**The results of this file represents the requested analysis from the following 3/4/16 email:**

For L6 between group comparisons of Lachnospira and Enterobacteriaceae:

-We want the GLM output for (1), controlling for BL and not controlling for BL (but controlling for BMI, Age, Sex)

For the clinical variable association with taxa for both models ), controlling for BL and not controlling for BL (but controlling for BMI, Age, Sex) and only for the clinical var assoc. with diet effect:

-We want (2) for Sutterella

- We want (2) for Peptostreptococcaceae

*\*\* We are only interested in the model with LPS\_TNF\_A . If it is easier to generate the output for this model only, do that.  Whatever is easiest*

**Between Group Comparisons, controlling for BL, BMI, Age, Sex**

**Between subject comparison (Group A vs. Group B at TimePoint==2)**

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Lachnospira"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-0.105360 -0.033926 -0.003405 0.019298 0.255032

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 0.0164368 0.0542410 0.303 0.7628

GROUPB 0.0327179 0.0130778 2.502 0.0147 \*

SEX 0.0011053 0.0133364 0.083 0.9342

RACE -0.0062264 0.0038552 -1.615 0.1107

BMI 0.0007336 0.0017694 0.415 0.6797

taxa.baseline 0.6272938 0.1016928 6.169 3.77e-08 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.05633 on 71 degrees of freedom

Multiple R-squared: 0.3852, Adjusted R-squared: 0.342

F-statistic: 8.899 on 5 and 71 DF, p-value: 1.349e-06

[1] "k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Enterobacteriales;f\_\_Enterobacteriaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-0.080829 -0.008007 -0.000785 0.008629 0.051609

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -0.0002368 0.0193571 -0.012 0.99027

GROUPB -0.0131721 0.0050528 -2.607 0.01113 \*

SEX -0.0034904 0.0050851 -0.686 0.49470

RACE 0.0042083 0.0014833 2.837 0.00593 \*\*

BMI -0.0002799 0.0006783 -0.413 0.68112

taxa.baseline 0.8922859 0.0665836 13.401 < 2e-16 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.02169 on 71 degrees of freedom

Multiple R-squared: 0.7331, Adjusted R-squared: 0.7143

F-statistic: 38.99 on 5 and 71 DF, p-value: < 2.2e-16

**Between subject comparison (DELTA\_Taxon, Group A vs. Group B)**

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Lachnospira"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-0.105360 -0.033926 -0.003405 0.019298 0.255032

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 0.0164368 0.0542410 0.303 0.762751

GROUPB 0.0327179 0.0130778 2.502 0.014663 \*

SEX 0.0011053 0.0133364 0.083 0.934182

RACE -0.0062264 0.0038552 -1.615 0.110733

BMI 0.0007336 0.0017694 0.415 0.679700

taxa.baseline -0.3727062 0.1016928 -3.665 0.000474 \*\*\*

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.05633 on 71 degrees of freedom

Multiple R-squared: 0.2864, Adjusted R-squared: 0.2361

F-statistic: 5.699 on 5 and 71 DF, p-value: 0.0001782

[1] "k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Enterobacteriales;f\_\_Enterobacteriaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-0.080829 -0.008007 -0.000785 0.008629 0.051609

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -0.0002368 0.0193571 -0.012 0.99027

GROUPB -0.0131721 0.0050528 -2.607 0.01113 \*

SEX -0.0034904 0.0050851 -0.686 0.49470

RACE 0.0042083 0.0014833 2.837 0.00593 \*\*

BMI -0.0002799 0.0006783 -0.413 0.68112

taxa.baseline -0.1077141 0.0665836 -1.618 0.11016

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.02169 on 71 degrees of freedom

Multiple R-squared: 0.2335, Adjusted R-squared: 0.1795

F-statistic: 4.325 on 5 and 71 DF, p-value: 0.001715

**Between Group Comparisons, not controlling for BL (but controlling for BMI, Age, Sex)**

**Between subject comparison (Group A vs. Group B at TimePoint==2)**

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Lachnospira"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-0.10513 -0.04922 -0.01549 0.03545 0.24109

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 0.1518917 0.0610387 2.488 0.0151 \*

GROUPB 0.0181911 0.0158316 1.149 0.2543

SEX -0.0103240 0.0162538 -0.635 0.5273

RACE -0.0071246 0.0047411 -1.503 0.1373

BMI -0.0009915 0.0021502 -0.461 0.6461

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.06932 on 72 degrees of freedom

Multiple R-squared: 0.05578, Adjusted R-squared: 0.003325

F-statistic: 1.063 on 4 and 72 DF, p-value: 0.381

[1] "k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Enterobacteriales;f\_\_Enterobacteriaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-0.033754 -0.018316 -0.006439 0.005096 0.212587

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 0.0421890 0.0356259 1.184 0.240

GROUPB 0.0002147 0.0092403 0.023 0.982

SEX -0.0035271 0.0094867 -0.372 0.711

RACE 0.0041879 0.0027672 1.513 0.135

BMI -0.0014479 0.0012550 -1.154 0.252

Residual standard error: 0.04046 on 72 degrees of freedom

Multiple R-squared: 0.05783, Adjusted R-squared: 0.005489

F-statistic: 1.105 on 4 and 72 DF, p-value: 0.3609

**Between subject comparison (DELTA\_Taxon, Group A vs. Group B)**

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Lachnospiraceae;g\_\_Lachnospira"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-0.140392 -0.028937 -0.001848 0.028711 0.263315

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -0.064044 0.053709 -1.192 0.23701

GROUPB 0.041349 0.013930 2.968 0.00406 \*\*

SEX 0.007896 0.014302 0.552 0.58260

RACE -0.005693 0.004172 -1.365 0.17664

BMI 0.001758 0.001892 0.929 0.35576

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.061 on 72 degrees of freedom

Multiple R-squared: 0.1514, Adjusted R-squared: 0.1043

F-statistic: 3.211 on 4 and 72 DF, p-value: 0.0175

[1] "k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Gammaproteobacteria;o\_\_Enterobacteriales;f\_\_Enterobacteriaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-0.088799 -0.007694 -0.000179 0.010651 0.048436

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -0.0053583 0.0193097 -0.277 0.78220

GROUPB -0.0147881 0.0050084 -2.953 0.00425 \*\*

SEX -0.0034860 0.0051419 -0.678 0.49998

RACE 0.0042107 0.0014999 2.807 0.00642 \*\*

BMI -0.0001389 0.0006802 -0.204 0.83877

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 0.02193 on 72 degrees of freedom

Multiple R-squared: 0.2052, Adjusted R-squared: 0.1611

F-statistic: 4.648 on 4 and 72 DF, p-value: 0.002149

**Clinical Var ~ Taxa Comparisons, controlling for BL, BMI, Age, Sex**

**Within GroupA comparison (DELTA\_clinicalvar ~ DELTA\_Taxon),**

"k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Alcaligenaceae;g\_\_Sutterella"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-9947.8 -4224.7 317.1 2478.0 19245.9

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -4.086e+03 8.372e+03 -0.488 0.62879

taxa 2.184e+04 1.840e+04 1.187 0.24398

SEX 3.556e+02 1.970e+03 0.180 0.85792

RACE -3.461e+02 5.987e+02 -0.578 0.56728

BMI 4.327e+02 3.127e+02 1.384 0.17594

LPS\_TNF\_A -4.142e-01 1.229e-01 -3.371 0.00197 \*\*

taxa.baseline -2.010e+04 2.113e+04 -0.951 0.34862

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5716 on 32 degrees of freedom

Multiple R-squared: 0.4284, Adjusted R-squared: 0.3213

F-statistic: 3.998 on 6 and 32 DF, p-value: 0.004259

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Peptostreptococcaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-10661.3 -3700.1 77.3 3381.6 19078.7

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -4.434e+03 8.277e+03 -0.536 0.595889

taxa -6.188e+05 3.146e+05 -1.967 0.057916 .

SEX 5.274e+02 1.899e+03 0.278 0.783039

RACE -2.155e+02 5.529e+02 -0.390 0.699298

BMI 3.798e+02 2.875e+02 1.321 0.195882

LPS\_TNF\_A -4.341e-01 1.170e-01 -3.710 0.000785 \*\*\*

taxa.baseline -5.268e+04 4.420e+05 -0.119 0.905865

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5618 on 32 degrees of freedom

Multiple R-squared: 0.4479, Adjusted R-squared: 0.3444

F-statistic: 4.327 on 6 and 32 DF, p-value: 0.002642

**Within GroupB comparison (DELTA\_clinicalvar ~ DELTA\_Taxon),**

[1] "k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Alcaligenaceae;g\_\_Sutterella"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-8477.4 -2595.4 -1.3 1557.1 15645.2

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 5.793e+03 7.124e+03 0.813 0.422

taxa 3.703e+04 2.201e+04 1.682 0.103

SEX -9.705e+02 1.811e+03 -0.536 0.596

RACE 7.904e+02 5.868e+02 1.347 0.188

BMI -2.508e+02 2.287e+02 -1.097 0.281

LPS\_TNF\_A -8.747e-02 1.132e-01 -0.773 0.445

taxa.baseline -1.104e+04 1.392e+04 -0.793 0.434

Residual standard error: 5312 on 31 degrees of freedom

Multiple R-squared: 0.2682, Adjusted R-squared: 0.1266

F-statistic: 1.894 on 6 and 31 DF, p-value: 0.1135

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Peptostreptococcaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-11339.6 -2451.2 323.2 2641.8 10547.5

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -1.084e+03 6.091e+03 -0.178 0.859907

taxa 1.133e+06 4.614e+05 2.456 0.019876 \*

SEX 1.464e+02 1.595e+03 0.092 0.927471

RACE 6.423e+02 5.018e+02 1.280 0.210074

BMI 2.279e+01 2.069e+02 0.110 0.912991

LPS\_TNF\_A -2.226e-01 1.003e-01 -2.219 0.033952 \*

taxa.baseline 2.205e+06 5.191e+05 4.247 0.000183 \*\*\*

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 4579 on 31 degrees of freedom

Multiple R-squared: 0.4561, Adjusted R-squared: 0.3509

F-statistic: 4.333 on 6 and 31 DF, p-value: 0.002755

**ALL Groups comparison (DELTA\_clinicalvar ~ DELTA\_Taxon),**

[1] "k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Alcaligenaceae;g\_\_Sutterella"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-11549.8 -3526.8 -770.9 2364.9 19875.9

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 4.688e+03 5.432e+03 0.863 0.39105

taxa 3.747e+04 1.394e+04 2.688 0.00896 \*\*

SEX -7.761e+02 1.356e+03 -0.572 0.56906

RACE -7.356e+01 4.000e+02 -0.184 0.85463

BMI -4.026e+01 1.852e+02 -0.217 0.82854

LPS\_TNF\_A -2.621e-01 8.408e-02 -3.117 0.00265 \*\*

taxa.baseline -5.100e+03 1.091e+04 -0.468 0.64150

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5745 on 70 degrees of freedom

Multiple R-squared: 0.2572, Adjusted R-squared: 0.1935

F-statistic: 4.039 on 6 and 70 DF, p-value: 0.001565

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Peptostreptococcaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars], taxa.baseline = otu.baseline[,

otu.ix]))

Residuals:

Min 1Q Median 3Q Max

-12422.3 -3319.4 99.4 2495.4 18748.6

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 1.096e+03 5.514e+03 0.199 0.842973

taxa -3.543e+05 2.686e+05 -1.319 0.191493

SEX -1.733e+02 1.363e+03 -0.127 0.899186

RACE -1.569e+02 4.026e+02 -0.390 0.697909

BMI 9.368e+01 1.906e+02 0.491 0.624673

LPS\_TNF\_A -2.897e-01 8.338e-02 -3.475 0.000883 \*\*\*

taxa.baseline 5.717e+05 3.430e+05 1.667 0.100037

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Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5747 on 70 degrees of freedom

Multiple R-squared: 0.2568, Adjusted R-squared: 0.1931

F-statistic: 4.032 on 6 and 70 DF, p-value: 0.001585

**Clinical Var ~ Taxa Comparisons, not controlling for BL, but controlling for BMI, Age, Sex**

**Within GroupA comparison (DELTA\_clinicalvar ~ DELTA\_Taxon),**

"k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Alcaligenaceae;g\_\_Sutterella"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-15658.9 -4006.8 237.4 3382.8 16851.6

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -4680.4 9364.9 -0.500 0.6204

taxa 46364.0 19950.7 2.324 0.0262 \*

SEX -547.4 2236.8 -0.245 0.8081

RACE -755.6 598.9 -1.262 0.2157

BMI 212.7 333.0 0.639 0.5274

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6667 on 34 degrees of freedom

Multiple R-squared: 0.1739, Adjusted R-squared: 0.07667

F-statistic: 1.789 on 4 and 34 DF, p-value: 0.1539

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Peptostreptococcaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-13043.8 -4071.9 832.9 3560.3 15124.9

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -6013.7 9197.7 -0.654 0.5176

taxa -868015.2 344408.7 -2.520 0.0166 \*

SEX 426.2 2181.5 0.195 0.8463

RACE -883.4 600.9 -1.470 0.1508

BMI 285.8 328.1 0.871 0.3899

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6588 on 34 degrees of freedom

Multiple R-squared: 0.1933, Adjusted R-squared: 0.09843

F-statistic: 2.037 on 4 and 34 DF, p-value: 0.1111

**Within GroupB comparison (DELTA\_clinicalvar ~ DELTA\_Taxon),**

"k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Alcaligenaceae;g\_\_Sutterella"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-9380.8 -2450.3 439.3 2120.7 15974.7

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 2432.1 5942.3 0.409 0.6850

taxa 48819.0 18089.0 2.699 0.0109 \*

SEX -919.1 1767.3 -0.520 0.6065

RACE 750.0 571.2 1.313 0.1982

BMI -218.8 209.8 -1.043 0.3044

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 5230 on 33 degrees of freedom

Multiple R-squared: 0.245, Adjusted R-squared: 0.1535

F-statistic: 2.677 on 4 and 33 DF, p-value: 0.04886

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Peptostreptococcaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-12004.8 -2354.5 163.4 1989.8 17518.8

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 1565.8 6529.8 0.240 0.812

taxa -434392.4 352741.1 -1.231 0.227

SEX -976.1 1921.4 -0.508 0.615

RACE 707.9 618.0 1.145 0.260

BMI -153.5 232.0 -0.662 0.513

Residual standard error: 5650 on 33 degrees of freedom

Multiple R-squared: 0.1188, Adjusted R-squared: 0.01201

F-statistic: 1.112 on 4 and 33 DF, p-value: 0.3672

**ALL Groups comparison (DELTA\_clinicalvar ~ DELTA\_Taxon),**

"k\_\_Bacteria;p\_\_Proteobacteria;c\_\_Betaproteobacteria;o\_\_Burkholderiales;f\_\_Alcaligenaceae;g\_\_Sutterella"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-16699.5 -3076.4 202.8 2374.6 19888.2

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) 1129.93 5257.86 0.215 0.830450

taxa 48292.49 13418.88 3.599 0.000583 \*\*\*

SEX -691.18 1425.03 -0.485 0.629129

RACE -222.12 414.30 -0.536 0.593527

BMI -63.53 187.60 -0.339 0.735863

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6047 on 72 degrees of freedom

Multiple R-squared: 0.1536, Adjusted R-squared: 0.1066

F-statistic: 3.267 on 4 and 72 DF, p-value: 0.01613

[1] "k\_\_Bacteria;p\_\_Firmicutes;c\_\_Clostridia;o\_\_Clostridiales;f\_\_Peptostreptococcaceae;g\_\_"

Call:

lm(formula = f, data = data.frame(taxa = taxa, map[, vars]))

Residuals:

Min 1Q Median 3Q Max

-13216.1 -2402.0 -109.1 3038.2 20993.2

Coefficients:

Estimate Std. Error t value Pr(>|t|)

(Intercept) -418.3 5409.9 -0.077 0.93858

taxa -703143.1 243657.4 -2.886 0.00515 \*\*

SEX -300.1 1458.7 -0.206 0.83757

RACE -295.1 430.1 -0.686 0.49479

BMI 18.2 194.0 0.094 0.92551

---

Signif. codes: 0 ‘\*\*\*’ 0.001 ‘\*\*’ 0.01 ‘\*’ 0.05 ‘.’ 0.1 ‘ ’ 1

Residual standard error: 6219 on 72 degrees of freedom

Multiple R-squared: 0.1049, Adjusted R-squared: 0.05515

F-statistic: 2.109 on 4 and 72 DF, p-value: 0.08846