Statistics/Data analysis

```
      name:  <unnamed>
       log:  C:\users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP repli
> cation files\Anoll Kam Marcellin Lucid Analyses.smcl
  log type:  smcl
 opened on:  10 Jan 2025, 14:29:04

1 .
2 . clear

3 . cd "C:/users/kamcd/Dropbox/CDK WORK/racial disparities essentialism/JOP replication
  > files"
  C:\users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP replication files

4 .
5 . *Saved csv file as an excel workbook
6 . *reading in the excel data
7 . use "Anoll Kam Marcellin Lucid March 2021 Survey.dta", clear
  (Cleaned with no consent, <18, failed ACs, speeders, non-finishers dropped)

8 .
9 . *****Coding Covariates*****
10. //age
11. gen age01 = (age-18)/(93-18)

12. lab var age01 "Age"

13.
14. //educ
15. gen ed6cat = (educ-1)/5

16. lab def ed6cat 0"Less HS" 1">BA"

17. lab val ed6cat ed6cat

18. lab var ed6cat "Education"

19.
20. //female
21. recode gender (1=1 "female")(2=0)(else=.), gen(female)
  (908 differences between gender and female)

22.
23. //race
24. gen race_all = .
  (1,975 missing values generated)

25. replace race_all = 1 if race_1==1
  (1,089 real changes made)

26. replace race_all = 2 if race_2==1
  (435 real changes made)

27. replace race_all = 4 if race_4==1|race_6==1
  (389 real changes made)

28. replace race_all = 3 if hisp_2==1|hisp_3==1|hisp_4==1|hisp_5==1
  (367 real changes made)

29. lab def race_all 1"White" 2"Black" 3"Hispanic any race" 4"AAPI"
```

```
30. lab val race_all race_all

31. tab race_all
```

race_all	Freq.	Percent	Cum.
White	831	42.42	42.42
Black	384	19.60	62.02
Hispanic any race	367	18.73	80.76
AAPI	377	19.24	100.00
Total	1,959	100.00	

```
32.
33. recode race_all (1=1)(2/4=0)(else=.), gen(white)
  (1,128 differences between race_all and white)

34. recode race_all (2=1)(1 3 4=0)(else=.), gen(black)
  (1,959 differences between race_all and black)

35. recode race_all (3=1)(1 2 4=0)(else=.), gen(hispanic)
  (1,959 differences between race_all and hispanic)

36. recode race_all (4=1)(1 2 3=0)(else=.), gen(api)
  (1,959 differences between race_all and api)

37. lab var black "Black"

38. lab var hispanic "Latino"

39. lab var api "Asian"

40.
41. //party
42. gen pid7cata = .
  (1,975 missing values generated)

43. replace pid7cata = 0 if demf==1
  (644 real changes made)

44. replace pid7cata = .17 if demf==2
  (362 real changes made)

45. replace pid7cata = .33 if indf==2
  (130 real changes made)

46. replace pid7cata = .5 if indf==3
  (218 real changes made)

47. replace pid7cata = .67 if indf==1
  (79 real changes made)

48. replace pid7cata = .83 if gopf==2
  (223 real changes made)

49. replace pid7cata = 1 if gopf==1
  (316 real changes made)

50. tab pid7cata
```

pid7cata	Freq.	Percent	Cum.
0	644	32.66	32.66
.17	362	18.36	51.01
.33	130	6.59	57.61
.5	218	11.05	68.66
.67	79	4.01	72.67
.83	223	11.31	83.98
1	316	16.02	100.00
Total	1,972	100.00	

```
51. lab var pid7cata "Party ID"

52.
53. recode pid7cata (0/.4=1)(.5/1=0)(else=.), gen(dem)
  (1,972 differences between pid7cata and dem)

54. recode pid7cata (0/.51=0)(.6/1=1)(else=.), gen(rep)
  (1,012 differences between pid7cata and rep)

55. recode pid7cata (0/.34=0)(.5=.5)(.6/1=1)(else=.), gen(pid3cata)
  (794 differences between pid7cata and pid3cata)

56. recode pid7cata (0/.34=0 "Dem")(.5=.)(.6/1=1 "GOP")(else=.), gen(pid2cata)
  (1,012 differences between pid7cata and pid2cata)

57. lab var pid2cata "Dem (0) or GOP (1)"

58.
59. //Five analytical groups
60. gen fivegroups = .
  (1,975 missing values generated)

61. replace fivegroups = 1 if api==1
  (377 real changes made)

62. replace fivegroups = 2 if black==1
  (384 real changes made)

63. replace fivegroups = 3 if hispanic==1
  (367 real changes made)

64. replace fivegroups = 4 if white==1 & pid2cata==0
  (410 real changes made)

65. replace fivegroups = 5 if white==1 & pid2cata==1
  (406 real changes made)

66. lab def fivegroups 1"Asian" 2"Black" 3"Latino" 4"White DEM" 5"White GOP"

67. lab val fivegroups fivegroups

68. tab fivegroups
```

fivegroups	Freq.	Percent	Cum.
Asian	**377**	**19.39**	**19.39**
Black	**384**	**19.75**	**39.15**
Latino	**367**	**18.88**	**58.02**
White DEM	**410**	**21.09**	**79.12**
White GOP	**406**	**20.88**	**100.00**
Total	**1,944**	**100.00**	

```
69.
70. //*Question 3: what determines your own race battery
71. recode moduleC_2_1 moduleC_2_2 moduleC_2_3 moduleC_2_4 moduleC_2_5 moduleC_2_6 modul
  > eC_2_7 (1=1)(2=0)(3=0)(4=0), gen(myrace_DNA myrace_culture myrace_history myrace_cho
  > ices myrace_forms myrace_toldme myrace_physical)
  (880 differences between moduleC_2_1 and myrace_DNA)
  (1,409 differences between moduleC_2_2 and myrace_culture)
  (1,370 differences between moduleC_2_3 and myrace_history)
  (1,503 differences between moduleC_2_4 and myrace_choices)
  (1,471 differences between moduleC_2_5 and myrace_forms)
  (1,827 differences between moduleC_2_6 and myrace_toldme)
  (1,175 differences between moduleC_2_7 and myrace_physical)
```

```
72. lab def myrace 1"Strongly" 0"Not strongly", modify

73. lab val myrace_DNA myrace_culture myrace_history myrace_choices myrace_forms myrace_
  > toldme myrace_physical myrace

74. sum myrace_DNA myrace_culture myrace_history myrace_choices myrace_forms myrace_told
  > me myrace_physical
```

Variable	Obs	Mean	Std. dev.	Min	Max
myrace_DNA	**1,975**	**.5544304**	**.4971544**	**0**	**1**
myrace_cul~e	**1,975**	**.2865823**	**.4522792**	**0**	**1**
myrace_his~y	**1,975**	**.3063291**	**.4610848**	**0**	**1**
myrace_cho~s	**1,975**	**.2389873**	**.426573**	**0**	**1**
myrace_forms	**1,975**	**.2551899**	**.4360783**	**0**	**1**
myrace_tol~e	**1,975**	**.0749367**	**.2633559**	**0**	**1**
myrace_phy~l	**1,975**	**.4050633**	**.4910286**	**0**	**1**

```
75.
76. //recoding to capture folks who state strongly or somewhat
77. //combining No and DK together
78. recode moduleC_2_1 moduleC_2_2 moduleC_2_3 moduleC_2_4 moduleC_2_5 moduleC_2_6 modul
  > eC_2_7 (1 2=1)(3 4=0), gen(myrace_DNA2 myrace_culture2 myrace_history2 myrace_choice
  > s2 myrace_forms2 myrace_toldme2 myrace_physical2)
  (880 differences between moduleC_2_1 and myrace_DNA2)
  (1,409 differences between moduleC_2_2 and myrace_culture2)
  (1,370 differences between moduleC_2_3 and myrace_history2)
  (1,503 differences between moduleC_2_4 and myrace_choices2)
  (1,471 differences between moduleC_2_5 and myrace_forms2)
  (1,827 differences between moduleC_2_6 and myrace_toldme2)
  (1,175 differences between moduleC_2_7 and myrace_physical2)

79. lab def myrace2 1"Strongly or somewhat" 0"Not at all"

80. lab val myrace_DNA2 myrace_culture2 myrace_history2 myrace_choices2 myrace_forms2 my
  > race_toldme2 myrace_physical2 myrace2

81.
82. //% DK/ref
83. tab1 moduleC_2_1- moduleC_2_7
```

-> tabulation of moduleC_2_1

Information contained in my DNA	Freq.	Percent	Cum.
Strongly determines my race	**1,095**	**55.44**	**55.44**
Somewhat determines my race	**600**	**30.38**	**85.82**
Does not at all determine my race	**179**	**9.06**	**94.89**
Don’t know/not sure	**101**	**5.11**	**100.00**
Total	**1,975**	**100.00**	

-> tabulation of moduleC_2_2

Culture shared with other members of my racial group	Freq.	Percent	Cum.
Strongly determines my race	**566**	**28.66**	**28.66**
Somewhat determines my race	**804**	**40.71**	**69.37**
Does not at all determine my race	**475**	**24.05**	**93.42**
Don’t know/not sure	**130**	**6.58**	**100.00**
Total	**1,975**	**100.00**	

-> tabulation of moduleC_2_3

History shared with other members of my racial group	Freq.	Percent	Cum.
Strongly determines my race	605	30.63	30.63
Somewhat determines my race	808	40.91	71.54
Does not at all determine my race	428	21.67	93.22
Don’t know/not sure	134	6.78	100.00
Total	1,975	100.00	

-> tabulation of moduleC_2_4

My own choices about my identity	Freq.	Percent	Cum.
Strongly determines my race	472	23.90	23.90
Somewhat determines my race	552	27.95	51.85
Does not at all determine my race	796	40.30	92.15
Don’t know/not sure	155	7.85	100.00
Total	1,975	100.00	

-> tabulation of moduleC_2_5

What race I select on official forms	Freq.	Percent	Cum.
Strongly determines my race	504	25.52	25.52
Somewhat determines my race	560	28.35	53.87
Does not at all determine my race	768	38.89	92.76
Don’t know/not sure	143	7.24	100.00
Total	1,975	100.00	

-> tabulation of moduleC_2_6

What someone else told me	Freq.	Percent	Cum.
Strongly determines my race	148	7.49	7.49
Somewhat determines my race	331	16.76	24.25
Does not at all determine my race	1,305	66.08	90.33
Don’t know/not sure	191	9.67	100.00
Total	1,975	100.00	

-> tabulation of moduleC_2_7

Physical traits like skin color	Freq.	Percent	Cum.
Strongly determines my race	800	40.51	40.51
Somewhat determines my race	744	37.67	78.18
Does not at all determine my race	350	17.72	95.90
Don’t know/not sure	81	4.10	100.00
Total	1,975	100.00	

84. egen ref_myrace = anycount(moduleC_2_1- moduleC_2_7), val(4)

85. tab ref_myrace

see notes	Freq.	Percent	Cum.
0	1,544	78.18	78.18
1	249	12.61	90.78
2	82	4.15	94.94
3	27	1.37	96.30
4	13	0.66	96.96
5	12	0.61	97.57
6	7	0.35	97.92
7	41	2.08	100.00
Total	1,975	100.00	

```
86.
87. forval v=1/7 {
    2. recode moduleC_2_`v' (1 2=1)(3 4 =0)(else=.), gen(myraceagree`v')
    3. }
  (880 differences between moduleC_2_1 and myraceagree1)
  (1,409 differences between moduleC_2_2 and myraceagree2)
  (1,370 differences between moduleC_2_3 and myraceagree3)
  (1,503 differences between moduleC_2_4 and myraceagree4)
  (1,471 differences between moduleC_2_5 and myraceagree5)
  (1,827 differences between moduleC_2_6 and myraceagree6)
  (1,175 differences between moduleC_2_7 and myraceagree7)

88.
89. set scheme s1mono

90. **********START FIGURE 1**********
91. //Figure 1. Agree + Strongly Agree, by racial group
92. forval v=1/7 {
    2. recode moduleC_2_`v' (1=1)(2 3 4 =0)(else=.), gen(myraceSTRagree`v')
    3. }
  (880 differences between moduleC_2_1 and myraceSTRagree1)
  (1,409 differences between moduleC_2_2 and myraceSTRagree2)
  (1,370 differences between moduleC_2_3 and myraceSTRagree3)
  (1,503 differences between moduleC_2_4 and myraceSTRagree4)
  (1,471 differences between moduleC_2_5 and myraceSTRagree5)
  (1,827 differences between moduleC_2_6 and myraceSTRagree6)
  (1,175 differences between moduleC_2_7 and myraceSTRagree7)

93.
94. forval v=1/7 {
    2. recode moduleC_2_`v' (2=1)(1 3 4 =0)(else=.), gen(myraceONLYagree`v')
    3. }
  (1,975 differences between moduleC_2_1 and myraceONLYagree1)
  (1,975 differences between moduleC_2_2 and myraceONLYagree2)
  (1,975 differences between moduleC_2_3 and myraceONLYagree3)
  (1,975 differences between moduleC_2_4 and myraceONLYagree4)
  (1,975 differences between moduleC_2_5 and myraceONLYagree5)
  (1,975 differences between moduleC_2_6 and myraceONLYagree6)
  (1,975 differences between moduleC_2_7 and myraceONLYagree7)

95.
96. //for text, % by fivegroups:
97. tab myraceagree1 fivegroups, col
```

Key
frequency *column percentage*

RECODE of moduleC_2_1 (Information contained in my DNA)	fivegroups					
	Asian	Black	Latino	White DEM	White GOP	Total
0	**45** **11.94**	**54** **14.06**	**67** **18.26**	**43** **10.49**	**63** **15.52**	**272** **13.99**
1	**332** **88.06**	**330** **85.94**	**300** **81.74**	**367** **89.51**	**343** **84.48**	**1,672** **86.01**
Total	**377** **100.00**	**384** **100.00**	**367** **100.00**	**410** **100.00**	**406** **100.00**	**1,944** **100.00**

98. tab myraceSTRagree1 fivegroups, col

Key
frequency *column percentage*

RECODE of moduleC_2_1 (Information contained in my DNA)	fivegroups					
	Asian	Black	Latino	White DEM	White GOP	Total
0	**186** **49.34**	**144** **37.50**	**183** **49.86**	**181** **44.15**	**167** **41.13**	**861** **44.29**
1	**191** **50.66**	**240** **62.50**	**184** **50.14**	**229** **55.85**	**239** **58.87**	**1,083** **55.71**
Total	**377** **100.00**	**384** **100.00**	**367** **100.00**	**410** **100.00**	**406** **100.00**	**1,944** **100.00**

99.
100 //% STRONGLY AGREE BY FIVEGROUPS
101 forval v=1/5 {
2. preserve
3. collapse myraceSTRagree1-myraceSTRagree7 if fivegroups==`v'
4. gen id = _n
5. reshape long myraceSTRagree, i(id) j(Q)
6. lab def Q 1 "DNA" 2 "Culture" 3 "History" 4 "My Choices" 5 "Select on Forms" 6 "W
> hat Someone Told Me" 7"Physical Traits"
7. lab val Q Q
8. gen myraceSTRagreepercent_`v' = myraceSTRagree*100
9. save myraceSTRagreepercent_`v', replace
10. restore
11. }
(j = 1 2 3 4 5 6 7)

Data	Wide	->	Long
Number of observations	**1**	->	**7**
Number of variables	**8**	->	**3**
j variable (7 values)		->	**Q**
xij variables:			
myraceSTRagree1 myraceSTRagree2 ... myraceSTRagree7->myraceSTRagree			

(file **myraceSTRagreepercent_1.dta** not found)
file **myraceSTRagreepercent_1.dta** saved
(j = 1 2 3 4 5 6 7)

Data	Wide	->	Long
Number of observations	**1**	->	**7**
Number of variables	**8**	->	**3**
j variable (7 values)		->	**Q**
xij variables:			
myraceSTRagree1 myraceSTRagree2 ... myraceSTRagree7->myraceSTRagree			

(file **myraceSTRagreepercent_2.dta** not found)
file **myraceSTRagreepercent_2.dta** saved
(j = 1 2 3 4 5 6 7)

```
Data                                Wide   ->   Long
-----------------------------------------------------------------------------
Number of observations                 1   ->   7
Number of variables                    8   ->   3
j variable (7 values)                      ->   Q
xij variables:
myraceSTRagree1 myraceSTRagree2 ... myraceSTRagree7->myraceSTRagree
-----------------------------------------------------------------------------
(file myraceSTRagreepercent_3.dta not found)
file myraceSTRagreepercent_3.dta saved
(j = 1 2 3 4 5 6 7)

Data                                Wide   ->   Long
-----------------------------------------------------------------------------
Number of observations                 1   ->   7
Number of variables                    8   ->   3
j variable (7 values)                      ->   Q
xij variables:
myraceSTRagree1 myraceSTRagree2 ... myraceSTRagree7->myraceSTRagree
-----------------------------------------------------------------------------
(file myraceSTRagreepercent_4.dta not found)
file myraceSTRagreepercent_4.dta saved
(j = 1 2 3 4 5 6 7)

Data                                Wide   ->   Long
-----------------------------------------------------------------------------
Number of observations                 1   ->   7
Number of variables                    8   ->   3
j variable (7 values)                      ->   Q
xij variables:
myraceSTRagree1 myraceSTRagree2 ... myraceSTRagree7->myraceSTRagree
-----------------------------------------------------------------------------
(file myraceSTRagreepercent_5.dta not found)
file myraceSTRagreepercent_5.dta saved

102
103 //% AGREE BY FIVEGROUPS
104 forval v=1/5 {
    2. preserve
    3. collapse myraceONLYagree1-myraceONLYagree7 if fivegroups==`v'
    4. gen id = _n
    5. reshape long myraceONLYagree, i(id) j(Q)
    6. lab def Q 1 "DNA" 2 "Culture" 3 "History" 4 "My Choices" 5 "Select on Forms" 6 "W
  > hat Someone Told Me" 7"Physical Traits"
    7. lab val Q Q
    8. gen myraceONLYagreepercent_`v' = myraceONLYagree*100
    9. save myraceONLYagreepercent_`v', replace
   10. restore
   11. }
  (j = 1 2 3 4 5 6 7)

Data                                Wide   ->   Long
-----------------------------------------------------------------------------
Number of observations                 1   ->   7
Number of variables                    8   ->   3
j variable (7 values)                      ->   Q
xij variables:
myraceONLYagree1 myraceONLYagree2 ... myraceONLYagree7->myraceONLYagree
-----------------------------------------------------------------------------
(file myraceONLYagreepercent_1.dta not found)
file myraceONLYagreepercent_1.dta saved
(j = 1 2 3 4 5 6 7)
```

```
Data                                Wide   ->   Long
-----------------------------------------------------------------------------
Number of observations                 1   ->   7
Number of variables                    8   ->   3
j variable (7 values)                      ->   Q
xij variables:
myraceONLYagree1 myraceONLYagree2 ... myraceONLYagree7->myraceONLYagree
-----------------------------------------------------------------------------
(file myraceONLYagreepercent_2.dta not found)
file myraceONLYagreepercent_2.dta saved
(j = 1 2 3 4 5 6 7)

Data                                Wide   ->   Long
-----------------------------------------------------------------------------
Number of observations                 1   ->   7
Number of variables                    8   ->   3
j variable (7 values)                      ->   Q
xij variables:
myraceONLYagree1 myraceONLYagree2 ... myraceONLYagree7->myraceONLYagree
-----------------------------------------------------------------------------
(file myraceONLYagreepercent_3.dta not found)
file myraceONLYagreepercent_3.dta saved
(j = 1 2 3 4 5 6 7)

Data                                Wide   ->   Long
-----------------------------------------------------------------------------
Number of observations                 1   ->   7
Number of variables                    8   ->   3
j variable (7 values)                      ->   Q
xij variables:
myraceONLYagree1 myraceONLYagree2 ... myraceONLYagree7->myraceONLYagree
-----------------------------------------------------------------------------
(file myraceONLYagreepercent_4.dta not found)
file myraceONLYagreepercent_4.dta saved
(j = 1 2 3 4 5 6 7)

Data                                Wide   ->   Long
-----------------------------------------------------------------------------
Number of observations                 1   ->   7
Number of variables                    8   ->   3
j variable (7 values)                      ->   Q
xij variables:
myraceONLYagree1 myraceONLYagree2 ... myraceONLYagree7->myraceONLYagree
-----------------------------------------------------------------------------
(file myraceONLYagreepercent_5.dta not found)
file myraceONLYagreepercent_5.dta saved

105
106 //PLOTTING %STR AGREE + AGREE BY FIVEGROUPS
107 forval v=1/5 {
    2. preserve
    3. clear
    4. use myraceSTRagreepercent_`v', clear
    5.          gen str10 group`v' = "Asian" if `v'==1
    6.          replace group`v' = "Black" if `v'==2
    7.          replace group`v' = "Latino" if `v'==3
    8.          replace group`v' = "White DEM" if `v'==4
    9.          replace group`v' = "White GOP" if `v'==5
   10.          local h = group`v'
   11. merge 1:1 Q using myraceONLYagreepercent_`v'
   12. recode Q (1=1 "DNA")(7=2 "Phys Traits")(3=3 "History")(2=4 "Culture") (5=5 "Forms
  > ")(4=6 "Choices")(6=7 "Told Me"), gen(graphorder)
   13. graph hbar myraceSTRagreepercent myraceONLYagreepercent, over(graphorder) ///
  > name(myraceboth_`v', replace) ///
  > title("`h' Respondents", size(medium)) ytitle(" ") xsize(5) ysize(4) graphregion(mar
  > gin(l+10)) stack asyvars legend(lab(1 "% Strongly") lab(2 "% Somewhat") symxsize(5)
  > keygap(.5) forcesize)
   14. restore
   15. }
  (0 real changes made)
  (0 real changes made)
  (0 real changes made)
```

```
(0 real changes made)
(label Q already defined)

    Result                      Number of obs
    ------------------------------------------
    Not matched                             0
    Matched                                 7  (_merge==3)
    ------------------------------------------

(4 differences between Q and graphorder)
(7 missing values generated)
(7 real changes made)
(0 real changes made)
(0 real changes made)
(0 real changes made)
(label Q already defined)

    Result                      Number of obs
    ------------------------------------------
    Not matched                             0
    Matched                                 7  (_merge==3)
    ------------------------------------------

(4 differences between Q and graphorder)
(7 missing values generated)
(0 real changes made)
(7 real changes made)
(0 real changes made)
(0 real changes made)
(label Q already defined)

    Result                      Number of obs
    ------------------------------------------
    Not matched                             0
    Matched                                 7  (_merge==3)
    ------------------------------------------

(4 differences between Q and graphorder)
(7 missing values generated)
(0 real changes made)
(0 real changes made)
(7 real changes made)
(0 real changes made)
(label Q already defined)

    Result                      Number of obs
    ------------------------------------------
    Not matched                             0
    Matched                                 7  (_merge==3)
    ------------------------------------------

(4 differences between Q and graphorder)
(7 missing values generated)
(0 real changes made)
(0 real changes made)
(0 real changes made)
(7 real changes made)
(label Q already defined)

    Result                      Number of obs
    ------------------------------------------
    Not matched                             0
    Matched                                 7  (_merge==3)
    ------------------------------------------

(4 differences between Q and graphorder)
```

```
108
109 graph combine myraceboth_1 myraceboth_2 myraceboth_3 myraceboth_4 myraceboth_5, row(
  > 2) title("To what extent do the following factors determine your race?", size(medium
  > )) xsize(6.5) ysize(4.5) imargin(medium) iscale(.55) ycommon xcommon

110 graph export Figure1.pdf, replace
  file Figure1.pdf saved as PDF format

111 **********END FIGURE 1**********
112
113 *****cleaning up directory*****
114 forval v=1/5 {
    2. erase myraceSTRagreepercent_`v'.dta
    3. erase myraceONLYagreepercent_`v'.dta
    4. }

115
116 *****FN 11: PAIRWISE COMPARISONS*****
117 //Difference of proportions test
118 //create comparison groups
119 gen AB = .
  (1,975 missing values generated)

120 replace AB=1 if fivegroups==1|fivegroups==2
  (761 real changes made)

121 gen AL = .
  (1,975 missing values generated)

122 replace AL=1 if fivegroups==1|fivegroups==3
  (744 real changes made)

123 gen AWD = .
  (1,975 missing values generated)

124 replace AWD=1 if fivegroups==1|fivegroups==4
  (787 real changes made)

125 gen AWR = .
  (1,975 missing values generated)

126 replace AWR=1 if fivegroups==1|fivegroups==5
  (783 real changes made)

127 gen BL = .
  (1,975 missing values generated)

128 replace BL=1 if fivegroups==2|fivegroups==3
  (751 real changes made)

129 gen BWD = .
  (1,975 missing values generated)

130 replace BWD=1 if fivegroups==2|fivegroups==4
  (794 real changes made)

131 gen BWR = .
  (1,975 missing values generated)

132 replace BWR=1 if fivegroups==2|fivegroups==5
  (790 real changes made)
```

```
133 gen LWD = .
  (1,975 missing values generated)

134 replace LWD=1 if fivegroups==3|fivegroups==4
  (777 real changes made)

135 gen LWR = .
  (1,975 missing values generated)

136 replace LWR=1 if fivegroups==3|fivegroups==5
  (773 real changes made)

137 gen WDR = .
  (1,975 missing values generated)

138 replace WDR=1 if fivegroups==4|fivegroups==5
  (816 real changes made)

139
140 *****Strongly or Somewhat: DNA*****
141 *****Multiple Factors*****
142 egen howmanyagree = anycount(myrace_DNA2 myrace_culture2 myrace_history2 myrace_choi
  > ces2 myrace_physical2 myrace_forms2 myrace_toldme2 ), val(1)

143 recode howmanyagree (0 1=0)(2/7=1 "Selected Agree with More than One Item"), gen(mor
  > ethanone)
  (1,913 differences between howmanyagree and morethanone)

144
145 *****"Opposing" Factors: DNA plus any constructivist (culture, history, choices, for
  > ms, told me)*****
146 egen anyconstructivist = anymatch(myrace_culture2 myrace_history2 myrace_choices2 my
  > race_forms2 myrace_toldme2), val(1)

147 gen DNAanycon= anyconstructivist +myrace_DNA2

148 replace DNAanycon = 0 if DNAanycon==1
  (368 real changes made)

149 replace DNAanycon =1 if DNAanycon==2
  (1,527 real changes made)

150
151 lab var morethanone "Proportion Agreeing with >1 Factor"

152 lab var DNAanycon "Proportion Agreeing with DNA + Any Constructivist Factor"

153 lab var myrace_DNA2 "Proportion Agreeing with DNA"

154 lab var myrace_DNA "Proportion Strongly Agreeing with DNA"

155 lab var fivegroups "Subgroups"

156
157 *****In text*****
158 tab fivegroups morethanone, row
```

Key
frequency *row percentage*

Subgroups	Proportion Agreeing with >1 Factor 0 Selected	Total
Asian	**13** **3.45**	**364** **96.55**	**377** **100.00**
Black	**22** **5.73**	**362** **94.27**	**384** **100.00**
Latino	**33** **8.99**	**334** **91.01**	**367** **100.00**
White DEM	**29** **7.07**	**381** **92.93**	**410** **100.00**
White GOP	**48** **11.82**	**358** **88.18**	**406** **100.00**
Total	**145** **7.46**	**1,799** **92.54**	**1,944** **100.00**

```
159 tab fivegroups DNAanycon, row
```

Key
frequency *row percentage*

Subgroups	Proportion Agreeing with DNA + Any Constructivist Factor 0	1	Total
Asian	**67** **17.77**	**310** **82.23**	**377** **100.00**
Black	**81** **21.09**	**303** **78.91**	**384** **100.00**
Latino	**89** **24.25**	**278** **75.75**	**367** **100.00**
White DEM	**73** **17.80**	**337** **82.20**	**410** **100.00**
White GOP	**125** **30.79**	**281** **69.21**	**406** **100.00**
Total	**435** **22.38**	**1,509** **77.62**	**1,944** **100.00**

```
160
161 *****PAIRWISE DIFFERENCE OF PROPORTIONS TESTS (FOR APPENDIX)*****
162 foreach y of varlist myrace_DNA2 myrace_DNA morethanone DNAanycon {
    2.          disp "TESTS FOR VARIABLE: `y'"
    3.          foreach v of varlist AB-WDR {
    4.                  prtest `y' if `v'==1, by(fivegroups)
    5.          }
    6.          }
  TESTS FOR VARIABLE: myrace_DNA2
```

Two-sample test of proportions — **Asian**: Number of obs = **377**; **Black**: Number of obs = **384**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.8806366**	**.016698**			**.8479092**	**.913364**
Black	**.859375**	**.0177401**			**.824605**	**.894145**
diff	**.0212616**	**.0243626**			**-.0264881**	**.0690113**
under H0:	**.0243903**	**0.87**	**0.383**			

diff = prop(**Asian**) - prop(**Black**) z = **0.8717**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.8083**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.3834**
Ha: diff > 0 — Pr(Z > z) = **0.1917**

Two-sample test of proportions — **Asian**: Number of obs = **377**; **Latino**: Number of obs = **367**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.8806366**	**.016698**			**.8479092**	**.913364**
Latino	**.8174387**	**.020165**			**.777916**	**.8569614**
diff	**.0631979**	**.0261811**			**.0118839**	**.1145119**
under H0:	**.0262227**	**2.41**	**0.016**			

diff = prop(**Asian**) - prop(**Latino**) z = **2.4100**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.9920**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.0160**
Ha: diff > 0 — Pr(Z > z) = **0.0080**

Two-sample test of proportions — **Asian**: Number of obs = **377**; **White DEM**: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.8806366**	**.016698**			**.8479092**	**.913364**
White DEM	**.895122**	**.0151318**			**.8654641**	**.9247798**
diff	**-.0144853**	**.0225343**			**-.0586517**	**.029681**
under H0:	**.0224869**	**-0.64**	**0.519**			

diff = prop(**Asian**) - prop(**White DEM**) z = **-0.6442**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.2597**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.5195**
Ha: diff > 0 — Pr(Z > z) = **0.7403**

Two-sample test of proportions — **Asian**: Number of obs = **377**; **White GOP**: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.8806366**	**.016698**			**.8479092**	**.913364**
White GOP	**.8448276**	**.0179692**			**.8096086**	**.8800465**
diff	**.035809**	**.0245298**			**-.0122686**	**.0838866**
under H0:	**.0246632**	**1.45**	**0.147**			

diff = prop(**Asian**) - prop(**White GOP**) z = **1.4519**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.9267**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.1465**
Ha: diff > 0 — Pr(Z > z) = **0.0733**

Two-sample test of proportions **Black**: Number of obs = **384**
Latino: Number of obs = **367**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.859375	.0177401			.824605	.894145
Latino	.8174387	.020165			.777916	.8569614
diff	.0419363	.0268578			-.010704	.0945766
	under H0:	.0268376	1.56	0.118		

diff = prop(**Black**) - prop(**Latino**) z = **1.5626**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9409** Pr(|Z| > |z|) = **0.1181** Pr(Z > z) = **0.0591**

Two-sample test of proportions **Black**: Number of obs = **384**
White DEM: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.859375	.0177401			.824605	.894145
White DEM	.895122	.0151318			.8654641	.9247798
diff	-.035747	.0233171			-.0814475	.0099536
	under H0:	.023256	-1.54	0.124		

diff = prop(**Black**) - prop(**White DEM**) z = **-1.5371**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.0621** Pr(|Z| > |z|) = **0.1243** Pr(Z > z) = **0.9379**

Two-sample test of proportions **Black**: Number of obs = **384**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.859375	.0177401			.824605	.894145
White GOP	.8448276	.0179692			.8096086	.8800465
diff	.0145474	.0252508			-.0349433	.0640381
	under H0:	.0252847	0.58	0.565		

diff = prop(**Black**) - prop(**White GOP**) z = **0.5753**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.7175** Pr(|Z| > |z|) = **0.5651** Pr(Z > z) = **0.2825**

Two-sample test of proportions **Latino**: Number of obs = **367**
White DEM: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Latino	.8174387	.020165			.777916	.8569614
White DEM	.895122	.0151318			.8654641	.9247798
diff	-.0776833	.0252111			-.1270962	-.0282704
	under H0:	.0250509	-3.10	0.002		

diff = prop(**Latino**) - prop(**White DEM**) z = **-3.1010**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.0010** Pr(|Z| > |z|) = **0.0019** Pr(Z > z) = **0.9990**

Two-sample test of proportions **Latino**: Number of obs = **367**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Latino	**.8174387**	**.020165**			**.777916**	**.8569614**
White GOP	**.8448276**	**.0179692**			**.8096086**	**.8800465**
diff	**-.0273889**	**.0270096**			**-.0803268**	**.025549**
under H0:	**.0269396**	**-1.02**	**0.309**			

diff = prop(**Latino**) - prop(**White GOP**) z = **-1.0167**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.1547** Pr(|Z| > |z|) = **0.3093** Pr(Z > z) = **0.8453**

Two-sample test of proportions **White DEM**: Number of obs = **410**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
White DEM	**.895122**	**.0151318**			**.8654641**	**.9247798**
White GOP	**.8448276**	**.0179692**			**.8096086**	**.8800465**
diff	**.0502944**	**.0234918**			**.0042513**	**.0963374**
under H0:	**.0235387**	**2.14**	**0.033**			

diff = prop(**White DEM**) - prop(**White GOP**) z = **2.1367**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9837** Pr(|Z| > |z|) = **0.0326** Pr(Z > z) = **0.0163**

TESTS FOR VARIABLE: myrace_DNA

Two-sample test of proportions **Asian**: Number of obs = **377**
Black: Number of obs = **384**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.5066313**	**.025749**			**.4561641**	**.5570985**
Black	**.625**	**.0247053**			**.5765785**	**.6734215**
diff	**-.1183687**	**.0356842**			**-.1883085**	**-.0484289**
under H0:	**.0359308**	**-3.29**	**0.001**			

diff = prop(**Asian**) - prop(**Black**) z = **-3.2944**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.0005** Pr(|Z| > |z|) = **0.0010** Pr(Z > z) = **0.9995**

Two-sample test of proportions **Asian**: Number of obs = **377**
Latino: Number of obs = **367**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.5066313**	**.025749**			**.4561641**	**.5570985**
Latino	**.5013624**	**.0260997**			**.4502079**	**.5525169**
diff	**.0052689**	**.0366634**			**-.0665901**	**.0771279**
under H0:	**.0366639**	**0.14**	**0.886**			

diff = prop(**Asian**) - prop(**Latino**) z = **0.1437**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.5571** Pr(|Z| > |z|) = **0.8857** Pr(Z > z) = **0.4429**

Two-sample test of proportions **Asian**: Number of obs = **377**
White DEM: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	.5066313	.025749			.4561641	.5570985
White DEM	.5585366	.0245234			.5104715	.6066016
diff	-.0519053	.0355586			-.1215988	.0177882
	under H0:	.0355965	-1.46	0.145		

diff = prop(**Asian**) - prop(**White DEM**) z = **-1.4582**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.0724** Pr(|Z| > |z|) = **0.1448** Pr(Z > z) = **0.9276**

Two-sample test of proportions **Asian**: Number of obs = **377**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	.5066313	.025749			.4561641	.5570985
White GOP	.58867	.0244213			.5408052	.6365347
diff	-.0820387	.0354882			-.1515942	-.0124831
	under H0:	.0355883	-2.31	0.021		

diff = prop(**Asian**) - prop(**White GOP**) z = **-2.3052**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.0106** Pr(|Z| > |z|) = **0.0212** Pr(Z > z) = **0.9894**

Two-sample test of proportions **Black**: Number of obs = **384**
Latino: Number of obs = **367**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.625	.0247053			.5765785	.6734215
Latino	.5013624	.0260997			.4502079	.5525169
diff	.1236376	.0359381			.0532003	.1940749
	under H0:	.0361941	3.42	0.001		

diff = prop(**Black**) - prop(**Latino**) z = **3.4160**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9997** Pr(|Z| > |z|) = **0.0006** Pr(Z > z) = **0.0003**

Two-sample test of proportions **Black**: Number of obs = **384**
White DEM: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.625	.0247053			.5765785	.6734215
White DEM	.5585366	.0245234			.5104715	.6066016
diff	.0664634	.0348102			-.0017633	.1346902
	under H0:	.0349189	1.90	0.057		

diff = prop(**Black**) - prop(**White DEM**) z = **1.9034**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9715** Pr(|Z| > |z|) = **0.0570** Pr(Z > z) = **0.0285**

Two-sample test of proportions **Black**: Number of obs = **384**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.625	.0247053			.5765785	.6734215
White GOP	.58867	.0244213			.5408052	.6365347
diff	.03633	.0347383			-.0317558	.1044159
	under H0:	.0347781	1.04	0.296		

diff = prop(**Black**) - prop(**White GOP**) z = **1.0446**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.8519** Pr(|Z| > |z|) = **0.2962** Pr(Z > z) = **0.1481**

Two-sample test of proportions **Latino**: Number of obs = **367**
White DEM: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Latino	.5013624	.0260997			.4502079	.5525169
White DEM	.5585366	.0245234			.5104715	.6066016
diff	-.0571742	.0358133			-.127367	.0130186
	under H0:	.0358583	-1.59	0.111		

diff = prop(**Latino**) - prop(**White DEM**) z = **-1.5944**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.0554** Pr(|Z| > |z|) = **0.1108** Pr(Z > z) = **0.9446**

Two-sample test of proportions **Latino**: Number of obs = **367**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Latino	.5013624	.0260997			.4502079	.5525169
White GOP	.58867	.0244213			.5408052	.6365347
diff	-.0873076	.0357434			-.1573634	-.0172517
	under H0:	.0358524	-2.44	0.015		

diff = prop(**Latino**) - prop(**White GOP**) z = **-2.4352**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.0074** Pr(|Z| > |z|) = **0.0149** Pr(Z > z) = **0.9926**

Two-sample test of proportions **White DEM**: Number of obs = **410**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
White DEM	.5585366	.0245234			.5104715	.6066016
White GOP	.58867	.0244213			.5408052	.6365347
diff	-.0301334	.0346092			-.0979662	.0376994
	under H0:	.0346268	-0.87	0.384		

diff = prop(**White DEM**) - prop(**White GOP**) z = **-0.8702**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.1921** Pr(|Z| > |z|) = **0.3842** Pr(Z > z) = **0.8079**

TESTS FOR VARIABLE: morethanone

Two-sample test of proportions — **Asian**: Number of obs = **377**; **Black**: Number of obs = **384**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.9655172**	**.0093975**			**.9470986**	**.9839359**
Black	**.9427083**	**.0118596**			**.919464**	**.9659527**
diff	**.0228089**	**.0151315**			**-.0068482**	**.0524661**
	under H0: **.0151871**		**1.50**	**0.133**		

diff = prop(**Asian**) - prop(**Black**) z = **1.5019**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.9334**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.1331**
Ha: diff > 0 — Pr(Z > z) = **0.0666**

Two-sample test of proportions — **Asian**: Number of obs = **377**; **Latino**: Number of obs = **367**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.9655172**	**.0093975**			**.9470986**	**.9839359**
Latino	**.9100817**	**.0149325**			**.8808147**	**.9393488**
diff	**.0554355**	**.0176434**			**.020855**	**.090016**
	under H0: **.017661**		**3.14**	**0.002**		

diff = prop(**Asian**) - prop(**Latino**) z = **3.1389**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.9992**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.0017**
Ha: diff > 0 — Pr(Z > z) = **0.0008**

Two-sample test of proportions — **Asian**: Number of obs = **377**; **White DEM**: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.9655172**	**.0093975**			**.9470986**	**.9839359**
White DEM	**.9292683**	**.0126615**			**.9044522**	**.9540844**
diff	**.0362489**	**.0157679**			**.0053445**	**.0671534**
	under H0: **.0160381**		**2.26**	**0.024**		

diff = prop(**Asian**) - prop(**White DEM**) z = **2.2602**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.9881**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.0238**
Ha: diff > 0 — Pr(Z > z) = **0.0119**

Two-sample test of proportions — **Asian**: Number of obs = **377**; **White GOP**: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.9655172**	**.0093975**			**.9470986**	**.9839359**
White GOP	**.8817734**	**.0160241**			**.8503668**	**.91318**
diff	**.0837438**	**.0185764**			**.0473347**	**.120153**
	under H0: **.0191699**		**4.37**	**0.000**		

diff = prop(**Asian**) - prop(**White GOP**) z = **4.3685**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **1.0000**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.0000**
Ha: diff > 0 — Pr(Z > z) = **0.0000**

Two-sample test of proportions **Black**: Number of obs = **384**
Latino: Number of obs = **367**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	**.9427083**	**.0118596**			**.919464**	**.9659527**
Latino	**.9100817**	**.0149325**			**.8808147**	**.9393488**
diff	**.0326266**	**.019069**			**-.004748**	**.0700012**
under H0:	**.0190181**	**1.72**	**0.086**			

diff = prop(**Black**) - prop(**Latino**) z = **1.7156**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9569** Pr(|Z| > |z|) = **0.0862** Pr(Z > z) = **0.0431**

Two-sample test of proportions **Black**: Number of obs = **384**
White DEM: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	**.9427083**	**.0118596**			**.919464**	**.9659527**
White DEM	**.9292683**	**.0126615**			**.9044522**	**.9540844**
diff	**.01344**	**.0173483**			**-.020562**	**.0474421**
under H0:	**.0174105**	**0.77**	**0.440**			

diff = prop(**Black**) - prop(**White DEM**) z = **0.7719**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.7799** Pr(|Z| > |z|) = **0.4401** Pr(Z > z) = **0.2201**

Two-sample test of proportions **Black**: Number of obs = **384**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	**.9427083**	**.0118596**			**.919464**	**.9659527**
White GOP	**.8817734**	**.0160241**			**.8503668**	**.91318**
diff	**.0609349**	**.0199354**			**.0218623**	**.1000076**
under H0:	**.0202289**	**3.01**	**0.003**			

diff = prop(**Black**) - prop(**White GOP**) z = **3.0123**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9987** Pr(|Z| > |z|) = **0.0026** Pr(Z > z) = **0.0013**

Two-sample test of proportions **Latino**: Number of obs = **367**
White DEM: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Latino	**.9100817**	**.0149325**			**.8808147**	**.9393488**
White DEM	**.9292683**	**.0126615**			**.9044522**	**.9540844**
diff	**-.0191865**	**.0195778**			**-.0575584**	**.0191853**
under H0:	**.0194721**	**-0.99**	**0.324**			

diff = prop(**Latino**) - prop(**White DEM**) z = **-0.9853**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.1622** Pr(|Z| > |z|) = **0.3245** Pr(Z > z) = **0.8378**

Two-sample test of proportions **Latino**: Number of obs = **367**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Latino	**.9100817**	**.0149325**			**.8808147**	**.9393488**
White GOP	**.8817734**	**.0160241**			**.8503668**	**.91318**
diff	**.0283083**	**.0219032**			**-.0146211**	**.0712378**
under H0:	**.0220602**	**1.28**	**0.199**			

diff = prop(**Latino**) - prop(**White GOP**) z = **1.2832**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9003** Pr(|Z| > |z|) = **0.1994** Pr(Z > z) = **0.0997**

Two-sample test of proportions **White DEM**: Number of obs = **410**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
White DEM	**.9292683**	**.0126615**			**.9044522**	**.9540844**
White GOP	**.8817734**	**.0160241**			**.8503668**	**.91318**
diff	**.0474949**	**.0204227**			**.0074672**	**.0875226**
under H0:	**.0204676**	**2.32**	**0.020**			

diff = prop(**White DEM**) - prop(**White GOP**) z = **2.3205**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9898** Pr(|Z| > |z|) = **0.0203** Pr(Z > z) = **0.0102**

TESTS FOR VARIABLE: DNAanycon

Two-sample test of proportions **Asian**: Number of obs = **377**
Black: Number of obs = **384**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.8222812**	**.0196882**			**.783693**	**.8608693**
Black	**.7890625**	**.0208193**			**.7482573**	**.8298677**
diff	**.0332187**	**.0286543**			**-.0229428**	**.0893801**
under H0:	**.0286967**	**1.16**	**0.247**			

diff = prop(**Asian**) - prop(**Black**) z = **1.1576**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.8765** Pr(|Z| > |z|) = **0.2470** Pr(Z > z) = **0.1235**

Two-sample test of proportions **Asian**: Number of obs = **377**
Latino: Number of obs = **367**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	**.8222812**	**.0196882**			**.783693**	**.8608693**
Latino	**.7574932**	**.0223727**			**.7136435**	**.8013429**
diff	**.064788**	**.0298021**			**.006377**	**.123199**
under H0:	**.0298511**	**2.17**	**0.030**			

diff = prop(**Asian**) - prop(**Latino**) z = **2.1704**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9850** Pr(|Z| > |z|) = **0.0300** Pr(Z > z) = **0.0150**

Two-sample test of proportions — **Asian**: Number of obs = **377**; **White DEM**: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	.8222812	.0196882			.783693	.8608693
White DEM	.8219512	.018893			.7849216	.8589808
diff	.0003299	.0272868			-.0531512	.0538111
	under H0:	.0272877	0.01	0.990		

diff = prop(**Asian**) - prop(**White DEM**) z = **0.0121**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.5048**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.9904**
Ha: diff > 0 — Pr(Z > z) = **0.4952**

Two-sample test of proportions — **Asian**: Number of obs = **377**; **White GOP**: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Asian	.8222812	.0196882			.783693	.8608693
White GOP	.6921182	.0229097			.6472161	.7370204
diff	.1301629	.0302073			.0709578	.1893681
	under H0:	.0307702	4.23	0.000		

diff = prop(**Asian**) - prop(**White GOP**) z = **4.2302**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **1.0000**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.0000**
Ha: diff > 0 — Pr(Z > z) = **0.0000**

Two-sample test of proportions — **Black**: Number of obs = **384**; **Latino**: Number of obs = **367**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.7890625	.0208193			.7482573	.8298677
Latino	.7574932	.0223727			.7136435	.8013429
diff	.0315693	.0305611			-.0283294	.091468
	under H0:	.0305488	1.03	0.301		

diff = prop(**Black**) - prop(**Latino**) z = **1.0334**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.8493**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.3014**
Ha: diff > 0 — Pr(Z > z) = **0.1507**

Two-sample test of proportions — **Black**: Number of obs = **384**; **White DEM**: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.7890625	.0208193			.7482573	.8298677
White DEM	.8219512	.018893			.7849216	.8589808
diff	-.0328887	.0281139			-.0879909	.0222135
	under H0:	.0280791	-1.17	0.241		

diff = prop(**Black**) - prop(**White DEM**) z = **-1.1713**
H0: diff = 0

Ha: diff < 0 — Pr(Z < z) = **0.1207**
Ha: diff != 0 — Pr(|Z| > |z|) = **0.2415**
Ha: diff > 0 — Pr(Z > z) = **0.8793**

Two-sample test of proportions **Black**: Number of obs = **384**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Black	.7890625	.0208193			.7482573	.8298677
White GOP	.6921182	.0229097			.6472161	.7370204
diff	.0969443	.0309564			.0362708	.1576177
	under H0:	.0312534	3.10	0.002		

diff = prop(**Black**) - prop(**White GOP**) z = **3.1019**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9990** Pr(|Z| > |z|) = **0.0019** Pr(Z > z) = **0.0010**

Two-sample test of proportions **Latino**: Number of obs = **367**
White DEM: Number of obs = **410**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Latino	.7574932	.0223727			.7136435	.8013429
White DEM	.8219512	.018893			.7849216	.8589808
diff	-.064458	.0292828			-.1218513	-.0070648
	under H0:	.0291917	-2.21	0.027		

diff = prop(**Latino**) - prop(**White DEM**) z = **-2.2081**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.0136** Pr(|Z| > |z|) = **0.0272** Pr(Z > z) = **0.9864**

Two-sample test of proportions **Latino**: Number of obs = **367**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
Latino	.7574932	.0223727			.7136435	.8013429
White GOP	.6921182	.0229097			.6472161	.7370204
diff	.065375	.0320217			.0026135	.1281364
	under H0:	.0322275	2.03	0.043		

diff = prop(**Latino**) - prop(**White GOP**) z = **2.0285**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **0.9787** Pr(|Z| > |z|) = **0.0425** Pr(Z > z) = **0.0213**

Two-sample test of proportions **White DEM**: Number of obs = **410**
White GOP: Number of obs = **406**

Group	Mean	Std. err.	z	P>|z|	[95% conf.	interval]
White DEM	.8219512	.018893			.7849216	.8589808
White GOP	.6921182	.0229097			.6472161	.7370204
diff	.129833	.0296951			.0716317	.1880343
	under H0:	.0300142	4.33	0.000		

diff = prop(**White DEM**) - prop(**White GOP**) z = **4.3257**
H0: diff = 0

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(Z < z) = **1.0000** Pr(|Z| > |z|) = **0.0000** Pr(Z > z) = **0.0000**

```
163
164 **********START FIGURE 2**********
165 foreach y of varlist morethanone DNAanycon {
    2. tempname memhold
    3. tempfile `y'
    4. postfile `memhold' fivegroups propagree seprop using `y', replace
    5. forval v=1/5 {
    6.         reg `y' if fivegroups==`v'
    7.         post `memhold ' (`v') (_b[_cons]) (_se[_cons])
    8. }
    9. postclose `memhold'
   10. }
  (file morethanone.dta not found)
```

Source	SS	df	MS		
Model	0	0	.	Number of obs	= 377
				F(0, 376)	= 0.00
Residual	12.5517241	376	.033382245	Prob > F	= .
				R-squared	= 0.0000
Total	12.5517241	376	.033382245	Adj R-squared	= 0.0000
				Root MSE	= .18271

morethanone	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.9655172	.0094099	102.61	0.000	.9470145	.98402

Source	SS	df	MS		
Model	0	0	.	Number of obs	= 384
				F(0, 383)	= 0.00
Residual	20.7395833	383	.054150348	Prob > F	= .
				R-squared	= 0.0000
Total	20.7395833	383	.054150348	Adj R-squared	= 0.0000
				Root MSE	= .2327

morethanone	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.9427083	.011875	79.39	0.000	.9193599	.9660568

Source	SS	df	MS		
Model	0	0	.	Number of obs	= 367
				F(0, 366)	= 0.00
Residual	30.0326975	366	.082056551	Prob > F	= .
				R-squared	= 0.0000
Total	30.0326975	366	.082056551	Adj R-squared	= 0.0000
				Root MSE	= .28646

morethanone	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.9100817	.0149528	60.86	0.000	.8806775	.939486

Source	SS	df	MS		
Model	0	0	.	Number of obs	= 410
				F(0, 409)	= 0.00
Residual	26.9487805	409	.065889439	Prob > F	= .
				R-squared	= 0.0000
Total	26.9487805	409	.065889439	Adj R-squared	= 0.0000
				Root MSE	= .25669

morethanone	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.9292683	.012677	73.30	0.000	.9043481	.9541885

Source	SS	df	MS	Number of obs	=	406
				F(0, 405)	=	0.00
Model	0	0	.	Prob > F	=	.
Residual	42.3251232	405	.104506477	R-squared	=	0.0000
				Adj R-squared	=	0.0000
Total	42.3251232	405	.104506477	Root MSE	=	.32327

morethanone	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.8817734	.0160438	54.96	0.000	.8502338	.913313

(file **DNAanycon.dta** not found)

Source	SS	df	MS	Number of obs	=	377
				F(0, 376)	=	0.00
Model	0	0	.	Prob > F	=	.
Residual	55.0928382	376	.146523506	R-squared	=	0.0000
				Adj R-squared	=	0.0000
Total	55.0928382	376	.146523506	Root MSE	=	.38278

DNAanycon	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.8222812	.0197144	41.71	0.000	.7835169	.8610454

Source	SS	df	MS	Number of obs	=	384
				F(0, 383)	=	0.00
Model	0	0	.	Prob > F	=	.
Residual	63.9140625	383	.166877448	R-squared	=	0.0000
				Adj R-squared	=	0.0000
Total	63.9140625	383	.166877448	Root MSE	=	.40851

DNAanycon	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.7890625	.0208465	37.85	0.000	.7480746	.8300504

Source	SS	df	MS	Number of obs	=	367
				F(0, 366)	=	0.00
Model	0	0	.	Prob > F	=	.
Residual	67.4168937	366	.184199163	R-squared	=	0.0000
				Adj R-squared	=	0.0000
Total	67.4168937	366	.184199163	Root MSE	=	.42918

DNAanycon	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.7574932	.0224032	33.81	0.000	.713438	.8015484

Source	SS	df	MS	Number of obs	=	410
				F(0, 409)	=	0.00
Model	0	0	.	Prob > F	=	.
Residual	60.002439	409	.14670523	R-squared	=	0.0000
				Adj R-squared	=	0.0000
Total	60.002439	409	.14670523	Root MSE	=	.38302

DNAanycon	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.8219512	.0189161	43.45	0.000	.7847664	.8591361

Source	SS	df	MS	Number of obs	=	406
				F(0, 405)	=	0.00
Model	0	0	.	Prob > F	=	.
Residual	86.5147783	405	.213616737	R-squared	=	0.0000
				Adj R-squared	=	0.0000
Total	86.5147783	405	.213616737	Root MSE	=	.46219

DNAanycon	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
_cons	.6921182	.022938	30.17	0.000	.6470259	.7372105

```
166
167 preserve

168 use morethanone, clear

169 lab def fivegroups 1"Asian" 2"Black" 3"Latino" 4"White DEM" 5"White GOP"

170 lab val fivegroups fivegroups

171 gen UB = propagree + 1.96*seprop

172 gen LB = propagree - 1.96*seprop

173 twoway (bar propagree fivegroups, fcolor(gs8)) (rcap UB LB fivegroups, lcolor(black)
  > ), xlabel(, valuelabel) xtitle(" ") legend(off) ylabel(0(.25)1) title("(a) Proportio
  > n Agree with >1 Factor to Define Race") name(morethanone, replace)

174
175 use DNAanycon, clear

176 lab def fivegroups 1"Asian" 2"Black" 3"Latino" 4"White DEM" 5"White GOP"

177 lab val fivegroups fivegroups

178 gen UB = propagree + 1.96*seprop

179 gen LB = propagree - 1.96*seprop

180 twoway (bar propagree fivegroups, fcolor(gs8)) (rcap UB LB fivegroups, lcolor(black)
  > ), xlabel(, valuelabel) xtitle(" ") legend(off) ylabel(0(.25)1) title("(b) Proportio
  > n Agree with 'Conflicting' Factors to Define Race") name(DNAanycon, replace)

181
182 graph combine morethanone DNAanycon, row(1) col(2) iscale(.7) imargin(r+10 l+5) xsiz
  > e(6.5) ysize(2.5)

183 graph export Figure2.pdf, replace
  file Figure2.pdf saved as PDF format

184 restore

185 **********END FIGURE 2**********
186 *****cleaning up directory*****
187 erase DNAanycon.dta

188 erase morethanone.dta
```

```
189
190 **********BIOLOGICAL DETERMINISM**********
191 recode moduleC_scale (1=1 "All biology")(2=.75)(3=.5)(4=.25)(5=0 "Identity totally s
  > eparate")(else=.), gen(race_bio_identity)
  (1,419 differences between moduleC_scale and race_bio_identity)

192
193 gen race_bio_graph= -1*(moduleC_scale-5)

194 lab def race_bio_graph 0 "Racial identity is totally separate from biology" 1 "Racia
  > l identity is somewhat separate from biology" 2 "Racial identity is tied to your bio
  > logy but not determined by it" 3 "Biology somewhat determines your racial identity"
  > 4 "Biology totally determines your racial identity", modify

195 lab val race_bio_graph race_bio_graph

196
197 *****in text*****
198 tab race_bio_graph fivegroups, col
```

Key
frequency *column percentage*

race_bio_graph	Subgroups: Asian	Black	Latino	White DEM	White GOP	Total
Racial identity is to	36	56	50	36	50	228
	9.55	14.58	13.62	8.78	12.32	11.73
Racial identity is so	15	31	32	34	20	132
	3.98	8.07	8.72	8.29	4.93	6.79
Racial identity is ti	118	130	114	126	114	602
	31.30	33.85	31.06	30.73	28.08	30.97
Biology somewhat dete	121	69	74	96	74	434
	32.10	17.97	20.16	23.41	18.23	22.33
Biology totally deter	87	98	97	118	148	548
	23.08	25.52	26.43	28.78	36.45	28.19
Total	377	384	367	410	406	1,944
	100.00	100.00	100.00	100.00	100.00	100.00

```
199 *range on somewhat + totally, Low & Hi: 34 to 55%
200 disp 17.97+25.52
  43.49

201 disp 32.10+23.08
  55.18

202
203 *****PAIRWISE DIFFERENCE OF MEANS TESTS
204 foreach v of varlist AB-WDR {
  2.                 ttest race_bio_identity if `v'==1, by(fivegroups)
  3.         }
```

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Asian	**377**	**.637931**	**.0150431**	**.2920834**	**.608352**	**.6675101**
Black	**384**	**.5794271**	**.0169647**	**.3324389**	**.5460715**	**.6127827**
Combined	**761**	**.60841**	**.0113918**	**.3142581**	**.5860468**	**.6307732**
diff		**.058504**	**.0227006**		**.0139406**	**.1030673**

diff = mean(**Asian**) - mean(**Black**) t = **2.5772**
H0: diff = 0 Degrees of freedom = **759**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.9949** Pr(|T| > |t|) = **0.0101** Pr(T > t) = **0.0051**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Asian	**377**	**.637931**	**.0150431**	**.2920834**	**.608352**	**.6675101**
Latino	**367**	**.5926431**	**.0173051**	**.3315188**	**.5586131**	**.626673**
Combined	**744**	**.6155914**	**.0114667**	**.3127702**	**.5930804**	**.6381024**
diff		**.045288**	**.0228907**		**.0003498**	**.0902261**

diff = mean(**Asian**) - mean(**Latino**) t = **1.9784**
H0: diff = 0 Degrees of freedom = **742**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.9759** Pr(|T| > |t|) = **0.0482** Pr(T > t) = **0.0241**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Asian	**377**	**.637931**	**.0150431**	**.2920834**	**.608352**	**.6675101**
White DE	**410**	**.6378049**	**.0152188**	**.3081573**	**.607888**	**.6677217**
Combined	**787**	**.6378653**	**.0107072**	**.3003743**	**.6168472**	**.6588834**
diff		**.0001262**	**.0214469**		**-.0419738**	**.0422262**

diff = mean(**Asian**) - mean(**White DE**) t = **0.0059**
H0: diff = 0 Degrees of freedom = **785**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.5023** Pr(|T| > |t|) = **0.9953** Pr(T > t) = **0.4977**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Asian	377	.637931	.0150431	.2920834	.608352	.6675101
White GO	406	.6539409	.016681	.3361132	.6211487	.6867331
Combined	783	.6462324	.011278	.3155829	.6240937	.6683712
diff		-.0160099	.0225787		-.060332	.0283123

diff = mean(**Asian**) - mean(**White GO**) t = **-0.7091**
H0: diff = 0 Degrees of freedom = **781**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.2392** Pr(|T| > |t|) = **0.4785** Pr(T > t) = **0.7608**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Black	384	.5794271	.0169647	.3324389	.5460715	.6127827
Latino	367	.5926431	.0173051	.3315188	.5586131	.626673
Combined	751	.5858855	.0121088	.3318341	.5621143	.6096567
diff		-.013216	.0242352		-.0607929	.0343609

diff = mean(**Black**) - mean(**Latino**) t = **-0.5453**
H0: diff = 0 Degrees of freedom = **749**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.2928** Pr(|T| > |t|) = **0.5857** Pr(T > t) = **0.7072**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Black	384	.5794271	.0169647	.3324389	.5460715	.6127827
White DE	410	.6378049	.0152188	.3081573	.607888	.6677217
Combined	794	.6095718	.011401	.3212567	.5871921	.6319514
diff		-.0583778	.0227341		-.1030041	-.0137515

diff = mean(**Black**) - mean(**White DE**) t = **-2.5678**
H0: diff = 0 Degrees of freedom = **792**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.0052** Pr(|T| > |t|) = **0.0104** Pr(T > t) = **0.9948**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Black	384	.5794271	.0169647	.3324389	.5460715	.6127827
White GO	406	.6539409	.016681	.3361132	.6211487	.6867331
Combined	790	.6177215	.0119612	.3361922	.594242	.641201
diff		-.0745138	.0237993		-.1212312	-.0277964

diff = mean(**Black**) - mean(**White GO**) t = **-3.1309**
H0: diff = 0 Degrees of freedom = **788**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.0009** Pr(|T| > |t|) = **0.0018** Pr(T > t) = **0.9991**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Latino	**367**	**.5926431**	**.0173051**	**.3315188**	**.5586131**	**.626673**
White DE	**410**	**.6378049**	**.0152188**	**.3081573**	**.607888**	**.6677217**
Combined	**777**	**.6164736**	**.0114797**	**.3199934**	**.5939387**	**.6390086**
diff		**-.0451618**	**.0229522**		**-.0902177**	**-.000106**

diff = mean(**Latino**) - mean(**White DE**) t = **-1.9676**
H0: diff = 0 Degrees of freedom = **775**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.0247** Pr(|T| > |t|) = **0.0495** Pr(T > t) = **0.9753**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
Latino	**367**	**.5926431**	**.0173051**	**.3315188**	**.5586131**	**.626673**
White GO	**406**	**.6539409**	**.016681**	**.3361132**	**.6211487**	**.6867331**
Combined	**773**	**.6248383**	**.0120537**	**.3351264**	**.6011765**	**.6485001**
diff		**-.0612978**	**.0240526**		**-.1085142**	**-.0140815**

diff = mean(**Latino**) - mean(**White GO**) t = **-2.5485**
H0: diff = 0 Degrees of freedom = **771**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.0055** Pr(|T| > |t|) = **0.0110** Pr(T > t) = **0.9945**

Two-sample t test with equal variances

Group	Obs	Mean	Std. err.	Std. dev.	[95% conf.	interval]
White DE	**410**	**.6378049**	**.0152188**	**.3081573**	**.607888**	**.6677217**
White GO	**406**	**.6539409**	**.016681**	**.3361132**	**.6211487**	**.6867331**
Combined	**816**	**.6458333**	**.0112818**	**.322273**	**.6236885**	**.6679782**
diff		**-.016136**	**.0225707**		**-.0604396**	**.0281676**

diff = mean(**White DE**) - mean(**White GO**) t = **-0.7149**
H0: diff = 0 Degrees of freedom = **814**

Ha: diff < 0 Ha: diff != 0 Ha: diff > 0
Pr(T < t) = **0.2374** Pr(|T| > |t|) = **0.4749** Pr(T > t) = **0.7626**

```
205
206 **********START FIGURE 3**********
207 catplot, over(race_bio_identity) over(fivegroups) percent(fivegroups) recast(hbar) s
  > tack asyvars legend(lab(1 "Racial identity totally separate from biology") lab(2 "Ra
  > cial identity somewhat separate from biology") lab(3 "Racial identity is tied to you
  > r biology but not determined by it") lab(4 "Biology somewhat determines your racial
  > identity") lab(5 "Biology totally determines your racial identity") row(5)) xsize(8)
  >  ysize(7) legend(size(*.7))
```

```
208 graph export Figure3.pdf, replace
  file Figure3.pdf saved as PDF format

209 **********END FIGURE 3**********
210
211 **********COVID-19 ATTRIBUTIONS**********
212 recode ModuleB_a ModuleB_b ModuleB_c ModuleB_d ModuleB_e ModuleB_f (1=1)(2=.67)(3=.3
  > 3)(4=0)(else=.), gen(covid_gene covid_preexisting covid_jobs covid_healthcare covid_
  > neighborhood covid_flout_protocols)
  (1,260 differences between ModuleB_a and covid_gene)
  (868 differences between ModuleB_b and covid_preexisting)
  (949 differences between ModuleB_c and covid_jobs)
  (945 differences between ModuleB_d and covid_healthcare)
  (963 differences between ModuleB_e and covid_neighborhood)
  (985 differences between ModuleB_f and covid_flout_protocols)

213
214 /*Taking out those who refuse the entire battery*/
215 egen ref_covid_battery = anycount(ModuleB_a-ModuleB_f), val(4)

216 tab ref_covid_battery
```

ModuleB_a, ModuleB_b, ModuleB_c, ModuleB_d, ModuleB_e, ModuleB_f == 4	Freq.	Percent	Cum.
0	1,630	82.53	82.53
1	199	10.08	92.61
2	70	3.54	96.15
3	25	1.27	97.42
4	20	1.01	98.43
5	8	0.41	98.84
6	23	1.16	100.00
Total	1,975	100.00	

```
217 //23 people refused to acknowledge any of the factors as accounting for racial dispa
  > rities
218
219 **********START FIGURE 4**********
220 /*ANALYSES WITH RAKED WEIGHTS*/
221 //creating weight - survey raking
222 //adjust for the five groups
223 //using CES 2021 as the benchmark for controls
224
225 svycal regress i.fivegroup, generate(fivegroup_weight) totals(909 3301 3320 6144 750
  > 8 21182, copy)

226 svyset [pweight=fivegroup_weight]

  Sampling weights: fivegroup_weight
               VCE: linearized
       Single unit: missing
          Strata 1: <one>
   Sampling unit 1: <observations>
             FPC 1: <zero>
```

```
227 recode fivegroups (4=1)(1/3 5=0)(else=.), gen(WDem)
  (1,944 differences between fivegroups and WDem)

228 recode fivegroups (5=1)(1/4 =0)(else=.), gen(WRep)
  (1,944 differences between fivegroups and WRep)

229
230 foreach v of varlist covid_gene covid_preexisting covid_jobs covid_healthcare covid_
  > neighborhood covid_flout_protocols {
    2. svy: reg `v' race_bio_identity pid7cata ed6cat age01 black hispanic api WDem if r
  > ef_covid_battery~=6
    3. est store `v'_wt
    4. }
  (running regress on estimation sample)

  Survey: Linear regression

  Number of strata =     1                        Number of obs    =      1,917
  Number of PSUs   = 1,917                        Population size = 20,895.419
                                                  Design df        =      1,916
                                                  F(8, 1909)       =       9.90
                                                  Prob > F         =     0.0000
                                                  R-squared        =     0.0351

------------------------------------------------------------------------------
             |             Linearized
   covid_gene | Coefficient  std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
race_bio_id~y |   .0984333   .0271588     3.62   0.000     .0451693    .1516973
      pid7cata |  -.1551406   .0353237    -4.39   0.000    -.2244175   -.0858637
        ed6cat |  -.0795426   .0259623    -3.06   0.002     -.13046   -.0286252
         age01 |  -.0272224   .0358219    -0.76   0.447    -.0974764    .0430315
         black |   -.019797   .0350534    -0.56   0.572    -.0885439    .0489498
      hispanic |  -.0263574   .0321397    -0.82   0.412     -.08939    .0366751
           api |  -.0952978   .0299959    -3.18   0.002     -.154126   -.0364697
          WDem |   -.085005   .0368552    -2.31   0.021    -.1572855   -.0127245
         _cons |   .7618239   .0453413    16.80   0.000     .6729004    .8507474
------------------------------------------------------------------------------

  (running regress on estimation sample)

  Survey: Linear regression

  Number of strata =     1                        Number of obs    =      1,918
  Number of PSUs   = 1,918                        Population size = 20,904.465
                                                  Design df        =      1,917
                                                  F(8, 1910)       =       8.07
                                                  Prob > F         =     0.0000
                                                  R-squared        =     0.0383

------------------------------------------------------------------------------
             |             Linearized
covid_preex~g | Coefficient  std. err.      t    P>|t|     [95% conf. interval]
-------------+----------------------------------------------------------------
race_bio_id~y |   .0037678   .0203518     0.19   0.853    -.0361462    .0436817
      pid7cata |  -.0842752    .026809    -3.14   0.002    -.1368531   -.0316972
        ed6cat |   .0272085    .019786     1.38   0.169    -.0115958    .0660127
         age01 |   .0930023   .0275264     3.38   0.001     .0390173    .1469872
         black |   .0464504   .0270986     1.71   0.087    -.0066954    .0995962
      hispanic |   .0361844   .0248984     1.45   0.146    -.0126463    .0850151
           api |  -.0139023   .0236251    -0.59   0.556    -.0602358    .0324313
          WDem |  -.0039737   .0288287    -0.14   0.890    -.0605127    .0525653
         _cons |   .7864648   .0358586    21.93   0.000     .7161389    .8567908
------------------------------------------------------------------------------

  (running regress on estimation sample)

  Survey: Linear regression
```

Number of strata = 1
Number of PSUs = 1,918

Number of obs = 1,918
Population size = 20,913.912
Design df = 1,917
F(8, 1910) = 25.86
Prob > F = 0.0000
R-squared = 0.1180

covid_jobs	Coefficient	Linearized std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0092167	.0217408	0.42	0.672	-.0334215	.0518548
pid7cata	-.1759918	.0290366	-6.06	0.000	-.2329383	-.1190452
ed6cat	.014672	.0213596	0.69	0.492	-.0272185	.0565625
age01	.0516579	.0295184	1.75	0.080	-.0062336	.1095494
black	.0924838	.0282939	3.27	0.001	.0369937	.1479739
hispanic	.0367335	.027005	1.36	0.174	-.0162288	.0896957
api	.0154891	.0256654	0.60	0.546	-.034846	.0658242
WDem	.0312084	.030561	1.02	0.307	-.0287279	.0911447
_cons	.7853123	.0376898	20.84	0.000	.711395	.8592295

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
Number of PSUs = 1,916

Number of obs = 1,916
Population size = 20,877.376
Design df = 1,915
F(8, 1908) = 33.02
Prob > F = 0.0000
R-squared = 0.1593

covid_healthcare	Coefficient	Linearized std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0175525	.0226086	-0.78	0.438	-.0618925	.0267876
pid7cata	-.2130158	.0305075	-6.98	0.000	-.2728472	-.1531844
ed6cat	.0272649	.0220817	1.23	0.217	-.0160419	.0705716
age01	.0115063	.0297323	0.39	0.699	-.0468049	.0698175
black	.0927743	.0295453	3.14	0.002	.03483	.1507187
hispanic	.0434475	.0288765	1.50	0.133	-.0131852	.1000802
api	.011617	.0264849	0.44	0.661	-.0403253	.0635594
WDem	.0459396	.0318099	1.44	0.149	-.0164461	.1083253
_cons	.8156273	.0399779	20.40	0.000	.7372226	.894032

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = 1
Number of PSUs = 1,918

Number of obs = 1,918
Population size = 20,913.912
Design df = 1,917
F(8, 1910) = 17.49
Prob > F = 0.0000
R-squared = 0.0781

covid_neighborh~d	Coefficient	Linearized std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0133618	.0210953	-0.63	0.527	-.0547339	.0280103
pid7cata	-.1765271	.0296803	-5.95	0.000	-.2347361	-.1183181
ed6cat	.009248	.0201844	0.46	0.647	-.0303378	.0488337
age01	.0041385	.0278903	0.15	0.882	-.05056	.0588371
black	.0240458	.029466	0.82	0.415	-.0337429	.0818346
hispanic	.0081421	.0274503	0.30	0.767	-.0456935	.0619777
api	-.0358463	.0248197	-1.44	0.149	-.0845228	.0128302
WDem	-.0224697	.0302206	-0.74	0.457	-.0817385	.036799
_cons	.8686381	.0371284	23.40	0.000	.7958219	.9414543

(running **regress** on estimation sample)

Survey: Linear regression

Number of strata = **1** Number of obs = **1,919**
Number of PSUs = **1,919** Population size = **20,922.958**
Design df = **1,918**
F(**8, 1911**) = **7.76**
Prob > F = **0.0000**
R-squared = **0.0313**

covid_flout_pro~s	Coefficient	Linearized std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0432885	.0223845	1.93	0.053	-.0006121	.0871891
pid7cata	-.1288173	.0309936	-4.16	0.000	-.1896019	-.0680326
ed6cat	-.0701042	.0224568	-3.12	0.002	-.1141465	-.0260619
age01	.0944697	.030763	3.07	0.002	.0341372	.1548021
black	-.0110932	.0310961	-0.36	0.721	-.0720789	.0498925
hispanic	.0105597	.0286414	0.37	0.712	-.0456119	.0667312
api	-.0351421	.0268043	-1.31	0.190	-.0877107	.0174265
WDem	-.0636017	.0321872	-1.98	0.048	-.1267274	-.0004761
_cons	.8132465	.0402597	20.20	0.000	.7342892	.8922039

```
231 coefplot covid_gene_wt covid_flout_protocols_wt covid_neighborhood_wt covid_jobs_wt
  > covid_healthcare_wt covid_preexisting_wt, keep(race_bio_identity) xline(0, lcolor(re
  > d) lpattern(dash) ) ///
  > legend(position(3) row(6) region(margin(r+5))) coeflabels(race_bio_identity=" ", not
  > icks) ///
  > plotlabels(`" " ""Genetic Differences"" ""' `" " ""Flout Protocols"" " "' `" " ""Nei
  > ghborhood Hot Spots"" " "'  `" " ""Occupational Hazards"" " "' `" " ""Healthcare Acc
  > ess"" " "' `" " ""Preexisting Conditions"" ""' ) ///
  > title("DVs: Explanations for COVID-19 Racial Disparities" "OLS Coefficient on Defini
  > ng Race as Biology", size(medium)) xsize(10) ysize(7)

232 graph export Figure4.pdf, replace
  file Figure4.pdf saved as PDF format

233 **********END FIGURE 4**********
234
235 **********FOR APPENDIX**********
236 est table covid_gene_wt covid_preexisting_wt covid_jobs_wt covid_healthcare_wt covid
  > _neighborhood_wt covid_flout_protocols_wt , b(%9.2f) se style(col) eq(1) stats(N) mo
  > delwidth(1)
```

Variable	covid_g~t	covid_p~t	covid_j~t	covid_h~t	covid_n~t	covid_f~t
race_bio_i~y	**0.10**	**0.00**	**0.01**	**-0.02**	**-0.01**	**0.04**
	0.03	**0.02**	**0.02**	**0.02**	**0.02**	**0.02**
pid7cata	**-0.16**	**-0.08**	**-0.18**	**-0.21**	**-0.18**	**-0.13**
	0.04	**0.03**	**0.03**	**0.03**	**0.03**	**0.03**
ed6cat	**-0.08**	**0.03**	**0.01**	**0.03**	**0.01**	**-0.07**
	0.03	**0.02**	**0.02**	**0.02**	**0.02**	**0.02**
age01	**-0.03**	**0.09**	**0.05**	**0.01**	**0.00**	**0.09**
	0.04	**0.03**	**0.03**	**0.03**	**0.03**	**0.03**
black	**-0.02**	**0.05**	**0.09**	**0.09**	**0.02**	**-0.01**
	0.04	**0.03**	**0.03**	**0.03**	**0.03**	**0.03**

hispanic	-0.03	0.04	0.04	0.04	0.01	0.01
	0.03	0.02	0.03	0.03	0.03	0.03
api	-0.10	-0.01	0.02	0.01	-0.04	-0.04
	0.03	0.02	0.03	0.03	0.02	0.03
WDem	-0.09	-0.00	0.03	0.05	-0.02	-0.06
	0.04	0.03	0.03	0.03	0.03	0.03
_cons	0.76	0.79	0.79	0.82	0.87	0.81
	0.05	0.04	0.04	0.04	0.04	0.04
N	1917	1918	1918	1916	1918	1919

Legend: b/

> se

237 est table covid_gene_wt covid_preexisting_wt covid_jobs_wt covid_healthcare_wt covid
> _neighborhood_wt covid_flout_protocols_wt , b(%9.2f) star(.05 .01 .001) style(col) e
> q(1) stats(N)

| Variable | covid_gene~t | covid_pree~t | covid_jobs~t | covid_heal~t | covid_nei
> g~t | covid_flou~t |
|---|---|---|---|---|---|
| race_bio_i~y | 0.10*** | 0.00 | 0.01 | -0.02 | -0.01
> 0.04 |
| pid7cata | -0.16*** | -0.08** | -0.18*** | -0.21*** | -0.18
> *** | -0.13*** |
| ed6cat | -0.08** | 0.03 | 0.01 | 0.03 | 0.01
> | -0.07** |
| age01 | -0.03 | 0.09*** | 0.05 | 0.01 | 0.00
> | 0.09** |
| black | -0.02 | 0.05 | 0.09** | 0.09** | 0.02
> | -0.01 |
| hispanic | -0.03 | 0.04 | 0.04 | 0.04 | 0.01
> | 0.01 |
| api | -0.10** | -0.01 | 0.02 | 0.01 | -0.04
> | -0.04 |
| WDem | -0.09* | -0.00 | 0.03 | 0.05 | -0.02
> | -0.06* |
| _cons | 0.76*** | 0.79*** | 0.79*** | 0.82*** | 0.87
> *** | 0.81*** |
| N | 1917 | 1918 | 1918 | 1916 | 1918
> | 1919 |

Legend: * p<.05;

> ** p<.01; *** p<.001

```
238
239 //New model separately by five groups
240 forval j=1/5 {
    2.         foreach v of varlist covid_gene covid_preexisting covid_jobs covid_health
  > care covid_neighborhood covid_flout_protocols {
    3.         reg `v' race_bio_identity pid7cata ed6cat age01 black hispanic api if fiv
  > egroups==`j' & ref_covid_battery~=6
    4. est store `v'_`j'
    5.         }
    6.         }
  note: black omitted because of collinearity.
  note: hispanic omitted because of collinearity.
  note: api omitted because of collinearity.
```

Source	SS	df	MS		
Model	.579246558	4	.14481164	Number of obs	= 371
				F(4, 366)	= 1.45
Residual	36.5315635	366	.099813015	Prob > F	= 0.2167
				R-squared	= 0.0156
				Adj R-squared	= 0.0049
Total	37.11081	370	.100299487	Root MSE	= .31593

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0324745	.0568972	0.57	0.569	-.079412	.144361
pid7cata	.0591964	.0527821	1.12	0.263	-.0445978	.1629905
ed6cat	.0742419	.0588599	1.26	0.208	-.0415041	.1899879
age01	-.1568964	.0781705	-2.01	0.045	-.3106161	-.0031768
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.5631289	.0609746	9.24	0.000	.4432244	.6830334

```
note: black omitted because of collinearity.
note: hispanic omitted because of collinearity.
note: api omitted because of collinearity.
```

Source	SS	df	MS		
Model	.81048245	4	.202620613	Number of obs	= 371
				F(4, 366)	= 3.60
Residual	20.6139349	366	.056322226	Prob > F	= 0.0068
				R-squared	= 0.0378
				Adj R-squared	= 0.0273
Total	21.4244173	370	.057903831	Root MSE	= .23732

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0398849	.0427403	-0.93	0.351	-.1239322	.0441624
pid7cata	-.0054818	.039649	-0.14	0.890	-.0834503	.0724867
ed6cat	.1194409	.0442146	2.70	0.007	.0324944	.2063875
age01	.1065469	.0587204	1.81	0.070	-.0089248	.2220186
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7016881	.0458031	15.32	0.000	.6116178	.7917585

```
note: black omitted because of collinearity.
note: hispanic omitted because of collinearity.
note: api omitted because of collinearity.
```

Source	SS	df	MS		
Model	1.67427775	4	.418569437	Number of obs	= 371
				F(4, 366)	= 5.93
Residual	25.8509623	366	.070631045	Prob > F	= 0.0001
				R-squared	= 0.0608
				Adj R-squared	= 0.0506
Total	27.5252401	370	.074392541	Root MSE	= .26577

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0009218	.0478625	-0.02	0.985	-.0950418	.0931982
pid7cata	-.1862137	.0444008	-4.19	0.000	-.2735264	-.0989011
ed6cat	.0851424	.0495135	1.72	0.086	-.0122242	.1825091
age01	-.0157478	.0657578	-0.24	0.811	-.1450582	.1135627
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.785093	.0512924	15.31	0.000	.6842281	.8859578

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 371
				F(4, 366)	= 7.39
Model	2.04979012	4	.512447531	Prob > F	= 0.0000
Residual	25.3731616	366	.069325578	R-squared	= 0.0747
				Adj R-squared	= 0.0646
Total	27.4229517	370	.074116086	Root MSE	= .2633

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0325693	.0474181	-0.69	0.493	-.1258154	.0606768
pid7cata	-.229716	.0439885	-5.22	0.000	-.316218	-.143214
ed6cat	.0089697	.0490538	0.18	0.855	-.087493	.1054323
age01	-.0278694	.0651472	-0.43	0.669	-.1559792	.1002405
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8691811	.0508162	17.10	0.000	.7692527	.9691094

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 371
				F(4, 366)	= 1.62
Model	.39584855	4	.098962138	Prob > F	= 0.1673
Residual	22.289605	366	.06090056	R-squared	= 0.0174
				Adj R-squared	= 0.0067
Total	22.6854535	370	.061312037	Root MSE	= .24678

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0167589	.0444435	0.38	0.706	-.0706377	.1041556
pid7cata	-.0870414	.0412291	-2.11	0.035	-.168117	-.0059658
ed6cat	.0454811	.0459766	0.99	0.323	-.0449302	.1358925
age01	-.0149529	.0610604	-0.24	0.807	-.1350262	.1051204
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7603401	.0476284	15.96	0.000	.6666804	.8539997

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 371
				F(4, 366)	= 0.73
Model	.234894137	4	.058723534	Prob > F	= 0.5689
Residual	29.2611228	366	.079948423	R-squared	= 0.0080
				Adj R-squared	= -0.0029
Total	29.4960169	370	.079718965	Root MSE	= .28275

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0684512	.0509216	1.34	0.180	-.0316845	.1685869
pid7cata	-.0430464	.0472387	-0.91	0.363	-.1359397	.0498468
ed6cat	-.033915	.0526782	-0.64	0.520	-.1375049	.0696749
age01	.0434023	.0699607	0.62	0.535	-.0941731	.1809777
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7210282	.0545708	13.21	0.000	.6137166	.8283399

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 380
				F(4, 375)	= 8.73
Model	3.71725623	4	.929314057	Prob > F	= 0.0000
Residual	39.9013221	375	.106403526	R-squared	= 0.0852
				Adj R-squared	= 0.0755
Total	43.6185783	379	.115088597	Root MSE	= .3262

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.1058281	.0510399	2.07	0.039	.0054678	.2061884
pid7cata	-.3057266	.0621366	-4.92	0.000	-.4279064	-.1835468
ed6cat	-.0999222	.0585648	-1.71	0.089	-.2150788	.0152345
age01	-.0823343	.0738895	-1.11	0.266	-.227624	.0629555
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7988455	.0514093	15.54	0.000	.6977589	.8999321

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 380
				F(4, 375)	= 4.60
Model	.953243977	4	.238310994	Prob > F	= 0.0012
Residual	19.4162107	375	.051776562	R-squared	= 0.0468
				Adj R-squared	= 0.0366
Total	20.3694547	379	.053745263	Root MSE	= .22754

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0313973	.035604	0.88	0.378	-.0386111	.1014058
pid7cata	-.1227863	.0433447	-2.83	0.005	-.2080154	-.0375572
ed6cat	.0112409	.0408532	0.28	0.783	-.0690891	.0915709
age01	.128478	.0515432	2.49	0.013	.027128	.2298279
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8195459	.0358617	22.85	0.000	.7490308	.890061

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 380
				F(4, 375)	= 8.43
Model	1.44288195	4	.360720487	Prob > F	= 0.0000
Residual	16.0441898	375	.042784506	R-squared	= 0.0825
				Adj R-squared	= 0.0727
Total	17.4870717	379	.046140031	Root MSE	= .20684

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0877688	.032365	2.71	0.007	.0241292	.1514083
pid7cata	-.1531162	.0394015	-3.89	0.000	-.2305918	-.0756407
ed6cat	.0199343	.0371366	0.54	0.592	-.0530878	.0929563
age01	.1145094	.0468542	2.44	0.015	.0223796	.2066392
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8019836	.0325992	24.60	0.000	.7378835	.8660838

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.40336645	4	.350841612	Number of obs	= 379
Residual	18.7894744	374	.050239236	F(4, 374)	= 6.98
Total	20.1928408	378	.053420214	Prob > F	= 0.0000
				R-squared	= 0.0695
				Adj R-squared	= 0.0595
				Root MSE	= .22414

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0318773	.0351275	0.91	0.365	-.0371948	.1009495
pid7cata	-.1167946	.0427444	-2.73	0.007	-.2008441	-.0327451
ed6cat	.0719376	.0402421	1.79	0.075	-.0071916	.1510667
age01	.1609723	.050811	3.17	0.002	.0610613	.2608834
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7835973	.0354449	22.11	0.000	.7139011	.8532935

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	2.03008062	4	.507520156	Number of obs	= 380
Residual	18.9610267	375	.050562738	F(4, 375)	= 10.04
Total	20.9911073	379	.055385507	Prob > F	= 0.0000
				R-squared	= 0.0967
				Adj R-squared	= 0.0871
				Root MSE	= .22486

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0517345	.0351842	1.47	0.142	-.0174484	.1209175
pid7cata	-.2347881	.0428336	-5.48	0.000	-.3190123	-.150564
ed6cat	.0607888	.0403714	1.51	0.133	-.018594	.1401715
age01	.0594472	.0509355	1.17	0.244	-.0407077	.1596022
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8220856	.0354388	23.20	0.000	.7524019	.8917692

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	2.64789078	4	.661972695	Number of obs	= 380
Residual	27.7336231	375	.073956328	F(4, 375)	= 8.95
Total	30.3815139	379	.080162306	Prob > F	= 0.0000
				R-squared	= 0.0872
				Adj R-squared	= 0.0774
				Root MSE	= .27195

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.1361745	.042552	3.20	0.001	.0525042	.2198449
pid7cata	-.2100863	.0518033	-4.06	0.000	-.3119475	-.108225
ed6cat	-.0753691	.0488255	-1.54	0.124	-.1713752	.020637
age01	.1183134	.0616017	1.92	0.056	-.0028146	.2394415
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7589043	.0428599	17.71	0.000	.6746284	.8431801

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.64947521	4	.412368804	Number of obs	= 360
Residual	35.9907439	355	.101382377	F(4, 355)	= 4.07
				Prob > F	= 0.0031
Total	37.6402192	359	.104847407	R-squared	= 0.0438
				Adj R-squared	= 0.0330
				Root MSE	= .31841

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0533694	.0519445	1.03	0.305	-.0487882	.1555271
pid7cata	-.1659894	.0508141	-3.27	0.001	-.2659238	-.066055
ed6cat	-.1071097	.0595468	-1.80	0.073	-.2242185	.0099992
age01	-.0473796	.0787381	-0.60	0.548	-.2022314	.1074722
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7841609	.0524649	14.95	0.000	.6809797	.8873421

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.653859767	4	.163464942	Number of obs	= 361
Residual	17.9907714	356	.050535875	F(4, 356)	= 3.23
				Prob > F	= 0.0126
Total	18.6446312	360	.051790642	R-squared	= 0.0351
				Adj R-squared	= 0.0242
				Root MSE	= .2248

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0029366	.0366683	-0.08	0.936	-.0750503	.069177
pid7cata	-.0704206	.0358637	-1.96	0.050	-.140952	.0001108
ed6cat	.0678801	.0420408	1.61	0.107	-.0147994	.1505597
age01	.1217662	.0555895	2.19	0.029	.0124411	.2310912
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7953463	.0370303	21.48	0.000	.7225206	.868172

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.54359277	4	.385898192	Number of obs	= 360
Residual	25.0849664	355	.070661877	F(4, 355)	= 5.46
				Prob > F	= 0.0003
Total	26.6285591	359	.074174259	R-squared	= 0.0580
				Adj R-squared	= 0.0474
				Root MSE	= .26582

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0197356	.0433662	-0.46	0.649	-.1050225	.0655512
pid7cata	-.1817085	.0424224	-4.28	0.000	-.2651393	-.0982777
ed6cat	.0333824	.049713	0.67	0.502	-.0643865	.1311514
age01	.1028598	.065735	1.56	0.119	-.0264191	.2321387
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8173275	.0438006	18.66	0.000	.7311862	.9034689

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 361
				F(4, 356)	= 11.92
Model	3.1784622	4	.79461555	Prob > F	= 0.0000
Residual	23.7387248	356	.066681811	R-squared	= 0.1181
				Adj R-squared	= 0.1082
Total	26.917187	360	.074769964	Root MSE	= .25823

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0067312	.0421206	0.16	0.873	-.0761052	.0895676
pid7cata	-.2833748	.0411964	-6.88	0.000	-.3643937	-.2023558
ed6cat	-.0040141	.048292	-0.08	0.934	-.0989875	.0909592
age01	.066689	.0638552	1.04	0.297	-.0588919	.1922699
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8653796	.0425365	20.34	0.000	.7817253	.9490339

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 360
				F(4, 355)	= 5.53
Model	1.41011266	4	.352528166	Prob > F	= 0.0002
Residual	22.6211965	355	.06372168	R-squared	= 0.0587
				Adj R-squared	= 0.0481
Total	24.0313092	359	.06693958	Root MSE	= .25243

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0356082	.0411815	-0.86	0.388	-.1165985	.0453822
pid7cata	-.1820329	.0402853	-4.52	0.000	-.2612607	-.1028051
ed6cat	-.0073862	.0472086	-0.16	0.876	-.1002298	.0854574
age01	.0604398	.0624234	0.97	0.334	-.0623263	.183206
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8818313	.0415941	21.20	0.000	.8000295	.9636331

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 361
				F(4, 356)	= 2.19
Model	.67025829	4	.167564573	Prob > F	= 0.0699
Residual	27.2619763	356	.076578585	R-squared	= 0.0240
				Adj R-squared	= 0.0130
Total	27.9322346	360	.077589541	Root MSE	= .27673

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0229041	.0451382	0.51	0.612	-.0658669	.1116751
pid7cata	-.1194934	.0441478	-2.71	0.007	-.2063168	-.0326701
ed6cat	-.0140755	.0517517	-0.27	0.786	-.115853	.0877021
age01	.1014652	.06843	1.48	0.139	-.0331126	.2360431
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8061818	.0455839	17.69	0.000	.7165342	.8958293

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	2.98877648	4	.74719412	Number of obs	407
Residual	40.467252	402	.100664806	F(4, 402)	7.42
				Prob > F	0.0000
Total	43.4560284	406	.107034553	R-squared	0.0688
				Adj R-squared	0.0595
				Root MSE	.31728

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.2133851	.0515421	4.14	0.000	.1120593	.3147108
pid7cata	.0846483	.1596313	0.53	0.596	-.2291681	.3984647
ed6cat	-.1760361	.0467479	-3.77	0.000	-.2679369	-.0841352
age01	.002533	.0659922	0.04	0.969	-.1271999	.132266
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.6271268	.0567527	11.05	0.000	.5155576	.738696

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.412443651	4	.103110913	Number of obs	407
Residual	18.1452058	402	.045137328	F(4, 402)	2.28
				Prob > F	0.0597
Total	18.5576495	406	.045708496	R-squared	0.0222
				Adj R-squared	0.0125
				Root MSE	.21246

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0573509	.0345137	1.66	0.097	-.010499	.1252007
pid7cata	-.1970412	.1068925	-1.84	0.066	-.4071793	.0130968
ed6cat	-.0019346	.0313034	-0.06	0.951	-.0634734	.0596041
age01	.0722703	.0441898	1.64	0.103	-.0146016	.1591422
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7817348	.0380028	20.57	0.000	.7070258	.8564439

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.404118445	4	.101029611	Number of obs	407
Residual	20.3488663	402	.05061907	F(4, 402)	2.00
				Prob > F	0.0944
Total	20.7529847	406	.051115726	R-squared	0.0195
				Adj R-squared	0.0097
				Root MSE	.22499

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0547933	.0365494	1.50	0.135	-.0170586	.1266452
pid7cata	-.182361	.1131974	-1.61	0.108	-.4048938	.0401717
ed6cat	.0407347	.0331497	1.23	0.220	-.0244338	.1059032
age01	.0324152	.0467962	0.69	0.489	-.0595807	.1244111
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7821882	.0402444	19.44	0.000	.7030725	.8613038

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 407
				F(4, 402)	= 1.12
Model	.217652612	4	.054413153	Prob > F	= 0.3462
Residual	19.5187075	402	.048553999	R-squared	= 0.0110
				Adj R-squared	= 0.0012
Total	19.7363601	406	.048611724	Root MSE	= .22035

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0252626	.0357961	0.71	0.481	-.0451084	.0956335
pid7cata	-.1203537	.1108643	-1.09	0.278	-.3382999	.0975925
ed6cat	.04375	.0324665	1.35	0.179	-.0200753	.1075754
age01	.0241993	.0458317	0.53	0.598	-.0659006	.1142991
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8130975	.0394149	20.63	0.000	.7356124	.8905826

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 407
				F(4, 402)	= 0.84
Model	.156200442	4	.039050111	Prob > F	= 0.4986
Residual	18.6263734	402	.046334262	R-squared	= 0.0083
				Adj R-squared	= -0.0016
Total	18.7825738	406	.046262497	Root MSE	= .21525

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0210827	.0349683	0.60	0.547	-.0476609	.0898262
pid7cata	-.1740544	.1083005	-1.61	0.109	-.3869605	.0388516
ed6cat	.0065647	.0317157	0.21	0.836	-.0557847	.068914
age01	-.0175605	.0447718	-0.39	0.695	-.1055767	.0704557
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8352892	.0385034	21.69	0.000	.7595961	.9109824

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 407
				F(4, 402)	= 4.09
Model	1.12909941	4	.282274851	Prob > F	= 0.0029
Residual	27.7268853	402	.068972351	R-squared	= 0.0391
				Adj R-squared	= 0.0296
Total	28.8559847	406	.071073854	Root MSE	= .26263

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.1066946	.0426639	2.50	0.013	.0228223	.1905669
pid7cata	.0273028	.1321347	0.21	0.836	-.2324584	.287064
ed6cat	-.1284749	.0386955	-3.32	0.001	-.2045458	-.0524041
age01	.0097445	.054625	0.18	0.859	-.0976418	.1171308
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7685589	.046977	16.36	0.000	.6762076	.8609102

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 399
				F(4, 394)	= 0.45
Model	.16765988	4	.04191497	Prob > F	= 0.7713
Residual	36.5800093	394	.092842663	R-squared	= 0.0046
				Adj R-squared	= -0.0055
Total	36.7476692	398	.092330827	Root MSE	= .3047

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0202144	.0471224	0.43	0.668	-.0724284	.1128572
pid7cata	-.0433427	.1512175	-0.29	0.775	-.3406367	.2539514
ed6cat	.0463857	.0489428	0.95	0.344	-.049836	.1426074
age01	-.0334925	.0656954	-0.51	0.610	-.16265	.0956649
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.6525041	.1469903	4.44	0.000	.3635206	.9414875

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 399
				F(4, 394)	= 0.69
Model	.196032421	4	.049008105	Prob > F	= 0.6004
Residual	28.0520814	394	.071198176	R-squared	= 0.0069
				Adj R-squared	= -0.0031
Total	28.2481138	398	.07097516	Root MSE	= .26683

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0396429	.0412656	-0.96	0.337	-.1207712	.0414854
pid7cata	.0040767	.1324228	0.03	0.975	-.2562669	.2644203
ed6cat	.0351898	.0428597	0.82	0.412	-.0490725	.1194522
age01	.0611691	.0575302	1.06	0.288	-.0519354	.1742737
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7447887	.128721	5.79	0.000	.4917228	.9978546

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 400
				F(4, 395)	= 0.59
Model	.204135447	4	.051033862	Prob > F	= 0.6728
Residual	34.3896577	395	.087062425	R-squared	= 0.0059
				Adj R-squared	= -0.0042
Total	34.5937932	399	.086701236	Root MSE	= .29506

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0357953	.0454922	-0.79	0.432	-.1252324	.0536418
pid7cata	-.15384	.1461748	-1.05	0.293	-.4412178	.1335378
ed6cat	-.030235	.0473005	-0.64	0.523	-.1232273	.0627573
age01	.0214798	.0634617	0.34	0.735	-.103285	.1462447
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8302587	.141955	5.85	0.000	.5511769	1.109341

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 398
				F(4, 393)	= 1.27
Model	.474133877	4	.118533469	Prob > F	= 0.2809
Residual	36.6621262	393	.093287853	R-squared	= 0.0128
				Adj R-squared	= 0.0027
Total	37.1362601	397	.093542217	Root MSE	= .30543

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0738527	.0472908	-1.56	0.119	-.1668272	.0191218
pid7cata	-.186725	.1516876	-1.23	0.219	-.4849457	.1114958
ed6cat	.0050121	.0490769	0.10	0.919	-.091474	.1014981
age01	-.0733142	.0659212	-1.11	0.267	-.2029165	.0562882
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8785729	.1474869	5.96	0.000	.5886109	1.168535

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 400
				F(4, 395)	= 0.63
Model	.192164455	4	.048041114	Prob > F	= 0.6404
Residual	30.0566097	395	.076092683	R-squared	= 0.0064
				Adj R-squared	= -0.0037
Total	30.2487742	399	.075811464	Root MSE	= .27585

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0590677	.0425298	-1.39	0.166	-.1426807	.0245452
pid7cata	-.0508728	.1366559	-0.37	0.710	-.3195367	.2177911
ed6cat	-.0032089	.0442204	-0.07	0.942	-.0901456	.0837278
age01	-.0432068	.0593291	-0.73	0.467	-.159847	.0734335
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8112967	.132711	6.11	0.000	.5503885	1.072205

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 400
				F(4, 395)	= 1.75
Model	.572786192	4	.143196548	Prob > F	= 0.1384
Residual	32.3348227	395	.081860311	R-squared	= 0.0174
				Adj R-squared	= 0.0075
Total	32.9076088	399	.08247521	Root MSE	= .28611

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0371037	.0441121	-0.84	0.401	-.1238276	.0496203
pid7cata	-.1245555	.1417404	-0.88	0.380	-.4032154	.1541045
ed6cat	-.023228	.0458656	-0.51	0.613	-.1133993	.0669433
age01	.1369735	.0615365	2.23	0.027	.0159935	.2579535
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8197742	.1376487	5.96	0.000	.5491585	1.09039

```
241
242 forval j=1/5 {
    2. est table covid_gene_`j' covid_preexisting_`j' covid_jobs_`j' covid_healthcare_`j
> '  covid_neighborhood_`j' covid_flout_protocols_`j' , b(%9.2f) se style(col) eq(1) s
> tats(N) keep(race_bio_identity pid7cata ed6cat age01 _cons)
    3. est table covid_gene_`j' covid_preexisting_`j' covid_jobs_`j' covid_healthcare_`j
> '  covid_neighborhood_`j' covid_flout_protocols_`j' , b(%9.2f) star(.05 .01 .001) st
> yle(col) eq(1) stats(N) keep(race_bio_identity pid7cata ed6cat age01 _cons)
    4. }
```

Variable	covid_g~1	covid_p~1	covid_j~1	covid_h~1	covid_n~1	covid_f~1
race_bio_i~y	0.03	-0.04	-0.00	-0.03	0.02	0.07
	0.06	0.04	0.05	0.05	0.04	0.05
pid7cata	0.06	-0.01	-0.19	-0.23	-0.09	-0.04
	0.05	0.04	0.04	0.04	0.04	0.05
ed6cat	0.07	0.12	0.09	0.01	0.05	-0.03
	0.06	0.04	0.05	0.05	0.05	0.05
age01	-0.16	0.11	-0.02	-0.03	-0.01	0.04
	0.08	0.06	0.07	0.07	0.06	0.07
_cons	0.56	0.70	0.79	0.87	0.76	0.72
	0.06	0.05	0.05	0.05	0.05	0.05
N	371	371	371	371	371	371

Legend: b/
> se

| Variable | covid_gene_1 | covid_pree~1 | covid_jobs_1 | covid_heal~1 | covid_nei
> g~1 | covid_flou~1 |
|---|---|---|---|---|---|
| race_bio_i~y | 0.03 | -0.04 | -0.00 | -0.03 | 0.02
> | 0.07 |
| pid7cata | 0.06 | -0.01 | -0.19*** | -0.23*** | -0.09
> * | -0.04 |
| ed6cat | 0.07 | 0.12** | 0.09 | 0.01 | 0.05
> | -0.03 |
| age01 | -0.16* | 0.11 | -0.02 | -0.03 | -0.01
> | 0.04 |

_cons	0.56***	0.70***	0.79***	0.87***	0.76***	0.72***
N	371	371	371	371	371	371

Legend: * p<.05; ** p<.01; *** p<.001

Variable	covid_g~2	covid_p~2	covid_j~2	covid_h~2	covid_n~2	covid_f~2
race_bio_i~y	0.11	0.03	0.09	0.03	0.05	0.14
	0.05	0.04	0.03	0.04	0.04	0.04
pid7cata	-0.31	-0.12	-0.15	-0.12	-0.23	-0.21
	0.06	0.04	0.04	0.04	0.04	0.05
ed6cat	-0.10	0.01	0.02	0.07	0.06	-0.08
	0.06	0.04	0.04	0.04	0.04	0.05
age01	-0.08	0.13	0.11	0.16	0.06	0.12
	0.07	0.05	0.05	0.05	0.05	0.06
_cons	0.80	0.82	0.80	0.78	0.82	0.76
	0.05	0.04	0.03	0.04	0.04	0.04
N	380	380	380	379	380	380

Legend: b/se

Variable	covid_gene_2	covid_pree~2	covid_jobs_2	covid_heal~2	covid_neig~2	covid_flou~2
race_bio_i~y	0.11*	0.03	0.09**	0.03	0.05	0.14**
pid7cata	-0.31***	-0.12**	-0.15***	-0.12**	-0.23***	-0.21***
ed6cat	-0.10	0.01	0.02	0.07	0.06	-0.08
age01	-0.08	0.13*	0.11*	0.16**	0.06	0.12
_cons	0.80***	0.82***	0.80***	0.78***	0.82***	0.76***
N	380	380	380	379	380	380

Legend: * p<.05; ** p<.01; *** p<.001

Variable	covid_g~3	covid_p~3	covid_j~3	covid_h~3	covid_n~3	covid_f~3
race_bio_i~y	0.05	-0.00	-0.02	0.01	-0.04	0.02
	0.05	0.04	0.04	0.04	0.04	0.05
pid7cata	-0.17	-0.07	-0.18	-0.28	-0.18	-0.12
	0.05	0.04	0.04	0.04	0.04	0.04
ed6cat	-0.11	0.07	0.03	-0.00	-0.01	-0.01
	0.06	0.04	0.05	0.05	0.05	0.05
age01	-0.05	0.12	0.10	0.07	0.06	0.10
	0.08	0.06	0.07	0.06	0.06	0.07
_cons	0.78	0.80	0.82	0.87	0.88	0.81
	0.05	0.04	0.04	0.04	0.04	0.05
N	360	361	360	361	360	361

Legend: b/se

Variable	covid_gene_3	covid_pree~3	covid_jobs_3	covid_heal~3	covid_neig~3	covid_flou~3
race_bio_i~y	0.05	-0.00	-0.02	0.01	-0.04	0.02
pid7cata	-0.17**	-0.07	-0.18***	-0.28***	-0.18***	-0.12**
ed6cat	-0.11	0.07	0.03	-0.00	-0.01	-0.01
age01	-0.05	0.12*	0.10	0.07	0.06	0.10
_cons	0.78***	0.80***	0.82***	0.87***	0.88***	0.81***
N	360	361	360	361	360	361

Legend: * p<.05; ** p<.01; *** p<.001

Variable	covid_g~4	covid_p~4	covid_j~4	covid_h~4	covid_n~4	covid_f~4
race_bio_i~y	0.21	0.06	0.05	0.03	0.02	0.11
	0.05	0.03	0.04	0.04	0.03	0.04
pid7cata	0.08	-0.20	-0.18	-0.12	-0.17	0.03

	0.16	0.11	0.11	0.11	0.11	0.13
ed6cat	-0.18	-0.00	0.04	0.04	0.01	-0.13
	0.05	0.03	0.03	0.03	0.03	0.04
age01	0.00	0.07	0.03	0.02	-0.02	0.01
	0.07	0.04	0.05	0.05	0.04	0.05
_cons	0.63	0.78	0.78	0.81	0.84	0.77
	0.06	0.04	0.04	0.04	0.04	0.05
N	407	407	407	407	407	407

Legend: b/se

Variable	covid_gene_4	covid_pree~4	covid_jobs_4	covid_heal~4	covid_neig~4	covid_flou~4
race_bio_i~y	0.21***	0.06	0.05	0.03	0.02	0.11*
pid7cata	0.08	-0.20	-0.18	-0.12	-0.17	0.03
ed6cat	-0.18***	-0.00	0.04	0.04	0.01	-0.13***
age01	0.00	0.07	0.03	0.02	-0.02	0.01
_cons	0.63***	0.78***	0.78***	0.81***	0.84***	0.77***
N	407	407	407	407	407	407

Legend: * p<.05; ** p<.01; *** p<.001

Variable	covid_g~5	covid_p~5	covid_j~5	covid_h~5	covid_n~5	covid_f~5
race_bio_i~y	0.02	-0.04	-0.04	-0.07	-0.06	-0.04
	0.05	0.04	0.05	0.05	0.04	0.04
pid7cata	-0.04	0.00	-0.15	-0.19	-0.05	-0.12
	0.15	0.13	0.15	0.15	0.14	0.14
ed6cat	0.05	0.04	-0.03	0.01	-0.00	-0.02
	0.05	0.04	0.05	0.05	0.04	0.05
age01	-0.03	0.06	0.02	-0.07	-0.04	0.14
	0.07	0.06	0.06	0.07	0.06	0.06
_cons	0.65	0.74	0.83	0.88	0.81	0.82

```
|                |       0.15 |       0.13 |       0.14 |       0.15 |       0.13 |       0.14
> |
|----------------+------------+------------+------------+------------+------------+------------
 _|
|              N |        399 |        399 |        400 |        398 |        400 |        400
> |
|----------------+------------+------------+------------+------------+------------+------------
 _|
                                                                                  Legend: b/
> se

 ----------------+----------------+----------------+----------------+----------------+----------
 ----+----------------+
|     Variable | covid_gene_5 | covid_pree~5 | covid_jobs_5 | covid_heal~5 | covid_nei
> g~5 | covid_flou~5 |
|----------------+----------------+----------------+----------------+----------------+----------
 ----+----------------+
| race_bio_i~y |       0.02    |      -0.04    |      -0.04    |      -0.07    |      -0.06
>     |      -0.04    |
|     pid7cata |      -0.04    |       0.00    |      -0.15    |      -0.19    |      -0.05
>     |      -0.12    |
|       ed6cat |       0.05    |       0.04    |      -0.03    |       0.01    |      -0.00
>     |      -0.02    |
|        age01 |      -0.03    |       0.06    |       0.02    |      -0.07    |      -0.04
>     |       0.14*   |
|        _cons |       0.65*** |       0.74*** |       0.83*** |       0.88*** |       0.81
> *** |       0.82*** |
|----------------+----------------+----------------+----------------+----------------+----------
 ----+----------------+
|              N |        399    |        399    |        400    |        398    |        400
>     |        400    |
|----------------+----------------+----------------+----------------+----------------+----------
 ----+----------------+
                                                                        Legend: * p<.05;
> ** p<.01; *** p<.001


**********FOOTNOTE - SEPARATE SAMPLE ESTIMATION
//pairwise comparisons:
//looking at the effect of race_bio_identity among:
//Asians vs. Blacks, Hispanics, W Dem, W GOP
//Blacks vs. Hispanics, W Dem, W GOP
//Hispanics vs. W Dem, W GOP
//W Dem vs. W GOP
*10 total comparisons

forval j=1/5 {
  2.         foreach v of varlist covid_gene covid_preexisting covid_jobs covid_health
> care covid_neighborhood covid_flout_protocols {
  3.         reg `v' race_bio_identity pid7cata ed6cat age01 black hispanic api if fiv
> egroups==`j' & ref_covid_battery~=6
  4. est store `v'`j'
  5.         }
  6.         }
note: black omitted because of collinearity.
note: hispanic omitted because of collinearity.
note: api omitted because of collinearity.

      Source |       SS           df       MS      Number of obs   =       371
-------------+----------------------------------   F(4, 366)       =      1.45
       Model |  .579246558         4  .14481164   Prob > F        =    0.2167
    Residual |  36.5315635       366  .099813015   R-squared       =    0.0156
-------------+----------------------------------   Adj R-squared   =    0.0049
       Total |    37.11081       370  .100299487   Root MSE        =    .31593
```

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0324745	.0568972	0.57	0.569	-.079412	.144361
pid7cata	.0591964	.0527821	1.12	0.263	-.0445978	.1629905
ed6cat	.0742419	.0588599	1.26	0.208	-.0415041	.1899879
age01	-.1568964	.0781705	-2.01	0.045	-.3106161	-.0031768
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.5631289	.0609746	9.24	0.000	.4432244	.6830334

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.81048245	4	.202620613	Number of obs	= 371
Residual	20.6139349	366	.056322226	F(4, 366)	= 3.60
				Prob > F	= 0.0068
				R-squared	= 0.0378
				Adj R-squared	= 0.0273
Total	21.4244173	370	.057903831	Root MSE	= .23732

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0398849	.0427403	-0.93	0.351	-.1239322	.0441624
pid7cata	-.0054818	.039649	-0.14	0.890	-.0834503	.0724867
ed6cat	.1194409	.0442146	2.70	0.007	.0324944	.2063875
age01	.1065469	.0587204	1.81	0.070	-.0089248	.2220186
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7016881	.0458031	15.32	0.000	.6116178	.7917585

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.67427775	4	.418569437	Number of obs	= 371
Residual	25.8509623	366	.070631045	F(4, 366)	= 5.93
				Prob > F	= 0.0001
				R-squared	= 0.0608
				Adj R-squared	= 0.0506
Total	27.5252401	370	.074392541	Root MSE	= .26577

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0009218	.0478625	-0.02	0.985	-.0950418	.0931982
pid7cata	-.1862137	.0444008	-4.19	0.000	-.2735264	-.0989011
ed6cat	.0851424	.0495135	1.72	0.086	-.0122242	.1825091
age01	-.0157478	.0657578	-0.24	0.811	-.1450582	.1135627
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.785093	.0512924	15.31	0.000	.6842281	.8859578

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	2.04979012	4	.512447531	Number of obs	= 371
Residual	25.3731616	366	.069325578	F(4, 366)	= 7.39
				Prob > F	= 0.0000
				R-squared	= 0.0747
				Adj R-squared	= 0.0646
Total	27.4229517	370	.074116086	Root MSE	= .2633

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0325693	.0474181	-0.69	0.493	-.1258154	.0606768
pid7cata	-.229716	.0439885	-5.22	0.000	-.316218	-.143214
ed6cat	.0089697	.0490538	0.18	0.855	-.087493	.1054323
age01	-.0278694	.0651472	-0.43	0.669	-.1559792	.1002405
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8691811	.0508162	17.10	0.000	.7692527	.9691094

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.39584855	4	.098962138	Number of obs	= 371
Residual	22.289605	366	.06090056	F(4, 366)	= 1.62
				Prob > F	= 0.1673
Total	22.6854535	370	.061312037	R-squared	= 0.0174
				Adj R-squared	= 0.0067
				Root MSE	= .24678

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0167589	.0444435	0.38	0.706	-.0706377	.1041556
pid7cata	-.0870414	.0412291	-2.11	0.035	-.168117	-.0059658
ed6cat	.0454811	.0459766	0.99	0.323	-.0449302	.1358925
age01	-.0149529	.0610604	-0.24	0.807	-.1350262	.1051204
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7603401	.0476284	15.96	0.000	.6666804	.8539997

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.234894137	4	.058723534	Number of obs	= 371
Residual	29.2611228	366	.079948423	F(4, 366)	= 0.73
				Prob > F	= 0.5689
Total	29.4960169	370	.079718965	R-squared	= 0.0080
				Adj R-squared	= -0.0029
				Root MSE	= .28275

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0684512	.0509216	1.34	0.180	-.0316845	.1685869
pid7cata	-.0430464	.0472387	-0.91	0.363	-.1359397	.0498468
ed6cat	-.033915	.0526782	-0.64	0.520	-.1375049	.0696749
age01	.0434023	.0699607	0.62	0.535	-.0941731	.1809777
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7210282	.0545708	13.21	0.000	.6137166	.8283399

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	3.71725623	4	.929314057	Number of obs	= 380
Residual	39.9013221	375	.106403526	F(4, 375)	= 8.73
				Prob > F	= 0.0000
Total	43.6185783	379	.115088597	R-squared	= 0.0852
				Adj R-squared	= 0.0755
				Root MSE	= .3262

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.1058281	.0510399	2.07	0.039	.0054678	.2061884
pid7cata	-.3057266	.0621366	-4.92	0.000	-.4279064	-.1835468
ed6cat	-.0999222	.0585648	-1.71	0.089	-.2150788	.0152345
age01	-.0823343	.0738895	-1.11	0.266	-.227624	.0629555
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7988455	.0514093	15.54	0.000	.6977589	.8999321

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.953243977	4	.238310994	Number of obs	= 380
Residual	19.4162107	375	.051776562	F(4, 375)	= 4.60
Total	20.3694547	379	.053745263	Prob > F	= 0.0012
				R-squared	= 0.0468
				Adj R-squared	= 0.0366
				Root MSE	= .22754

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0313973	.035604	0.88	0.378	-.0386111	.1014058
pid7cata	-.1227863	.0433447	-2.83	0.005	-.2080154	-.0375572
ed6cat	.0112409	.0408532	0.28	0.783	-.0690891	.0915709
age01	.128478	.0515432	2.49	0.013	.027128	.2298279
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8195459	.0358617	22.85	0.000	.7490308	.890061

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.44288195	4	.360720487	Number of obs	= 380
Residual	16.0441898	375	.042784506	F(4, 375)	= 8.43
Total	17.4870717	379	.046140031	Prob > F	= 0.0000
				R-squared	= 0.0825
				Adj R-squared	= 0.0727
				Root MSE	= .20684

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0877688	.032365	2.71	0.007	.0241292	.1514083
pid7cata	-.1531162	.0394015	-3.89	0.000	-.2305918	-.0756407
ed6cat	.0199343	.0371366	0.54	0.592	-.0530878	.0929563
age01	.1145094	.0468542	2.44	0.015	.0223796	.2066392
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8019836	.0325992	24.60	0.000	.7378835	.8660838

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.40336645	4	.350841612	Number of obs	= 379
Residual	18.7894744	374	.050239236	F(4, 374)	= 6.98
Total	20.1928408	378	.053420214	Prob > F	= 0.0000
				R-squared	= 0.0695
				Adj R-squared	= 0.0595
				Root MSE	= .22414

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0318773	.0351275	0.91	0.365	-.0371948	.1009495
pid7cata	-.1167946	.0427444	-2.73	0.007	-.2008441	-.0327451
ed6cat	.0719376	.0402421	1.79	0.075	-.0071916	.1510667
age01	.1609723	.050811	3.17	0.002	.0610613	.2608834
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7835973	.0354449	22.11	0.000	.7139011	.8532935

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	2.03008062	4	.507520156	Number of obs	380
				F(4, 375)	10.04
Residual	18.9610267	375	.050562738	Prob > F	0.0000
				R-squared	0.0967
				Adj R-squared	0.0871
Total	20.9911073	379	.055385507	Root MSE	.22486

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0517345	.0351842	1.47	0.142	-.0174484	.1209175
pid7cata	-.2347881	.0428336	-5.48	0.000	-.3190123	-.150564
ed6cat	.0607888	.0403714	1.51	0.133	-.018594	.1401715
age01	.0594472	.0509355	1.17	0.244	-.0407077	.1596022
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8220856	.0354388	23.20	0.000	.7524019	.8917692

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	2.64789078	4	.661972695	Number of obs	380
				F(4, 375)	8.95
Residual	27.7336231	375	.073956328	Prob > F	0.0000
				R-squared	0.0872
				Adj R-squared	0.0774
Total	30.3815139	379	.080162306	Root MSE	.27195

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.1361745	.042552	3.20	0.001	.0525042	.2198449
pid7cata	-.2100863	.0518033	-4.06	0.000	-.3119475	-.108225
ed6cat	-.0753691	.0488255	-1.54	0.124	-.1713752	.020637
age01	.1183134	.0616017	1.92	0.056	-.0028146	.2394415
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7589043	.0428599	17.71	0.000	.6746284	.8431801

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.64947521	4	.412368804	Number of obs	360
				F(4, 355)	4.07
Residual	35.9907439	355	.101382377	Prob > F	0.0031
				R-squared	0.0438
				Adj R-squared	0.0330
Total	37.6402192	359	.104847407	Root MSE	.31841

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0533694	.0519445	1.03	0.305	-.0487882	.1555271
pid7cata	-.1659894	.0508141	-3.27	0.001	-.2659238	-.066055
ed6cat	-.1071097	.0595468	-1.80	0.073	-.2242185	.0099992
age01	-.0473796	.0787381	-0.60	0.548	-.2022314	.1074722
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7841609	.0524649	14.95	0.000	.6809797	.8873421

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.653859767	4	.163464942	Number of obs	= 361
Residual	17.9907714	356	.050535875	F(4, 356)	= 3.23
				Prob > F	= 0.0126
Total	18.6446312	360	.051790642	R-squared	= 0.0351
				Adj R-squared	= 0.0242
				Root MSE	= .2248

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0029366	.0366683	-0.08	0.936	-.0750503	.069177
pid7cata	-.0704206	.0358637	-1.96	0.050	-.140952	.0001108
ed6cat	.0678801	.0420408	1.61	0.107	-.0147994	.1505597
age01	.1217662	.0555895	2.19	0.029	.0124411	.2310912
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7953463	.0370303	21.48	0.000	.7225206	.868172

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.54359277	4	.385898192	Number of obs	= 360
Residual	25.0849664	355	.070661877	F(4, 355)	= 5.46
				Prob > F	= 0.0003
Total	26.6285591	359	.074174259	R-squared	= 0.0580
				Adj R-squared	= 0.0474
				Root MSE	= .26582

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0197356	.0433662	-0.46	0.649	-.1050225	.0655512
pid7cata	-.1817085	.0424224	-4.28	0.000	-.2651393	-.0982777
ed6cat	.0333824	.049713	0.67	0.502	-.0643865	.1311514
age01	.1028598	.065735	1.56	0.119	-.0264191	.2321387
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8173275	.0438006	18.66	0.000	.7311862	.9034689

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	3.1784622	4	.79461555	Number of obs	= 361
Residual	23.7387248	356	.066681811	F(4, 356)	= 11.92
				Prob > F	= 0.0000
Total	26.917187	360	.074769964	R-squared	= 0.1181
				Adj R-squared	= 0.1082
				Root MSE	= .25823

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0067312	.0421206	0.16	0.873	-.0761052	.0895676
pid7cata	-.2833748	.0411964	-6.88	0.000	-.3643937	-.2023558
ed6cat	-.0040141	.048292	-0.08	0.934	-.0989875	.0909592
age01	.066689	.0638552	1.04	0.297	-.0588919	.1922699
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8653796	.0425365	20.34	0.000	.7817253	.9490339

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 360
				F(4, 355)	= 5.53
Model	1.41011266	4	.352528166	Prob > F	= 0.0002
Residual	22.6211965	355	.06372168	R-squared	= 0.0587
				Adj R-squared	= 0.0481
Total	24.0313092	359	.06693958	Root MSE	= .25243

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0356082	.0411815	-0.86	0.388	-.1165985	.0453822
pid7cata	-.1820329	.0402853	-4.52	0.000	-.2612607	-.1028051
ed6cat	-.0073862	.0472086	-0.16	0.876	-.1002298	.0854574
age01	.0604398	.0624234	0.97	0.334	-.0623263	.183206
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8818313	.0415941	21.20	0.000	.8000295	.9636331

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 361
				F(4, 356)	= 2.19
Model	.67025829	4	.167564573	Prob > F	= 0.0699
Residual	27.2619763	356	.076578585	R-squared	= 0.0240
				Adj R-squared	= 0.0130
Total	27.9322346	360	.077589541	Root MSE	= .27673

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0229041	.0451382	0.51	0.612	-.0658669	.1116751
pid7cata	-.1194934	.0441478	-2.71	0.007	-.2063168	-.0326701
ed6cat	-.0140755	.0517517	-0.27	0.786	-.115853	.0877021
age01	.1014652	.06843	1.48	0.139	-.0331126	.2360431
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8061818	.0455839	17.69	0.000	.7165342	.8958293

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
				Number of obs	= 407
				F(4, 402)	= 7.42
Model	2.98877648	4	.74719412	Prob > F	= 0.0000
Residual	40.467252	402	.100664806	R-squared	= 0.0688
				Adj R-squared	= 0.0595
Total	43.4560284	406	.107034553	Root MSE	= .31728

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.2133851	.0515421	4.14	0.000	.1120593	.3147108
pid7cata	.0846483	.1596313	0.53	0.596	-.2291681	.3984647
ed6cat	-.1760361	.0467479	-3.77	0.000	-.2679369	-.0841352
age01	.002533	.0659922	0.04	0.969	-.1271999	.132266
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.6271268	.0567527	11.05	0.000	.5155576	.738696

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.412443651	4	.103110913	Number of obs	= 407
Residual	18.1452058	402	.045137328	F(4, 402)	= 2.28
				Prob > F	= 0.0597
Total	18.5576495	406	.045708496	R-squared	= 0.0222
				Adj R-squared	= 0.0125
				Root MSE	= .21246

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0573509	.0345137	1.66	0.097	-.010499	.1252007
pid7cata	-.1970412	.1068925	-1.84	0.066	-.4071793	.0130968
ed6cat	-.0019346	.0313034	-0.06	0.951	-.0634734	.0596041
age01	.0722703	.0441898	1.64	0.103	-.0146016	.1591422
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7817348	.0380028	20.57	0.000	.7070258	.8564439

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.404118445	4	.101029611	Number of obs	= 407
Residual	20.3488663	402	.05061907	F(4, 402)	= 2.00
				Prob > F	= 0.0944
Total	20.7529847	406	.051115726	R-squared	= 0.0195
				Adj R-squared	= 0.0097
				Root MSE	= .22499

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0547933	.0365494	1.50	0.135	-.0170586	.1266452
pid7cata	-.182361	.1131974	-1.61	0.108	-.4048938	.0401717
ed6cat	.0407347	.0331497	1.23	0.220	-.0244338	.1059032
age01	.0324152	.0467962	0.69	0.489	-.0595807	.1244111
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7821882	.0402444	19.44	0.000	.7030725	.8613038

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.217652612	4	.054413153	Number of obs	= 407
Residual	19.5187075	402	.048553999	F(4, 402)	= 1.12
				Prob > F	= 0.3462
Total	19.7363601	406	.048611724	R-squared	= 0.0110
				Adj R-squared	= 0.0012
				Root MSE	= .22035

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0252626	.0357961	0.71	0.481	-.0451084	.0956335
pid7cata	-.1203537	.1108643	-1.09	0.278	-.3382999	.0975925
ed6cat	.04375	.0324665	1.35	0.179	-.0200753	.1075754
age01	.0241993	.0458317	0.53	0.598	-.0659006	.1142991
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8130975	.0394149	20.63	0.000	.7356124	.8905826

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.156200442	4	.039050111	Number of obs	= 407
Residual	18.6263734	402	.046334262	F(4, 402)	= 0.84
Total	18.7825738	406	.046262497	Prob > F	= 0.4986
				R-squared	= 0.0083
				Adj R-squared	= -0.0016
				Root MSE	= .21525

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0210827	.0349683	0.60	0.547	-.0476609	.0898262
pid7cata	-.1740544	.1083005	-1.61	0.109	-.3869605	.0388516
ed6cat	.0065647	.0317157	0.21	0.836	-.0557847	.068914
age01	-.0175605	.0447718	-0.39	0.695	-.1055767	.0704557
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8352892	.0385034	21.69	0.000	.7595961	.9109824

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	1.12909941	4	.282274851	Number of obs	= 407
Residual	27.7268853	402	.068972351	F(4, 402)	= 4.09
Total	28.8559847	406	.071073854	Prob > F	= 0.0029
				R-squared	= 0.0391
				Adj R-squared	= 0.0296
				Root MSE	= .26263

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.1066946	.0426639	2.50	0.013	.0228223	.1905669
pid7cata	.0273028	.1321347	0.21	0.836	-.2324584	.287064
ed6cat	-.1284749	.0386955	-3.32	0.001	-.2045458	-.0524041
age01	.0097445	.054625	0.18	0.859	-.0976418	.1171308
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7685589	.046977	16.36	0.000	.6762076	.8609102

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.16765988	4	.04191497	Number of obs	= 399
Residual	36.5800093	394	.092842663	F(4, 394)	= 0.45
Total	36.7476692	398	.092330827	Prob > F	= 0.7713
				R-squared	= 0.0046
				Adj R-squared	= -0.0055
				Root MSE	= .3047

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	.0202144	.0471224	0.43	0.668	-.0724284	.1128572
pid7cata	-.0433427	.1512175	-0.29	0.775	-.3406367	.2539514
ed6cat	.0463857	.0489428	0.95	0.344	-.049836	.1426074
age01	-.0334925	.0656954	-0.51	0.610	-.16265	.0956649
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.6525041	.1469903	4.44	0.000	.3635206	.9414875

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.196032421	4	.049008105	Number of obs	= 399
Residual	28.0520814	394	.071198176	F(4, 394)	= 0.69
				Prob > F	= 0.6004
Total	28.2481138	398	.07097516	R-squared	= 0.0069
				Adj R-squared	= -0.0031
				Root MSE	= .26683

covid_preexisting	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0396429	.0412656	-0.96	0.337	-.1207712	.0414854
pid7cata	.0040767	.1324228	0.03	0.975	-.2562669	.2644203
ed6cat	.0351898	.0428597	0.82	0.412	-.0490725	.1194522
age01	.0611691	.0575302	1.06	0.288	-.0519354	.1742737
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7447887	.128721	5.79	0.000	.4917228	.9978546

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.204135447	4	.051033862	Number of obs	= 400
Residual	34.3896577	395	.087062425	F(4, 395)	= 0.59
				Prob > F	= 0.6728
Total	34.5937932	399	.086701236	R-squared	= 0.0059
				Adj R-squared	= -0.0042
				Root MSE	= .29506

covid_jobs	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0357953	.0454922	-0.79	0.432	-.1252324	.0536418
pid7cata	-.15384	.1461748	-1.05	0.293	-.4412178	.1335378
ed6cat	-.030235	.0473005	-0.64	0.523	-.1232273	.0627573
age01	.0214798	.0634617	0.34	0.735	-.103285	.1462447
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8302587	.141955	5.85	0.000	.5511769	1.109341

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.474133877	4	.118533469	Number of obs	= 398
Residual	36.6621262	393	.093287853	F(4, 393)	= 1.27
				Prob > F	= 0.2809
Total	37.1362601	397	.093542217	R-squared	= 0.0128
				Adj R-squared	= 0.0027
				Root MSE	= .30543

covid_healthcare	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0738527	.0472908	-1.56	0.119	-.1668272	.0191218
pid7cata	-.186725	.1516876	-1.23	0.219	-.4849457	.1114958
ed6cat	.0050121	.0490769	0.10	0.919	-.091474	.1014981
age01	-.0733142	.0659212	-1.11	0.267	-.2029165	.0562882
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8785729	.1474869	5.96	0.000	.5886109	1.168535

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.192164455	4	.048041114	Number of obs	= 400
Residual	30.0566097	395	.076092683	F(4, 395)	= 0.63
				Prob > F	= 0.6404
Total	30.2487742	399	.075811464	R-squared	= 0.0064
				Adj R-squared	= -0.0037
				Root MSE	= .27585

covid_neighborh~d	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0590677	.0425298	-1.39	0.166	-.1426807	.0245452
pid7cata	-.0508728	.1366559	-0.37	0.710	-.3195367	.2177911
ed6cat	-.0032089	.0442204	-0.07	0.942	-.0901456	.0837278
age01	-.0432068	.0593291	-0.73	0.467	-.159847	.0734335
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8112967	.132711	6.11	0.000	.5503885	1.072205

note: **black** omitted because of collinearity.
note: **hispanic** omitted because of collinearity.
note: **api** omitted because of collinearity.

Source	SS	df	MS		
Model	.572786192	4	.143196548	Number of obs	= 400
Residual	32.3348227	395	.081860311	F(4, 395)	= 1.75
				Prob > F	= 0.1384
Total	32.9076088	399	.08247521	R-squared	= 0.0174
				Adj R-squared	= 0.0075
				Root MSE	= .28611

covid_flout_pro~s	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	-.0371037	.0441121	-0.84	0.401	-.1238276	.0496203
pid7cata	-.1245555	.1417404	-0.88	0.380	-.4032154	.1541045
ed6cat	-.023228	.0458656	-0.51	0.613	-.1133993	.0669433
age01	.1369735	.0615365	2.23	0.027	.0159935	.2579535
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.8197742	.1376487	5.96	0.000	.5491585	1.09039

```
256 suest covid_gene1 covid_gene2

  Simultaneous results for covid_gene1, covid_gene2

                                                      Number of obs = 751
```

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene1_mean						
race_bio_identity	.0324745	.0588925	0.55	0.581	-.0829528	.1479018
pid7cata	.0591964	.0519622	1.14	0.255	-.0426477	.1610405
ed6cat	.0742419	.0603236	1.23	0.218	-.0439903	.1924741
age01	-.1568964	.0785664	-2.00	0.046	-.3108838	-.0029091
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.5631289	.0647317	8.70	0.000	.436257	.6900008
covid_gene1_lnvar						
_cons	-2.304457	.0588589	-39.15	0.000	-2.419818	-2.189095
covid_gene2_mean						
race_bio_identity	.1058281	.0504032	2.10	0.036	.0070397	.2046165
pid7cata	-.3057266	.0647003	-4.73	0.000	-.4325369	-.1789163
ed6cat	-.0999222	.0624064	-1.60	0.109	-.2222365	.0223921
age01	-.0823343	.0742211	-1.11	0.267	-.227805	.0631364
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7988455	.051267	15.58	0.000	.6983641	.8993269
covid_gene2_lnvar						
_cons	-2.240517	.0690139	-32.46	0.000	-2.375781	-2.105252

```
257 test [covid_gene1_mean]race_bio_identity = [covid_gene2_mean]race_bio_identity

  ( 1)  [covid_gene1_mean]race_bio_identity - [covid_gene2_mean]race_bio_identity = 0

           chi2(  1) =    0.90
         Prob > chi2 =    0.3440

258 suest covid_gene1 covid_gene3

  Simultaneous results for covid_gene1, covid_gene3

                                                      Number of obs = 731
```

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene1_mean						
race_bio_identity	.0324745	.0588936	0.55	0.581	-.0829549	.1479039
pid7cata	.0591964	.0519632	1.14	0.255	-.0426496	.1610423
ed6cat	.0742419	.0603247	1.23	0.218	-.0439924	.1924762
age01	-.1568964	.0785678	-2.00	0.046	-.3108866	-.0029063
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.5631289	.0647329	8.70	0.000	.4362547	.6900031
covid_gene1_lnvar						
_cons	-2.304457	.05886	-39.15	0.000	-2.41982	-2.189093
covid_gene3_mean						
race_bio_identity	.0533694	.0545696	0.98	0.328	-.0535851	.160324
pid7cata	-.1659894	.0517784	-3.21	0.001	-.2674732	-.0645056
ed6cat	-.1071097	.0601568	-1.78	0.075	-.2250147	.0107954
age01	-.0473796	.0795404	-0.60	0.551	-.2032758	.1085167

black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7841609	.0533217	14.71	0.000	.6796522	.8886696
covid_gene3_lnvar						
_cons	-2.288856	.0695194	-32.92	0.000	-2.425112	-2.1526

259 test [covid_gene1_mean]race_bio_identity = [covid_gene3_mean]race_bio_identity

(1) **[covid_gene1_mean]race_bio_identity - [covid_gene3_mean]race_bio_identity = 0**

chi2(1) = **0.07**
Prob > chi2 = **0.7947**

260 suest covid_gene1 covid_gene4

Simultaneous results for covid_gene1, covid_gene4

Number of obs = **778**

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene1_mean						
race_bio_identity	.0324745	.0588912	0.55	0.581	-.0829501	.1478991
pid7cata	.0591964	.051961	1.14	0.255	-.0426454	.1610381
ed6cat	.0742419	.0603222	1.23	0.218	-.0439875	.1924713
age01	-.1568964	.0785646	-2.00	0.046	-.3108802	-.0029126
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.5631289	.0647302	8.70	0.000	.4362599	.6899978
covid_gene1_lnvar						
_cons	-2.304457	.0588575	-39.15	0.000	-2.419815	-2.189098
covid_gene4_mean						
race_bio_identity	.2133851	.0559133	3.82	0.000	.1037971	.3229731
pid7cata	.0846483	.1566252	0.54	0.589	-.2223315	.3916281
ed6cat	-.1760361	.0463263	-3.80	0.000	-.2668339	-.0852383
age01	.002533	.0667182	0.04	0.970	-.1282323	.1332984
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.6271268	.0585173	10.72	0.000	.512435	.7418186
covid_gene4_lnvar						
_cons	-2.295959	.0609061	-37.70	0.000	-2.415333	-2.176585

261 test [covid_gene1_mean]race_bio_identity = [covid_gene4_mean]race_bio_identity

(1) **[covid_gene1_mean]race_bio_identity - [covid_gene4_mean]race_bio_identity = 0**

chi2(1) = **4.96**
Prob > chi2 = **0.0259**

```
262 /*p=0.026*/
263 suest covid_gene1 covid_gene5
```

Simultaneous results for covid_gene1, covid_gene5

Number of obs = **770**

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene1_mean						
race_bio_identity	**.0324745**	**.0588916**	**0.55**	**0.581**	**-.0829509**	**.1478999**
pid7cata	**.0591964**	**.0519614**	**1.14**	**0.255**	**-.0426461**	**.1610388**
ed6cat	**.0742419**	**.0603227**	**1.23**	**0.218**	**-.0439883**	**.1924721**
age01	**-.1568964**	**.0785651**	**-2.00**	**0.046**	**-.3108812**	**-.0029116**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.5631289**	**.0647307**	**8.70**	**0.000**	**.4362591**	**.6899987**
covid_gene1_lnvar						
_cons	**-2.304457**	**.0588579**	**-39.15**	**0.000**	**-2.419816**	**-2.189097**
covid_gene5_mean						
race_bio_identity	**.0202144**	**.050721**	**0.40**	**0.690**	**-.079197**	**.1196257**
pid7cata	**-.0433427**	**.1518907**	**-0.29**	**0.775**	**-.341043**	**.2543577**
ed6cat	**.0463857**	**.0471054**	**0.98**	**0.325**	**-.0459393**	**.1387106**
age01	**-.0334925**	**.0673052**	**-0.50**	**0.619**	**-.1654083**	**.0984232**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.6525041**	**.1451583**	**4.50**	**0.000**	**.367999**	**.9370091**
covid_gene5_lnvar						
_cons	**-2.376849**	**.0582718**	**-40.79**	**0.000**	**-2.49106**	**-2.262638**

```
264 test [covid_gene1_mean]race_bio_identity = [covid_gene5_mean]race_bio_identity
```

(1) **[covid_gene1_mean]race_bio_identity - [covid_gene5_mean]race_bio_identity = 0**

chi2(1) = **0.02**
Prob > chi2 = **0.8747**

```
265 suest covid_gene2 covid_gene3
```

Simultaneous results for covid_gene2, covid_gene3

Number of obs = **740**

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene2_mean						
race_bio_identity	**.1058281**	**.0504037**	**2.10**	**0.036**	**.0070387**	**.2046175**
pid7cata	**-.3057266**	**.064701**	**-4.73**	**0.000**	**-.4325382**	**-.178915**
ed6cat	**-.0999222**	**.062407**	**-1.60**	**0.109**	**-.2222377**	**.0223933**
age01	**-.0823343**	**.0742218**	**-1.11**	**0.267**	**-.2278064**	**.0631379**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.7988455**	**.0512675**	**15.58**	**0.000**	**.6983631**	**.8993279**
covid_gene2_lnvar						
_cons	**-2.240517**	**.0690146**	**-32.46**	**0.000**	**-2.375783**	**-2.10525**
covid_gene3_mean						
race_bio_identity	**.0533694**	**.0545692**	**0.98**	**0.328**	**-.0535842**	**.1603231**
pid7cata	**-.1659894**	**.051778**	**-3.21**	**0.001**	**-.2674724**	**-.0645064**
ed6cat	**-.1071097**	**.0601563**	**-1.78**	**0.075**	**-.2250137**	**.0107944**

age01	-.0473796	.0795397	-0.60	0.551	-.2032745	.1085154
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7841609	.0533213	14.71	0.000	.6796531	.8886687
covid_gene3_lnvar						
_cons	-2.288856	.0695188	-32.92	0.000	-2.42511	-2.152602

266 test [covid_gene2_mean]race_bio_identity = [covid_gene3_mean]race_bio_identity

(1) **[covid_gene2_mean]race_bio_identity - [covid_gene3_mean]race_bio_identity = 0**

chi2(1) = **0.50**
Prob > chi2 = **0.4801**

267 suest covid_gene2 covid_gene4

Simultaneous results for covid_gene2, covid_gene4

Number of obs = **787**

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene2_mean						
race_bio_identity	.1058281	.0504016	2.10	0.036	.0070427	.2046135
pid7cata	-.3057266	.0646984	-4.73	0.000	-.4325331	-.1789201
ed6cat	-.0999222	.0624045	-1.60	0.109	-.2222327	.0223884
age01	-.0823343	.0742188	-1.11	0.267	-.2278005	.063132
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.7988455	.0512654	15.58	0.000	.6983672	.8993238
covid_gene2_lnvar						
_cons	-2.240517	.0690118	-32.47	0.000	-2.375777	-2.105256
covid_gene4_mean						
race_bio_identity	.2133851	.0559129	3.82	0.000	.1037979	.3229723
pid7cata	.0846483	.1566241	0.54	0.589	-.2223293	.3916258
ed6cat	-.1760361	.0463259	-3.80	0.000	-.2668332	-.085239
age01	.002533	.0667177	0.04	0.970	-.1282313	.1332974
black	0	(omitted)				
hispanic	0	(omitted)				
api	0	(omitted)				
_cons	.6271268	.0585169	10.72	0.000	.5124358	.7418178
covid_gene4_lnvar						
_cons	-2.295959	.0609056	-37.70	0.000	-2.415332	-2.176586

268 test [covid_gene2_mean]race_bio_identity = [covid_gene4_mean]race_bio_identity

(1) **[covid_gene2_mean]race_bio_identity - [covid_gene4_mean]race_bio_identity = 0**

chi2(1) = **2.04**
Prob > chi2 = **0.1531**

```
269 suest covid_gene2 covid_gene5
```

Simultaneous results for covid_gene2, covid_gene5

Number of obs = **779**

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene2_mean						
race_bio_identity	**.1058281**	**.050402**	**2.10**	**0.036**	**.0070421**	**.2046141**
pid7cata	**-.3057266**	**.0646988**	**-4.73**	**0.000**	**-.4325339**	**-.1789193**
ed6cat	**-.0999222**	**.0624049**	**-1.60**	**0.109**	**-.2222335**	**.0223892**
age01	**-.0823343**	**.0742193**	**-1.11**	**0.267**	**-.2278015**	**.0631329**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.7988455**	**.0512657**	**15.58**	**0.000**	**.6983665**	**.8993245**
covid_gene2_lnvar						
_cons	**-2.240517**	**.0690123**	**-32.47**	**0.000**	**-2.375778**	**-2.105255**
covid_gene5_mean						
race_bio_identity	**.0202144**	**.0507206**	**0.40**	**0.690**	**-.0791962**	**.1196249**
pid7cata	**-.0433427**	**.1518896**	**-0.29**	**0.775**	**-.3410408**	**.2543554**
ed6cat	**.0463857**	**.0471051**	**0.98**	**0.325**	**-.0459386**	**.1387099**
age01	**-.0334925**	**.0673047**	**-0.50**	**0.619**	**-.1654073**	**.0984222**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.6525041**	**.1451572**	**4.50**	**0.000**	**.3680011**	**.937007**
covid_gene5_lnvar						
_cons	**-2.376849**	**.0582714**	**-40.79**	**0.000**	**-2.491059**	**-2.262639**

```
270 test [covid_gene2_mean]race_bio_identity = [covid_gene5_mean]race_bio_identity
```

(1) **[covid_gene2_mean]race_bio_identity - [covid_gene5_mean]race_bio_identity = 0**

chi2(1) = **1.43**
Prob > chi2 = **0.2312**

```
271 suest covid_gene3 covid_gene4
```

Simultaneous results for covid_gene3, covid_gene4

Number of obs = **767**

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene3_mean						
race_bio_identity	**.0533694**	**.0545679**	**0.98**	**0.328**	**-.0535816**	**.1603205**
pid7cata	**-.1659894**	**.0517768**	**-3.21**	**0.001**	**-.26747**	**-.0645088**
ed6cat	**-.1071097**	**.0601548**	**-1.78**	**0.075**	**-.2250109**	**.0107916**
age01	**-.0473796**	**.0795378**	**-0.60**	**0.551**	**-.2032708**	**.1085117**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.7841609**	**.05332**	**14.71**	**0.000**	**.6796556**	**.8886662**
covid_gene3_lnvar						
_cons	**-2.288856**	**.0695172**	**-32.93**	**0.000**	**-2.425107**	**-2.152605**
covid_gene4_mean						
race_bio_identity	**.2133851**	**.0559138**	**3.82**	**0.000**	**.103796**	**.3229741**
pid7cata	**.0846483**	**.1566267**	**0.54**	**0.589**	**-.2223343**	**.3916309**
ed6cat	**-.1760361**	**.0463267**	**-3.80**	**0.000**	**-.2668347**	**-.0852375**
age01	**.002533**	**.0667188**	**0.04**	**0.970**	**-.1282335**	**.1332996**

black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.6271268**	**.0585178**	**10.72**	**0.000**	**.5124339**	**.7418197**
covid_gene4_lnvar						
_cons	**-2.295959**	**.0609066**	**-37.70**	**0.000**	**-2.415334**	**-2.176584**

```
272 test [covid_gene3_mean]race_bio_identity = [covid_gene4_mean]race_bio_identity

 ( 1)  [covid_gene3_mean]race_bio_identity - [covid_gene4_mean]race_bio_identity = 0

           chi2(  1) =    4.19
         Prob > chi2 =    0.0405

273 /*p=0.0405*/
274 suest covid_gene3 covid_gene5

Simultaneous results for covid_gene3, covid_gene5

                                                     Number of obs =     759
```

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene3_mean						
race_bio_identity	**.0533694**	**.0545683**	**0.98**	**0.328**	**-.0535824**	**.1603212**
pid7cata	**-.1659894**	**.0517771**	**-3.21**	**0.001**	**-.2674707**	**-.0645081**
ed6cat	**-.1071097**	**.0601552**	**-1.78**	**0.075**	**-.2250118**	**.0107924**
age01	**-.0473796**	**.0795384**	**-0.60**	**0.551**	**-.2032719**	**.1085127**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.7841609**	**.0533204**	**14.71**	**0.000**	**.6796549**	**.888667**
covid_gene3_lnvar						
_cons	**-2.288856**	**.0695176**	**-32.92**	**0.000**	**-2.425108**	**-2.152604**
covid_gene5_mean						
race_bio_identity	**.0202144**	**.0507215**	**0.40**	**0.690**	**-.0791979**	**.1196266**
pid7cata	**-.0433427**	**.1518922**	**-0.29**	**0.775**	**-.3410458**	**.2543605**
ed6cat	**.0463857**	**.0471059**	**0.98**	**0.325**	**-.0459402**	**.1387115**
age01	**-.0334925**	**.0673058**	**-0.50**	**0.619**	**-.1654095**	**.0984244**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.6525041**	**.1451597**	**4.50**	**0.000**	**.3679963**	**.9370118**
covid_gene5_lnvar						
_cons	**-2.376849**	**.0582724**	**-40.79**	**0.000**	**-2.491061**	**-2.262637**

```
275 test [covid_gene3_mean]race_bio_identity = [covid_gene5_mean]race_bio_identity

 ( 1)  [covid_gene3_mean]race_bio_identity - [covid_gene5_mean]race_bio_identity = 0

           chi2(  1) =    0.20
         Prob > chi2 =    0.6563
```

```
276 suest covid_gene4 covid_gene5
```

Simultaneous results for covid_gene4, covid_gene5

Number of obs = **806**

	Coefficient	Robust std. err.	z	P>|z|	[95% conf.	interval]
covid_gene4_mean						
race_bio_identity	**.2133851**	**.055912**	**3.82**	**0.000**	**.1037995**	**.3229707**
pid7cata	**.0846483**	**.1566217**	**0.54**	**0.589**	**-.2223247**	**.3916212**
ed6cat	**-.1760361**	**.0463252**	**-3.80**	**0.000**	**-.2668319**	**-.0852403**
age01	**.002533**	**.0667167**	**0.04**	**0.970**	**-.1282294**	**.1332954**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.6271268**	**.058516**	**10.72**	**0.000**	**.5124376**	**.741816**
covid_gene4_lnvar						
_cons	**-2.295959**	**.0609047**	**-37.70**	**0.000**	**-2.41533**	**-2.176588**
covid_gene5_mean						
race_bio_identity	**.0202144**	**.0507195**	**0.40**	**0.690**	**-.0791941**	**.1196228**
pid7cata	**-.0433427**	**.1518863**	**-0.29**	**0.775**	**-.3410344**	**.254349**
ed6cat	**.0463857**	**.0471041**	**0.98**	**0.325**	**-.0459366**	**.1387079**
age01	**-.0334925**	**.0673032**	**-0.50**	**0.619**	**-.1654044**	**.0984194**
black	**0**	(omitted)				
hispanic	**0**	(omitted)				
api	**0**	(omitted)				
_cons	**.6525041**	**.1451541**	**4.50**	**0.000**	**.3680073**	**.9370009**
covid_gene5_lnvar						
_cons	**-2.376849**	**.0582701**	**-40.79**	**0.000**	**-2.491056**	**-2.262642**

```
277 test [covid_gene4_mean]race_bio_identity = [covid_gene5_mean]race_bio_identity
```

(1) **[covid_gene4_mean]race_bio_identity - [covid_gene5_mean]race_bio_identity = 0**

chi2(1) = **6.55**
Prob > chi2 = **0.0105**

```
278 /*p=0.0105*/
279
280 //analyzing the four other groups together, without WDem//
281 reg covid_gene race_bio_identity pid7cata ed6cat age01 black hispanic api if fivegro
  > ups~=4 & ref_covid_battery~=6
```

Source	SS	df	MS		
Model	**6.25250139**	**7**	**.893214484**	Number of obs	= **1,524**
Residual	**153.199941**	**1,516**	**.10105537**	F(7, 1516)	= **8.84**
				Prob > F	= **0.0000**
				R-squared	= **0.0392**
				Adj R-squared	= **0.0348**
Total	**159.452442**	**1,523**	**.104696285**	Root MSE	= **.31789**

covid_gene	Coefficient	Std. err.	t	P>|t|	[95% conf.	interval]
race_bio_identity	**.0642775**	**.0255792**	**2.51**	**0.012**	**.0141033**	**.1144518**
pid7cata	**-.1286343**	**.0300906**	**-4.27**	**0.000**	**-.187658**	**-.0696107**
ed6cat	**-.0300365**	**.0276248**	**-1.09**	**0.277**	**-.0842234**	**.0241504**
age01	**-.0699894**	**.0364037**	**-1.92**	**0.055**	**-.1413963**	**.0014175**
black	**-.0082752**	**.0310293**	**-0.27**	**0.790**	**-.06914**	**.0525897**
hispanic	**-.0182544**	**.0290388**	**-0.63**	**0.530**	**-.0752149**	**.038706**
api	**-.0983064**	**.0284479**	**-3.46**	**0.001**	**-.1541078**	**-.0425049**
_cons	**.7565476**	**.0410345**	**18.44**	**0.000**	**.6760572**	**.837038**

```
282
283 log close
       name:  <unnamed>
        log:  C:\users\kamcd\Dropbox\CDK WORK\racial disparities essentialism\JOP repli
> cation files\Anoll Kam Marcellin Lucid Analyses.smcl
   log type:  smcl
  closed on:  10 Jan 2025, 14:29:19
```