MASThesis

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I. Running Variable and Cutoff

What: Use school-level FRPM eligibility % as the running variable. Define one or more cutoffs (e.g., 75%, 85%, 90%) where eligibility for food or afterschool programs changes.

Why it's important: RDD depends on a predictable rule where treatment assignment discontinuously changes at a threshold. This makes it possible to estimate causal effects near the cutoff.

How it supports your thesis: These cutoffs create a natural experiment. Schools just above and just below the FRPM threshold are comparable, allowing you to isolate the effect of the program (food or BTB) from confounding factors.

```
##
## 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(rdrobust)
library(rddensity)

merged <- merged %>%
  mutate(
    frpm_rate = ifelse(frpm_rate <= 1, frpm_rate * 100, frpm_rate),
    running   = frpm_rate - 75,
    treated   = ifelse(frpm_rate >= 75, 1, 0)
  )

# ggplot(merged, aes(frpm_rate, chronic_absenteeism)) +
#   geom_point(alpha = .4) +
#   geom_vline(xintercept = 75, linetype = "dashed") +
#   labs(x = "FRPM eligibility rate (%)",
#        y = "Chronic absenteeism rate (%)")
```

II. Identify Treatment Assignment and Outcome Variables

What: - **Treatment:** School participation in the food program (CEP) or BTB afterschool program - **Outcomes:** Chronic absenteeism (primary), possibly test scores or graduation rates later

Why it's important: You need clear and measurable definitions of both the intervention (treatment) and the outcomes it is supposed to influence.

How it supports your thesis: Establishes a cause-and-effect structure — you're asking: "Do schools just above the FRPM threshold, who get the program, show better outcomes than those just below?"

III. Estimate the Treatment Effect with Local Linear Regression

What: Use local linear regression (with a small bandwidth around the cutoff) to estimate the treatment effect at the threshold.

Why it's important: This is the core of RDD — using only schools close to the cutoff, fit a regression model that separately estimates trends from either side and captures the jump at the cutoff.

How it supports your thesis: This gives you the local average treatment effect (LATE) — the causal effect of the program on schools near the threshold. This is your key result.

```
# 2. Sharp RD estimate
rd75 <- rdrobust(merged$chronic_absenteeism,
                 merged$frpm_rate,
                 c          = 75,
                 masspoints = "adjust")
```

```
## Warning in rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, :
## Mass points detected in the running variable.
```

```
summary(rd75)
```

```
## Sharp RD estimates using local polynomial regression.
##
## Number of Obs.                 8391
## BW type                       mserd
## Kernel                   Triangular
## VCE method                       NN
##
## Number of Obs.                 2615         5776
## Eff. Number of Obs.             252          309
## Order est. (p)                    1            1
## Order bias  (q)                   2            2
## BW est. (h)                   4.443        4.443
## BW bias (b)                   7.426        7.426
## rho (h/b)                     0.598        0.598
## Unique Obs.                     176          433
##
## ===============================================================================
##         Method     Coef. Std. Err.         z     P>|z|      [ 95% C.I. ]
## ===============================================================================
##   Conventional    10.368     1.734     5.978     0.000     [6.969 , 13.767]
##         Robust          -         -     5.446     0.000     [7.169 , 15.229]
## ===============================================================================
```

IV. Choose and Justify Bandwidth

What: Use data-driven methods (e.g., Imbens-Kalyanaraman or Calonico-Cattaneo-Titiunik (CCT)) to select optimal bandwidths.

Why it's important: Bandwidth determines how many schools around the cutoff are included in the regression. Too wide = biased; too narrow = noisy.

How it supports your thesis: Justifying bandwidths ensures credible identification and protects against cherry-picking results. It gives your estimates scientific rigor.

```r
# Load package
library(rdrobust)

# Declare models
m1  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 2, p = 1, masspoints = "adjus
m2  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 2, p = 2, masspoints = "adjus
m3  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 2, p = 3, masspoints = "adjus
m4  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 3, p = 1, masspoints = "adjus
m5  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 3, p = 2, masspoints = "adjus
m6  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 3, p = 3, masspoints = "adjus
m7  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 4, p = 1, masspoints = "adjus
m8  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 4, p = 2, masspoints = "adjus
m9  <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 4, p = 3, masspoints = "adjus
m10 <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 5, p = 1, masspoints = "adjus
m11 <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 5, p = 2, masspoints = "adjus
m12 <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 5, p = 3, masspoints = "adjus
m13 <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 6, p = 1, masspoints = "adjus
m14 <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 6, p = 2, masspoints = "adjus
m15 <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 6, p = 3, masspoints = "adjus

# Store models with correct metadata manually
model_info <- data.frame(
  name = paste0("m", 1:15),
  cutoff = 75,
  bandwidth = rep(2:6, each = 3),
  poly_order = rep(1:3, times = 5),
  stringsAsFactors = FALSE
)

models <- list(m1, m2, m3, m4, m5, m6, m7, m8, m9, m10, m11, m12, m13, m14, m15)

# Extract results and build table
robust_results <- do.call(rbind, Map(function(model, info) {
  data.frame(
    cutoff = info$cutoff,
    bandwidth = info$bandwidth,
    poly_order = info$poly_order,
    coef = model$coef[1, 1],
    se = model$se[1, 1],
    pval = model$pv[1, 1],
    ci_lower = model$ci[1, 1],
    ci_upper = model$ci[1, 2]
  )
}, models, split(model_info, seq(nrow(model_info)))))
```

```r
# Show result
print(robust_results)
```

```
##    cutoff bandwidth poly_order       coef        se         pval   ci_lower
## 1      75         2          1  -2.428590  2.811263 3.876546e-01  -7.938566
## 2      75         2          2 -31.283435  5.056396 6.135728e-10 -41.193789
## 3      75         2          3 -40.774795 10.145976 5.849172e-05 -60.660543
## 4      75         3          1   8.075415  2.070939 9.643238e-05   4.016449
## 5      75         3          2  -7.387688  3.629974 4.183172e-02 -14.502306
## 6      75         3          3 -42.998963  6.160372 2.953283e-12 -55.073070
## 7      75         4          1   9.984008  1.862172 8.254047e-08   6.334218
## 8      75         4          2   1.781048  2.765611 5.195767e-01  -3.639449
## 9      75         4          3 -13.602781  4.368021 1.844601e-03 -22.163945
## 10     75         5          1  10.174908  1.625776 3.887195e-10   6.988444
## 11     75         5          2   7.326720  2.440236 2.678041e-03   2.543945
## 12     75         5          3  -8.064500  3.650360 2.715838e-02 -15.219075
## 13     75         6          1   8.156506  1.441245 1.519510e-08   5.331717
## 14     75         6          2  10.897604  2.233584 1.066379e-06   6.519859
## 15     75         6          3  -2.008942  3.159919 5.249345e-01  -8.202270
##       ci_upper
## 1    3.0813847
## 2  -21.3730818
## 3  -20.8890472
## 4   12.1343814
## 5   -0.2730700
## 6  -30.9248554
## 7   13.6337982
## 8    7.2015449
## 9   -5.0416172
## 10  13.3613709
## 11  12.1094953
## 12  -0.9099248
## 13  10.9812952
## 14  15.2753484
## 15   4.1843856
```

```r
bw <- rdbwselect(merged$chronic_absenteeism, merged$frpm_rate, c = 75)
```

```
## Warning in rdbwselect(merged$chronic_absenteeism, merged$frpm_rate, c = 75):
## Mass points detected in the running variable.
```

```r
summary(bw)
```

```
## Call: rdbwselect
##
## Number of Obs.                 8391
## BW type                       mserd
## Kernel                   Triangular
## VCE method                       NN
##
## Number of Obs.                 2615         5776
```

```
## Order est. (p)                    1            1
## Order bias  (q)                   2            2
## Unique Obs.                     176          433
##
## ===================================================
##                   BW est. (h)    BW bias (b)
##             Left of c Right of c  Left of c Right of c
## ===================================================
##      mserd     4.443      4.443      7.426      7.426
## ===================================================
```

V. Interpret and Contextualize the Results

What: Quantify the effect size (e.g., "BTB increases attendance by 1.5% for schools near 75% FRPM cutoff") and discuss policy implications.

Why it's important: You're connecting statistical results to real-world meaning — which is the goal of your thesis.

How it supports your thesis: You can now confidently argue that FRPM-based eligibility cutoffs caused changes in outcomes — backing your case that these programs have measurable benefits (or not).

This means the optimal comparison window is ±4.443 percentage points around the cutoff — i.e., schools with FRPM between 70.56% and 79.44%.

```
main <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 4.443, p = 1, masspoints = "a
summary(main)
```

```
## Sharp RD estimates using local polynomial regression.
##
## Number of Obs.                 8391
## BW type                      Manual
## Kernel                   Triangular
## VCE method                       NN
##
## Number of Obs.                 2615         5776
## Eff. Number of Obs.             252          309
## Order est. (p)                    1            1
## Order bias  (q)                   2            2
## BW est. (h)                   4.443        4.443
## BW bias (b)                   4.443        4.443
## rho (h/b)                     1.000        1.000
## Unique Obs.                    2615         5776
##
## ================================================================================
##         Method     Coef. Std. Err.         z     P>|z|      [ 95% C.I. ]
## ================================================================================
##   Conventional    10.368     1.734     5.979     0.000     [6.969 , 13.767]
##         Robust         -         -     1.992     0.046     [0.085 , 10.317]
## ================================================================================
```

VI. Visualize the Discontinuity (RDD Plots)

What: Plot outcome vs. FRPM %, and check for a visible jump at the cutoff.

Why it's important: A visual RDD plot helps validate the first sign of a causal effect. It shows whether there's a discontinuity in outcomes at the eligibility threshold.

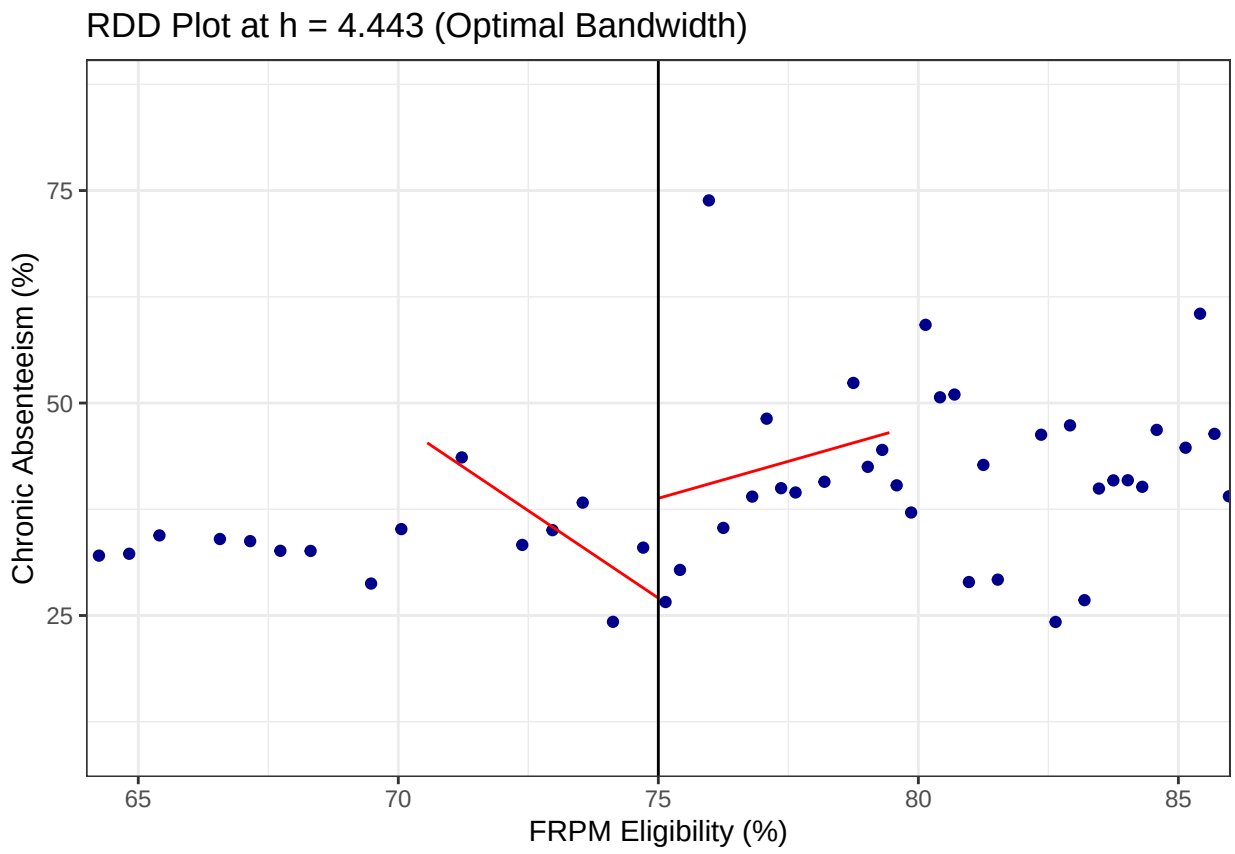
How it supports your thesis: If you observe a clear jump in outcomes right at the cutoff, it's strong preliminary evidence that the program has a measurable effect.

Identification: Quick Visual Check

- Schools with similar FRPM can have different absenteeism — typical heterogeneity.
- The dashed line at 75% is the policy threshold for program eligibility.
- A visible jump suggests program participation may increase absenteeism.

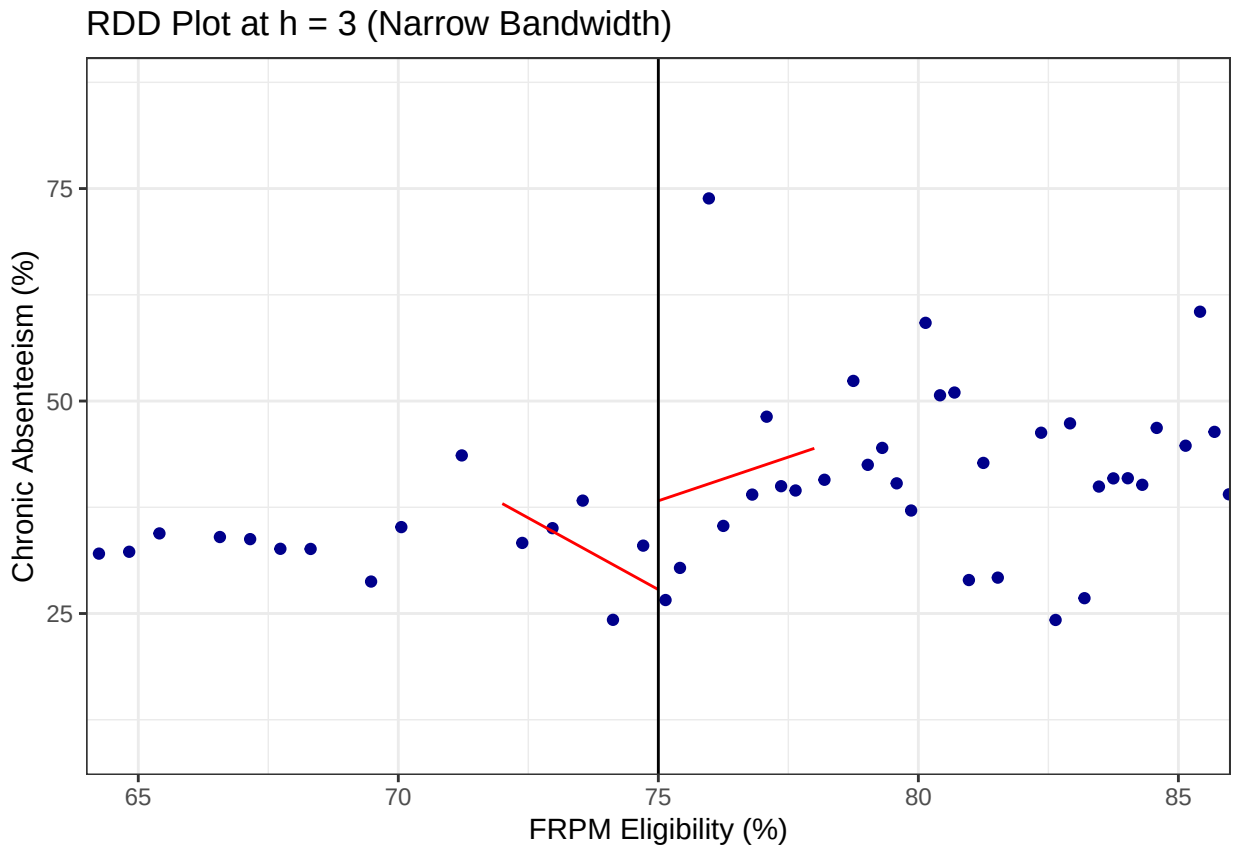
```
library(rdrobust)

# Optimal bandwidth from rdbwselect (rounded for clarity)
rdplot(merged$chronic_absenteeism, merged$frpm_rate,
       c = 75, h = 4.443, p = 1,
       x.lim = c(65, 85),
       title = "RDD Plot at h = 4.443 (Optimal Bandwidth)",
       x.label = "FRPM Eligibility (%)",
       y.label = "Chronic Absenteeism (%)")
```

```
## [1] "Mass points detected in the running variable."
```



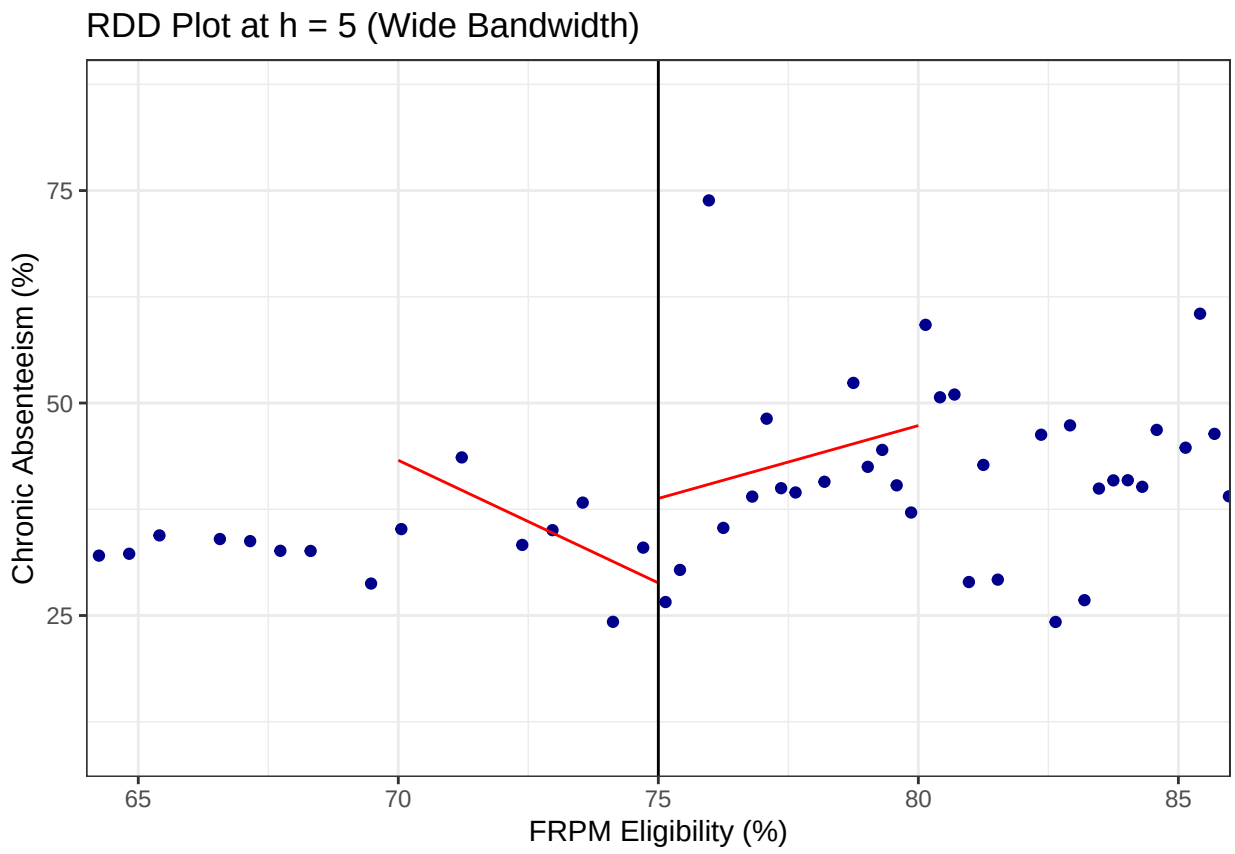

```
# Sensitivity: Narrower
rdplot(merged$chronic_absenteeism, merged$frpm_rate,
       c = 75, h = 3, p = 1,
       x.lim = c(65, 85),
       title = "RDD Plot at h = 3 (Narrow Bandwidth)",
       x.label = "FRPM Eligibility (%)",
       y.label = "Chronic Absenteeism (%)")
```

```
## [1] "Mass points detected in the running variable."
```



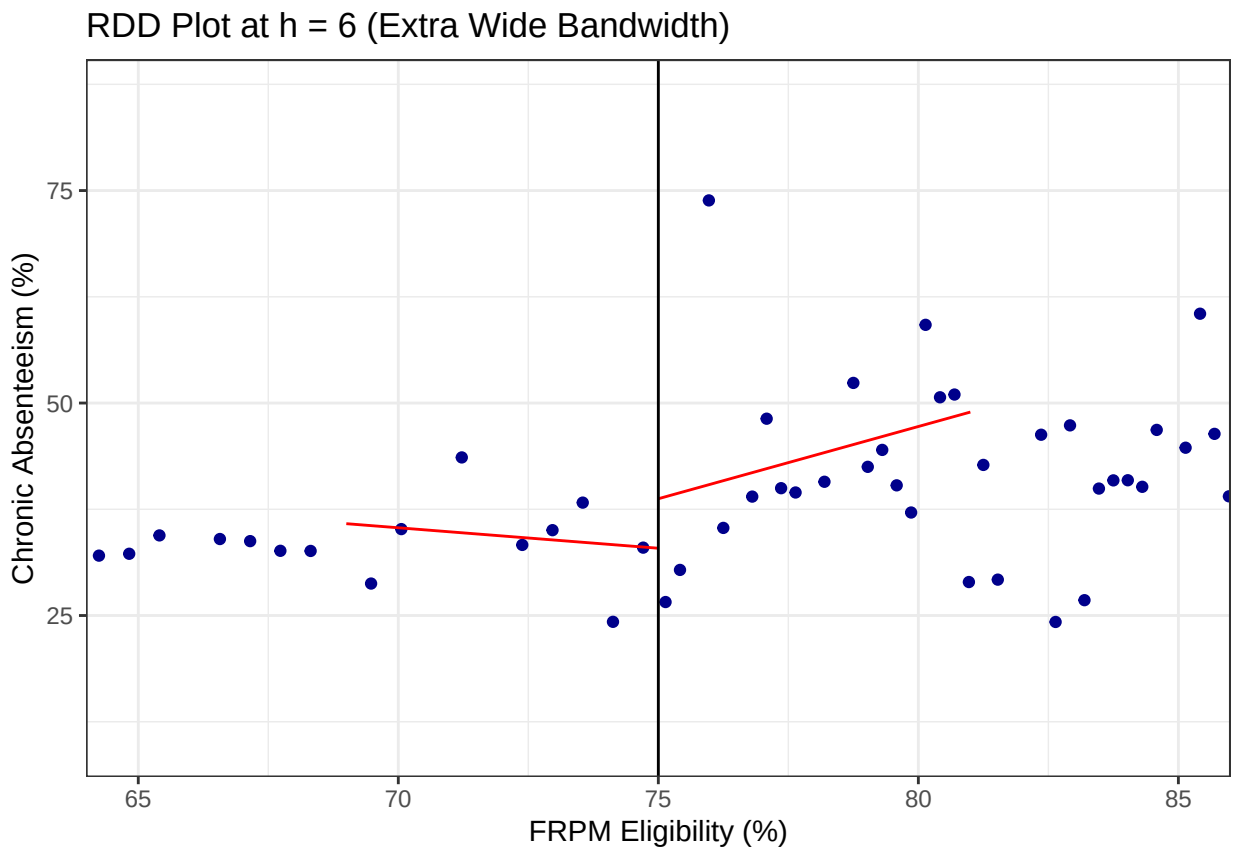

```
# Sensitivity: Wider
rdplot(merged$chronic_absenteeism, merged$frpm_rate,
       c = 75, h = 5, p = 1,
       x.lim = c(65, 85),
       title = "RDD Plot at h = 5 (Wide Bandwidth)",
       x.label = "FRPM Eligibility (%)",
       y.label = "Chronic Absenteeism (%)")
```

```
## [1] "Mass points detected in the running variable."
```




```
# Sensitivity: Even wider
rdplot(merged$chronic_absenteeism, merged$frpm_rate,
       c = 75, h = 6, p = 1,
       x.lim = c(65, 85),
       title = "RDD Plot at h = 6 (Extra Wide Bandwidth)",
       x.label = "FRPM Eligibility (%)",
       y.label = "Chronic Absenteeism (%)")
```

```
## [1] "Mass points detected in the running variable."
```



VII. Run the McCrary Density Test

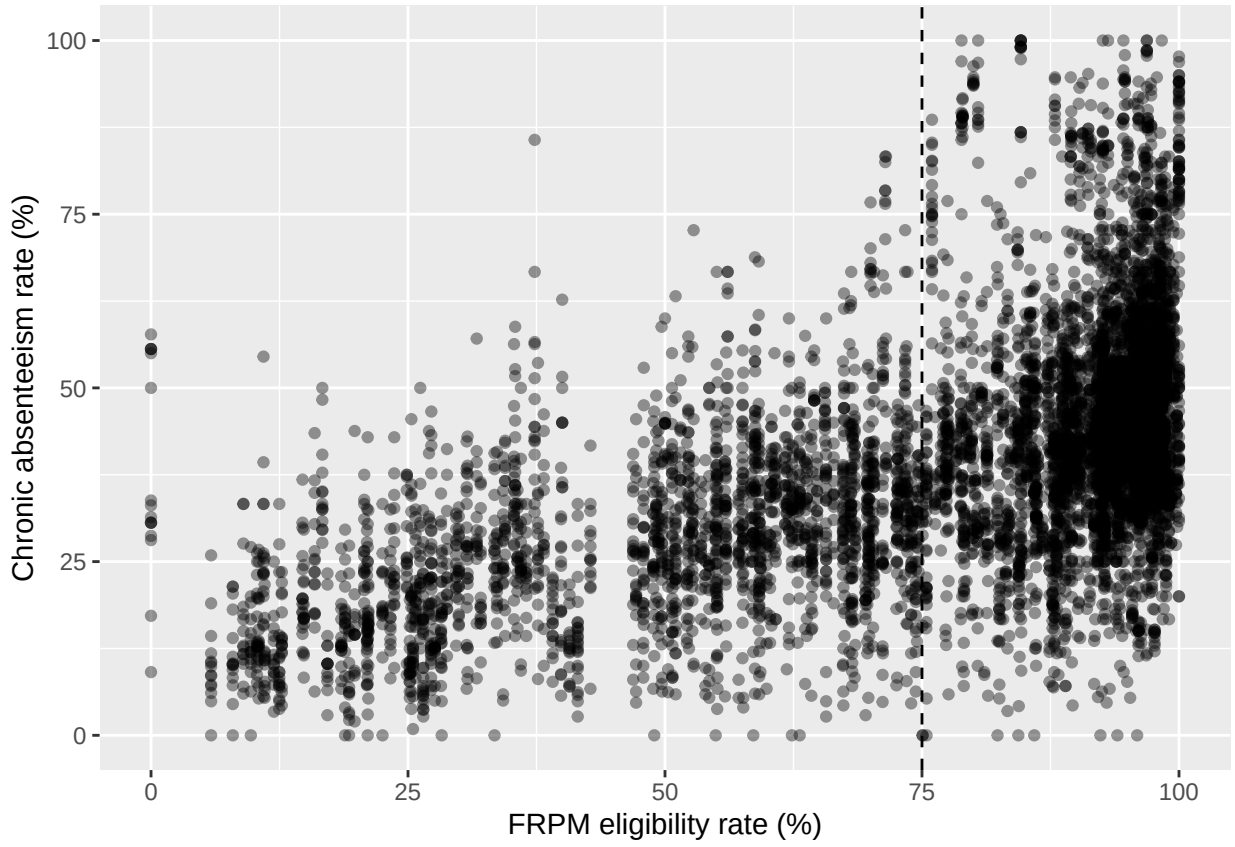
What: Check whether schools are manipulating FRPM % to qualify.

Why it's important: RDD assumes schools cannot manipulate assignment. Bunching invalidates causal claims.

How it supports your thesis: If there's no manipulation, the assignment can be seen as as-good-as-random, strengthening causal identification.

```
library(rdrobust)
library(rddensity)

merged <- merged %>%
  mutate(
    frpm_rate = ifelse(frpm_rate <= 1, frpm_rate * 100, frpm_rate),
    running   = frpm_rate - 75,
    treated   = ifelse(frpm_rate >= 75, 1, 0)
  )

ggplot(merged, aes(frpm_rate, chronic_absenteeism)) +
  geom_point(alpha = .4) +
  geom_vline(xintercept = 75, linetype = "dashed") +
  labs(x = "FRPM eligibility rate (%)",
       y = "Chronic absenteeism rate (%)")
```

```
## Warning: Removed 4710 rows containing missing values or values outside the scale range
## (`geom_point()`).
```




```
library(rddensity)

# 1. McCrary density test
dens75 <- rddensity(merged$frpm_rate, c = 75)
dens75$test             # prints t_jk and p_jk
```

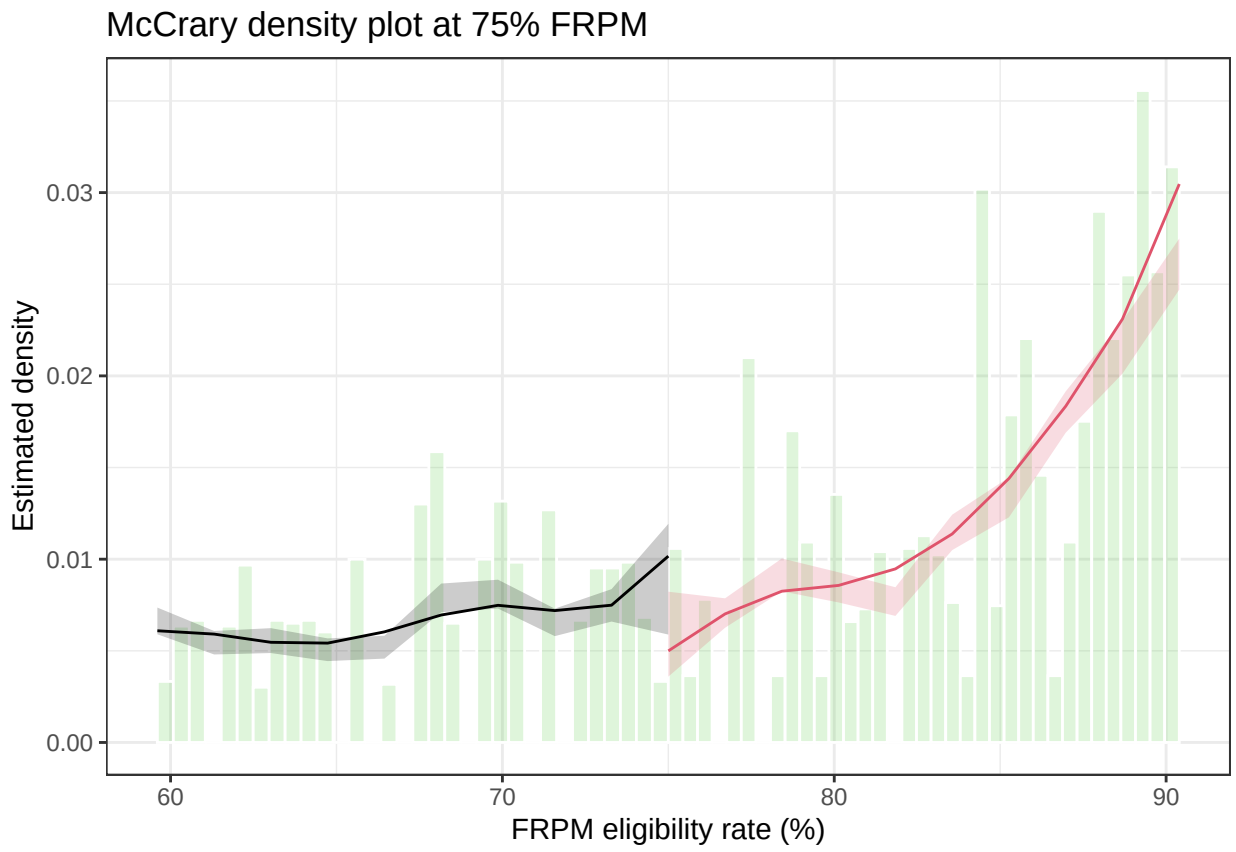
```
## $t_asy
## [1] NA
##
## $t_jk
## [1] -1.545891
##
## $p_asy
## [1] NA
##
## $p_jk
## [1] 0.1221309
```

```
# 3. Density test statistics (use the right object)
dens75$test             # NOT rd75$test
```

```
## $t_asy
```

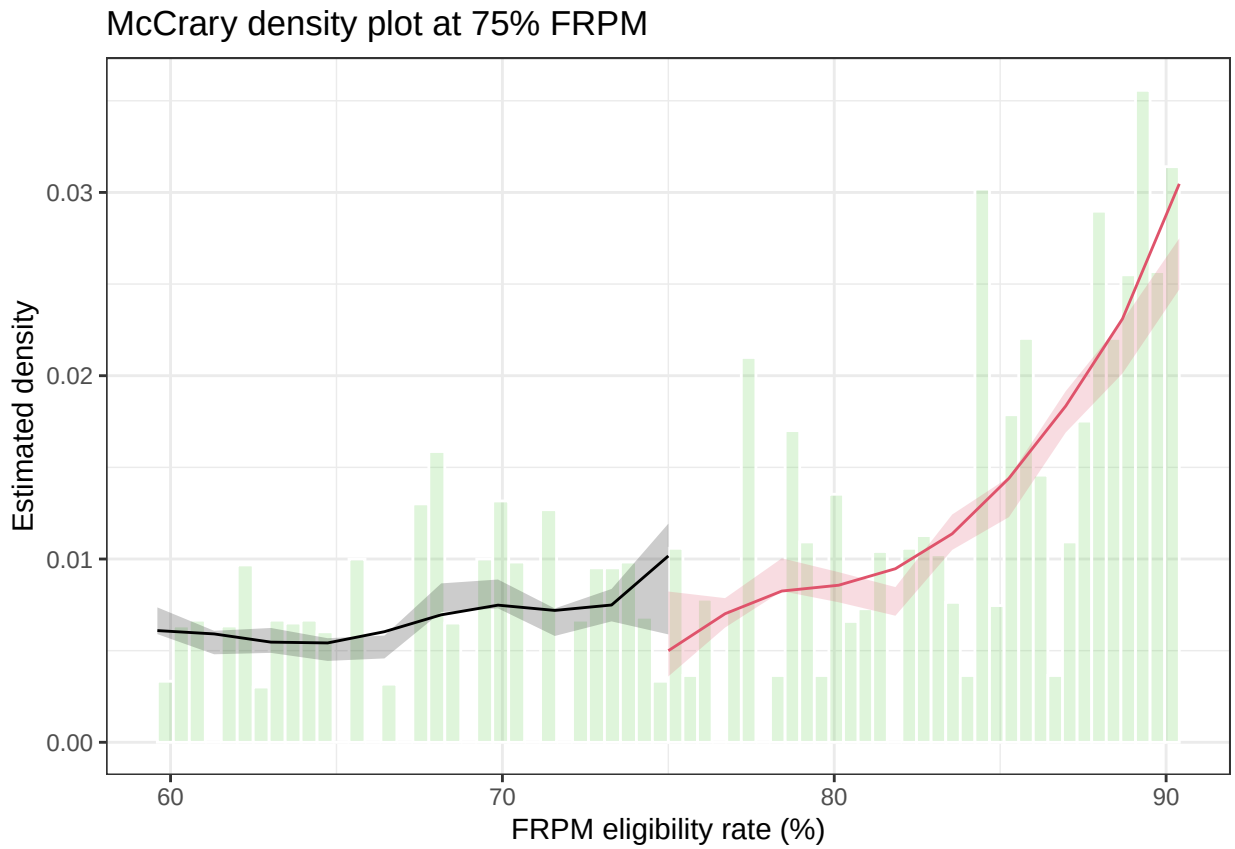
```
## [1] NA
##
## $t_jk
## [1] -1.545891
##
## $p_asy
## [1] NA
##
## $p_jk
## [1] 0.1221309
```

```r
# 4. McCrary density plot
# McCrary density test object
dens75 <- rddensity(merged$frpm_rate, c = 75)

# Density plot    rdd object first, X second
rdplotdensity(
  dens75,                 # ← rdd    (object returned by rddensity)
  merged$frpm_rate,       # ← X      (numeric running-variable vector)
  title  = "McCrary density plot at 75% FRPM",
  xlabel = "FRPM eligibility rate (%)",
  ylabel = "Estimated density"
)
```




```
## $Estl
```

```
## Call: lpdensity
##
## Sample size                                    3583
## Polynomial order for point estimation    (p=)  2
## Order of derivative estimated            (v=)  1
## Polynomial order for confidence interval (q=)  3
## Kernel function                                triangular
## Scaling factor                                 0.273511450381679
## Bandwidth method                               user provided
##
## Use summary(...) to show estimates.
##
## $Estr
## Call: lpdensity
##
## Sample size                                    9518
## Polynomial order for point estimation    (p=)  2
## Order of derivative estimated            (v=)  1
## Polynomial order for confidence interval (q=)  3
## Kernel function                                triangular
## Scaling factor                                 0.726564885496183
## Bandwidth method                               user provided
##
## Use summary(...) to show estimates.
##
## $Estplot
```



VIII. Covariate Balance Checks

What: Test if school characteristics (e.g., enrollment) are smooth across the cutoff.

Why: Ensures groups just above and below the cutoff are comparable.

How it supports your thesis: No discontinuity in covariates = credible causal design.

> Consider expanding this section: Include more covariates if available (e.g., ELL %, foster youth %, total enrollment).

IX. Robustness Checks

1. Bandwidth Sensitivity

Try different bandwidths (e.g., h = 2 to h = 6). Linear results are most credible. Avoid high-order polynomials due to overfitting.

```
# Fit models
bw_models <- list(
  h2 = rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 2, p = 1),
  h3 = rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 3, p = 1),
  h4 = rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 4.443, p = 1),
  h5 = rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 5, p = 1),
  h6 = rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 75, h = 6, p = 1)
)

# Create table
bw_results <- do.call(rbind, Map(function(model, h) {
  data.frame(
    Bandwidth = h,
    Coef = model$coef[1, 1],
    SE = model$se[1, 1],
    Pval = model$pv[1, 1],
    CI_Lower = model$ci[1, 1],
    CI_Upper = model$ci[1, 2]
  )
}, bw_models, c(2, 3, 4.443, 5, 6)))
knitr::kable(bw_results, digits = 3, caption = "Bandwidth Sensitivity: Local Linear RDD Estimates")
```

Table 1: Bandwidth Sensitivity: Local Linear RDD Estimates

	Bandwidth	Coef	SE	Pval	CI_Lower	CI_Upper
h2	2.000	-2.429	2.811	0.388	-7.939	3.081
h3	3.000	8.075	2.071	0.000	4.016	12.134
h4	4.443	10.368	1.734	0.000	6.969	13.767
h5	5.000	10.175	1.626	0.000	6.988	13.361
h6	6.000	8.157	1.441	0.000	5.332	10.981

2. Polynomial Order Sensitivity

Include results but de-emphasize cubic and quadratic fits. Note they are unstable and reverse sign — a common RDD issue.

```
# Models: m7, m8, m9 (h = 4, p = 1-3)
poly_models <- list(m7, m8, m9)
poly_info <- data.frame(Poly_Order = 1:3, Bandwidth = 4)

poly_table <- do.call(rbind, Map(function(model, spec) {
  data.frame(
    Poly_Order = spec$Poly_Order,
    Coef = model$coef[1,1],
    SE = model$se[1,1],
    Pval = model$pv[1,1],
    CI_Lower = model$ci[1,1],
    CI_Upper = model$ci[1,2]
  )
}, poly_models, split(poly_info, seq(nrow(poly_info)))))

knitr::kable(poly_table, digits = 3, caption = "Polynomial Order Sensitivity at h = 4")
```

Table 2: Polynomial Order Sensitivity at h = 4

Poly_Order	Coef	SE	Pval	CI_Lower	CI_Upper
1	9.984	1.862	0.000	6.334	13.634
2	1.781	2.766	0.520	-3.639	7.202
3	-13.603	4.368	0.002	-22.164	-5.042

3. Placebo Cutoffs (Next Step Suggestion)

Try cutoffs at 85% or 90% where no program change should occur. Null effects there will further validate your 75% results.

```
# Placebo cutoffs at 85% and 90%
p70 <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 85, h = 4, p = 1, masspoints = "adjus
p80 <- rdrobust(merged$chronic_absenteeism, merged$frpm_rate, c = 90, h = 4, p = 1, masspoints = "adjus

placebo_results <- do.call(rbind, Map(function(model, cutoff) {
  data.frame(
    Placebo_Cutoff = cutoff,
    Coef = model$coef[1,1],
    SE = model$se[1,1],
    Pval = model$pv[1,1],
    CI_Lower = model$ci[1,1],
    CI_Upper = model$ci[1,2]
  )
}, list(p70, p80), c(70, 80)))

knitr::kable(placebo_results, digits = 3, caption = "Placebo Cutoffs (No Expected Treatment Effect)")
```

Table 3: Placebo Cutoffs (No Expected Treatment Effect)

Placebo_Cutoff	Coef	SE	Pval	CI_Lower	CI_Upper
70	0.102	1.245	0.935	-2.339	2.543
80	-0.358	1.046	0.732	-2.407	1.692

4. Covariate Balance Across Bandwidths

(Optional) Repeat balance checks using different bandwidths to confirm results hold locally.

X. Final RDD Plots

Use `rdplot()` for h = 3 to 6, `p = 1`. Zoom in (65–85%) for interpretability.

> Use `fig.cap` for titles. Reference plots in the text: e.g., "Figure 2 shows a local linear RDD plot at h = 4."