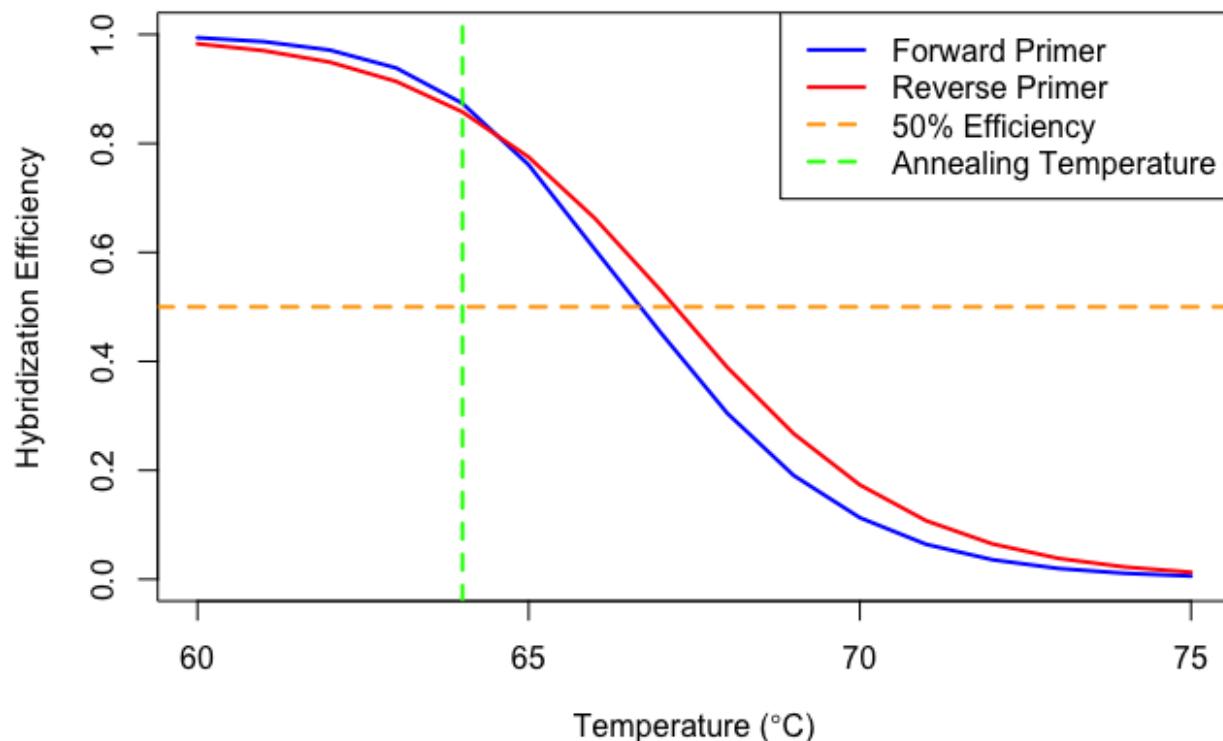
Denaturation Plot



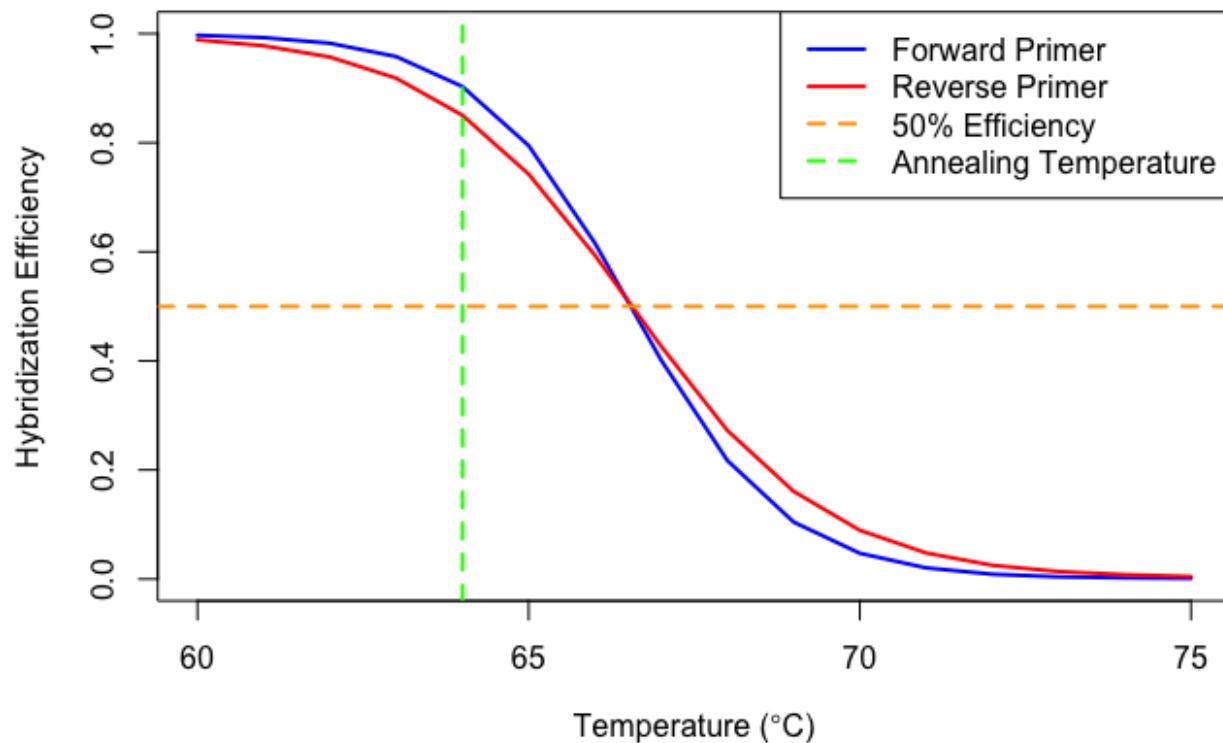
Denaturation Plot



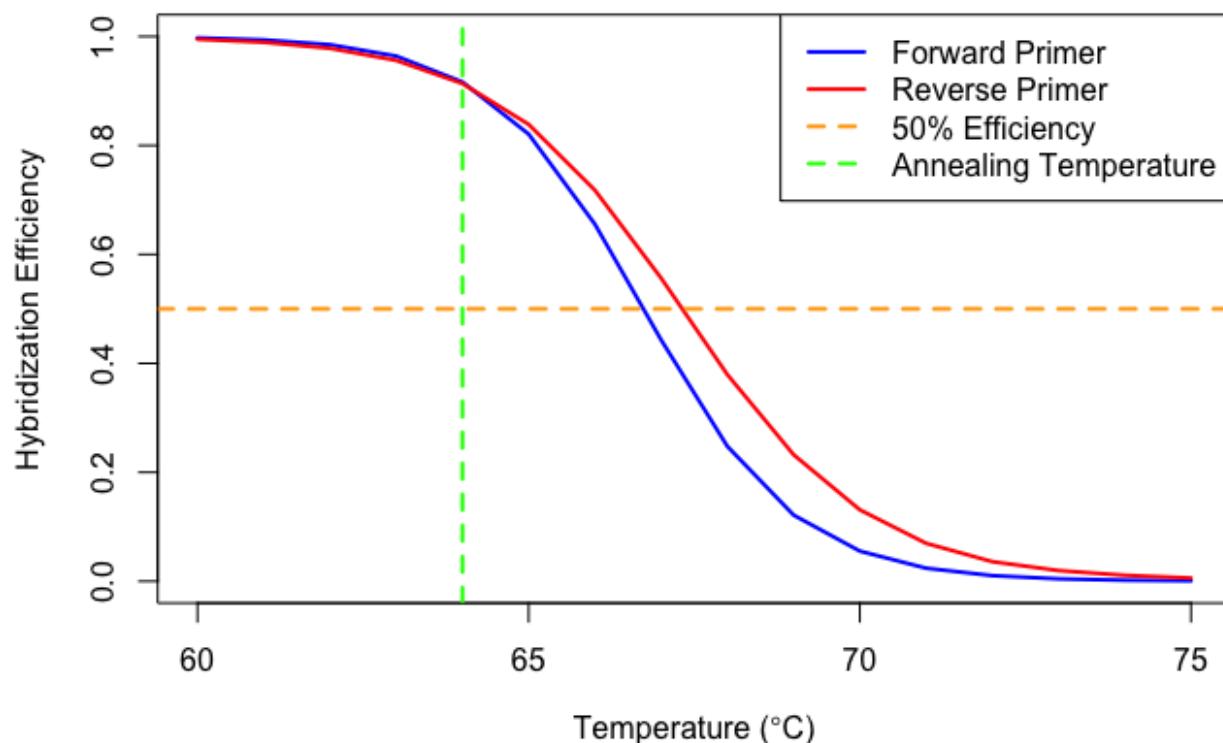
Denaturation Plot



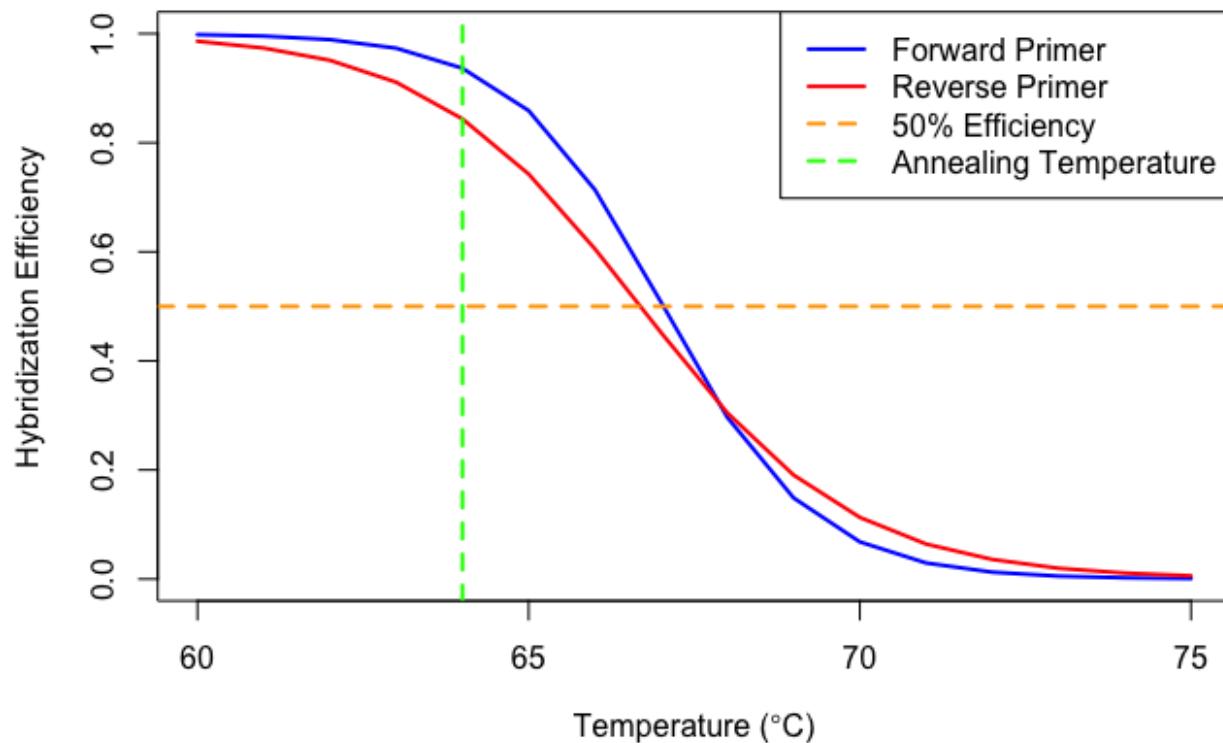
Denaturation Plot



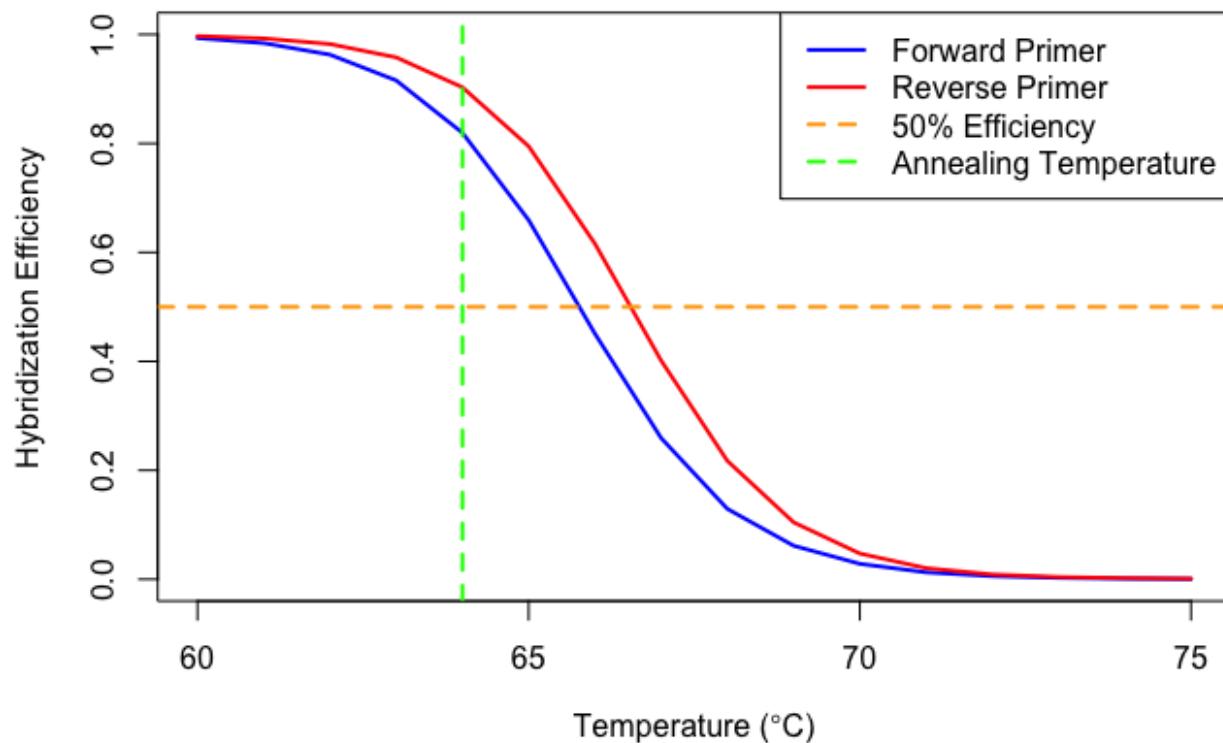
Denaturation Plot



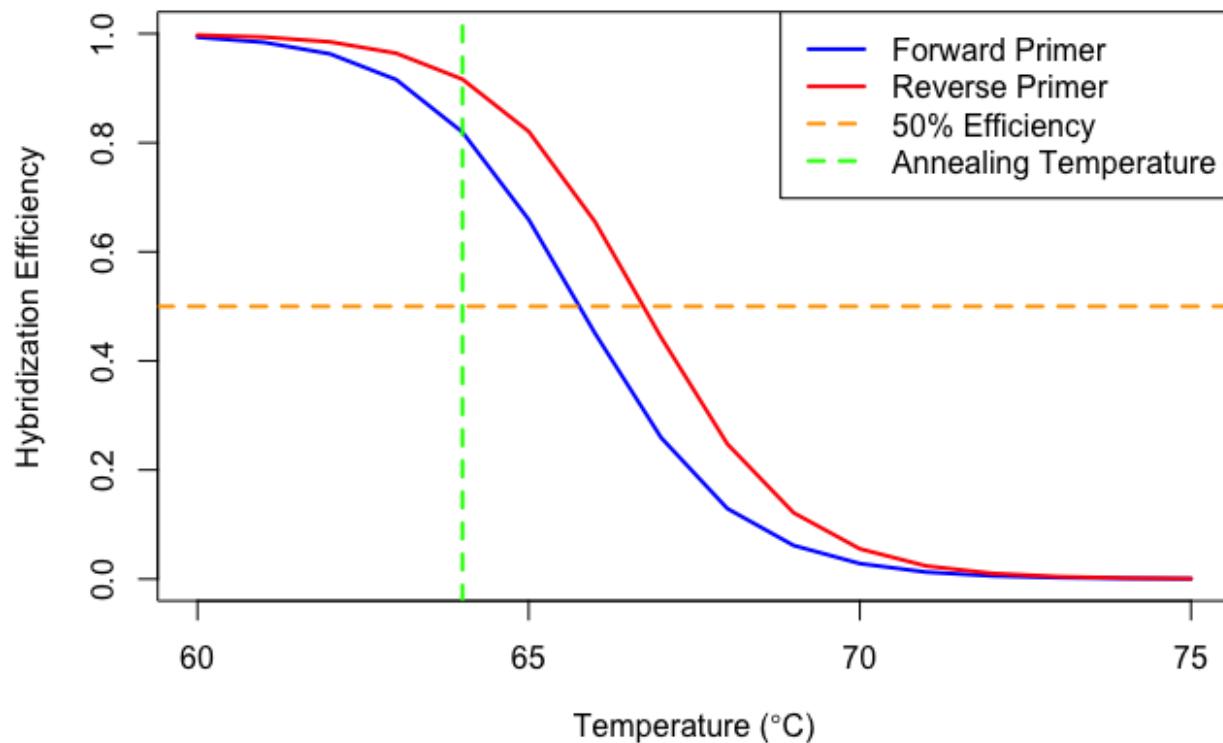
Denaturation Plot



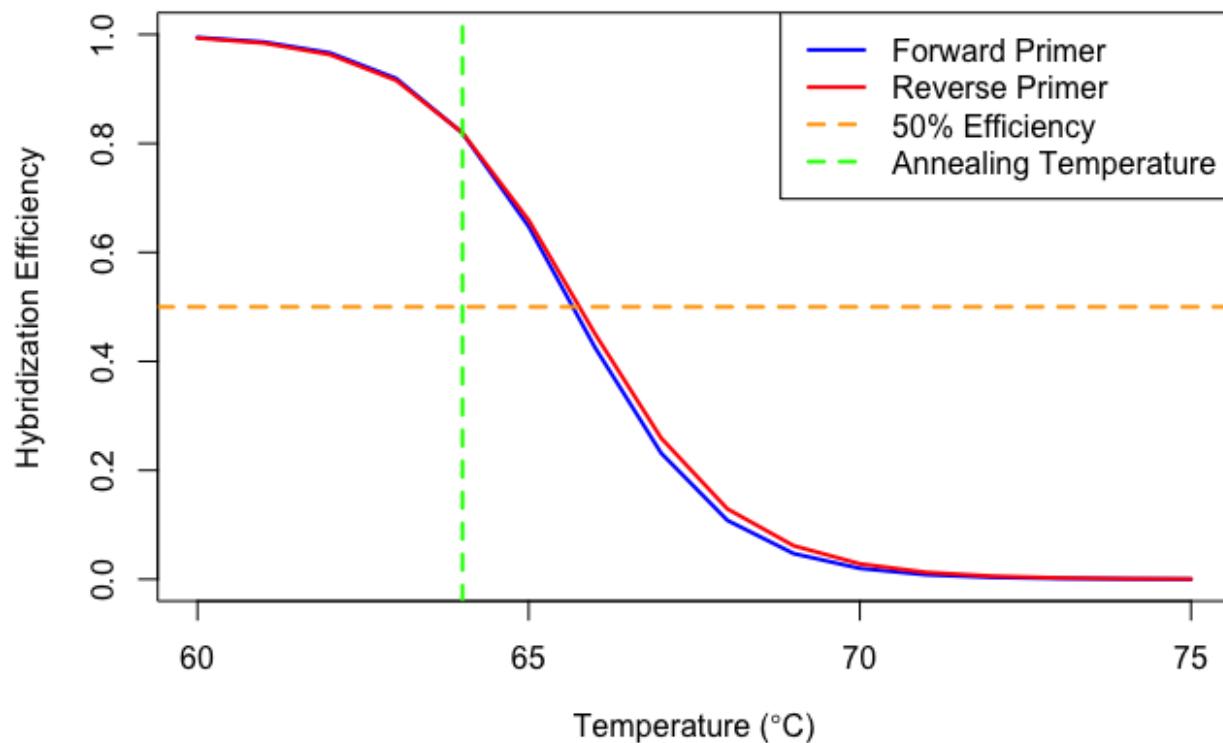
Denaturation Plot



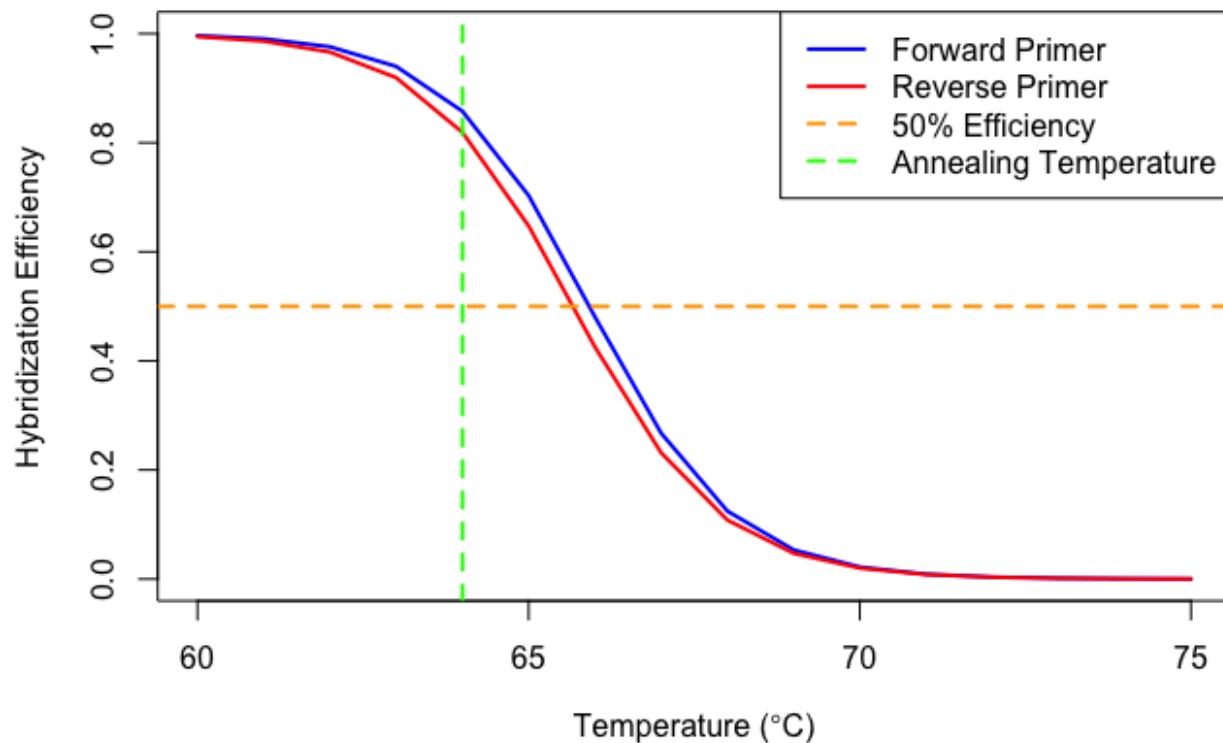
Denaturation Plot



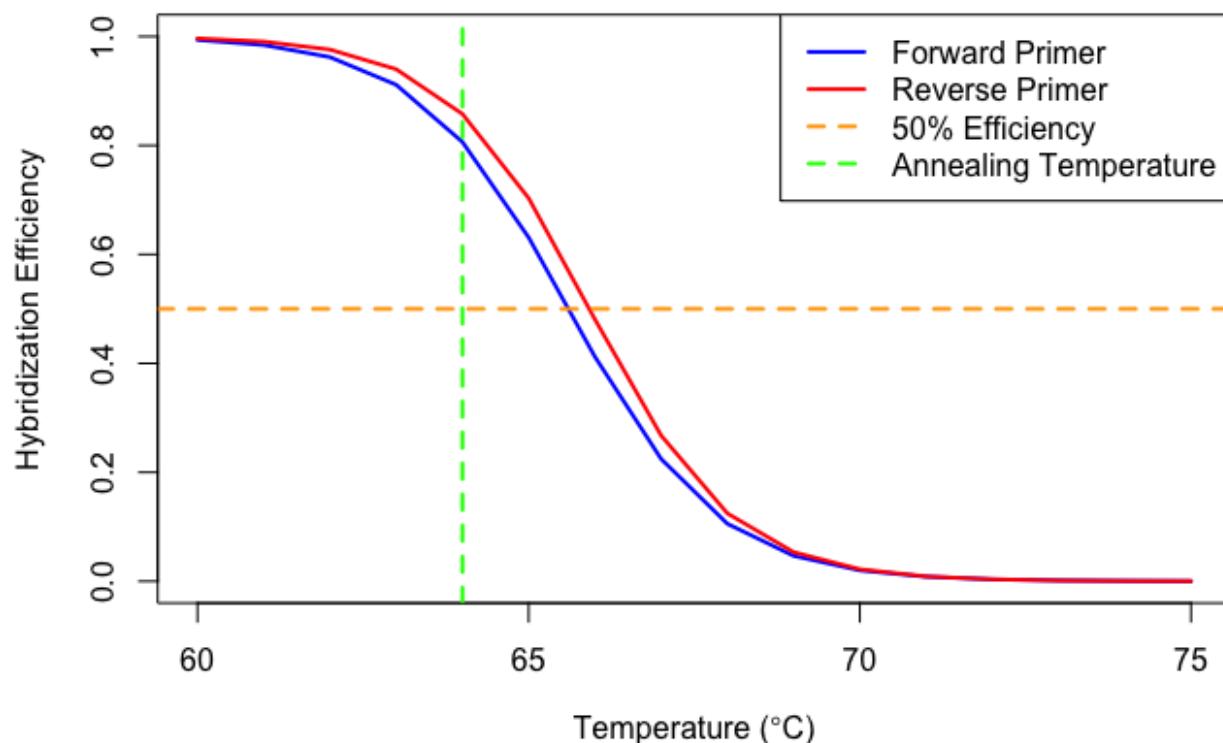
Denaturation Plot



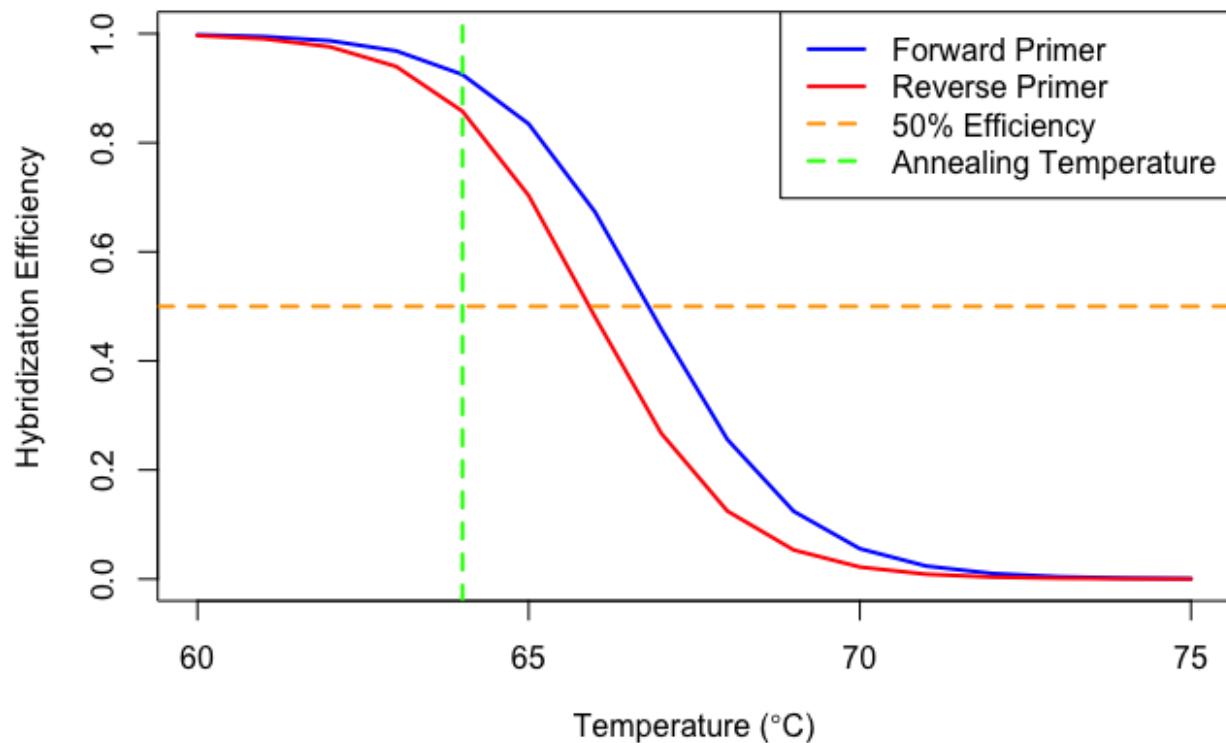
Denaturation Plot



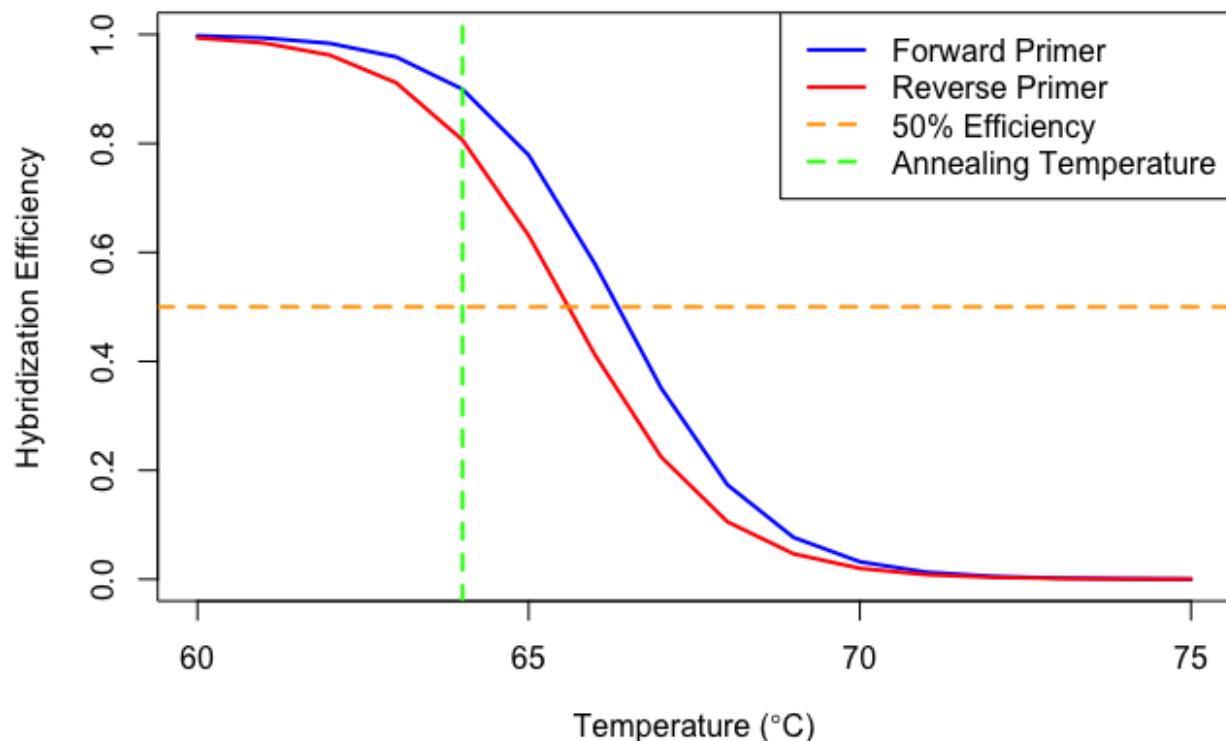
Denaturation Plot



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 0.47 secs
## 
## Designing primer sequences based on the group 'HPV18':
## =====
## 
## Time difference of 62.38 secs
## 
## Selecting the most common primer sequences:
## =====
## 
## Time difference of 14.01 secs
## 
## Determining PCR products from each group:
## =====
## 
## Time difference of 6.48 secs
## 
## Scoring primer pair combinations:
## =====
## 
## Time difference of 0.01 secs
## 
## Choosing optimal forward and reverse pairs:
```

```
## =====
## 
## Time difference of 1.66 secs

##          forward_primer          reverse_primer score coverage proc
## 1 CCAACGACGCAGAGAAACACAA ATGTCTTCAATGTTGCCCTAGGT 0 0.2
## 2 CCAACGACGCAGAGAAACACAAG ATGTCTTCAATGTTGCCCTAGGT 0 0.2
## 3 GCTTGAGGATCCAACACGGC GCAGTGAAGTGTTCAGTCCGT 0 0.2
## 4 GCTTGAGGATCCAACACGGC GTGTTCAGTCCGTGCACAGAT 0 0.2
## 5 GCTTGAGGATCCAACACGGC GCAGTGAAGTGTTCAGTCCGTG 0 0.2
## 6 GCTTGAGGATCCAACACGGC AGTGTTCAGTCCGTGCACAG 0 0.2
## 7 GCTTGAGGATCCAACACGGC AGTGAAGTGTTCAGTCCGTGC 0 0.2
## 8 GCTTGAGGATCCAACACGGC GTGTTCAGTCCGTGCACAGA 0 0.2
## 9 GCTTGAGGATCCAACACGGC GTGAAGTGTTCAGTCCGTGCA 0 0.2
## 10 GCTTGAGGATCCAACACGGC GAAGTGTTCAGTCCGTGCACA 0 0.2
## 11 TCGTCTGCAACCGAGC ATGTCTTCAATGTTGCCCTAGGT 0 0.2
## 12 TCGTCTGCAACCGAGC GTTGCCTTAGGTCCATGCATACTTA 0 0.2
## 13 CAGGAAMGACTCCAACGACGC ATGTCTTCAATGTTGCCCTAGGT 0 0.2
## 14 CAGGAAMGACTCCAACGACGC GTTGCCTTAGGTCCATGCATACTTA 0 0.2
## 15 GGAAMGACTCCAACGACGC ATGTCTTCAATGTTGCCCTAGGT 0 0.2
## 16 GGAAMGACTCCAACGACGC GTTGCCTTAGGTCCATGCATACTTA 0 0.2
## 17 CCCCCCGCCAACCTACTA GTGCAGCATCCTTTGACAGGT 0 0.2
## 18 CCCCCCGCCAACCTACTA CCTTATTTTCAGCYGGTGCAGCAT 0 0.2
## 19 CCCCCCGCCAACCTACTA TTTCAGCYGGTGCAGCAT 0 0.2
## 20 CCCCCCGCCAACCTACTA GTGCAGCATCCTTTGACAGGTAA 0 0.2
## 21 CCCCCCGCCAACCTACTA CCTTATTTTCAGCYGGTGCAGCATC 0 0.2
## 22 CCCCCCGCCAACCTACTA TCCTTATTTTCAGCYGGTGCAGC 0 0.2
## 23 CCCCCCGCCAACCTACTA CCTTATTTTCAGCYGGTGCAGC 0 0.2
## 24 CCCCCCGCCAACCTACTA GTGCAGCATCCTTTGACAGGTAA 0 0.2
## 25 CCCCCCGCCAACCTACTA CCTTATTTTCAGCYGGTGCAGCA 0 0.2
## 26 CCCCCCGCCAACCTACTA TTTCAGCYGGTGCAGCA 0 0.2
## 27 CCCCCCGCCAACCTACTA GTGCAGCATCCTTTGACAGGTAA 0 0.2
## 28 TCTCCTGTACCTGGCAATATGAT TCYTCACATGTCTGCTATACTGCT 0 0.2
## 29 TCTCCTGTACCTGGCAATATGAT CCTCAACATGTCTGCTATACTGCC 0 0.2
## 30 GCATGCTGCATGCCATAATGTATA TCYATGTGTCTCCATACACAGAGT 0 0.2
## 31 TGCCGCCACGTCTAACATGTTTC GGCACAGCCCCAAATACATAACTGT 0 0.2
## 32 TGCCGCCACGTCTAACATGTTTC GGGCACAGCCCCAAATACATAACT 0 0.2
## 33 TGCCGCCACGTCTAACATGTTTC GGGCACAGCCCCAAATACATAACTG 0 0.2
## 34 TGCCGCCACGTCTAACATGTTTC CAATAGCAGGGGCACAGGCC 0 0.2
## 35 TGCCGCCACGTCTAACATGTTTC GGGGCACAGCCCCAAATACATAAC 0 0.2
## 36 TGCCGCCACGTCTAACATGTTTC GCAGGGKYACAGCCCC 0 0.2
## 37 CAACGACGCAGAGAAACACAAGTAT ATGTCTTCAATGTTGCCCTAGGT 0 0.2
## 38 GATGTGAGAACRCACCCACAATACT GCTTGTAGGGTCGCCGTGTT 0 0.2
## 39 GATGTGAGAACRCACCCACAATACT GCTTGTAGGGTCGCCGTGT 0 0.2
## 40 GATGTGAGAACRCACCCACAATACT CACAGATCAGGTAGCTGTAGGGT 0 0.2
## 41 GATGTGAGAACRCACCCACAATACT AGTTCCGTGCACAGATCAGGT 0 0.2
## 42 GATGTGAGAACRCACCCACAATACT GTGTTCAGTCCGTGCACAGAT 0 0.2
## 43 GATGTGAGAACRCACCCACAATACT CTTGTAGGGTCGCCGTGTTG 0 0.2
## 44 GATGTGAGAACRCACCCACAATACT GCTTGTAGGGTCGCCGTG 0 0.2
## 45 GATGTGAGAACRCACCCACAATACT GTAGGGTCGCCGTGTTGG 0 0.2
## 46 GATGTGAGAACRCACCCACAATACT GCACAGATCAGGTAGCTGTAGGG 0 0.2
```

## 47	GATGTGAGAACRCACCAACAATCT	CAGTCCGTGCACAGATCAGG	0	0.2
## 48	GATGTGAGAACRCACCAACAATCT	AGATCAGGTAGCTTAGGGTCG	0	0.2
## 49	GATGTGAGAACRCACCAACAATCT	GTAGCTTAGGGTCGCCG	0	0.2
## 50	GATGTGAGAACRCACCAACAATCT	GTTCCGTGCACAGATCAGGTAG	0	0.2
## 51	GATGTGAGAACRCACCAACAATCT	GTTCAGTCCGTGCACAGATCAG	0	0.2
## 52	GATGTGAGAACRCACCAACAATCT	ACAGATCAGGTAGCTTAGGGTC	0	0.2
## 53	GATGTGAGAACRCACCAACAATCT	TGTTCAGTCCGTGCACAGATC	0	0.2
## 54	GATGTGAGAACRCACCAACAATCT	TCAGGTAGCTTAGGGTCGC	0	0.2
## 55	GATGTGAGAACRCACCAACAATCT	AGGTAGCTTAGGGTCGCC	0	0.2
## 56	GATGTGAGAACRCACCAACAATCT	AGTTCCGTGCACAGATCAGGTAG	0	0.2
## 57	GATGTGAGAACRCACCAACAATCT	GTGTTCAGTCCGTGCACAGA	0	0.2
## 58	GATGTGAGAACRCACCAACAATCT	GTTCAGTCCGTGCACAGATC	0	0.2
## 59	TCTGAGGACGTTAGGGACAATGTG	GGCACAGCCAAAATACATAACTGT	0	0.2
## 60	TCTGAGGACGTTAGGGACAATGTG	GGGCACAGCCAAAATACATAACT	0	0.2
## 61	TCTGAGGACGTTAGGGACAATGTG	GGGCACAGCCAAAATACATAACTG	0	0.2
## 62	TCTGAGGACGTTAGGGACAATGTG	CAATAGCAGGGGCACAGCC	0	0.2
## 63	TCTGAGGACGTTAGGGACAATGTG	GGGGCACAGCCAAAATACATAAC	0	0.2
## 64	TCTGAGGACGTTAGGGACAATGTG	GCAGGGKYACAGCCC	0	0.2
## 65	CAACGACGCGAGAACACAAGT	ATGTCTTGAATGTTGCCCTAGGT	0	0.2
## 66	GCAGGTACTATGGGTGACACTGTG	GCACGCATACTGTGCCCTTAATAT	0	0.2
## 67	GCAGGTACTATGGGTGACACTGTG	GCACGCATACTGTGCCCTTAAT	0	0.2
## 68	GCAGGTACTATGGGTGACACTGTG	GCACGCATACTGTGCCCTTA	0	0.2
## 69	CGGCTGGTTTATGTACAGGCTA	CCATATCCGACCCTGTGTCTGT	0	0.2
## 70	CGGCTGGTTTATGTACAGGCTA	CCATATCCGACCCTGTGTCTGT	0	0.2
## 71	CGGCTGGTTTATGTACAGGCTA	ACCATATCCGACCCTGTGTCTG	0	0.2
## 72	CGGCTGGTTTATGTACAGGCTA	CGACCCCTGTGTCTGTTGCATTTC	0	0.2
## 73	ACTCTGTGTATGGAGACACATTGGA	GCACCGCAGGCACCTTATTAAT	0	0.2
## 74	ACTCTGTGTATGGAGACACATTGGA	GCACCGCAGGCACCTTATTAA	0	0.2
## 75	ACTCTGTGTATGGAGACACATTGGA	GCACCGCAGGCACCTTATTAATAAA	0	0.2
## 76	AGATGTGAGAACRCACCAAT	GCTTGTAGGGTCGCCGTGTT	0	0.2
## 77	AGATGTGAGAACRCACCAAT	GCTTGTAGGGTCGCCGTG	0	0.2
## 78	AGATGTGAGAACRCACCAAT	CACAGATCAGGTAGCTTAGGGT	0	0.2
## 79	AGATGTGAGAACRCACCAAT	AGTTCCGTGCACAGATCAGGTAG	0	0.2
## 80	AGATGTGAGAACRCACCAAT	GTGTTCAGTCCGTGCACAGAT	0	0.2
## 81	AGATGTGAGAACRCACCAAT	CTTGAGGGTCGCCGTGTT	0	0.2
## 82	AGATGTGAGAACRCACCAAT	GCTTGTAGGGTCGCCGTG	0	0.2
## 83	AGATGTGAGAACRCACCAAT	GTAGGGTCGCCGTGTTGG	0	0.2
## 84	AGATGTGAGAACRCACCAAT	GCACAGATCAGGTAGCTTAGGG	0	0.2
## 85	AGATGTGAGAACRCACCAAT	CAGTTCCGTGCACAGATCAGG	0	0.2
## 86	AGATGTGAGAACRCACCAAT	AGATCAGGTAGCTTAGGGTCG	0	0.2
## 87	AGATGTGAGAACRCACCAAT	GTAGCTTGTAGGGTCGCCG	0	0.2
## 88	AGATGTGAGAACRCACCAAT	GTTCCGTGCACAGATCAGGTAG	0	0.2
## 89	AGATGTGAGAACRCACCAAT	GTTCAGTCCGTGCACAGATC	0	0.2
## 90	AGATGTGAGAACRCACCAAT	AGTGTTCAGTCCGTGCACAG	0	0.2
## 91	AGATGTGAGAACRCACCAAT	ACAGATCAGGTAGCTTAGGGTC	0	0.2
## 92	AGATGTGAGAACRCACCAAT	TGTTCAGTCCGTGCACAGATC	0	0.2
## 93	AGATGTGAGAACRCACCAAT	AGTGAAGTGTTCAGTCCGTG	0	0.2
## 94	AGATGTGAGAACRCACCAAT	TCAGGTAGCTTAGGGTCGC	0	0.2
## 95	AGATGTGAGAACRCACCAAT	AGGTAGCTTAGGGTCGCC	0	0.2
## 96	AGATGTGAGAACRCACCAAT	TGAAGTGTTCAGTCCGTGCAC	0	0.2
## 97	AGATGTGAGAACRCACCAAT	AGTTCCGTGCACAGATCAGGTAG	0	0.2

## 98	AGATGTGAGAACRCACCAAT	GTGTTCAGTCCGTGCACAGA	0	0.2
## 99	AGATGTGAGAACRCACCAAT	GTTCAAGTCCGTGCACAGATCA	0	0.2
## 100	AGATGTGAGAACRCACCAAT	GTGAAGTGTTCAGTCCGTGCA	0	0.2
	## 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(Oral.L1.seqs)
data(Oral.L1.vars)

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

print(Oral.L1.seqs)
```

```
##   A DNAStringSet instance of length 31
##       width seq                               names
## [1] 313 GGTATACATGGTACACATTATTA...ATATAGAGTATTTAGGGTGCAG gi|944543704|gt
## [2] 312 TATACCGCATGCTGCATGCCATA...CACAAGTATAATATTAAGTATG gi|944543703|gt
## [3] 316 ATTAGAGTTAATAAACACAGTTA...TTTAGCCAGTTCAAATTATTTT gi|944543701|gt
## [4] 321 TATCACAGGGCGATTGCCCCCCT...ACAGGTATGCGTGCTTCACCTG gi|944543699|gt
## [5] 313 CGGATGAATATGTTGCACGCACA...CTTTATTAAATAAATTGGATGA gi|944543697|gt
## ...
## [27] ... ...
## [28] 437 TTGAAGTACGGAATGGGCAGGAC...GTTAATAAACTCCATTATCGAA gi|440573440|gt
## [29] 437 TTAATGTATATGAAGGTAACGAG...GTTAGTTAACAGCACTATTCAAG gi|440573438|gt
## [30] 440 ATGATGTCAGATCTAGTGTGGC...ATTAAAAATACAGTAATTGAA gi|440573436|gt
## [31] 437 TTGATGTTAGAGACACTGTGGAT...ATTAGTAAATACTGTAATTGAA gi|440573434|gt
## [31] 440 TTGAAGTGCCTAATGGTTGGGT...GTTAATAAAATACAGTAATTGAA gi|440573432|gt
```

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

```
## Adding 31 sequences to the database.
##
## 31 total sequences in table Seqs.
## Time difference of 0.05 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 Seas add column SVAR INTEGER
```

```
##  
## Expression:  
## update Seqs set SVAR = :SVAR where row_names = :row_names  
  
## Warning: Factors converted to character  
  
## 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  
  
## Warning: Factors converted to character  
  
## Expression:  
## update Seqs set identifier = :identifier where row_names = :row_names  
  
## Warning: Factors converted to character  
  
## Added to table Seqs: "GI" and "SVAR" and "ISO" and "GENE" and "identifier"  
##  
## Time difference of 0.04 secs
```

```
dbGetQuery(dbConn, "select * from Seqs") %>% head(4)
```

```
##   row_names identifier  
## 1      1      HPV18  
## 2      2      HPV18  
## 3      3      HPV16  
## 4      4      HPV18  
##  
## 1 gi|944543704|gb|KT365847.1| Human papillomavirus isolate HPV18-14 L1 prot  
## 2 gi|944543703|gb|KT365846.1| Human papillomavirus isolate HPV18-13 L1 prot  
## 3 gi|944543701|gb|KT365845.1| Human papillomavirus isolate HPV16-5 L1 prot  
## 4 gi|944543699|gb|KT365844.1| Human papillomavirus isolate HPV18-12 L1 prot  
##       GI  SVAR ISO  GENE  
## 1 944543704 HPV18  14    L1  
## 2 944543703 HPV18  13    L1  
## 3 944543701 HPV16  5     L1  
## 4 944543699 HPV18  12    L1
```

```
data(RESTRICTION_ENZYMES)

FOCUS_ID <- 'HPV11'

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,
      identifier = '',
      focusID = FOCUS_ID,
      enzymes = RESTRICTION_ENZYMES[i],
      minProductSize = MIN_SIZE,
      maxProductSize = MAX_SIZE,
      resolution = RESOLUTION,
      levels = LEVELS
    )
  ) %>% print
```

```
## Tallying 8-mers for 5 groups:
## =====
##
## Time difference of 0.37 secs
##
## Designing primer sequences based on the group 'HPV11':
## =====
##
## Time difference of 17.67 secs
##
## Selecting the most common primer sequences:
## =====
##
## Time difference of 3.75 secs
##
## Determining PCR products from each group:
## =====
##
## Time difference of 2.58 secs
##
```

```
## Scoring primer pair combinations:  
## =====  
##  
## Time difference of 0.01 secs  
##  
## Choosing optimal forward and reverse pairs:  
## =====  
##  
## Time difference of 1.61 secs  
##  
## Finding the best restriction enzyme:  
## =====  
##  
## Time difference of 3.52 secs  
## Tallying 8-mers for 5 groups:  
## =====  
##  
## Time difference of 0.32 secs  
##  
## Designing primer sequences based on the group 'HPV11':  
## =====  
##  
## Time difference of 17.39 secs  
##  
## Selecting the most common primer sequences:  
## =====  
##  
## Time difference of 3.61 secs  
##  
## Determining PCR products from each group:  
## =====  
##  
## Time difference of 2.33 secs  
##  
## Scoring primer pair combinations:  
## =====  
##  
## Time difference of 0.01 secs  
##  
## Choosing optimal forward and reverse pairs:  
## =====  
##  
## Time difference of 1.92 secs  
##  
## Finding the best restriction enzyme:  
## =====  
##  
## Time difference of 1.89 secs  
## Tallying 8-mers for 5 groups:  
## =====  
##  
## Time difference of 0.34 secs
```

```
##  
## Designing primer sequences based on the group 'HPV11':  
## =====  
##  
## Time difference of 25.14 secs  
##  
## Selecting the most common primer sequences:  
## =====  
##  
## Time difference of 4.29 secs  
##  
## Determining PCR products from each group:  
## =====  
##  
## Time difference of 2.87 secs  
##  
## Scoring primer pair combinations:  
## =====  
##  
## Time difference of 0.01 secs  
##  
## Choosing optimal forward and reverse pairs:  
## =====  
##  
## Time difference of 1.77 secs  
##  
## Finding the best restriction enzyme:  
## =====  
##  
## Time difference of 2.37 secs  
## Tallying 8-mers for 5 groups:  
## =====  
##  
## Time difference of 0.35 secs  
##  
## Designing primer sequences based on the group 'HPV11':  
## =====  
##  
## Time difference of 18.83 secs  
##  
## Selecting the most common primer sequences:  
## =====  
##  
## Time difference of 4 secs  
##  
## Determining PCR products from each group:  
## =====  
##  
## Time difference of 2.26 secs  
##  
## Scoring primer pair combinations:
```

```
## =====
## 
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
## =====
##
## Time difference of 1.45 secs
##
## Finding the best restriction enzyme:
## =====
##
## Time difference of 1.86 secs
## Tallying 8-mers for 5 groups:
## =====
##
## Time difference of 0.35 secs
##
## Designing primer sequences based on the group 'HPV11':
## =====
##
## Time difference of 16.88 secs

##
## Selecting the most common primer sequences:
## =====
##
## Time difference of 3.92 secs
##
## Determining PCR products from each group:
## =====
##
## Time difference of 2.15 secs
##
## Scoring primer pair combinations:
## =====
##
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
## =====
##
## Time difference of 1.4 secs
##
## Finding the best restriction enzyme:
## =====
##
## Time difference of 1.38 secs
## Tallying 8-mers for 5 groups:
## =====
##
## Time difference of 0.3 secs
```

```
##  
## Designing primer sequences based on the group 'HPV11':  
## =====  
##  
## Time difference of 14.48 secs  
##  
## Selecting the most common primer sequences:  
## =====  
##  
## Time difference of 3.01 secs  
##  
## Determining PCR products from each group:  
## =====  
##  
## Time difference of 2.04 secs  
##  
## Scoring primer pair combinations:  
## =====  
##  
## Time difference of 0.01 secs  
##  
## Choosing optimal forward and reverse pairs:  
## =====  
##  
## Time difference of 1.39 secs  
##  
## Finding the best restriction enzyme:  
## =====  
##  
## Time difference of 1.71 secs  
## Tallying 8-mers for 5 groups:  
## =====  
##  
## Time difference of 0.31 secs  
##  
## Designing primer sequences based on the group 'HPV11':  
## =====  
##  
## Time difference of 14.82 secs  
##  
## Selecting the most common primer sequences:  
## =====  
##  
## Time difference of 3.09 secs  
##  
## Determining PCR products from each group:  
## =====  
##  
## Time difference of 2.44 secs  
##  
## Scoring primer pair combinations:
```

```
## =====
## 
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
## =====
##
## Time difference of 1.44 secs
##
## Finding the best restriction enzyme:
## =====
##
## Time difference of 1.64 secs
## Tallying 8-mers for 5 groups:
## =====
##
## Time difference of 0.32 secs
##
## Designing primer sequences based on the group 'HPV11':
## =====
##
## Time difference of 14.62 secs

##
## Selecting the most common primer sequences:
## =====
##
## Time difference of 3.23 secs
##
## Determining PCR products from each group:
## =====
##
## Time difference of 2.15 secs
##
## Scoring primer pair combinations:
## =====
##
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
## =====
##
## Time difference of 1.36 secs
##
## Finding the best restriction enzyme:
## =====
##
## Time difference of 1.65 secs
## Tallying 8-mers for 5 groups:
## =====
##
## Time difference of 0.32 secs
```

```
##
## Designing primer sequences based on the group 'HPV11':
## =====
##
## Time difference of 14.51 secs
##
## Selecting the most common primer sequences:
## =====
##
## Time difference of 3.29 secs
##
## Determining PCR products from each group:
## =====
##
## Time difference of 1.9 secs
##
## Scoring primer pair combinations:
## =====
##
## Time difference of 0.01 secs
##
## Choosing optimal forward and reverse pairs:
## =====
##
## Time difference of 1.36 secs
##
## Finding the best restriction enzyme:
## =====
##
## Time difference of 1.63 secs
## [[1]]
#>      forward_primer      reverse_primer score coverage product
#> 1  GTTTGACCCCCTACACAGCG  CCTAAAGGGTTGACCCCTGCC 0 0.2
#> 2  TGACCCCCTACACAGCGTT  CCTAAAGGGTTGACCCCTGCC 0 0.2
#> 3  GTTTGACCCCCTACACAGCG CACTAACACCAACGCCTAAAGGTT 0 0.2
#> 4  GTTTGACCCCCTACACAGCG CACTAACACCAACGCCTAAAGGT 0 0.2
#> 5  GTTTGACCCCCTACACAGCG CCTAAAGGGTTGACCCCTGCCT 0 0.2
#> 6  GTTTGACCCCCTACACAGCG ACGCCTAACAGGTTGACCCCT 0 0.2
#> 7  GTTTGACCCCCTACACAGCG GGCTGACCMCKGCCTACCT 0 0.2
#> 8  GTTTGACCCCCTACACAGCG TTGTTTAGCAATGGATGCCACT 0 0.2
#> 9  GTTTGACCCCCTACACAGCG ACTAACACCAACGCCTAAAGGTTG 0 0.2
#> 10 GTTTGACCCCCTACACAGCG CGCCTAACAGGTTGACCCCTG 0 0.2
#> 11 GTTTGACCCCCTACACAGCG CCACTAACRCCAACRCCTAAAGG 0 0.2
#> 12 GTTTGACCCCCTACACAGCG GGATGCCACTAACACCAACG 0 0.2
#> 13 GTTTGACCCCCTACACAGCG CCCACTAACACCAACGCCTAAAG 0 0.2
#> 14 GTTTGACCCCCTACACAGCG GGCTGACCMCKGCCTACCTC 0 0.2
#> 15 GTTTGACCCCCTACACAGCG GCCTAACAGGTTGACCCCTGC 0 0.2
#> 16 GTTTGACCCCCTACACAGCG TGCCCCTAACACCAACGC 0 0.2
#> 17 GTTTGACCCCCTACACAGCG TGACCCCTGCCTACCTCC 0 0.2
#> 18 GTTTGACCCCCTACACAGCG CAACGCCTAACAGGTTGACCCC 0 0.2
#> 19 GTTTGACCCCCTACACAGCG CCAACGCCTAACAGGTTGACCC 0 0.2
```

## 20	GTTTGACCCC ACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC CACTAACACC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC CACTAACAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	ATGGATGCC CACTAACACCAAC	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 40	GTTTGACCCC ACTACACAGCG	CCCACTAACACCAACGCC AAA	0	0.2
## 41	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACT	0	0.2
## 45	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC CACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC CACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC CACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCC TACCTCCAACCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCC CATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2			
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2			
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2			
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2			
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2			
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2			
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2			
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2			
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCCATACTAACGCTGTGTAG	0	0.2			
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2			
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2			
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2			
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2			
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2			
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2			
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2			
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2			
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2			
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2			
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2			
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2			
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2			
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2			
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCCATACTAACGCTGTGA	0	0.2			
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGA	0	0.2			
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2			
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATATA	0	0.2			
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2			
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2			
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2			
## similar_signatures		missing_signatures	enzyme	digest_score	fragme		
## 1		HPV18, HPV16, HPV4, HPV17	Acc65I		0		
## 2		HPV18, HPV16, HPV4, HPV17	Acc65I		0		
## 3		HPV18, HPV16, HPV4, HPV17			0		
## 4		HPV18, HPV16, HPV4, HPV17			0		
## 5		HPV18, HPV16, HPV4, HPV17			0		
## 6		HPV18, HPV16, HPV4, HPV17			0		
## 7		HPV18, HPV16, HPV4, HPV17			0		
## 8		HPV18, HPV16, HPV4, HPV17			0		
## 9		HPV18, HPV16, HPV4, HPV17			0		
## 10		HPV18, HPV16, HPV4, HPV17			0		
## 11		HPV18, HPV16, HPV4, HPV17			0		
## 12		HPV18, HPV16, HPV4, HPV17			0		
## 13		HPV18, HPV16, HPV4, HPV17			0		
## 14		HPV18, HPV16, HPV4, HPV17			0		
## 15		HPV18, HPV16, HPV4, HPV17			0		
## 16		HPV18, HPV16, HPV4, HPV17			0		
## 17		HPV18, HPV16, HPV4, HPV17			0		
## 18		HPV18, HPV16, HPV4, HPV17			0		
## 19		HPV18, HPV16, HPV4, HPV17			0		
## 20		HPV18, HPV16, HPV4, HPV17			0		

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72		HPV18, HPV16, HPV4, HPV17			0
## 73		HPV18, HPV16, HPV4, HPV17			0
## 74		HPV18, HPV16, HPV4, HPV17			0
## 75		HPV18, HPV16, HPV4, HPV17			0
## 76		HPV18, HPV16, HPV4, HPV17			0
## 77		HPV18, HPV16, HPV4, HPV17			0
## 78		HPV18, HPV16, HPV4, HPV17			0
## 79		HPV18, HPV16, HPV4, HPV17			0
## 80		HPV18, HPV16, HPV4, HPV17			0
## 81		HPV18, HPV16, HPV4, HPV17			0
## 82		HPV18, HPV16, HPV4, HPV17			0
## 83		HPV18, HPV16, HPV4, HPV17			0
## 84		HPV18, HPV16, HPV4, HPV17			0
## 85		HPV18, HPV16, HPV4, HPV17			0
## 86		HPV18, HPV16, HPV4, HPV17			0
## 87		HPV18, HPV16, HPV4, HPV17			0
## 88		HPV18, HPV16, HPV4, HPV17			0
## 89		HPV18, HPV16, HPV4, HPV17			0
## 90		HPV18, HPV16, HPV4, HPV17			0
## 91		HPV18, HPV16, HPV4, HPV17			0
## 92		HPV18, HPV16, HPV4, HPV17			0
## 93		HPV18, HPV16, HPV4, HPV17			0
## 94		HPV18, HPV16, HPV4, HPV17			0
## 95		HPV18, HPV16, HPV4, HPV17			0
## 96		HPV18, HPV16, HPV4, HPV17			0
## 97		HPV18, HPV16, HPV4, HPV17			0
## 98		HPV18, HPV16, HPV4, HPV17			0
## 99		HPV18, HPV16, HPV4, HPV17			0
## 100		HPV18, HPV16, HPV4, HPV17			0
##					
## [[2]]					
##	forward_primer		reverse_primer	score	coverage product
## 1	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGTT	0	0.2	
## 2	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGT	0	0.2	
## 3	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCCT	0	0.2	
## 4	GTTTGACCCCCTACTACACAGCG	ACGCCCTAAAGGTTGACCCCT	0	0.2	
## 5	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCT	0	0.2	
## 6	GTTTGACCCCCTACTACACAGCG	TTGTTTAGCAATGGATGCCACT	0	0.2	
## 7	GTTTGACCCCCTACTACACAGCG	ACTAACACCAACGCCCTAAAGGTTG	0	0.2	
## 8	GTTTGACCCCCTACTACACAGCG	CGCCTAAAGGTTGACCCCTG	0	0.2	
## 9	GTTTGACCCCCTACTACACAGCG	CCACTAACRCCAACRCCTAAAGG	0	0.2	
## 10	GTTTGACCCCCTACTACACAGCG	GGATGCCACTAACACCAACG	0	0.2	
## 11	GTTTGACCCCCTACTACACAGCG	CCCACTAACACCAACGCCCTAAAG	0	0.2	
## 12	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCTC	0	0.2	
## 13	GTTTGACCCCCTACTACACAGCG	GCCTAAAGGTTGACCCCTGC	0	0.2	
## 14	GTTTGACCCCCTACTACACAGCG	TGCCCACTAACACCAACGC	0	0.2	
## 15	GTTTGACCCCCTACTACACAGCG	TGACCCCTGCCTACCTCC	0	0.2	
## 16	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCC	0	0.2	
## 17	GTTTGACCCCCTACTACACAGCG	CAACGCCCTAAAGGTTGACCC	0	0.2	
## 18	GTTTGACCCCCTACTACACAGCG	CCAACGCCCTAAAGGTTGACCC	0	0.2	
## 19	GTTTGACCCCCTACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2	

## 20	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC ACTAACACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC ACTAACAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC ACTAAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ATGGATGCC ACTAACACCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC ACTA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CAATGGATGCC ACTAACACCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC ACTAACAA	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC ACTAA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCAAC	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	CAATGGATGCC ACTAACACCAA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CCC ACTAACACCAACGCC TAAA	0	0.2
## 40	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 41	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 45	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC ACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC ACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC ACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC ACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC ACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC ACTAACAA	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC ACTAACACCAA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCC TACCTCCAACCCCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCCCATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2			
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2			
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2			
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2			
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2			
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2			
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2			
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2			
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGTAG	0	0.2			
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2			
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2			
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2			
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2			
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2			
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2			
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2			
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2			
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2			
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2			
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2			
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2			
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2			
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2			
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGA	0	0.2			
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGTA	0	0.2			
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2			
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCATA	0	0.2			
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2			
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2			
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2			
## similar_signatures		missing_signatures	enzyme	digest_score	fragme		
## 1		HPV18, HPV16, HPV4, HPV17			0		
## 2		HPV18, HPV16, HPV4, HPV17			0		
## 3		HPV18, HPV16, HPV4, HPV17			0		
## 4		HPV18, HPV16, HPV4, HPV17			0		
## 5		HPV18, HPV16, HPV4, HPV17			0		
## 6		HPV18, HPV16, HPV4, HPV17			0		
## 7		HPV18, HPV16, HPV4, HPV17			0		
## 8		HPV18, HPV16, HPV4, HPV17			0		
## 9		HPV18, HPV16, HPV4, HPV17			0		
## 10		HPV18, HPV16, HPV4, HPV17			0		
## 11		HPV18, HPV16, HPV4, HPV17			0		
## 12		HPV18, HPV16, HPV4, HPV17			0		
## 13		HPV18, HPV16, HPV4, HPV17			0		
## 14		HPV18, HPV16, HPV4, HPV17			0		
## 15		HPV18, HPV16, HPV4, HPV17			0		
## 16		HPV18, HPV16, HPV4, HPV17			0		
## 17		HPV18, HPV16, HPV4, HPV17			0		
## 18		HPV18, HPV16, HPV4, HPV17			0		
## 19		HPV18, HPV16, HPV4, HPV17			0		
## 20		HPV18, HPV16, HPV4, HPV17			0		

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72		HPV18, HPV16, HPV4, HPV17			0
## 73		HPV18, HPV16, HPV4, HPV17			0
## 74		HPV18, HPV16, HPV4, HPV17			0
## 75		HPV18, HPV16, HPV4, HPV17			0
## 76		HPV18, HPV16, HPV4, HPV17			0
## 77		HPV18, HPV16, HPV4, HPV17			0
## 78		HPV18, HPV16, HPV4, HPV17			0
## 79		HPV18, HPV16, HPV4, HPV17			0
## 80		HPV18, HPV16, HPV4, HPV17			0
## 81		HPV18, HPV16, HPV4, HPV17			0
## 82		HPV18, HPV16, HPV4, HPV17			0
## 83		HPV18, HPV16, HPV4, HPV17			0
## 84		HPV18, HPV16, HPV4, HPV17			0
## 85		HPV18, HPV16, HPV4, HPV17			0
## 86		HPV18, HPV16, HPV4, HPV17			0
## 87		HPV18, HPV16, HPV4, HPV17			0
## 88		HPV18, HPV16, HPV4, HPV17			0
## 89		HPV18, HPV16, HPV4, HPV17			0
## 90		HPV18, HPV16, HPV4, HPV17			0
## 91		HPV18, HPV16, HPV4, HPV17			0
## 92		HPV18, HPV16, HPV4, HPV17			0
## 93		HPV18, HPV16, HPV4, HPV17			0
## 94		HPV18, HPV16, HPV4, HPV17			0
## 95		HPV18, HPV16, HPV4, HPV17			0
## 96		HPV18, HPV16, HPV4, HPV17			0
## 97		HPV18, HPV16, HPV4, HPV17			0
## 98		HPV18, HPV16, HPV4, HPV17			0
## 99		HPV18, HPV16, HPV4, HPV17			0
## 100		HPV18, HPV16, HPV4, HPV17			0
##					
## [[3]]					
##	forward_primer		reverse_primer	score	coverage product
## 1	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGTT	0	0.2	
## 2	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGT	0	0.2	
## 3	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCCT	0	0.2	
## 4	GTTTGACCCCCTACTACACAGCG	ACGCCCTAAAGGTTGACCCCT	0	0.2	
## 5	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCT	0	0.2	
## 6	GTTTGACCCCCTACTACACAGCG	TTGTTTAGCAATGGATGCCACT	0	0.2	
## 7	GTTTGACCCCCTACTACACAGCG	ACTAACACCAACGCCCTAAAGGTTG	0	0.2	
## 8	GTTTGACCCCCTACTACACAGCG	CGCCTAAAGGTTGACCCCTG	0	0.2	
## 9	GTTTGACCCCCTACTACACAGCG	CCACTAACRCCAACRCCTAAAGG	0	0.2	
## 10	GTTTGACCCCCTACTACACAGCG	GGATGCCACTAACACCAACG	0	0.2	
## 11	GTTTGACCCCCTACTACACAGCG	CCCACTAACACCAACGCCCTAAAG	0	0.2	
## 12	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCTC	0	0.2	
## 13	GTTTGACCCCCTACTACACAGCG	GCCTAAAGGTTGACCCCTGC	0	0.2	
## 14	GTTTGACCCCCTACTACACAGCG	TGCCCACTAACACCAACGC	0	0.2	
## 15	GTTTGACCCCCTACTACACAGCG	TGACCCCTGCCTACCTCC	0	0.2	
## 16	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCC	0	0.2	
## 17	GTTTGACCCCCTACTACACAGCG	CAACGCCCTAAAGGTTGACCC	0	0.2	
## 18	GTTTGACCCCCTACTACACAGCG	CCAACGCCCTAAAGGTTGACCC	0	0.2	
## 19	GTTTGACCCCCTACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2	

## 20	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC CACTAACACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC CACTAACAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ATGGATGCC CACTAACACCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCAAC	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCAA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CCC ACTAACACCAACGCC TAAA	0	0.2
## 40	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 41	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 45	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC CACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC CACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC CACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCAA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCCCATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2			
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2			
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2			
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2			
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2			
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2			
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2			
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2			
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGTAG	0	0.2			
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2			
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2			
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2			
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2			
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2			
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2			
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2			
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2			
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2			
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2			
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2			
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2			
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2			
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2			
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGA	0	0.2			
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGTA	0	0.2			
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2			
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATATA	0	0.2			
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2			
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2			
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2			
## similar_signatures		missing_signatures	enzyme	digest_score	fragme		
## 1		HPV18, HPV16, HPV4, HPV17			0		
## 2		HPV18, HPV16, HPV4, HPV17			0		
## 3		HPV18, HPV16, HPV4, HPV17			0		
## 4		HPV18, HPV16, HPV4, HPV17			0		
## 5		HPV18, HPV16, HPV4, HPV17			0		
## 6		HPV18, HPV16, HPV4, HPV17			0		
## 7		HPV18, HPV16, HPV4, HPV17			0		
## 8		HPV18, HPV16, HPV4, HPV17			0		
## 9		HPV18, HPV16, HPV4, HPV17			0		
## 10		HPV18, HPV16, HPV4, HPV17			0		
## 11		HPV18, HPV16, HPV4, HPV17			0		
## 12		HPV18, HPV16, HPV4, HPV17			0		
## 13		HPV18, HPV16, HPV4, HPV17			0		
## 14		HPV18, HPV16, HPV4, HPV17			0		
## 15		HPV18, HPV16, HPV4, HPV17			0		
## 16		HPV18, HPV16, HPV4, HPV17			0		
## 17		HPV18, HPV16, HPV4, HPV17			0		
## 18		HPV18, HPV16, HPV4, HPV17			0		
## 19		HPV18, HPV16, HPV4, HPV17			0		
## 20		HPV18, HPV16, HPV4, HPV17			0		

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72		HPV18, HPV16, HPV4, HPV17			0
## 73		HPV18, HPV16, HPV4, HPV17			0
## 74		HPV18, HPV16, HPV4, HPV17			0
## 75		HPV18, HPV16, HPV4, HPV17			0
## 76		HPV18, HPV16, HPV4, HPV17			0
## 77		HPV18, HPV16, HPV4, HPV17			0
## 78		HPV18, HPV16, HPV4, HPV17			0
## 79		HPV18, HPV16, HPV4, HPV17			0
## 80		HPV18, HPV16, HPV4, HPV17			0
## 81		HPV18, HPV16, HPV4, HPV17			0
## 82		HPV18, HPV16, HPV4, HPV17			0
## 83		HPV18, HPV16, HPV4, HPV17			0
## 84		HPV18, HPV16, HPV4, HPV17			0
## 85		HPV18, HPV16, HPV4, HPV17			0
## 86		HPV18, HPV16, HPV4, HPV17			0
## 87		HPV18, HPV16, HPV4, HPV17			0
## 88		HPV18, HPV16, HPV4, HPV17			0
## 89		HPV18, HPV16, HPV4, HPV17			0
## 90		HPV18, HPV16, HPV4, HPV17			0
## 91		HPV18, HPV16, HPV4, HPV17			0
## 92		HPV18, HPV16, HPV4, HPV17			0
## 93		HPV18, HPV16, HPV4, HPV17			0
## 94		HPV18, HPV16, HPV4, HPV17			0
## 95		HPV18, HPV16, HPV4, HPV17			0
## 96		HPV18, HPV16, HPV4, HPV17			0
## 97		HPV18, HPV16, HPV4, HPV17			0
## 98		HPV18, HPV16, HPV4, HPV17			0
## 99		HPV18, HPV16, HPV4, HPV17			0
## 100		HPV18, HPV16, HPV4, HPV17			0
##					
## [[4]]					
##	forward_primer		reverse_primer	score	coverage product
## 1	GTTTGACCCCCTACTACACAGCG		CCTAAAGGTTGACCCCTGCC	0	0.2
## 2	TGACCCCCTACTACACAGCGTT		CCTAAAGGTTGACCCCTGCC	0	0.2
## 3	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCTAAAGGTT		0	0.2
## 4	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCTAAAGGT		0	0.2
## 5	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCCT		0	0.2
## 6	GTTTGACCCCCTACTACACAGCG	ACGCCTAAAGGTTGACCCCT		0	0.2
## 7	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCT		0	0.2
## 8	GTTTGACCCCCTACTACACAGCG	TTGTTTAGCAATGGATGCCACT		0	0.2
## 9	GTTTGACCCCCTACTACACAGCG	ACTAACACCAACGCCTAAAGGTTG		0	0.2
## 10	GTTTGACCCCCTACTACACAGCG	CGCCTAAAGGTTGACCCCTG		0	0.2
## 11	GTTTGACCCCCTACTACACAGCG	CCACTAACRCCAACRCCTAAAGG		0	0.2
## 12	GTTTGACCCCCTACTACACAGCG	GGATGCCACTAACACCAACG		0	0.2
## 13	GTTTGACCCCCTACTACACAGCG	CCCACTAACACCAACGCCTAAAG		0	0.2
## 14	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCTC		0	0.2
## 15	GTTTGACCCCCTACTACACAGCG	GCCTAAAGGTTGACCCCTGC		0	0.2
## 16	GTTTGACCCCCTACTACACAGCG	TGCCCACTAACACCAACGC		0	0.2
## 17	GTTTGACCCCCTACTACACAGCG	TGACCCCTGCCTACCTCC		0	0.2
## 18	GTTTGACCCCCTACTACACAGCG	CAACGCCTAAAGGTTGACCCC		0	0.2
## 19	GTTTGACCCCCTACTACACAGCG	CCAAAGCCTAAAGGTTGACCC		0	0.2

## 20	GTTTGACCCC ACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC CACTAACACC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC CACTAACAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	ATGGATGCC CACTAACACCAAC	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 40	GTTTGACCCC ACTACACAGCG	CCC ACTAACACCAACGCC AAA	0	0.2
## 41	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACT	0	0.2
## 45	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC CACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC CACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC CACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCC TACCTCCAACCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCC CATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2			
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2			
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2			
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2			
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2			
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2			
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2			
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2			
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGTAG	0	0.2			
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2			
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2			
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2			
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2			
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2			
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2			
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2			
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2			
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2			
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2			
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2			
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2			
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2			
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2			
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGA	0	0.2			
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGA	0	0.2			
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2			
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATATA	0	0.2			
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2			
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2			
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2			
## similar_signatures		missing_signatures	enzyme	digest_score	fragme		
## 1		HPV18, HPV16, HPV4, HPV17	Acc65I		0		
## 2		HPV18, HPV16, HPV4, HPV17	Acc65I		0		
## 3		HPV18, HPV16, HPV4, HPV17			0		
## 4		HPV18, HPV16, HPV4, HPV17			0		
## 5		HPV18, HPV16, HPV4, HPV17			0		
## 6		HPV18, HPV16, HPV4, HPV17			0		
## 7		HPV18, HPV16, HPV4, HPV17			0		
## 8		HPV18, HPV16, HPV4, HPV17			0		
## 9		HPV18, HPV16, HPV4, HPV17			0		
## 10		HPV18, HPV16, HPV4, HPV17			0		
## 11		HPV18, HPV16, HPV4, HPV17			0		
## 12		HPV18, HPV16, HPV4, HPV17			0		
## 13		HPV18, HPV16, HPV4, HPV17			0		
## 14		HPV18, HPV16, HPV4, HPV17			0		
## 15		HPV18, HPV16, HPV4, HPV17			0		
## 16		HPV18, HPV16, HPV4, HPV17			0		
## 17		HPV18, HPV16, HPV4, HPV17			0		
## 18		HPV18, HPV16, HPV4, HPV17			0		
## 19		HPV18, HPV16, HPV4, HPV17			0		
## 20		HPV18, HPV16, HPV4, HPV17			0		

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72		HPV18, HPV16, HPV4, HPV17			0
## 73		HPV18, HPV16, HPV4, HPV17			0
## 74		HPV18, HPV16, HPV4, HPV17			0
## 75		HPV18, HPV16, HPV4, HPV17			0
## 76		HPV18, HPV16, HPV4, HPV17			0
## 77		HPV18, HPV16, HPV4, HPV17			0
## 78		HPV18, HPV16, HPV4, HPV17			0
## 79		HPV18, HPV16, HPV4, HPV17			0
## 80		HPV18, HPV16, HPV4, HPV17			0
## 81		HPV18, HPV16, HPV4, HPV17			0
## 82		HPV18, HPV16, HPV4, HPV17			0
## 83		HPV18, HPV16, HPV4, HPV17			0
## 84		HPV18, HPV16, HPV4, HPV17			0
## 85		HPV18, HPV16, HPV4, HPV17			0
## 86		HPV18, HPV16, HPV4, HPV17			0
## 87		HPV18, HPV16, HPV4, HPV17			0
## 88		HPV18, HPV16, HPV4, HPV17			0
## 89		HPV18, HPV16, HPV4, HPV17			0
## 90		HPV18, HPV16, HPV4, HPV17			0
## 91		HPV18, HPV16, HPV4, HPV17			0
## 92		HPV18, HPV16, HPV4, HPV17			0
## 93		HPV18, HPV16, HPV4, HPV17			0
## 94		HPV18, HPV16, HPV4, HPV17			0
## 95		HPV18, HPV16, HPV4, HPV17			0
## 96		HPV18, HPV16, HPV4, HPV17			0
## 97		HPV18, HPV16, HPV4, HPV17			0
## 98		HPV18, HPV16, HPV4, HPV17			0
## 99		HPV18, HPV16, HPV4, HPV17			0
## 100		HPV18, HPV16, HPV4, HPV17			0
##					
## [[5]]					
##	forward_primer		reverse_primer	score	coverage product
## 1	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGTT	0	0.2	
## 2	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGT	0	0.2	
## 3	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCCT	0	0.2	
## 4	GTTTGACCCCCTACTACACAGCG	ACGCCCTAAAGGTTGACCCCT	0	0.2	
## 5	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCT	0	0.2	
## 6	GTTTGACCCCCTACTACACAGCG	TTGTTTAGCAATGGATGCCACT	0	0.2	
## 7	GTTTGACCCCCTACTACACAGCG	ACTAACACCAACGCCCTAAAGGTTG	0	0.2	
## 8	GTTTGACCCCCTACTACACAGCG	CGCCTAAAGGTTGACCCCTG	0	0.2	
## 9	GTTTGACCCCCTACTACACAGCG	CCACTAACRCCAACRCCTAAAGG	0	0.2	
## 10	GTTTGACCCCCTACTACACAGCG	GGATGCCACTAACACCAACG	0	0.2	
## 11	GTTTGACCCCCTACTACACAGCG	CCCACTAACACCAACGCCCTAAAG	0	0.2	
## 12	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCTC	0	0.2	
## 13	GTTTGACCCCCTACTACACAGCG	GCCTAAAGGTTGACCCCTGC	0	0.2	
## 14	GTTTGACCCCCTACTACACAGCG	TGCCCACTAACACCAACGC	0	0.2	
## 15	GTTTGACCCCCTACTACACAGCG	TGACCCCTGCCTACCTCC	0	0.2	
## 16	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCC	0	0.2	
## 17	GTTTGACCCCCTACTACACAGCG	CAACGCCCTAAAGGTTGACCC	0	0.2	
## 18	GTTTGACCCCCTACTACACAGCG	CCAACGCCCTAAAGGTTGACCC	0	0.2	
## 19	GTTTGACCCCCTACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2	

## 20	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC CACTAACACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC CACTAACAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ATGGATGCC CACTAACACCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCAAC	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCAA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CCC ACTAACACCAACGCC TAAA	0	0.2
## 40	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 41	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 45	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC CACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC CACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC CACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCAA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCC TACCTCCAACCCCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCCCATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2		
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2		
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2		
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2		
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2		
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2		
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2		
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2		
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCCATACTAACGCTGTGTAG	0	0.2		
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2		
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2		
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2		
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2		
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2		
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2		
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2		
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2		
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2		
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2		
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2		
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2		
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2		
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2		
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCCATACTAACGCTGTGA	0	0.2		
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2		
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2		
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCATA	0	0.2		
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2		
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2		
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2		
## similar_signatures		missing_signatures	enzyme	digest_score	fragme	
## 1		HPV18, HPV16, HPV4, HPV17			0	
## 2		HPV18, HPV16, HPV4, HPV17			0	
## 3		HPV18, HPV16, HPV4, HPV17			0	
## 4		HPV18, HPV16, HPV4, HPV17			0	
## 5		HPV18, HPV16, HPV4, HPV17			0	
## 6		HPV18, HPV16, HPV4, HPV17			0	
## 7		HPV18, HPV16, HPV4, HPV17			0	
## 8		HPV18, HPV16, HPV4, HPV17			0	
## 9		HPV18, HPV16, HPV4, HPV17			0	
## 10		HPV18, HPV16, HPV4, HPV17			0	
## 11		HPV18, HPV16, HPV4, HPV17			0	
## 12		HPV18, HPV16, HPV4, HPV17			0	
## 13		HPV18, HPV16, HPV4, HPV17			0	
## 14		HPV18, HPV16, HPV4, HPV17			0	
## 15		HPV18, HPV16, HPV4, HPV17			0	
## 16		HPV18, HPV16, HPV4, HPV17			0	
## 17		HPV18, HPV16, HPV4, HPV17			0	
## 18		HPV18, HPV16, HPV4, HPV17			0	
## 19		HPV18, HPV16, HPV4, HPV17			0	
## 20		HPV18, HPV16, HPV4, HPV17			0	

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72		HPV18, HPV16, HPV4, HPV17			0
## 73		HPV18, HPV16, HPV4, HPV17			0
## 74		HPV18, HPV16, HPV4, HPV17			0
## 75		HPV18, HPV16, HPV4, HPV17			0
## 76		HPV18, HPV16, HPV4, HPV17			0
## 77		HPV18, HPV16, HPV4, HPV17			0
## 78		HPV18, HPV16, HPV4, HPV17			0
## 79		HPV18, HPV16, HPV4, HPV17			0
## 80		HPV18, HPV16, HPV4, HPV17			0
## 81		HPV18, HPV16, HPV4, HPV17			0
## 82		HPV18, HPV16, HPV4, HPV17			0
## 83		HPV18, HPV16, HPV4, HPV17			0
## 84		HPV18, HPV16, HPV4, HPV17			0
## 85		HPV18, HPV16, HPV4, HPV17			0
## 86		HPV18, HPV16, HPV4, HPV17			0
## 87		HPV18, HPV16, HPV4, HPV17			0
## 88		HPV18, HPV16, HPV4, HPV17			0
## 89		HPV18, HPV16, HPV4, HPV17			0
## 90		HPV18, HPV16, HPV4, HPV17			0
## 91		HPV18, HPV16, HPV4, HPV17			0
## 92		HPV18, HPV16, HPV4, HPV17			0
## 93		HPV18, HPV16, HPV4, HPV17			0
## 94		HPV18, HPV16, HPV4, HPV17			0
## 95		HPV18, HPV16, HPV4, HPV17			0
## 96		HPV18, HPV16, HPV4, HPV17			0
## 97		HPV18, HPV16, HPV4, HPV17			0
## 98		HPV18, HPV16, HPV4, HPV17			0
## 99		HPV18, HPV16, HPV4, HPV17			0
## 100		HPV18, HPV16, HPV4, HPV17			0
##					
## [[6]]					
##	forward_primer		reverse_primer	score	coverage product
## 1	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGTT	0	0.2	
## 2	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGT	0	0.2	
## 3	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCCT	0	0.2	
## 4	GTTTGACCCCCTACTACACAGCG	ACGCCCTAAAGGTTGACCCCT	0	0.2	
## 5	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCT	0	0.2	
## 6	GTTTGACCCCCTACTACACAGCG	TTGTTTAGCAATGGATGCCACT	0	0.2	
## 7	GTTTGACCCCCTACTACACAGCG	ACTAACACCAACGCCCTAAAGGTTG	0	0.2	
## 8	GTTTGACCCCCTACTACACAGCG	CGCCTAAAGGTTGACCCCTG	0	0.2	
## 9	GTTTGACCCCCTACTACACAGCG	CCACTAACRCCAACRCCTAAAGG	0	0.2	
## 10	GTTTGACCCCCTACTACACAGCG	GGATGCCACTAACACCAACG	0	0.2	
## 11	GTTTGACCCCCTACTACACAGCG	CCCACTAACACCAACGCCCTAAAG	0	0.2	
## 12	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCTC	0	0.2	
## 13	GTTTGACCCCCTACTACACAGCG	GCCTAAAGGTTGACCCCTGC	0	0.2	
## 14	GTTTGACCCCCTACTACACAGCG	TGCCCACTAACACCAACGC	0	0.2	
## 15	GTTTGACCCCCTACTACACAGCG	TGACCCCTGCCTACCTCC	0	0.2	
## 16	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCC	0	0.2	
## 17	GTTTGACCCCCTACTACACAGCG	CAACGCCCTAAAGGTTGACCC	0	0.2	
## 18	GTTTGACCCCCTACTACACAGCG	CCAACGCCCTAAAGGTTGACCC	0	0.2	
## 19	GTTTGACCCCCTACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2	

## 20	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC ACTAACACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC ACTAACAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC ACTAAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ATGGATGCC ACTAACACCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC ACTA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CAATGGATGCC ACTAACACCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC ACTAACAA	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC ACTAA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCAAC	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	CAATGGATGCC ACTAACACCAA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CCC ACTAACACCAACGCC TAAA	0	0.2
## 40	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 41	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 45	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC ACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC ACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC ACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC ACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC ACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC ACTAACAA	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC ACTAACACCAA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCCCATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2			
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2			
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2			
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2			
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2			
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2			
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2			
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2			
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGTAG	0	0.2			
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2			
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2			
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2			
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2			
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2			
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2			
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2			
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2			
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2			
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2			
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2			
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2			
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2			
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2			
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGA	0	0.2			
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGTA	0	0.2			
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2			
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCATA	0	0.2			
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2			
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2			
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2			
## similar_signatures		missing_signatures	enzyme	digest_score	fragme		
## 1		HPV18, HPV16, HPV4, HPV17			0		
## 2		HPV18, HPV16, HPV4, HPV17			0		
## 3		HPV18, HPV16, HPV4, HPV17			0		
## 4		HPV18, HPV16, HPV4, HPV17			0		
## 5		HPV18, HPV16, HPV4, HPV17			0		
## 6		HPV18, HPV16, HPV4, HPV17			0		
## 7		HPV18, HPV16, HPV4, HPV17			0		
## 8		HPV18, HPV16, HPV4, HPV17			0		
## 9		HPV18, HPV16, HPV4, HPV17			0		
## 10		HPV18, HPV16, HPV4, HPV17			0		
## 11		HPV18, HPV16, HPV4, HPV17			0		
## 12		HPV18, HPV16, HPV4, HPV17			0		
## 13		HPV18, HPV16, HPV4, HPV17			0		
## 14		HPV18, HPV16, HPV4, HPV17			0		
## 15		HPV18, HPV16, HPV4, HPV17			0		
## 16		HPV18, HPV16, HPV4, HPV17			0		
## 17		HPV18, HPV16, HPV4, HPV17			0		
## 18		HPV18, HPV16, HPV4, HPV17			0		
## 19		HPV18, HPV16, HPV4, HPV17			0		
## 20		HPV18, HPV16, HPV4, HPV17			0		

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72		HPV18, HPV16, HPV4, HPV17			0
## 73		HPV18, HPV16, HPV4, HPV17			0
## 74		HPV18, HPV16, HPV4, HPV17			0
## 75		HPV18, HPV16, HPV4, HPV17			0
## 76		HPV18, HPV16, HPV4, HPV17			0
## 77		HPV18, HPV16, HPV4, HPV17			0
## 78		HPV18, HPV16, HPV4, HPV17			0
## 79		HPV18, HPV16, HPV4, HPV17			0
## 80		HPV18, HPV16, HPV4, HPV17			0
## 81		HPV18, HPV16, HPV4, HPV17			0
## 82		HPV18, HPV16, HPV4, HPV17			0
## 83		HPV18, HPV16, HPV4, HPV17			0
## 84		HPV18, HPV16, HPV4, HPV17			0
## 85		HPV18, HPV16, HPV4, HPV17			0
## 86		HPV18, HPV16, HPV4, HPV17			0
## 87		HPV18, HPV16, HPV4, HPV17			0
## 88		HPV18, HPV16, HPV4, HPV17			0
## 89		HPV18, HPV16, HPV4, HPV17			0
## 90		HPV18, HPV16, HPV4, HPV17			0
## 91		HPV18, HPV16, HPV4, HPV17			0
## 92		HPV18, HPV16, HPV4, HPV17			0
## 93		HPV18, HPV16, HPV4, HPV17			0
## 94		HPV18, HPV16, HPV4, HPV17			0
## 95		HPV18, HPV16, HPV4, HPV17			0
## 96		HPV18, HPV16, HPV4, HPV17			0
## 97		HPV18, HPV16, HPV4, HPV17			0
## 98		HPV18, HPV16, HPV4, HPV17			0
## 99		HPV18, HPV16, HPV4, HPV17			0
## 100		HPV18, HPV16, HPV4, HPV17			0
##					
## [[7]]					
##	forward_primer		reverse_primer	score	coverage product
## 1	GTTTGACCCCCTACTACACAGCG		CCTAAAGGTTGACCCCTGCC	0	0.2
## 2	TGACCCCCTACTACACAGCGTT		CCTAAAGGTTGACCCCTGCC	0	0.2
## 3	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCTAAAGGTT		0	0.2
## 4	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCTAAAGGT		0	0.2
## 5	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCCT		0	0.2
## 6	GTTTGACCCCCTACTACACAGCG	ACGCCTAAAGGTTGACCCCT		0	0.2
## 7	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCT		0	0.2
## 8	GTTTGACCCCCTACTACACAGCG	TTGTTTAGCAATGGATGCCACT		0	0.2
## 9	GTTTGACCCCCTACTACACAGCG	ACTAACACCAACGCCTAAAGGTTG		0	0.2
## 10	GTTTGACCCCCTACTACACAGCG	CGCCTAAAGGTTGACCCCTG		0	0.2
## 11	GTTTGACCCCCTACTACACAGCG	CCACTAACRCCAACRCCTAAAGG		0	0.2
## 12	GTTTGACCCCCTACTACACAGCG	GGATGCCACTAACACCAACG		0	0.2
## 13	GTTTGACCCCCTACTACACAGCG	CCCACTAACACCAACGCCTAAAG		0	0.2
## 14	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCTC		0	0.2
## 15	GTTTGACCCCCTACTACACAGCG	GCCTAAAGGTTGACCCCTGC		0	0.2
## 16	GTTTGACCCCCTACTACACAGCG	TGCCCACTAACACCAACGC		0	0.2
## 17	GTTTGACCCCCTACTACACAGCG	TGACCCCTGCCTACCTCC		0	0.2
## 18	GTTTGACCCCCTACTACACAGCG	CAACGCCTAAAGGTTGACCCC		0	0.2
## 19	GTTTGACCCCCTACTACACAGCG	CCAAACGCCTAAAGGTTGACCC		0	0.2

## 20	GTTTGACCCC ACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC CACTAACACC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC CACTAACAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	ATGGATGCC CACTAACACCAAC	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 40	GTTTGACCCC ACTACACAGCG	CCCACTAACACCAACGCC AAA	0	0.2
## 41	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACT	0	0.2
## 45	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC CACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC CACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC CACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCC TACCTCCAACCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCC CATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2		
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2		
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2		
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2		
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2		
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2		
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2		
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2		
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCCATACTAACGCTGTGTAG	0	0.2		
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2		
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2		
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2		
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2		
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2		
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2		
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2		
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2		
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2		
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2		
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2		
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2		
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2		
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2		
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCCATACTAACGCTGTGA	0	0.2		
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2		
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2		
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCATA	0	0.2		
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2		
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2		
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2		
## similar_signatures		missing_signatures	enzyme	digest_score	fragme	
## 1		HPV18, HPV16, HPV4, HPV17	Acc65I	0		
## 2		HPV18, HPV16, HPV4, HPV17	Acc65I	0		
## 3		HPV18, HPV16, HPV4, HPV17		0		
## 4		HPV18, HPV16, HPV4, HPV17		0		
## 5		HPV18, HPV16, HPV4, HPV17		0		
## 6		HPV18, HPV16, HPV4, HPV17		0		
## 7		HPV18, HPV16, HPV4, HPV17		0		
## 8		HPV18, HPV16, HPV4, HPV17		0		
## 9		HPV18, HPV16, HPV4, HPV17		0		
## 10		HPV18, HPV16, HPV4, HPV17		0		
## 11		HPV18, HPV16, HPV4, HPV17		0		
## 12		HPV18, HPV16, HPV4, HPV17		0		
## 13		HPV18, HPV16, HPV4, HPV17		0		
## 14		HPV18, HPV16, HPV4, HPV17		0		
## 15		HPV18, HPV16, HPV4, HPV17		0		
## 16		HPV18, HPV16, HPV4, HPV17		0		
## 17		HPV18, HPV16, HPV4, HPV17		0		
## 18		HPV18, HPV16, HPV4, HPV17		0		
## 19		HPV18, HPV16, HPV4, HPV17		0		
## 20		HPV18, HPV16, HPV4, HPV17		0		

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72		HPV18, HPV16, HPV4, HPV17			0
## 73		HPV18, HPV16, HPV4, HPV17			0
## 74		HPV18, HPV16, HPV4, HPV17			0
## 75		HPV18, HPV16, HPV4, HPV17			0
## 76		HPV18, HPV16, HPV4, HPV17			0
## 77		HPV18, HPV16, HPV4, HPV17			0
## 78		HPV18, HPV16, HPV4, HPV17			0
## 79		HPV18, HPV16, HPV4, HPV17			0
## 80		HPV18, HPV16, HPV4, HPV17			0
## 81		HPV18, HPV16, HPV4, HPV17			0
## 82		HPV18, HPV16, HPV4, HPV17			0
## 83		HPV18, HPV16, HPV4, HPV17			0
## 84		HPV18, HPV16, HPV4, HPV17			0
## 85		HPV18, HPV16, HPV4, HPV17			0
## 86		HPV18, HPV16, HPV4, HPV17			0
## 87		HPV18, HPV16, HPV4, HPV17			0
## 88		HPV18, HPV16, HPV4, HPV17			0
## 89		HPV18, HPV16, HPV4, HPV17			0
## 90		HPV18, HPV16, HPV4, HPV17			0
## 91		HPV18, HPV16, HPV4, HPV17			0
## 92		HPV18, HPV16, HPV4, HPV17			0
## 93		HPV18, HPV16, HPV4, HPV17			0
## 94		HPV18, HPV16, HPV4, HPV17			0
## 95		HPV18, HPV16, HPV4, HPV17			0
## 96		HPV18, HPV16, HPV4, HPV17			0
## 97		HPV18, HPV16, HPV4, HPV17			0
## 98		HPV18, HPV16, HPV4, HPV17			0
## 99		HPV18, HPV16, HPV4, HPV17			0
## 100		HPV18, HPV16, HPV4, HPV17			0
##					
## [[8]]					
##	forward_primer		reverse_primer	score	coverage product
## 1	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGTT	0	0.2	
## 2	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGT	0	0.2	
## 3	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCCT	0	0.2	
## 4	GTTTGACCCCCTACTACACAGCG	ACGCCCTAAAGGTTGACCCCT	0	0.2	
## 5	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCT	0	0.2	
## 6	GTTTGACCCCCTACTACACAGCG	TTGTTTAGCAATGGATGCCACT	0	0.2	
## 7	GTTTGACCCCCTACTACACAGCG	ACTAACACCAACGCCCTAAAGGTTG	0	0.2	
## 8	GTTTGACCCCCTACTACACAGCG	CGCCTAAAGGTTGACCCCTG	0	0.2	
## 9	GTTTGACCCCCTACTACACAGCG	CCACTAACRCCAACRCCTAAAGG	0	0.2	
## 10	GTTTGACCCCCTACTACACAGCG	GGATGCCACTAACACCAACG	0	0.2	
## 11	GTTTGACCCCCTACTACACAGCG	CCCACTAACACCAACGCCCTAAAG	0	0.2	
## 12	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCTC	0	0.2	
## 13	GTTTGACCCCCTACTACACAGCG	GCCTAAAGGTTGACCCCTGC	0	0.2	
## 14	GTTTGACCCCCTACTACACAGCG	TGCCCACTAACACCAACGC	0	0.2	
## 15	GTTTGACCCCCTACTACACAGCG	TGACCCCTGCCTACCTCC	0	0.2	
## 16	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCC	0	0.2	
## 17	GTTTGACCCCCTACTACACAGCG	CAACGCCCTAAAGGTTGACCC	0	0.2	
## 18	GTTTGACCCCCTACTACACAGCG	CCAACGCCCTAAAGGTTGACCC	0	0.2	
## 19	GTTTGACCCCCTACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2	

## 20	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC CACTAACACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC CACTAACAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ATGGATGCC CACTAACACCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCAAC	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	CAATGGATGCC CACTAACACCAA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CCC ACTAACACCAACGCC TAAA	0	0.2
## 40	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 41	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 45	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC CACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC CACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC CACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC CACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC CACTAAC	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC CACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC CACTAACACCAA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCC TACCTCCAACCCCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCCCATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2		
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2		
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2		
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2		
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2		
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2		
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2		
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2		
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCCATACTAACGCTGTGTAG	0	0.2		
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2		
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2		
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2		
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2		
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2		
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2		
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2		
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2		
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2		
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2		
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2		
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2		
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2		
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2		
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCCATACTAACGCTGTGA	0	0.2		
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2		
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2		
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCATA	0	0.2		
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2		
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2		
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2		
## similar_signatures		missing_signatures	enzyme	digest_score	fragme	
## 1		HPV18, HPV16, HPV4, HPV17			0	
## 2		HPV18, HPV16, HPV4, HPV17			0	
## 3		HPV18, HPV16, HPV4, HPV17			0	
## 4		HPV18, HPV16, HPV4, HPV17			0	
## 5		HPV18, HPV16, HPV4, HPV17			0	
## 6		HPV18, HPV16, HPV4, HPV17			0	
## 7		HPV18, HPV16, HPV4, HPV17			0	
## 8		HPV18, HPV16, HPV4, HPV17			0	
## 9		HPV18, HPV16, HPV4, HPV17			0	
## 10		HPV18, HPV16, HPV4, HPV17			0	
## 11		HPV18, HPV16, HPV4, HPV17			0	
## 12		HPV18, HPV16, HPV4, HPV17			0	
## 13		HPV18, HPV16, HPV4, HPV17			0	
## 14		HPV18, HPV16, HPV4, HPV17			0	
## 15		HPV18, HPV16, HPV4, HPV17			0	
## 16		HPV18, HPV16, HPV4, HPV17			0	
## 17		HPV18, HPV16, HPV4, HPV17			0	
## 18		HPV18, HPV16, HPV4, HPV17			0	
## 19		HPV18, HPV16, HPV4, HPV17			0	
## 20		HPV18, HPV16, HPV4, HPV17			0	

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72		HPV18, HPV16, HPV4, HPV17			0
## 73		HPV18, HPV16, HPV4, HPV17			0
## 74		HPV18, HPV16, HPV4, HPV17			0
## 75		HPV18, HPV16, HPV4, HPV17			0
## 76		HPV18, HPV16, HPV4, HPV17			0
## 77		HPV18, HPV16, HPV4, HPV17			0
## 78		HPV18, HPV16, HPV4, HPV17			0
## 79		HPV18, HPV16, HPV4, HPV17			0
## 80		HPV18, HPV16, HPV4, HPV17			0
## 81		HPV18, HPV16, HPV4, HPV17			0
## 82		HPV18, HPV16, HPV4, HPV17			0
## 83		HPV18, HPV16, HPV4, HPV17			0
## 84		HPV18, HPV16, HPV4, HPV17			0
## 85		HPV18, HPV16, HPV4, HPV17			0
## 86		HPV18, HPV16, HPV4, HPV17			0
## 87		HPV18, HPV16, HPV4, HPV17			0
## 88		HPV18, HPV16, HPV4, HPV17			0
## 89		HPV18, HPV16, HPV4, HPV17			0
## 90		HPV18, HPV16, HPV4, HPV17			0
## 91		HPV18, HPV16, HPV4, HPV17			0
## 92		HPV18, HPV16, HPV4, HPV17			0
## 93		HPV18, HPV16, HPV4, HPV17			0
## 94		HPV18, HPV16, HPV4, HPV17			0
## 95		HPV18, HPV16, HPV4, HPV17			0
## 96		HPV18, HPV16, HPV4, HPV17			0
## 97		HPV18, HPV16, HPV4, HPV17			0
## 98		HPV18, HPV16, HPV4, HPV17			0
## 99		HPV18, HPV16, HPV4, HPV17			0
## 100		HPV18, HPV16, HPV4, HPV17			0
##					
## [[9]]					
##	forward_primer		reverse_primer	score	coverage product
## 1	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGTT	0	0.2	
## 2	GTTTGACCCCCTACTACACAGCG	CACTAACACCAACGCCCTAAAGGT	0	0.2	
## 3	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCCT	0	0.2	
## 4	GTTTGACCCCCTACTACACAGCG	ACGCCCTAAAGGTTGACCCCT	0	0.2	
## 5	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCT	0	0.2	
## 6	GTTTGACCCCCTACTACACAGCG	TTGTTTAGCAATGGATGCCACT	0	0.2	
## 7	GTTTGACCCCCTACTACACAGCG	ACTAACACCAACGCCCTAAAGGTTG	0	0.2	
## 8	GTTTGACCCCCTACTACACAGCG	CGCCTAAAGGTTGACCCCTG	0	0.2	
## 9	GTTTGACCCCCTACTACACAGCG	CCACTAACRCCAACRCCTAAAGG	0	0.2	
## 10	GTTTGACCCCCTACTACACAGCG	GGATGCCACTAACACCAACG	0	0.2	
## 11	GTTTGACCCCCTACTACACAGCG	CCCACTAACACCAACGCCCTAAAG	0	0.2	
## 12	GTTTGACCCCCTACTACACAGCG	GGCTGACCMCKGCCTACCTC	0	0.2	
## 13	GTTTGACCCCCTACTACACAGCG	GCCTAAAGGTTGACCCCTGC	0	0.2	
## 14	GTTTGACCCCCTACTACACAGCG	TGCCCACTAACACCAACGC	0	0.2	
## 15	GTTTGACCCCCTACTACACAGCG	TGACCCCTGCCTACCTCC	0	0.2	
## 16	GTTTGACCCCCTACTACACAGCG	CCTAAAGGTTGACCCCTGCC	0	0.2	
## 17	GTTTGACCCCCTACTACACAGCG	CAACGCCCTAAAGGTTGACCC	0	0.2	
## 18	GTTTGACCCCCTACTACACAGCG	CCAACGCCCTAAAGGTTGACCC	0	0.2	
## 19	GTTTGACCCCCTACTACACAGCG	AGGTTGACCCCTGCCTACC	0	0.2	

## 20	GTTTGACCCC ACTACACAGCG	ACCAACGCC TAAAGGTTGACC	0	0.2
## 21	GTTTGACCCC ACTACACAGCG	GCAATGGATGCC ACTAACACC	0	0.2
## 22	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 23	GTTTGACCCC ACTACACAGCG	ACACCAACGCC TAAAGGTTGAC	0	0.2
## 24	GTTTGACCCC ACTACACAGCG	AGCAATGGATGCC ACTAACAC	0	0.2
## 25	GTTTGACCCC ACTACACAGCG	TGTTTAGCAATGGATGCC ACTAAC	0	0.2
## 26	GTTTGACCCC ACTACACAGCG	ACCCCTGCC TACCTCCAAC	0	0.2
## 27	GTTTGACCCC ACTACACAGCG	ATGGATGCC ACTAACACCAAC	0	0.2
## 28	GTTTGACCCC ACTACACAGCG	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 29	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 30	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC ACTA	0	0.2
## 31	GTTTGACCCC ACTACACAGCG	CTAACACCAACGCC TAAAGGTTGA	0	0.2
## 32	GTTTGACCCC ACTACACAGCG	CACCYCTRCC TACCTCCA	0	0.2
## 33	GTTTGACCCC ACTACACAGCG	CAATGGATGCC ACTAACACCA	0	0.2
## 34	GTTTGACCCC ACTACACAGCG	GTTTAGCAATGGATGCC ACTAACAA	0	0.2
## 35	GTTTGACCCC ACTACACAGCG	GCCC ACTAACACCAACGCC TAA	0	0.2
## 36	GTTTGACCCC ACTACACAGCG	TTGTTTAGCAATGGATGCC ACTAA	0	0.2
## 37	GTTTGACCCC ACTACACAGCG	GACCCCTGCC TACCTCCAAC	0	0.2
## 38	GTTTGACCCC ACTACACAGCG	CAATGGATGCC ACTAACACCAA	0	0.2
## 39	GTTTGACCCC ACTACACAGCG	CCC ACTAACACCAACGCC TAAA	0	0.2
## 40	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCT	0	0.2
## 41	TGACCCC ACTACACAGCGTT	ACGCC TAAAGGTTGACCCCT	0	0.2
## 42	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCT	0	0.2
## 43	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACT	0	0.2
## 44	TGACCCC ACTACACAGCGTT	CGCCTAAAGGTTGACCCCTG	0	0.2
## 45	TGACCCC ACTACACAGCGTT	GGCTGACCMCKGCC TACCTC	0	0.2
## 46	TGACCCC ACTACACAGCGTT	GCCTAAAGGTTGACCCCTGC	0	0.2
## 47	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCC	0	0.2
## 48	TGACCCC ACTACACAGCGTT	AGGTTGACCCCTGCC TACC	0	0.2
## 49	TGACCCC ACTACACAGCGTT	GCAATGGATGCC ACTAACACC	0	0.2
## 50	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTAC	0	0.2
## 51	TGACCCC ACTACACAGCGTT	AGCAATGGATGCC ACTAACAC	0	0.2
## 52	TGACCCC ACTACACAGCGTT	TGTTTAGCAATGGATGCC ACTAAC	0	0.2
## 53	TGACCCC ACTACACAGCGTT	ATGGATGCC ACTAACACCAAC	0	0.2
## 54	TGACCCC ACTACACAGCGTT	CCTAAAGGTTGACCCCTGCCTA	0	0.2
## 55	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACTA	0	0.2
## 56	TGACCCC ACTACACAGCGTT	CAATGGATGCC ACTAACACCA	0	0.2
## 57	TGACCCC ACTACACAGCGTT	GTTTAGCAATGGATGCC ACTAACAA	0	0.2
## 58	TGACCCC ACTACACAGCGTT	TTGTTTAGCAATGGATGCC ACTAA	0	0.2
## 59	TGACCCC ACTACACAGCGTT	CAATGGATGCC ACTAACACCAA	0	0.2
## 60	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGT	0	0.2
## 61	TCCTTGCTGTGGGACATCCAT	CACGCCCATACTAAACGCTGT	0	0.2
## 62	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCCTGT	0	0.2
## 63	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGGT	0	0.2
## 64	TCCTTGCTGTGGGACATCCAT	CGCCCATACTAAACGCTGTGTAGT	0	0.2
## 65	TCCTTGCTGTGGGACATCCAT	GCACGCCCATACTAAACGCT	0	0.2
## 66	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCCT	0	0.2
## 67	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCC CACT	0	0.2
## 68	TCCTTGCTGTGGGACATCCAT	TGTGTA GTGGGTCAAACAGAGAT	0	0.2
## 69	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGAAT	0	0.2
## 70	TCCTTGCTGTGGGACATCCAT	ACGCCCATACTAAACGCTGTG	0	0.2

## 71	TCCTTGCTGTGGGACATCCAT	TGCCTACCTCCAACCCTGTG	0	0.2			
## 72	TCCTTGCTGTGGGACATCCAT	GCCCCATAACTAACGCTGTAGTG	0	0.2			
## 73	TCCTTGCTGTGGGACATCCAT	GCACGCCATACTAACGCTG	0	0.2			
## 74	TCCTTGCTGTGGGACATCCAT	CCTGCCTACCTCCAACCCTG	0	0.2			
## 75	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGATG	0	0.2			
## 76	TCCTTGCTGTGGGACATCCAT	CATACTAACGCTGTAGTGGG	0	0.2			
## 77	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGG	0	0.2			
## 78	TCCTTGCTGTGGGACATCCAT	CCTCCAACCCTGTGCACG	0	0.2			
## 79	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGTAG	0	0.2			
## 80	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGAG	0	0.2			
## 81	TCCTTGCTGTGGGACATCCAT	GTGGGGTCAAACAGAGATGAATCAG	0	0.2			
## 82	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAG	0	0.2			
## 83	TCCTTGCTGTGGGACATCCAT	CTAAACGCTGTGTAGTGGGTC	0	0.2			
## 84	TCCTTGCTGTGGGACATCCAT	GCCTACCTCCAACCCTGTGC	0	0.2			
## 85	TCCTTGCTGTGGGACATCCAT	TCCAACCCTGTGCACGC	0	0.2			
## 86	TCCTTGCTGTGGGACATCCAT	CCAACCCTGTGCACGCC	0	0.2			
## 87	TCCTTGCTGTGGGACATCCAT	CCCTGCCTACCTCCAACCC	0	0.2			
## 88	TCCTTGCTGTGGGACATCCAT	CCCCTGCCTACCTCCAACC	0	0.2			
## 89	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATAC	0	0.2			
## 90	TCCTTGCTGTGGGACATCCAT	CCTACCTCCAACCCTGTGCAC	0	0.2			
## 91	TCCTTGCTGTGGGACATCCAT	ACCCCTGCCTACCTCCAAC	0	0.2			
## 92	TCCTTGCTGTGGGACATCCAT	CCTGTGCACGCCCATACTAAC	0	0.2			
## 93	TCCTTGCTGTGGGACATCCAT	CGCTGTGTAGTGGGTCAAAC	0	0.2			
## 94	TCCTTGCTGTGGGACATCCAT	CGCCCATACAAACGCTGTGA	0	0.2			
## 95	TCCTTGCTGTGGGACATCCAT	GGGGTCAAACAGAGATGAATCAGTA	0	0.2			
## 96	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATACTA	0	0.2			
## 97	TCCTTGCTGTGGGACATCCAT	CCCTGTGCACGCCCATATA	0	0.2			
## 98	TCCTTGCTGTGGGACATCCAT	TGTAGTGGGTCAAACAGAGATGA	0	0.2			
## 99	TCCTTGCTGTGGGACATCCAT	TGTGTAGTGGGTCAAACAGAGA	0	0.2			
## 100	TCCTTGCTGTGGGACATCCAT	GCTGTGTAGTGGGTCAAACAGA	0	0.2			
## similar_signatures		missing_signatures	enzyme	digest_score	fragme		
## 1		HPV18, HPV16, HPV4, HPV17			0		
## 2		HPV18, HPV16, HPV4, HPV17			0		
## 3		HPV18, HPV16, HPV4, HPV17			0		
## 4		HPV18, HPV16, HPV4, HPV17			0		
## 5		HPV18, HPV16, HPV4, HPV17			0		
## 6		HPV18, HPV16, HPV4, HPV17			0		
## 7		HPV18, HPV16, HPV4, HPV17			0		
## 8		HPV18, HPV16, HPV4, HPV17			0		
## 9		HPV18, HPV16, HPV4, HPV17			0		
## 10		HPV18, HPV16, HPV4, HPV17			0		
## 11		HPV18, HPV16, HPV4, HPV17			0		
## 12		HPV18, HPV16, HPV4, HPV17			0		
## 13		HPV18, HPV16, HPV4, HPV17			0		
## 14		HPV18, HPV16, HPV4, HPV17			0		
## 15		HPV18, HPV16, HPV4, HPV17			0		
## 16		HPV18, HPV16, HPV4, HPV17			0		
## 17		HPV18, HPV16, HPV4, HPV17			0		
## 18		HPV18, HPV16, HPV4, HPV17			0		
## 19		HPV18, HPV16, HPV4, HPV17			0		
## 20		HPV18, HPV16, HPV4, HPV17			0		

## 21	HPV18, HPV16, HPV4, HPV17	0
## 22	HPV18, HPV16, HPV4, HPV17	0
## 23	HPV18, HPV16, HPV4, HPV17	0
## 24	HPV18, HPV16, HPV4, HPV17	0
## 25	HPV18, HPV16, HPV4, HPV17	0
## 26	HPV18, HPV16, HPV4, HPV17	0
## 27	HPV18, HPV16, HPV4, HPV17	0
## 28	HPV18, HPV16, HPV4, HPV17	0
## 29	HPV18, HPV16, HPV4, HPV17	0
## 30	HPV18, HPV16, HPV4, HPV17	0
## 31	HPV18, HPV16, HPV4, HPV17	0
## 32	HPV18, HPV16, HPV4, HPV17	0
## 33	HPV18, HPV16, HPV4, HPV17	0
## 34	HPV18, HPV16, HPV4, HPV17	0
## 35	HPV18, HPV16, HPV4, HPV17	0
## 36	HPV18, HPV16, HPV4, HPV17	0
## 37	HPV18, HPV16, HPV4, HPV17	0
## 38	HPV18, HPV16, HPV4, HPV17	0
## 39	HPV18, HPV16, HPV4, HPV17	0
## 40	HPV18, HPV16, HPV4, HPV17	0
## 41	HPV18, HPV16, HPV4, HPV17	0
## 42	HPV18, HPV16, HPV4, HPV17	0
## 43	HPV18, HPV16, HPV4, HPV17	0
## 44	HPV18, HPV16, HPV4, HPV17	0
## 45	HPV18, HPV16, HPV4, HPV17	0
## 46	HPV18, HPV16, HPV4, HPV17	0
## 47	HPV18, HPV16, HPV4, HPV17	0
## 48	HPV18, HPV16, HPV4, HPV17	0
## 49	HPV18, HPV16, HPV4, HPV17	0
## 50	HPV18, HPV16, HPV4, HPV17	0
## 51	HPV18, HPV16, HPV4, HPV17	0
## 52	HPV18, HPV16, HPV4, HPV17	0
## 53	HPV18, HPV16, HPV4, HPV17	0
## 54	HPV18, HPV16, HPV4, HPV17	0
## 55	HPV18, HPV16, HPV4, HPV17	0
## 56	HPV18, HPV16, HPV4, HPV17	0
## 57	HPV18, HPV16, HPV4, HPV17	0
## 58	HPV18, HPV16, HPV4, HPV17	0
## 59	HPV18, HPV16, HPV4, HPV17	0
## 60	HPV18, HPV16, HPV4, HPV17	0
## 61	HPV18, HPV16, HPV4, HPV17	0
## 62	HPV18, HPV16, HPV4, HPV17	0
## 63	HPV18, HPV16, HPV4, HPV17	0
## 64	HPV18, HPV16, HPV4, HPV17	0
## 65	HPV18, HPV16, HPV4, HPV17	0
## 66	HPV18, HPV16, HPV4, HPV17	0
## 67	HPV18, HPV16, HPV4, HPV17	0
## 68	HPV18, HPV16, HPV4, HPV17	0
## 69	HPV18, HPV16, HPV4, HPV17	0
## 70	HPV18, HPV16, HPV4, HPV17	0
## 71	HPV18, HPV16, HPV4, HPV17	0

## 72	HPV18, HPV16, HPV4, HPV17	0
## 73	HPV18, HPV16, HPV4, HPV17	0
## 74	HPV18, HPV16, HPV4, HPV17	0
## 75	HPV18, HPV16, HPV4, HPV17	0
## 76	HPV18, HPV16, HPV4, HPV17	0
## 77	HPV18, HPV16, HPV4, HPV17	0
## 78	HPV18, HPV16, HPV4, HPV17	0
## 79	HPV18, HPV16, HPV4, HPV17	0
## 80	HPV18, HPV16, HPV4, HPV17	0
## 81	HPV18, HPV16, HPV4, HPV17	0
## 82	HPV18, HPV16, HPV4, HPV17	0
## 83	HPV18, HPV16, HPV4, HPV17	0
## 84	HPV18, HPV16, HPV4, HPV17	0
## 85	HPV18, HPV16, HPV4, HPV17	0
## 86	HPV18, HPV16, HPV4, HPV17	0
## 87	HPV18, HPV16, HPV4, HPV17	0
## 88	HPV18, HPV16, HPV4, HPV17	0
## 89	HPV18, HPV16, HPV4, HPV17	0
## 90	HPV18, HPV16, HPV4, HPV17	0
## 91	HPV18, HPV16, HPV4, HPV17	0
## 92	HPV18, HPV16, HPV4, HPV17	0
## 93	HPV18, HPV16, HPV4, HPV17	0
## 94	HPV18, HPV16, HPV4, HPV17	0
## 95	HPV18, HPV16, HPV4, HPV17	0
## 96	HPV18, HPV16, HPV4, HPV17	0
## 97	HPV18, HPV16, HPV4, HPV17	0
## 98	HPV18, HPV16, HPV4, HPV17	0
## 99	HPV18, HPV16, HPV4, HPV17	0
## 100	HPV18, HPV16, HPV4, HPV17	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
```

RFLP optimization by grid search

```

FOCUS_ID <- 'HPV18'

params <- expand.grid(
  enzymes = lapply(1:3, function(x)
    RESTRICTION_ENZYMES[
      sample(1:length(RESTRICTION_ENZYMES), 3)
    ]
  ),
  minProductSize = seq(80, 150, length.out = 3),
  maxProductSize = seq(500, 5000, length.out = 3),
  resolution = seq(1, 2, length.out = 3),
  levels = seq(5, 20, length.out = 3)
) %>% mutate(type = rep('melt', 243))

gridsearch <- apply(params, 1, function(...)

  list(
    arg = as.list(...),
    out = do.call(
      DesignSignatures,
      append(
        list(
          dbFile = dbConn,
          tblName = 'Seqs',
          identifier = '',
          focusID = FOCUS_ID
        ),
        as.list(...)
      )
    )
  )
) %>% bind_rows

objective <- function(x) {
  print(x)
}

```

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)
```