

Symbolic Incentives in High-Stakes Prosocial Behavior

Supplementary Tables S1-S10

June 22, 2025

Contents

Data Loading	1
Table S1: Study Sample Representativeness	2
Table S2: Balance Check	3
Table S3: Attrition Information	8
Table S4: Main Analysis (Average Marginal Effects)	8
Table S5: Intent-to-Treat (ITT) Analysis	16
Table S6: OLS Regressions	19
Table S7: Different Time Windows	22
Table S8: Unsubscription and Total Donations	24
Table S9: Heterogeneous Treatment Effects	25
Table S10: Intention-Behavior Gap	28

Data Loading

```
# Load the dataset
df <- read_csv('final_dataset.csv')

## Rows: 20916 Columns: 28
## -- Column specification -----
## Delimiter: ","
## chr  (5): participant_id, treatment_group, race, bloodtype_group, us_region
## dbl (20): wave, is_female, age, prior_plasma_donation, avg_annual_donations,...
## lgl  (3): is_study_sample, is_ab_blood_type, high_prior_donations
```

```
##
## i Use `spec()` to retrieve the full column specification for this data.
## i Specify the column types or set `show_col_types = FALSE` to quiet this message.
```

```
# Define the two main analysis samples
baseline_sample <- df
study_sample <- df %>% filter(is_study_sample == TRUE)

# Show sample sizes
print(paste("Baseline sample size:", nrow(baseline_sample)))
```

```
## [1] "Baseline sample size: 20916"
```

```
print(paste("Study sample size:", nrow(study_sample)))
```

```
## [1] "Study sample size: 2322"
```

Table S1: Study Sample Representativeness

```
# Calculate means for each characteristic in the study sample
table_s1_results <- study_sample %>%
  summarise(
    female_prop = mean(is_female, na.rm = TRUE),
    white_prop = mean(race == "White", na.rm = TRUE),
    hispanic_prop = mean(race == "Hispanic", na.rm = TRUE),
    other_prop = mean(race == "Other", na.rm = TRUE),
    black_prop = mean(race == "Black", na.rm = TRUE),
    asian_prop = mean(race == "Asian", na.rm = TRUE),
    age_mean = mean(age, na.rm = TRUE),
    prior_plasma_prop = mean(prior_plasma_donation, na.rm = TRUE),
    ab_blood_prop = mean(is_ab_blood_type, na.rm = TRUE),
    annual_donations_mean = mean(avg_annual_donations, na.rm = TRUE),
    median_income_mean = mean(zip_median_income, na.rm = TRUE),
    midwest_prop = mean(us_region == "Midwest", na.rm = TRUE),
    northeast_prop = mean(us_region == "Northeast", na.rm = TRUE),
    south_prop = mean(us_region == "South", na.rm = TRUE),
    west_prop = mean(us_region == "West", na.rm = TRUE),
    urban_prop = mean(is_urban, na.rm = TRUE),
    covid_incidence_mean = mean(county_covid_per_100k, na.rm = TRUE)
  )

# Print results
print("Table S1 Results - Study Sample Characteristics:")
```

```
## [1] "Table S1 Results - Study Sample Characteristics:"
```

```
print(t(table_s1_results))
```

```
##                                [,1]
## female_prop                  5.004e-01
## white_prop                   8.730e-01
## hispanic_prop                6.245e-02
## other_prop                   2.153e-02
## black_prop                   2.110e-02
## asian_prop                   1.852e-02
## age_mean                     4.648e+01
## prior_plasma_prop            3.015e-02
## ab_blood_prop                4.522e-02
## annual_donations_mean       1.727e+00
## median_income_mean          7.498e+04
## midwest_prop                 4.070e-01
## northeast_prop              1.593e-01
## south_prop                   2.808e-01
## west_prop                    1.529e-01
## urban_prop                   9.039e-01
## covid_incidence_mean        4.426e+03
```

Table S2: Balance Check

```
# Panel A: Study Sample Balance Check
```

```
# For continuous variables (age, annual donations, income, covid incidence)
print("Panel A - Continuous Variables Balance:")
```

```
## [1] "Panel A - Continuous Variables Balance:"
```

```
# Age
```

```
age_control <- study_sample %>% filter(treatment_group == "Control") %>% pull(age)
age_treatment <- study_sample %>% filter(treatment_group == "Symbolic Incentives") %>% pull(age)
age_test <- t.test(age_control, age_treatment)
print(paste("Age - Control mean:", round(mean(age_control, na.rm=TRUE), 2),
           "Treatment mean:", round(mean(age_treatment, na.rm=TRUE), 2),
           "Difference:", round(mean(age_treatment, na.rm=TRUE) - mean(age_control, na.rm=TRUE), 2),
           "p-value:", round(age_test$p.value, 3)))
```

```
## [1] "Age - Control mean: 45.71 Treatment mean: 47.25 Difference: 1.54 p-value: 0.02"
```

```
# Annual donations
```

```
donations_control <- study_sample %>% filter(treatment_group == "Control") %>% pull(avg_annual_donations)
donations_treatment <- study_sample %>% filter(treatment_group == "Symbolic Incentives") %>% pull(avg_annual_donations)
donations_test <- t.test(donations_control, donations_treatment)
print(paste("Annual Donations - Control mean:", round(mean(donations_control, na.rm=TRUE), 2),
           "Treatment mean:", round(mean(donations_treatment, na.rm=TRUE), 2),
           "Difference:", round(mean(donations_treatment, na.rm=TRUE) - mean(donations_control, na.rm=TRUE), 2),
           "p-value:", round(donations_test$p.value, 3)))
```

```
## [1] "Annual Donations - Control mean: 1.74 Treatment mean: 1.72 Difference: -0.02 p-value: 0.808"
```

```
# Median income
income_control <- study_sample %>% filter(treatment_group == "Control") %>% pull(zip_median_income)
income_treatment <- study_sample %>% filter(treatment_group == "Symbolic Incentives") %>% pull(zip_median_income)
income_test <- t.test(income_control, income_treatment)
print(paste("Median Income - Control mean:", round(mean(income_control, na.rm=TRUE), 2),
            "Treatment mean:", round(mean(income_treatment, na.rm=TRUE), 2),
            "Difference:", round(mean(income_treatment, na.rm=TRUE) - mean(income_control, na.rm=TRUE), 2),
            "p-value:", round(income_test$p.value, 3)))
```

```
## [1] "Median Income - Control mean: 74992.82 Treatment mean: 74964.26 Difference: -28.56 p-value: 0.95"
```

```
# COVID-19 incidence
covid_control <- study_sample %>% filter(treatment_group == "Control") %>% pull(county_covid_per_100k)
covid_treatment <- study_sample %>% filter(treatment_group == "Symbolic Incentives") %>% pull(county_covid_per_100k)
covid_test <- t.test(covid_control, covid_treatment)
print(paste("COVID-19 Incidence - Control mean:", round(mean(covid_control, na.rm=TRUE), 2),
            "Treatment mean:", round(mean(covid_treatment, na.rm=TRUE), 2),
            "Difference:", round(mean(covid_treatment, na.rm=TRUE) - mean(covid_control, na.rm=TRUE), 2),
            "p-value:", round(covid_test$p.value, 3)))
```

```
## [1] "COVID-19 Incidence - Control mean: 4370.78 Treatment mean: 4481.73 Difference: 110.95 p-value: 0.0001"
```

```
# For binary variables
print("\nPanel A - Binary Variables Balance:")
```

```
## [1] "\nPanel A - Binary Variables Balance:"
```

```
# Female
female_table <- table(study_sample$is_female, study_sample$treatment_group)
female_test <- chisq.test(female_table)
female_props <- prop.table(female_table, 2)
print(paste("Female - Control prop:", round(female_props[2,1], 3),
            "Treatment prop:", round(female_props[2,2], 3),
            "Difference:", round(female_props[2,2] - female_props[2,1], 3),
            "p-value:", round(female_test$p.value, 3)))
```

```
## [1] "Female - Control prop: 0.494 Treatment prop: 0.506 Difference: 0.012 p-value: 0.589"
```

```
# Prior plasma donation
prior_table <- table(study_sample$prior_plasma_donation, study_sample$treatment_group)
prior_test <- chisq.test(prior_table)
prior_props <- prop.table(prior_table, 2)
print(paste("Prior Plasma - Control prop:", round(prior_props[2,1], 3),
            "Treatment prop:", round(prior_props[2,2], 3),
            "Difference:", round(prior_props[2,2] - prior_props[2,1], 3),
            "p-value:", round(prior_test$p.value, 3)))
```

```
## [1] "Prior Plasma - Control prop: 0.036 Treatment prop: 0.024 Difference: -0.012 p-value: 0.122"
```

```
# Urban region
urban_table <- table(study_sample$is_urban, study_sample$treatment_group)
urban_test <- chisq.test(urban_table)
urban_props <- prop.table(urban_table, 2)
print(paste("Urban Region - Control prop:", round(urban_props[2,1], 3),
            "Treatment prop:", round(urban_props[2,2], 3),
            "Difference:", round(urban_props[2,2] - urban_props[2,1], 3),
            "p-value:", round(urban_test$p.value, 3)))
```

```
## [1] "Urban Region - Control prop: 0.905 Treatment prop: 0.903 Difference: -0.002 p-value: 0.933"
```

```
# For categorical variables
print("\nPanel A - Categorical Variables Balance:")
```

```
## [1] "\nPanel A - Categorical Variables Balance:"
```

```
# Race
race_table <- table(study_sample$race, study_sample$treatment_group)
race_test <- chisq.test(race_table)
```

```
## Warning in chisq.test(race_table): Chi-squared approximation may be incorrect
```

```
print("Race proportions by treatment:")
```

```
## [1] "Race proportions by treatment:"
```

```
print(prop.table(race_table, 2))
```

```
##
##           Control Symbolic Incentives
##   Asian      0.018884      0.018150
##   Black      0.021459      0.020743
##   Hispanic    0.063519      0.061366
##   Missing/Other 0.002575      0.004322
##   Other      0.026609      0.016422
##   White      0.866953      0.878997
```

```
print(paste("Race chi-squared p-value:", round(race_test$p.value, 3)))
```

```
## [1] "Race chi-squared p-value: 0.626"
```

```
# Blood type
bloodtype_table <- table(study_sample$bloodtype_group, study_sample$treatment_group)
bloodtype_test <- chisq.test(bloodtype_table)
print("\nBlood type proportions by treatment:")
```

```
## [1] "\nBlood type proportions by treatment:"
```

```
print(prop.table(bloodtype_table, 2))
```

```
##
##           Control Symbolic Incentives
##   A-  0.066953           0.081245
##   A+  0.287554           0.230769
##   AB- 0.008584           0.007779
##   AB+ 0.034335           0.039758
##   B-   0.020601           0.022472
##   B+   0.082403           0.082973
##   O-   0.121030           0.126188
##   O+   0.378541           0.408816
```

```
print(paste("Blood type chi-squared p-value:", round(bloodtype_test$p.value, 3)))
```

```
## [1] "Blood type chi-squared p-value: 0.143"
```

```
# US Region
region_table <- table(study_sample$us_region, study_sample$treatment_group)
region_test <- chisq.test(region_table)
print("\nUS Region proportions by treatment:")
```

```
## [1] "\nUS Region proportions by treatment:"
```

```
print(prop.table(region_table, 2))
```

```
##
##           Control Symbolic Incentives
##   Midwest  0.3991           0.4149
##   Northeast 0.1691           0.1495
##   South     0.2738           0.2878
##   West      0.1579           0.1478
```

```
print(paste("US Region chi-squared p-value:", round(region_test$p.value, 3)))
```

```
## [1] "US Region chi-squared p-value: 0.467"
```

```
# Wave
wave_table <- table(study_sample$wave, study_sample$treatment_group)
wave_test <- chisq.test(wave_table)
print("\nWave proportions by treatment:")
```

```
## [1] "\nWave proportions by treatment:"
```

```
print(prop.table(wave_table, 2))
```

```
##
##      Control Symbolic Incentives
##  1 0.116738          0.114952
##  2 0.398283          0.399309
##  3 0.181116          0.184097
##  4 0.294421          0.294728
##  5 0.009442          0.006914
```

```
print(paste("Wave chi-squared p-value:", round(wave_test$p.value, 3)))
```

```
## [1] "Wave chi-squared p-value: 0.974"
```

```
# Sample sizes
print("\nPanel A - Sample Sizes:")
```

```
## [1] "\nPanel A - Sample Sizes:"
```

```
print(table(study_sample$treatment_group))
```

```
##
##      Control Symbolic Incentives
##      1165          1157
```

```
# Panel B: Baseline Sample Balance
print("\n\nPanel B - Baseline Sample Selection Criteria:")
```

```
## [1] "\n\nPanel B - Baseline Sample Selection Criteria:"
```

```
# Email opened
opened_table <- table(baseline_sample$email_opened, baseline_sample$treatment_group)
opened_test <- chisq.test(opened_table)
opened_props <- prop.table(opened_table, 2)
print(paste("Email Opened - Control prop:", round(opened_props[2,1], 3),
            "Treatment prop:", round(opened_props[2,2], 3),
            "Difference:", round(opened_props[2,2] - opened_props[2,1], 3),
            "p-value:", round(opened_test$p.value, 3)))
```

```
## [1] "Email Opened - Control prop: 0.445 Treatment prop: 0.446 Difference: 0.001 p-value: 0.93"
```

```
# No phone contact
phone_table <- table(baseline_sample$no_phone_contact, baseline_sample$treatment_group)
phone_test <- chisq.test(phone_table)
phone_props <- prop.table(phone_table, 2)
print(paste("No Phone Contact - Control prop:", round(phone_props[2,1], 3),
            "Treatment prop:", round(phone_props[2,2], 3),
            "Difference:", round(phone_props[2,2] - phone_props[2,1], 3),
            "p-value:", round(phone_test$p.value, 3)))
```

```
## [1] "No Phone Contact - Control prop: 0.228 Treatment prop: 0.227 Difference: 0 p-value: 0.952"
```

```
print("\nPanel B - Sample Sizes:")
```

```
## [1] "\nPanel B - Sample Sizes:"
```

```
print(table(baseline_sample$treatment_group))
```

```
##
##           Control Symbolic Incentives
##           10529           10387
```

Table S3: Attrition Information

```
# Calculate attrition by treatment group
attrition_summary <- baseline_sample %>%
  group_by(treatment_group) %>%
  summarise(
    enrolled = n(),
    analyzed = sum(is_study_sample, na.rm = TRUE),
    excluded_total = enrolled - analyzed,
    # Criterion 1 only: did not open email, but no phone contact
    excluded_crit1_only = sum(email_opened == 0 & no_phone_contact == 1, na.rm = TRUE),
    # Criterion 2 only: had phone contact, but did open email
    excluded_crit2_only = sum(email_opened == 1 & no_phone_contact == 0, na.rm = TRUE),
    # Both criteria: neither opened email nor phone contact
    excluded_both = sum(email_opened == 0 & no_phone_contact == 0, na.rm = TRUE),
    # Calculate proportions
    prop_crit1 = excluded_crit1_only / excluded_total,
    prop_crit2 = excluded_crit2_only / excluded_total,
    prop_both = excluded_both / excluded_total
  )

print("Table S3 - Attrition Information:")
```

```
## [1] "Table S3 - Attrition Information:"
```

```
print(attrition_summary)
```

```
## # A tibble: 2 x 10
##   treatment_group   enrolled analyzed excluded_total excluded_crit1_only
##   <chr>           <int>    <int>         <int>          <int>
## 1 Control         10529    1165          9364           1235
## 2 Symbolic Incentives 10387    1157          9230           1206
## # i 5 more variables: excluded_crit2_only <int>, excluded_both <int>,
## #   prop_crit1 <dbl>, prop_crit2 <dbl>, prop_both <dbl>
```

Table S4: Main Analysis (Average Marginal Effects)


```

# Model 1: Appointment creation without controls
modell1 <- glm(appointment_within_48h ~ treatment_group + factor(wave),
              data = study_sample, family = "binomial")
print("Model 1 - Appointment Creation (No Controls):")

## [1] "Model 1 - Appointment Creation (No Controls):"

summary(modell1)

##
## Call:
## glm(formula = appointment_within_48h ~ treatment_group + factor(wave),
##      family = "binomial", data = study_sample)
##
## Coefficients:
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -4.701      0.595  -7.90 2.7e-15 ***
## treatment_groupSymbolic Incentives    0.397      0.218    1.82  0.068 .
## factor(wave)2       1.186      0.607    1.95  0.051 .
## factor(wave)3       1.529      0.622    2.46  0.014 *
## factor(wave)4       1.534      0.607    2.53  0.011 *
## factor(wave)5     -12.047     549.025  -0.02  0.982
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 767.94  on 2321  degrees of freedom
## Residual deviance: 751.99  on 2316  degrees of freedom
## AIC: 764
##
## Number of Fisher Scoring iterations: 15

# Calculate AME for Model 1
margins1 <- margins(modell1)
print("\nAME for Model 1:")

## [1] "\nAME for Model 1:"

summary(margins1)

##              factor      AME      SE      z      p      lower
## treatment_groupSymbolic Incentives 0.0147 0.0080 1.8343 0.0666 -0.0010
##              wave2 0.0245 0.0088 2.7669 0.0057 0.0071
##              wave3 0.0383 0.0123 3.1092 0.0019 0.0142
##              wave4 0.0385 0.0105 3.6737 0.0002 0.0180
##              wave5 -0.0112 0.0064 -1.7422 0.0815 -0.0237
## upper
## 0.0305
## 0.0418

```

```
## 0.0624
## 0.0591
## 0.0014
```

```
# Model 2: Appointment creation with controls
```

```
model2 <- glm(appointment_within_48h ~ treatment_group + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = study_sample, family = "binomial")
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
print("\n\nModel 2 - Appointment Creation (With Controls):")
```

```
## [1] "\n\nModel 2 - Appointment Creation (With Controls):"
```

```
summary(model2)
```

```
##
## Call:
## glm(formula = appointment_within_48h ~ treatment_group + factor(wave) +
##      is_female + age + race + prior_plasma_donation + bloodtype_group +
##      avg_annual_donations + zip_median_income + us_region + is_urban +
##      county_covid_per_100k, family = "binomial", data = study_sample)
##
## Coefficients:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -7.41e+00   1.48e+00  -5.00  5.8e-07 ***
## treatment_groupSymbolic Incentives  5.92e-01   2.51e-01   2.36  0.01845 *
## factor(wave)2      1.57e+00   6.31e-01   2.48  0.01310 *
## factor(wave)3      1.85e+00   6.62e-01   2.80  0.00514 **
## factor(wave)4      2.53e+00   6.60e-01   3.83  0.00013 ***
## factor(wave)5     -1.29e+01   1.39e+03  -0.01  0.99258
## is_female         2.31e-01   2.48e-01   0.93  0.35254
## age               3.98e-03   8.35e-03   0.48  0.63405
## raceBlack        -1.54e+01   9.04e+02  -0.02  0.98639
## raceHispanic     -1.24e+00   8.32e-01  -1.49  0.13611
## raceMissing/Other -1.52e+01   2.60e+03  -0.01  0.99532
## raceOther        -1.05e+00   1.02e+00  -1.03  0.30379
## raceWhite        -3.28e-01   6.88e-01  -0.48  0.63298
## prior_plasma_donation -1.62e+01   8.23e+02  -0.02  0.98426
## bloodtype_groupA+  1.74e+00   7.48e-01   2.33  0.01977 *
## bloodtype_groupAB- 1.60e+00   1.29e+00   1.24  0.21569
## bloodtype_groupAB+ 1.22e+00   1.03e+00   1.18  0.23891
## bloodtype_groupB-  1.14e+00   1.25e+00   0.91  0.36179
## bloodtype_groupB+  2.15e+00   7.91e-01   2.71  0.00667 **
## bloodtype_group0-  7.25e-01   8.39e-01   0.86  0.38765
## bloodtype_group0+  9.70e-01   7.58e-01   1.28  0.20046
## avg_annual_donations 1.03e-01   5.98e-02   1.73  0.08386 .
## zip_median_income  3.52e-06   4.94e-06   0.71  0.47653
## us_regionNortheast  7.52e-01   4.13e-01   1.82  0.06881 .
```

```
## us_regionSouth          -8.61e-01  4.16e-01  -2.07  0.03848 *
## us_regionWest           1.33e+00  3.24e-01   4.12  3.8e-05 ***
## is_urban                1.27e+00  7.42e-01   1.71  0.08746 .
## county_covid_per_100k   -2.53e-04  8.28e-05  -3.05  0.00225 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 665.71  on 2085  degrees of freedom
## Residual deviance: 551.03  on 2058  degrees of freedom
## (236 observations deleted due to missingness)
## AIC: 607
##
## Number of Fisher Scoring iterations: 17
```

```
# Calculate AME for Model 2
margins2 <- margins(model2)
print("\nAME for Model 2:")
```

```
## [1] "\nAME for Model 2:"
```

```
summary(margins2)
```

```
##               factor      AME      SE      z      p      lower
##               age  0.0001  0.0003  0.4759  0.6341  -0.0004
##   avg_annual_donations  0.0034  0.0020  1.7190  0.0856  -0.0005
##   bloodtype_groupA+  0.0440  0.0120  3.6648  0.0002   0.0205
##   bloodtype_groupAB-  0.0375  0.0462  0.8117  0.4170  -0.0530
##   bloodtype_groupAB+  0.0235  0.0244  0.9624  0.3359  -0.0244
##   bloodtype_groupB-  0.0213  0.0311  0.6833  0.4944  -0.0397
##   bloodtype_groupB+  0.0662  0.0215  3.0829  0.0020   0.0241
##   bloodtype_group0-  0.0109  0.0116  0.9378  0.3484  -0.0119
##   bloodtype_group0+  0.0165  0.0096  1.7206  0.0853  -0.0023
##   county_covid_per_100k -0.0000  0.0000 -2.9903  0.0028  -0.0000
##   is_female  0.0076  0.0082  0.9282  0.3533  -0.0084
##   is_urban  0.0417  0.0247  1.6922  0.0906  -0.0066
##   prior_plasma_donation -0.5344 27.0942 -0.0197  0.9843 -53.6382
##   raceBlack -0.0543  0.0306 -1.7750  0.0759  -0.1143
##   raceHispanic -0.0364  0.0313 -1.1635  0.2446  -0.0977
##   raceMissing/Other -0.0543  0.0306 -1.7750  0.0759  -0.1143
##   raceOther -0.0329  0.0339 -0.9717  0.3312  -0.0992
##   raceWhite -0.0134  0.0313 -0.4270  0.6693  -0.0746
##   treatment_groupSymbolic Incentives  0.0193  0.0081  2.3793  0.0173   0.0034
##   us_regionNortheast  0.0290  0.0185  1.5683  0.1168  -0.0072
##   us_regionSouth -0.0165  0.0076 -2.1607  0.0307  -0.0314
##   us_regionWest  0.0665  0.0190  3.5001  0.0005   0.0293
##   wave2  0.0246  0.0072  3.4229  0.0006   0.0105
##   wave3  0.0338  0.0107  3.1477  0.0016   0.0128
##   wave4  0.0654  0.0143  4.5634  0.0000   0.0373
##   wave5 -0.0073  0.0042 -1.7218  0.0851  -0.0156
##   zip_median_income  0.0000  0.0000  0.7066  0.4798  -0.0000
##   upper
```

```
## 0.0007
## 0.0073
## 0.0675
## 0.1280
## 0.0714
## 0.0823
## 0.1083
## 0.0337
## 0.0353
## -0.0000
## 0.0236
## 0.0901
## 52.5693
## 0.0057
## 0.0249
## 0.0057
## 0.0335
## 0.0479
## 0.0351
## 0.0652
## -0.0015
## 0.1038
## 0.0387
## 0.0549
## 0.0935
## 0.0010
## 0.0000
```

```
# Model 3: Donation without controls
```

```
model3 <- glm(donated_within_13d ~ treatment_group + factor(wave),
              data = study_sample, family = "binomial")
print("\n\nModel 3 - Donation (No Controls):")
```

```
## [1] "\n\nModel 3 - Donation (No Controls):"
```

```
summary(model3)
```

```
##
## Call:
## glm(formula = donated_within_13d ~ treatment_group + factor(wave),
##      family = "binomial", data = study_sample)
##
## Coefficients:
##
##              Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -4.897      0.818   -5.99 2.1e-09 ***
## treatment_groupSymbolic Incentives    0.711      0.869    0.82  0.413
## factor(wave)2     -1.655      0.916   -1.81  0.071 .
## factor(wave)3    -17.074    1410.016   -0.01  0.990
## factor(wave)4     -2.046      1.157   -1.77  0.077 .
## factor(wave)5    -17.017    6659.427    0.00  0.998
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
##
```

```
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 83.486 on 2321 degrees of freedom
## Residual deviance: 75.832 on 2316 degrees of freedom
## AIC: 87.83
##
## Number of Fisher Scoring iterations: 20
```

```
# Calculate AME for Model 3
margins3 <- margins(model3)
print("\nAME for Model 3:")
```

```
## [1] "\nAME for Model 3:"
```

```
summary(margins3)
```

```
##               factor      AME      SE      z      p      lower
## treatment_groupSymbolic Incentives  0.0018 0.0021  0.8343 0.4041 -0.0024
##                               wave2 -0.0090 0.0066 -1.3683 0.1712 -0.0219
##                               wave3 -0.0112 0.0064 -1.7429 0.0813 -0.0238
##                               wave4 -0.0097 0.0066 -1.4773 0.1396 -0.0226
##                               wave5 -0.0112 0.0064 -1.7429 0.0813 -0.0238
## upper
## 0.0059
## 0.0039
## 0.0014
## 0.0032
## 0.0014
```

```
# Model 4: Donation with controls
model4 <- glm(donated_within_13d ~ treatment_group + factor(wave) +
             is_female + age + race + prior_plasma_donation + bloodtype_group +
             avg_annual_donations + zip_median_income + us_region + is_urban +
             county_covid_per_100k,
             data = study_sample, family = "binomial")
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
print("\n\nModel 4 - Donation (With Controls):")
```

```
## [1] "\n\nModel 4 - Donation (With Controls):"
```

```
summary(model4)
```

```
##
## Call:
## glm(formula = donated_within_13d ~ treatment_group + factor(wave) +
##      is_female + age + race + prior_plasma_donation + bloodtype_group +
##      avg_annual_donations + zip_median_income + us_region + is_urban +
##      county_covid_per_100k, family = "binomial", data = study_sample)
```

```
##
## Coefficients:
##               Estimate Std. Error z value Pr(>|z|)
## (Intercept)      -6.35e+01  2.05e+04   0.00   1.00
## treatment_groupSymbolic Incentives  7.69e-01  1.14e+00   0.68   0.50
## factor(wave)2      -1.06e+00  1.10e+00  -0.97   0.33
## factor(wave)3      -1.98e+01  4.76e+03   0.00   1.00
## factor(wave)4      -1.90e+01  3.73e+03  -0.01   1.00
## factor(wave)5      -1.75e+01  2.48e+04   0.00   1.00
## is_female          1.72e+00  1.20e+00   1.44   0.15
## age                6.71e-02  4.24e-02   1.58   0.11
## raceBlack           1.12e+00  2.33e+04   0.00   1.00
## raceHispanic        -3.00e-01  1.99e+04   0.00   1.00
## raceMissing/Other   -2.27e+00  4.45e+04   0.00   1.00
## raceOther            1.99e+01  1.76e+04   0.00   1.00
## raceWhite            1.79e+01  1.76e+04   0.00   1.00
## prior_plasma_donation -1.89e+01  1.18e+04   0.00   1.00
## bloodtype_groupA+    1.78e+01  7.97e+03   0.00   1.00
## bloodtype_groupAB-   2.46e+00  2.28e+04   0.00   1.00
## bloodtype_groupAB+  -2.06e+00  1.28e+04   0.00   1.00
## bloodtype_groupB-    1.49e+00  1.80e+04   0.00   1.00
## bloodtype_groupB+    1.87e+01  7.97e+03   0.00   1.00
## bloodtype_groupO-   -2.49e-01  9.83e+03   0.00   1.00
## bloodtype_groupO+    1.81e+01  7.97e+03   0.00   1.00
## avg_annual_donations  2.10e-01  2.38e-01   0.88   0.38
## zip_median_income    1.85e-05  1.69e-05   1.09   0.27
## us_regionNortheast    8.36e-01  1.64e+00   0.51   0.61
## us_regionSouth       -1.73e+01  3.98e+03   0.00   1.00
## us_regionWest         1.68e+00  1.49e+00   1.13   0.26
## is_urban              1.75e+01  6.76e+03   0.00   1.00
## county_covid_per_100k -6.22e-04  5.59e-04  -1.11   0.27
##
## (Dispersion parameter for binomial family taken to be 1)
##
## Null deviance: 70.324 on 2085 degrees of freedom
## Residual deviance: 36.994 on 2058 degrees of freedom
## (236 observations deleted due to missingness)
## AIC: 92.99
##
## Number of Fisher Scoring iterations: 23

# Calculate AME for Model 4
margins4 <- margins(model4)
print("\nAME for Model 4:")

## [1] "\nAME for Model 4:"

summary(margins4)

##               factor      AME      SE      z      p      lower
##               age 0.0001 0.0001 1.4089 0.1589 -0.0001
##      avg_annual_donations 0.0004 0.0005 0.8509 0.3948 -0.0006
##      bloodtype_groupA+ 0.0026 0.0018 1.4414 0.1495 -0.0009
```

##	bloodtype_groupAB-	0.0000	0.0000	0.0000	1.0000	-0.0000
##	bloodtype_groupAB+	-0.0000	0.0000	-0.0001	0.9999	-0.0000
##	bloodtype_groupB-	0.0000	0.0000	0.0000	1.0000	-0.0000
##	bloodtype_groupB+	0.0057	0.0048	1.1749	0.2400	-0.0038
##	bloodtype_groupO-	-0.0000	0.0000	-0.0000	1.0000	-0.0000
##	bloodtype_groupO+	0.0036	0.0023	1.5806	0.1140	-0.0009
##	county_covid_per_100k	-0.0000	0.0000	-1.0455	0.2958	-0.0000
##	is_female	0.0036	0.0027	1.3157	0.1883	-0.0018
##	is_urban	0.0366	14.0887	0.0026	0.9979	-27.5768
##	prior_plasma_donation	-0.0394	24.6602	-0.0016	0.9987	-48.3726
##	raceBlack	0.0000	0.0000	0.0000	1.0000	-0.0000
##	raceHispanic	-0.0000	0.0000	-0.0000	1.0000	-0.0000
##	raceMissing/Other	-0.0000	0.0000	-0.0000	1.0000	-0.0000
##	raceOther	0.0120	0.0124	0.9688	0.3326	-0.0123
##	raceWhite	0.0023	0.0011	2.0095	0.0445	0.0001
##	treatment_groupSymbolic Incentives	0.0016	0.0023	0.6904	0.4899	-0.0029
##	us_regionNortheast	0.0017	0.0033	0.4999	0.6172	-0.0049
##	us_regionSouth	-0.0015	0.0016	-0.9343	0.3502	-0.0046
##	us_regionWest	0.0050	0.0046	1.0757	0.2821	-0.0041
##	wave2	-0.0038	0.0044	-0.8470	0.3970	-0.0125
##	wave3	-0.0065	0.0040	-1.6333	0.1024	-0.0143
##	wave4	-0.0065	0.0040	-1.6333	0.1024	-0.0143
##	wave5	-0.0065	0.0040	-1.6333	0.1024	-0.0143
##	zip_median_income	0.0000	0.0000	1.0347	0.3008	-0.0000
##	upper					
##	0.0003					
##	0.0014					
##	0.0062					
##	0.0000					
##	0.0000					
##	0.0000					
##	0.0151					
##	0.0000					
##	0.0080					
##	0.0000					
##	0.0089					
##	27.6499					
##	48.2938					
##	0.0000					
##	0.0000					
##	0.0000					
##	0.0364					
##	0.0045					
##	0.0060					
##	0.0082					
##	0.0016					
##	0.0141					
##	0.0049					
##	0.0013					
##	0.0013					
##	0.0013					
##	0.0000					

Table S5: Intent-to-Treat (ITT) Analysis

```
# Repeat main analysis on baseline sample
print("Table S5 - ITT Analysis on Full Baseline Sample")

## [1] "Table S5 - ITT Analysis on Full Baseline Sample"

# Model 1: Appointment creation without controls (ITT)
modell1_itt <- glm(appointment_within_48h ~ treatment_group + factor(wave),
  data = baseline_sample, family = "binomial")
margins1_itt <- margins(modell1_itt)
print("Model 1 ITT - Appointment Creation (No Controls):")

## [1] "Model 1 ITT - Appointment Creation (No Controls):"

summary(margins1_itt)

##               factor      AME      SE      z      p      lower
## treatment_groupSymbolic Incentives  0.0026 0.0016  1.6648 0.0959 -0.0005
##                               wave2 -0.0024 0.0021 -1.1293 0.2588 -0.0065
##                               wave3 -0.0063 0.0025 -2.5325 0.0113 -0.0112
##                               wave4 -0.0051 0.0025 -2.0721 0.0383 -0.0099
##                               wave5 -0.0083 0.0058 -1.4315 0.1523 -0.0196
##      upper
##      0.0057
##      0.0018
##     -0.0014
##     -0.0003
##      0.0031

# Model 2: Appointment creation with controls (ITT)
modell2_itt <- glm(appointment_within_48h ~ treatment_group + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = baseline_sample, family = "binomial")
margins2_itt <- margins(modell2_itt)
print("\nModel 2 ITT - Appointment Creation (With Controls):")

## [1] "\nModel 2 ITT - Appointment Creation (With Controls):"

summary(margins2_itt)

##               factor      AME      SE      z      p      lower
##                               age  0.0002 0.0001  4.2140 0.0000  0.0001
##      avg_annual_donations  0.0009 0.0004  2.2015 0.0277  0.0001
##      bloodtype_groupA+    0.0019 0.0036  0.5280 0.5975 -0.0052
##      bloodtype_groupAB- -0.0001 0.0097 -0.0152 0.9879 -0.0192
##      bloodtype_groupAB+  0.0036 0.0057  0.6293 0.5291 -0.0076
```



```

##          bloodtype_groupB- -0.0062 0.0052 -1.1944 0.2323 -0.0163
##          bloodtype_groupB+  0.0038 0.0043  0.8775 0.3802 -0.0047
##          bloodtype_group0- -0.0043 0.0040 -1.0579 0.2901 -0.0122
##          bloodtype_group0+ -0.0043 0.0035 -1.2457 0.2129 -0.0111
##          county_covid_per_100k -0.0000 0.0000 -3.2818 0.0010 -0.0000
##              is_female  0.0031 0.0016  1.8873 0.0591 -0.0001
##              is_urban   0.0062 0.0042  1.4726 0.1409 -0.0021
##          prior_plasma_donation 0.0005 0.0052  0.0907 0.9277 -0.0097
##              raceBlack -0.0026 0.0062 -0.4255 0.6705 -0.0147
##              raceHispanic -0.0037 0.0050 -0.7399 0.4593 -0.0134
##          raceMissing/Other -0.0131 0.0045 -2.9481 0.0032 -0.0219
##              raceOther -0.0030 0.0063 -0.4858 0.6271 -0.0153
##              raceWhite -0.0003 0.0046 -0.0644 0.9487 -0.0093
## treatment_groupSymbolic Incentives 0.0033 0.0016  2.0420 0.0412  0.0001
##          us_regionNortheast 0.0107 0.0038  2.7897 0.0053  0.0032
##          us_regionSouth -0.0031 0.0016 -1.9279 0.0539 -0.0063
##          us_regionWest  0.0135 0.0032  4.1722 0.0000  0.0072
##              wave2 -0.0001 0.0019 -0.0739 0.9411 -0.0040
##              wave3 -0.0029 0.0026 -1.1007 0.2710 -0.0080
##              wave4  0.0030 0.0035  0.8503 0.3952 -0.0039
##              wave5 -0.0030 0.0070 -0.4196 0.6748 -0.0168
##          zip_median_income 0.0000 0.0000  2.9042 0.0037  0.0000
## upper
## 0.0003
## 0.0017
## 0.0091
## 0.0189
## 0.0147
## 0.0040
## 0.0123
## 0.0036
## 0.0025
## -0.0000
## 0.0063
## 0.0145
## 0.0106
## 0.0095
## 0.0060
## -0.0044
## 0.0092
## 0.0087
## 0.0064
## 0.0182
## 0.0001
## 0.0199
## 0.0037
## 0.0022
## 0.0098
## 0.0109
## 0.0000

```

```

# Model 3: Donation without controls (ITT)
model3_itt <- glm(donated_within_13d ~ treatment_group + factor(wave),
                  data = baseline_sample, family = "binomial")

```

```
margins3_itt <- margins(model3_itt)
print("\nModel 3 ITT - Donation (No Controls):")
```

```
## [1] "\nModel 3 ITT - Donation (No Controls):"
```

```
summary(margins3_itt)
```

```
##               factor      AME      SE      z      p      lower
## treatment_groupSymbolic Incentives  0.0009 0.0011  0.7946 0.4268 -0.0013
##               wave2 -0.0140 0.0019 -7.3788 0.0000 -0.0177
##               wave3 -0.0166 0.0019 -8.8481 0.0000 -0.0203
##               wave4 -0.0164 0.0019 -8.7798 0.0000 -0.0201
##               wave5 -0.0098 0.0058 -1.6795 0.0930 -0.0211
##      upper
##      0.0031
##     -0.0103
##     -0.0129
##     -0.0128
##      0.0016
```

```
# Model 4: Donation with controls (ITT)
model4_itt <- glm(donated_within_13d ~ treatment_group + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = baseline_sample, family = "binomial")
margins4_itt <- margins(model4_itt)
print("\nModel 4 ITT - Donation (With Controls):")
```

```
## [1] "\nModel 4 ITT - Donation (With Controls):"
```

```
summary(margins4_itt)
```

```
##               factor      AME      SE      z      p      lower
##               age  0.0001 0.0000  3.6969 0.0002  0.0001
## avg_annual_donations 0.0009 0.0003  3.6552 0.0003  0.0004
## bloodtype_groupA+ -0.0026 0.0031 -0.8411 0.4003 -0.0087
## bloodtype_groupAB- -0.0098 0.0029 -3.3635 0.0008 -0.0156
## bloodtype_groupAB+  0.0041 0.0049  0.8357 0.4033 -0.0056
## bloodtype_groupB- -0.0045 0.0047 -0.9505 0.3418 -0.0138
## bloodtype_groupB+ -0.0032 0.0034 -0.9413 0.3466 -0.0098
## bloodtype_group0- -0.0050 0.0034 -1.4664 0.1425 -0.0117
## bloodtype_group0+ -0.0063 0.0030 -2.0795 0.0376 -0.0122
## county_covid_per_100k -0.0000 0.0000 -3.7834 0.0002 -0.0000
## is_female  0.0020 0.0012  1.6826 0.0924 -0.0003
## is_urban  0.0112 0.0060  1.8638 0.0623 -0.0006
## prior_plasma_donation 0.0037 0.0026  1.4279 0.1533 -0.0014
## raceBlack -0.0040 0.0042 -0.9439 0.3452 -0.0122
## raceHispanic -0.0029 0.0038 -0.7627 0.4456 -0.0104
## raceMissing/Other -0.0082 0.0034 -2.3970 0.0165 -0.0150
## raceOther -0.0021 0.0048 -0.4374 0.6619 -0.0116
```

```
##               raceWhite -0.0021 0.0035 -0.5830 0.5599 -0.0090
## treatment_groupSymbolic Incentives 0.0015 0.0011 1.3249 0.1852 -0.0007
##               us_regionNortheast 0.0039 0.0022 1.7738 0.0761 -0.0004
##               us_regionSouth -0.0007 0.0012 -0.6128 0.5400 -0.0031
##               us_regionWest 0.0053 0.0020 2.6321 0.0085 0.0013
##               wave2 -0.0087 0.0016 -5.4252 0.0000 -0.0118
##               wave3 -0.0109 0.0016 -6.6141 0.0000 -0.0141
##               wave4 -0.0101 0.0019 -5.2967 0.0000 -0.0138
##               wave5 0.0004 0.0094 0.0424 0.9662 -0.0180
##               zip_median_income 0.0000 0.0000 1.9225 0.0545 -0.0000
## upper
## 0.0002
## 0.0014
## 0.0035
## -0.0041
## 0.0138
## 0.0048
## 0.0034
## 0.0017
## -0.0004
## -0.0000
## 0.0042
## 0.0230
## 0.0087
## 0.0043
## 0.0046
## -0.0015
## 0.0073
## 0.0049
## 0.0037
## 0.0082
## 0.0016
## 0.0092
## -0.0055
## -0.0077
## -0.0064
## 0.0188
## 0.0000
```

```
print(paste("\nSample size for ITT analysis:", nrow(baseline_sample)))
```

```
## [1] "\nSample size for ITT analysis: 20916"
```

Table S6: OLS Regressions

```
# OLS models with robust standard errors
print("Table S6 - OLS Regressions with Robust Standard Errors")
```

```
## [1] "Table S6 - OLS Regressions with Robust Standard Errors"
```

```

# Model 1: Appointment creation without controls (OLS)
ols1 <- lm(appointment_within_48h ~ treatment_group + factor(wave),
           data = study_sample)
print("Model 1 OLS - Appointment Creation (No Controls):")

## [1] "Model 1 OLS - Appointment Creation (No Controls):"

coeftest(ols1, vcov = vcovHC(ols1, type = "HC1"))

##
## t test of coefficients:
##
##
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.00387   0.00733    0.53  0.59789
## treatment_groupSymbolic Incentives 0.01474   0.00805    1.83  0.06723 .
## factor(wave)2      0.02442   0.00885    2.76  0.00582 **
## factor(wave)3      0.03826   0.01236    3.10  0.00199 **
## factor(wave)4      0.03849   0.01049    3.67  0.00025 ***
## factor(wave)5     -0.01007   0.00662   -1.52  0.12804
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

# Model 2: Appointment creation with controls (OLS)
ols2 <- lm(appointment_within_48h ~ treatment_group + factor(wave) +
           is_female + age + race + prior_plasma_donation + bloodtype_group +
           avg_annual_donations + zip_median_income + us_region + is_urban +
           county_covid_per_100k,
           data = study_sample)
print("\nModel 2 OLS - Appointment Creation (With Controls):")

## [1] "\nModel 2 OLS - Appointment Creation (With Controls):"

coeftest(ols2, vcov = vcovHC(ols2, type = "HC1"))

##
## t test of coefficients:
##
##
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)     -4.04e-02  5.74e-02   -0.70  0.48193
## treatment_groupSymbolic Incentives 1.76e-02  8.28e-03    2.13  0.03332 *
## factor(wave)2     3.92e-02  1.05e-02    3.73  0.00020 ***
## factor(wave)3     5.29e-02  1.52e-02    3.47  0.00052 ***
## factor(wave)4     7.41e-02  1.54e-02    4.80  1.7e-06 ***
## factor(wave)5     3.25e-02  2.04e-02    1.59  0.11088
## is_female         9.36e-03  8.29e-03    1.13  0.25903
## age               2.13e-04  2.85e-04    0.75  0.45416
## raceBlack        -6.16e-02  5.08e-02   -1.21  0.22556
## raceHispanic     -6.46e-02  5.31e-02   -1.22  0.22355
## raceMissing/Other -7.57e-02  5.30e-02   -1.43  0.15324
## raceOther        -4.16e-02  5.82e-02   -0.71  0.47470
## raceWhite        -2.50e-02  5.09e-02   -0.49  0.62386

```

```
## prior_plasma_donation      -7.32e-02  1.28e-02  -5.71  1.3e-08 ***
## bloodtype_groupA+         4.87e-02  1.37e-02   3.55  0.00039 ***
## bloodtype_groupAB-        4.74e-02  5.07e-02   0.93  0.35014
## bloodtype_groupAB+        2.77e-02  2.19e-02   1.27  0.20562
## bloodtype_groupB-         2.07e-02  2.43e-02   0.85  0.39418
## bloodtype_groupB+         6.90e-02  2.26e-02   3.06  0.00227 **
## bloodtype_groupO-         1.15e-02  1.31e-02   0.88  0.37732
## bloodtype_groupO+         1.95e-02  1.10e-02   1.78  0.07574 .
## avg_annual_donations      3.85e-03  2.90e-03   1.33  0.18489
## zip_median_income         1.41e-07  1.53e-07   0.92  0.35662
## us_regionNortheast        3.85e-02  2.37e-02   1.62  0.10435
## us_regionSouth            -1.63e-02  9.47e-03  -1.72  0.08547 .
## us_regionWest             7.06e-02  2.01e-02   3.51  0.00046 ***
## is_urban                  2.19e-02  8.74e-03   2.50  0.01240 *
## county_covid_per_100k     -8.57e-06  3.13e-06  -2.74  0.00615 **
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Model 3: Donation without controls (OLS)
ols3 <- lm(donated_within_13d ~ treatment_group + factor(wave),
  data = study_sample)
print("\nModel 3 OLS - Donation (No Controls):")
```

```
## [1] "\nModel 3 OLS - Donation (No Controls):"
```

```
coeftest(ols3, vcov = vcovHC(ols3, type = "HC1"))
```

```
##
## t test of coefficients:
##
##              Estimate Std. Error t value Pr(>|t|)
## (Intercept)      0.01028   0.00624    1.65   0.100 .
## treatment_groupSymbolic Incentives  0.00176   0.00211    0.83   0.405
## factor(wave)2     -0.00900   0.00659   -1.37   0.172
## factor(wave)3     -0.01117   0.00641   -1.74   0.082 .
## factor(wave)4     -0.00970   0.00658   -1.47   0.140
## factor(wave)5     -0.01102   0.00638   -1.73   0.084 .
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

```
# Model 4: Donation with controls (OLS)
ols4 <- lm(donated_within_13d ~ treatment_group + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = study_sample)
print("\nModel 4 OLS - Donation (With Controls):")
```

```
## [1] "\nModel 4 OLS - Donation (With Controls):"
```

```
coeftest(ols4, vcov = vcovHC(ols4, type = "HC1"))
```

```
##
## t test of coefficients:
##
##               Estimate Std. Error t value Pr(>|t|)
## (Intercept)      -6.32e-03   7.61e-03   -0.83   0.406
## treatment_groupSymbolic Incentives  1.29e-03   2.03e-03    0.64   0.524
## factor(wave)2      -9.12e-03   7.16e-03   -1.27   0.203
## factor(wave)3      -1.14e-02   6.93e-03   -1.64   0.101
## factor(wave)4      -1.08e-02   6.95e-03   -1.55   0.122
## factor(wave)5      -1.03e-02   6.29e-03   -1.64   0.102
## is_female          3.10e-03   2.15e-03    1.44   0.150
## age                1.25e-04   6.24e-05    2.01   0.044 *
## raceBlack           5.31e-04   2.45e-03    0.22   0.829
## raceHispanic        1.52e-04   2.34e-03    0.06   0.948
## raceMissing/Other  -3.62e-03   5.08e-03   -0.71   0.477
## raceOther           2.16e-02   2.09e-02    1.04   0.300
## raceWhite           3.49e-03   3.35e-03    1.04   0.298
## prior_plasma_donation -3.97e-03   2.12e-03   -1.87   0.062 .
## bloodtype_groupA+    3.72e-03   2.51e-03    1.48   0.138
## bloodtype_groupAB-    6.74e-04   1.36e-03    0.50   0.620
## bloodtype_groupAB+   -5.04e-04   1.34e-03   -0.38   0.707
## bloodtype_groupB-    1.78e-03   1.40e-03    1.27   0.203
## bloodtype_groupB+    5.97e-03   6.38e-03    0.94   0.350
## bloodtype_groupO-    6.62e-04   9.32e-04    0.71   0.477
## bloodtype_groupO+    3.08e-03   2.02e-03    1.52   0.128
## avg_annual_donations  4.48e-04   3.41e-04    1.32   0.188
## zip_median_income    5.32e-08   4.92e-08    1.08   0.280
## us_regionNortheast    6.79e-03   7.81e-03    0.87   0.385
## us_regionSouth       -2.11e-03   1.62e-03   -1.30   0.193
## us_regionWest         3.35e-03   5.56e-03    0.60   0.546
## is_urban              9.37e-04   1.35e-03    0.70   0.487
## county_covid_per_100k -5.50e-07   5.28e-07   -1.04   0.297
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Table S7: Different Time Windows

```
print("Table S7 - Different Time Windows (Logistic Regression)")
```

```
## [1] "Table S7 - Different Time Windows (Logistic Regression)"
```

```
# 24-hour window
model_24h <- glm(appointment_within_24h ~ treatment_group + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = study_sample, family = "binomial")
```

```
## Warning: glm.fit: fitted probabilities numerically 0 or 1 occurred
```

```
print("Appointment within 24 hours:")
```

```
## [1] "Appointment within 24 hours:"
```

```
summary(model_24h)$coefficients["treatment_groupSymbolic Incentives",]
```

```
##      Estimate Std. Error      z value    Pr(>|z|)
##      0.56325     0.26257      2.14515     0.03194
```

```
# 7-day window
```

```
model_7d <- glm(appointment_within_7d ~ treatment_group + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = study_sample, family = "binomial")
print("\nAppointment within 7 days:")
```

```
## [1] "\nAppointment within 7 days:"
```

```
summary(model_7d)$coefficients["treatment_groupSymbolic Incentives",]
```

```
##      Estimate Std. Error      z value    Pr(>|z|)
##      0.38199     0.21599      1.76857     0.07697
```

```
# Anytime appointment
```

```
model_anytime <- glm(appointment_anytime ~ treatment_group + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = study_sample, family = "binomial")
print("\nAppointment anytime:")
```

```
## [1] "\nAppointment anytime:"
```

```
summary(model_anytime)$coefficients["treatment_groupSymbolic Incentives",]
```

```
##      Estimate Std. Error      z value    Pr(>|z|)
##      0.1385     0.1681      0.8237     0.4101
```

```
# Anytime donation
```

```
model_donate_anytime <- glm(donated_anytime ~ treatment_group + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = study_sample, family = "binomial")
print("\nDonation anytime:")
```

```
## [1] "\nDonation anytime:"
```

```
summary(model_donate_anytime)$coefficients["treatment_groupSymbolic Incentives",]
```

```
##      Estimate Std. Error      z value    Pr(>|z|)
##      0.05376     0.19637     0.27376     0.78427
```

Table S8: Unsubscription and Total Donations

```
print("Table S8 - Secondary Outcomes (OLS with Robust SEs)")
```

```
## [1] "Table S8 - Secondary Outcomes (OLS with Robust SEs)"
```

```
# Unsubscription without controls
```

```
unsub1 <- lm(unsubscribe ~ treatment_group + factor(wave), data = study_sample)
print("Unsubscription (No Controls):")
```

```
## [1] "Unsubscription (No Controls):"
```

```
coeftest(unsub1, vcov = vcovHC(unsub1, type = "HC1"))["treatment_groupSymbolic Incentives",]
```

```
##      Estimate Std. Error      t value    Pr(>|t|)
##     -0.001703   0.002111   -0.807064     0.419712
```

```
# Unsubscription with controls
```

```
unsub2 <- lm(unsubscribe ~ treatment_group + factor(wave) +
             is_female + age + race + prior_plasma_donation + bloodtype_group +
             avg_annual_donations + zip_median_income + us_region + is_urban +
             county_covid_per_100k,
             data = study_sample)
print("\nUnsubscription (With Controls):")
```

```
## [1] "\nUnsubscription (With Controls):"
```

```
coeftest(unsub2, vcov = vcovHC(unsub2, type = "HC1"))["treatment_groupSymbolic Incentives",]
```

```
##      Estimate Std. Error      t value    Pr(>|t|)
##     -0.001681   0.001746   -0.962452     0.335936
```

```
# Total donations without controls
```

```
total1 <- lm(total_donations_post_treatment ~ treatment_group + factor(wave),
             data = study_sample)
print("\nTotal Donations (No Controls):")
```

```
## [1] "\nTotal Donations (No Controls):"
```



```
coeftest(total1, vcov = vcovHC(total1, type = "HC1"))["treatment_groupSymbolic Incentives",]
```

```
##      Estimate Std. Error    t value    Pr(>|t|)
##      0.02291    0.02947    0.77737    0.43702
```

```
# Total donations with controls
```

```
total2 <- lm(total_donations_post_treatment ~ treatment_group + factor(wave) +
             is_female + age + race + prior_plasma_donation + bloodtype_group +
             avg_annual_donations + zip_median_income + us_region + is_urban +
             county_covid_per_100k,
             data = study_sample)
print("\nTotal Donations (With Controls):")
```

```
## [1] "\nTotal Donations (With Controls):"
```

```
coeftest(total2, vcov = vcovHC(total2, type = "HC1"))["treatment_groupSymbolic Incentives",]
```

```
##      Estimate Std. Error    t value    Pr(>|t|)
##      0.008261    0.030044    0.274950    0.783382
```

Table S9: Heterogeneous Treatment Effects

```
print("Table S9 - Heterogeneous Treatment Effects")
```

```
## [1] "Table S9 - Heterogeneous Treatment Effects"
```

```
# Female interaction
```

```
print("\n1. FEMALE INTERACTION:")
```

```
## [1] "\n1. FEMALE INTERACTION:"
```

```
# Appointment outcome
```

```
hte_female_appt <- lm(appointment_within_48h ~ treatment_group * is_female + factor(wave) +
                     age + race + prior_plasma_donation + bloodtype_group +
                     avg_annual_donations + zip_median_income + us_region + is_urban +
                     county_covid_per_100k,
                     data = study_sample)
print("Appointment Creation:")
```

```
## [1] "Appointment Creation:"
```

```
coeftest(hte_female_appt, vcov = vcovHC(hte_female_appt, type = "HC1"))[c("is_female", "treatment_groupSymbolic Incentives:is_female"),]
```

```
##              Estimate Std. Error t value
## is_female      -0.001612    0.01054 -0.1529
## treatment_groupSymbolic Incentives:is_female  0.021921    0.01599  1.3707
##              Pr(>|t|)
## is_female              0.8785
## treatment_groupSymbolic Incentives:is_female  0.1706
```

```
# Donation outcome
hte_female_donate <- lm(donated_within_13d ~ treatment_group * is_female + factor(wave) +
  age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban +
  county_covid_per_100k,
  data = study_sample)

print("\nDonation:")
```

```
## [1] "\nDonation:"
```

```
coeftest(hte_female_donate, vcov = vcovHC(hte_female_donate, type = "HC1"))[c("is_female", "treatment_g
```

```
##                                Estimate Std. Error t value
## is_female                      0.000204   0.002611  0.07814
## treatment_groupSymbolic Incentives:is_female 0.005788   0.004155  1.39300
##                                Pr(>|t|)
## is_female                      0.9377
## treatment_groupSymbolic Incentives:is_female 0.1638
```

```
# Annual donations interaction
print("\n\n2. ANNUAL DONATIONS INTERACTION:")
```

```
## [1] "\n\n2. ANNUAL DONATIONS INTERACTION:"
```

```
# Appointment outcome
hte_donations_appt <- lm(appointment_within_48h ~ treatment_group * avg_annual_donations + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  zip_median_income + us_region + is_urban + county_covid_per_100k,
  data = study_sample)

print("Appointment Creation:")
```

```
## [1] "Appointment Creation:"
```

```
coeftest(hte_donations_appt, vcov = vcovHC(hte_donations_appt, type = "HC1"))[c("avg_annual_donations",
```

```
##                                Estimate Std. Error
## avg_annual_donations           0.0004245   0.004208
## treatment_groupSymbolic Incentives:avg_annual_donations 0.0068391   0.005600
##                                t value Pr(>|t|)
## avg_annual_donations           0.1009   0.9196
## treatment_groupSymbolic Incentives:avg_annual_donations 1.2213   0.2221
```

```
# Donation outcome
hte_donations_donate <- lm(donated_within_13d ~ treatment_group * avg_annual_donations + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  zip_median_income + us_region + is_urban + county_covid_per_100k,
  data = study_sample)

print("\nDonation:")
```

```
## [1] "\nDonation:"
```

```
coeftest(hte_donations_donate, vcov = vcovHC(hte_donations_donate, type = "HC1"))[c("avg_annual_donations", "treatment_groupSymbolic Incentives:avg_annual_donations")]
```

```
##
## avg_annual_donations -0.0001802 0.0001620
## treatment_groupSymbolic Incentives:avg_annual_donations 0.0012555 0.0007621
## t value Pr(>|t|)
## avg_annual_donations -1.113 0.26605
## treatment_groupSymbolic Incentives:avg_annual_donations 1.647 0.09962
```

```
# Urban interaction
print("\n\n3. URBAN INTERACTION:")
```

```
## [1] "\n\n3. URBAN INTERACTION:"
```

```
# Appointment outcome
hte_urban_appt <- lm(appointment_within_48h ~ treatment_group * is_urban + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + county_covid_per_100k,
  data = study_sample)
print("Appointment Creation:")
```

```
## [1] "Appointment Creation:"
```

```
coeftest(hte_urban_appt, vcov = vcovHC(hte_urban_appt, type = "HC1"))[c("is_urban", "treatment_groupSymbolic Incentives:is_urban")]
```

```
##
## is_urban Estimate Std. Error t value
## is_urban 0.01130 0.01203 0.9396
## treatment_groupSymbolic Incentives:is_urban 0.02095 0.01742 1.2024
## Pr(>|t|)
## is_urban 0.3475
## treatment_groupSymbolic Incentives:is_urban 0.2293
```

```
# Donation outcome
hte_urban_donate <- lm(donated_within_13d ~ treatment_group * is_urban + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + county_covid_per_100k,
  data = study_sample)
print("\nDonation:")
```

```
## [1] "\nDonation:"
```

```
coeftest(hte_urban_donate, vcov = vcovHC(hte_urban_donate, type = "HC1"))[c("is_urban", "treatment_groupSymbolic Incentives:is_urban")]
```

```
##
## is_urban Estimate Std. Error t value
## is_urban 7.013e-05 0.001394 0.05029
## treatment_groupSymbolic Incentives:is_urban 1.718e-03 0.002726 0.63022
## Pr(>|t|)
## is_urban 0.9599
## treatment_groupSymbolic Incentives:is_urban 0.5286
```

```

# Democratic county interaction
print("\n\n4. DEMOCRATIC COUNTY INTERACTION:")

## [1] "\n\n4. DEMOCRATIC COUNTY INTERACTION:"

# Appointment outcome
hte_dem_appt <- lm(appointment_within_48h ~ treatment_group * is_majority_dem_county + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban + county_covid_per_1000
  data = study_sample)
print("Appointment Creation:")

## [1] "Appointment Creation:"

coeftest(hte_dem_appt, vcov = vcovHC(hte_dem_appt, type = "HC1"))[c("is_majority_dem_county", "treatment_groupSymbolic Incentives:is_majority_dem_county")]

##
## is_majority_dem_county Estimate Std. Error
## treatment_groupSymbolic Incentives:is_majority_dem_county -0.002155 0.01614
## t value Pr(>|t|)
## is_majority_dem_county 2.0948 0.03631
## treatment_groupSymbolic Incentives:is_majority_dem_county -0.1335 0.89380

# Donation outcome
hte_dem_donate <- lm(donated_within_13d ~ treatment_group * is_majority_dem_county + factor(wave) +
  is_female + age + race + prior_plasma_donation + bloodtype_group +
  avg_annual_donations + zip_median_income + us_region + is_urban + county_covid_per_1000
  data = study_sample)
print("\nDonation:")

## [1] "\nDonation:"

coeftest(hte_dem_donate, vcov = vcovHC(hte_dem_donate, type = "HC1"))[c("is_majority_dem_county", "treatment_groupSymbolic Incentives:is_majority_dem_county")]

##
## is_majority_dem_county Estimate Std. Error
## treatment_groupSymbolic Incentives:is_majority_dem_county 0.002289 0.004455
## t value Pr(>|t|)
## is_majority_dem_county 1.0606 0.2890
## treatment_groupSymbolic Incentives:is_majority_dem_county 0.5139 0.6074

```

Table S10: Intention-Behavior Gap

```

print("Table S10 - Intention-Behavior Gap Analysis")

## [1] "Table S10 - Intention-Behavior Gap Analysis"

```

```

# Filter to those who made appointments
gap_sample <- study_sample %>% filter(!is.na(intention_behavior_gap))
print(paste("Sample size for gap analysis:", nrow(gap_sample)))

## [1] "Sample size for gap analysis: 91"

print(paste("Control group size:", sum(gap_sample$treatment_group == "Control")))

## [1] "Control group size: 37"

print(paste("Treatment group size:", sum(gap_sample$treatment_group == "Symbolic Incentives")))

## [1] "Treatment group size: 54"

# Model without controls
gap_model1 <- glm(intention_behavior_gap ~ treatment_group + factor(wave),
                  data = gap_sample, family = "binomial")
print("\nModel 1 - No Controls:")

## [1] "\nModel 1 - No Controls:"

summary(gap_model1)$coefficients["treatment_groupSymbolic Incentives",]

##      Estimate Std. Error    z value    Pr(>|z|)
##      0.2735     0.4956     0.5519     0.5810

# Model with controls
gap_model2 <- glm(intention_behavior_gap ~ treatment_group + factor(wave) +
                  is_female + age + race,
                  data = gap_sample, family = "binomial")
print("\nModel 2 - With Controls:")

## [1] "\nModel 2 - With Controls:"

summary(gap_model2)$coefficients["treatment_groupSymbolic Incentives",]

##      Estimate Std. Error    z value    Pr(>|z|)
##      0.3534     0.5182     0.6821     0.4952

# Show the actual gap rates by treatment
gap_rates <- gap_sample %>%
  group_by(treatment_group) %>%
  summarise(
    n = n(),
    gap_rate = mean(intention_behavior_gap, na.rm = TRUE),
    donated_rate = 1 - gap_rate
  )
print("\nGap rates by treatment group:")

## [1] "\nGap rates by treatment group:"

```

```
print(gap_rates)
```

```
## # A tibble: 2 x 4
##   treatment_group      n gap_rate donated_rate
##   <chr>          <int>   <dbl>      <dbl>
## 1 Control           37    0.270      0.730
## 2 Symbolic Incentives 54    0.370      0.630
```