

```
summary(glm(x.scot ~ x1.scot + g.scot[, 1] + g.scot[, 2] +
g.scot[, 3] + g.scot[, 4] +
+ g.scot[, 5] + g.scot[, 6] + nsg.scot[, 1] +
nsg.scot[, 2], family="gaussian"))
```

Call:

```
glm(formula = x.scot ~ x1.scot + g.scot[, 1] + g.scot[, 2] +
g.scot[, 3] + g.scot[, 4] + g.scot[, 5] + g.scot[, 6] +
nsg.scot[, 1] + nsg.scot[, 2], family = "gaussian")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-5.2141	-0.4902	0.1030	0.6404	2.2760

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.056936	0.171497	-0.332	0.7401
x1.scot	0.028336	0.053221	0.532	0.5947
g.scot[, 1]	-0.056796	0.732052	-0.078	0.9382
g.scot[, 2]	0.299388	0.260737	1.148	0.2516
g.scot[, 3]	0.157389	0.429150	0.367	0.7140
g.scot[, 4]	-0.153697	0.410871	-0.374	0.7085
g.scot[, 5]	-0.008457	0.735931	-0.011	0.9908
g.scot[, 6]	0.309254	0.167818	1.843	0.0661 .
nsg.scot[, 1]	-0.064399	0.095807	-0.672	0.5019
nsg.scot[, 2]	-0.266848	0.143094	-1.865	0.0629 .

---

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

(Dispersion parameter for gaussian family taken to be 0.9856182)

Null deviance: 452.79 on 408 degrees of freedom  
Residual deviance: 393.26 on 399 degrees of freedom  
(413 observations deleted due to missingness)  
AIC: 1166.6

Number of Fisher Scoring iterations: 2

>

```
> summary(glm(x.vis ~ x1.vis + g.vis[, 1] + g.vis[, 2] + g.vis[,
3] + g.vis[, 4] + g.vis[, 5] +
+ g.vis[, 6] + nsg.vis[, 1] + nsg.vis[, 2],
family="gaussian"))
```

Call:

```
glm(formula = x.vis ~ x1.vis + g.vis[, 1] + g.vis[, 2] + g.vis[,
3] + g.vis[, 4] + g.vis[, 5] + g.vis[, 6] + nsg.vis[, 1] +
nsg.vis[, 2], family = "gaussian")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.73136	-0.56041	-0.05767	0.51437	3.20312

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.07811	0.36402	-0.215	0.830
x1.vis	-0.04048	0.06067	-0.667	0.505
g.vis[, 1]	-0.09465	1.08102	-0.088	0.930
g.vis[, 2]	-0.02495	0.44986	-0.055	0.956
g.vis[, 3]	0.32182	0.71165	0.452	0.651
g.vis[, 4]	-0.41433	0.54635	-0.758	0.449
g.vis[, 5]	0.25095	0.90027	0.279	0.781
g.vis[, 6]	0.94044	0.19909	4.724	3.35e-06 ***
nsg.vis[, 1]	-0.25028	0.19123	-1.309	0.191
nsg.vis[, 2]	0.10626	0.17753	0.599	0.550

---

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

(Dispersion parameter for gaussian family taken to be 0.8000532)

Null deviance: 412.73 on 362 degrees of freedom  
Residual deviance: 282.42 on 353 degrees of freedom  
(124 observations deleted due to missingness)  
AIC: 961.03

Number of Fisher Scoring iterations: 2

>

```
> summary(glm(y.scot ~ x.scot + x1.scot + g.scot[, 1] + g.scot[, 2] + g.scot[, 3] + g.scot[, 4] + g.scot[, 5] +  
+           + g.scot[, 6] + nsg.scot[, 1] + nsg.scot[, 2] +  
indel.scot, family="binomial"))
```

Call:

```
glm(formula = y.scot ~ x.scot + x1.scot + g.scot[, 1] + g.scot[, 2] + g.scot[, 3] + g.scot[, 4] + g.scot[, 5] + +g.scot[, 6] + nsg.scot[, 1] + nsg.scot[, 2] + indel.scot, family = "binomial")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.8155	-0.9180	-0.5655	1.0918	2.2021

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	1.66378	0.88518	1.880	0.060163 .
x.scot	-0.03436	0.11132	-0.309	0.757574
x1.scot	-0.51523	0.13644	-3.776	0.000159 ***
g.scot[, 1]	-13.87360	596.12296	-0.023	0.981432
g.scot[, 2]	1.66888	0.97454	1.712	0.086809 .
g.scot[, 3]	-0.66862	1.12766	-0.593	0.553230
g.scot[, 4]	-0.97077	1.01989	-0.952	0.341181
g.scot[, 5]	14.94336	596.12356	0.025	0.980001
g.scot[, 6]	0.89031	0.78657	1.132	0.257680
nsg.scot[, 1]	0.50594	0.21575	2.345	0.019029 *
nsg.scot[, 2]	-0.42182	0.34712	-1.215	0.224296

```
indel.scot      -2.19242      0.79126  -2.771 0.005592 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 527.36 on 397 degrees of freedom
Residual deviance: 457.85 on 386 degrees of freedom
(424 observations deleted due to missingness)
AIC: 481.85
```

Number of Fisher Scoring iterations: 13

```
>
> summary(glm(y.scot ~ x.scot + x1.scot, family="binomial"))
```

```
Call:
glm(formula = y.scot ~ x.scot + x1.scot, family = "binomial")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.3297	-0.9635	-0.8225	1.3223	1.8282

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )	
(Intercept)	-0.57625	0.09386	-6.139	8.28e-10	***
x.scot	-0.22820	0.09330	-2.446	0.014444	*
x1.scot	-0.33419	0.09815	-3.405	0.000662	***

```
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

(Dispersion parameter for binomial family taken to be 1)

```
Null deviance: 670.11 on 510 degrees of freedom
Residual deviance: 653.87 on 508 degrees of freedom
(311 observations deleted due to missingness)
AIC: 659.87
```

Number of Fisher Scoring iterations: 4

```
>
> summary(glm(x1.scot ~ indel.scot, family="gaussian"))
```

```
Call:
glm(formula = x1.scot ~ indel.scot, family = "gaussian")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.4228	-0.5870	-0.0908	0.4578	3.4320

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )	
(Intercept)	0.99782	0.11121	8.973	<2e-16	***

```

indel.scot  -0.75556    0.07844   -9.633   <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.8500721)

Null deviance: 495.41  on 491  degrees of freedom
Residual deviance: 416.54  on 490  degrees of freedom
(330 observations deleted due to missingness)
AIC: 1320.3

Number of Fisher Scoring iterations: 2

> summary(glm(x1.vis ~ indel.vis, family="gaussian"))

Call:
glm(formula = x1.vis ~ indel.vis, family = "gaussian")

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-3.915040  -0.405676   0.009906   0.469534   2.364874

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  1.53901    0.10684   14.40  <2e-16 ***
indel.vis   -1.10396    0.07122  -15.50  <2e-16 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.6101309)

Null deviance: 381.51  on 386  degrees of freedom
Residual deviance: 234.90  on 385  degrees of freedom
(100 observations deleted due to missingness)
AIC: 911.04

Number of Fisher Scoring iterations: 2

>
> summary(glm(x.scot ~ g.scot[, 3], family="gaussian"))

Call:
glm(formula = x.scot ~ g.scot[, 3], family = "gaussian")

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-5.2787  -0.5436   0.1129   0.6453   2.4109

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.24651    0.05780  -4.265 2.37e-05 ***
g.scot[, 3]  0.38050    0.06303   6.036 3.00e-09 ***
---

```

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

(Dispersion parameter for gaussian family taken to be 0.9397393)

Null deviance: 521.97 on 520 degrees of freedom  
Residual deviance: 487.72 on 519 degrees of freedom  
(301 observations deleted due to missingness)  
AIC: 1450.1

Number of Fisher Scoring iterations: 2

```
> summary(glm(x.vis ~ g.vis[, 3], family="gaussian"))
```

Call:  
glm(formula = x.vis ~ g.vis[, 3], family = "gaussian")

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.87872	-0.64918	-0.06501	0.63584	3.75794

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	-0.51748	0.07542	-6.861	2.17e-11 ***
g.vis[, 3]	0.61085	0.06923	8.824	< 2e-16 ***

---  
Signif. codes: 0 '\*\*\*' 0.001 '\*\*' 0.01 '\*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 1.059121)

Null deviance: 579.19 on 470 degrees of freedom  
Residual deviance: 496.73 on 469 degrees of freedom  
(16 observations deleted due to missingness)  
AIC: 1367.7

Number of Fisher Scoring iterations: 2

```
>  
> summary(glm(y.scot ~ g.scot[, 3] + nsg.scot[, 1] + nsg.scot[,  
2], family="binomial"))
```

Call:  
glm(formula = y.scot ~ g.scot[, 3] + nsg.scot[, 1] + nsg.scot[,  
2], family = "binomial")

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.2419	-0.8181	-0.7224	1.2035	2.1695

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-0.9226	0.2065	-4.469	7.87e-06 ***
g.scot[, 3]	-0.7183	0.1813	-3.963	7.41e-05 ***
nsg.scot[, 1]	0.4307	0.1370	3.143	0.00167 **

```

nsg.scot[, 2]    0.1057      0.1895    0.558  0.57701
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 871.55  on 725  degrees of freedom
Residual deviance: 816.88  on 722  degrees of freedom
(96 observations deleted due to missingness)
AIC: 824.88

Number of Fisher Scoring iterations: 4

>
> summary(glm(y.scot ~ x.scot + xl.scot + g.scot[, 3] + nsg.scot[,
1] + nsg.scot[, 2] + indel.scot, family="binomial"))

Call:
glm(formula = y.scot ~ x.scot + xl.scot + g.scot[, 3] + nsg.scot[,
1] + nsg.scot[, 2] + indel.scot, family = "binomial")

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-1.6982  -0.9110  -0.5835   1.0816   2.1818

Coefficients:
            Estimate Std. Error z value Pr(>|z|)
(Intercept)  0.73922    0.49899   1.481  0.13849
x.scot      -0.04733    0.10801  -0.438  0.66124
xl.scot     -0.54618    0.13282  -4.112 3.92e-05 ***
g.scot[, 3] -0.15133    0.33027  -0.458  0.64680
nsg.scot[, 1]  0.47047    0.17347   2.712  0.00668 **
nsg.scot[, 2] -0.28298    0.31024  -0.912  0.36170
indel.scot   -1.21954    0.38379  -3.178  0.00148 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 555.64  on 423  degrees of freedom
Residual deviance: 491.25  on 417  degrees of freedom
(398 observations deleted due to missingness)
AIC: 505.25

Number of Fisher Scoring iterations: 4

>
> # indel lowers CFHR1, lowers AMD risk, but lower CFHR1 is
associated with higher AMD risk.
>
> ## g3 raises CFH, lowers AMD risk, and higher CFH is associated
with lower AMD risk
>

```

```

> cor(x.scot, x1.scot, use="pairwise")
[1] -0.1320983
> cor(x.vis, x1.vis, use="pairwise")
[1] -0.3761947
>
> summary(glm(x.scot ~ x1.scot + g.scot[, 3] + indel.scot,
family="gaussian"))

Call:
glm(formula = x.scot ~ x1.scot + g.scot[, 3] + indel.scot, family =
"gaussian")

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-5.1786  -0.5352   0.0972   0.6290   2.4160

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -0.75284     0.12971  -5.804 1.17e-08 ***
x1.scot      -0.01000     0.04744  -0.211  0.833
g.scot[, 3]  0.14365     0.08051   1.784  0.075 .
indel.scot   0.50766     0.10930   4.645 4.40e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 0.92723)

Null deviance: 502.75  on 485  degrees of freedom
Residual deviance: 446.92  on 482  degrees of freedom
(336 observations deleted due to missingness)
AIC: 1348.5

Number of Fisher Scoring iterations: 2

> summary(glm(x.vis ~ x1.vis + g.vis[, 3] + indel.vis,
family="gaussian"))

Call:
glm(formula = x.vis ~ x1.vis + g.vis[, 3] + indel.vis, family =
"gaussian")

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-2.78831  -0.55960  -0.01779   0.51117   3.22524

Coefficients:
              Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.31017     0.15589  -8.404 9.11e-16 ***
x1.vis      -0.09279     0.06012  -1.543 0.123583
g.vis[, 3]  0.27423     0.07907   3.468 0.000585 ***
indel.vis   0.74410     0.11754   6.331 6.99e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

(Dispersion parameter for gaussian family taken to be 0.8340849)

Null deviance: 446.17 on 377 degrees of freedom  
Residual deviance: 311.95 on 374 degrees of freedom  
(109 observations deleted due to missingness)  
AIC: 1010.1

Number of Fisher Scoring iterations: 2

```
>
> tapply(phenotypes.scot$cfhrl, indel.scot, mean, na.rm=TRUE)
      1      2      3
1.0013031 0.8961789 0.5493750
> tapply(phenotypes.vis$cfhrlraw, indel.vis, mean, na.rm=TRUE)
      1      2      3
1.0274699 0.8404839 0.3750000
>
> xnomiss <- x.scot
> xnomiss[is.na(x1.scot)] <- NA
> xlnomiss <- x1.scot
> xlnomiss[is.na(x.scot)] <- NA
> xres <- glm(xnomiss ~ age.scot + sex.scot + g.scot[, 6] +
indel.scot, family="gaussian")$residuals
> xlres <- glm(xlnomiss ~ age.scot + sex.scot + g.scot[, 6] +
indel.scot, family="gaussian")$residuals
> cor(xres, xlres, use="pairwise")
[1] 0.00222619
>
> xfit <- glm(xnomiss ~ age.scot + sex.scot +
+           g.scot[, 1] + g.scot[, 2] + g.scot[, 3] + g.scot[,
4] + g.scot[, 5] + g.scot[, 6] +
+           + indel.scot, family="gaussian")$fitted.values
> x1fit <- glm(xlnomiss ~ age.scot + sex.scot +
+           g.scot[, 1] + g.scot[, 2] + g.scot[, 3] + g.scot[,
4] + g.scot[, 5] + g.scot[, 6] +
+           + indel.scot, family="gaussian")$fitted.values
> cor(xfit, x1fit)
[1] -0.916143
>
> xnomiss <- x.vis
> xnomiss[is.na(x1.vis)] <- NA
> xlnomiss <- x1.vis
> xlnomiss[is.na(x.vis)] <- NA
> xres <- glm(xnomiss ~ age.vis + sex.vis + g.vis[, 6] +
indel.vis, family="gaussian")$residuals
> xlres <- glm(xlnomiss ~ age.vis + sex.vis + g.vis[, 6] +
indel.vis, family="gaussian")$residuals
> cor(xres, xlres, use="pairwise")
[1] -0.03194020
>
> xfit <- glm(xnomiss ~ age.vis + sex.vis +
+           g.vis[, 1] + g.vis[, 2] + g.vis[, 3] + g.vis[, 4] +
```



```

g.vis[, 5] + g.vis[, 6] +
+           + indel.vis, family="gaussian")$fitted.values
> x1fit <- glm(xlnomiss ~ age.vis + sex.vis +
+           g.vis[, 1] + g.vis[, 2] + g.vis[, 3] + g.vis[, 4] +
+           g.vis[, 5] + g.vis[, 6] +
+           + indel.vis, family="gaussian")$fitted.values
>
> cor(data.frame(phenotypes.vis$cfh, phenotypes.vis$cfhrlraw,
phenotypes.vis$newcfh), use="pair")
              phenotypes.vis.cfh phenotypes.vis.cfhrlraw
phenotypes.vis.cfh           1.00000000          -0.37619468
phenotypes.vis.cfhrlraw      -0.37619468           1.00000000
phenotypes.vis.newcfh        -0.04608352          -0.02779138
              phenotypes.vis.newcfh
phenotypes.vis.cfh           -0.04608352
phenotypes.vis.cfhrlraw      -0.02779138
phenotypes.vis.newcfh         1.00000000
>
> cor(data.frame(phenotypes.scot$Plasma.CFH.Normalised.to.VIS,
phenotypes.scot$cfhrl,
phenotypes.scot$Plasma.CFH.Rank.Transformed,
phenotypes.scot$CFHnew), use="pair")
              phenotypes.scot.Plasm
a.CFH.Normalised.to.VIS
phenotypes.scot.Plasma.CFH.Normalised.to.VIS
1.00000000
phenotypes.scot.cfhrl
-0.132098301
phenotypes.scot.Plasma.CFH.Rank.Transformed
0.975310562
phenotypes.scot.CFHnew
-0.004374329
              phenotypes.scot.cfhrl
phenotypes.scot.Plasma.CFH.Normalised.to.VIS          -0.13209830
phenotypes.scot.cfhrl                                1.00000000
phenotypes.scot.Plasma.CFH.Rank.Transformed          -0.16023060
phenotypes.scot.CFHnew                               -0.03360623
              phenotypes.scot.Plasm
a.CFH.Rank.Transformed
phenotypes.scot.Plasma.CFH.Normalised.to.VIS
0.97531056
phenotypes.scot.cfhrl
-0.16023060
phenotypes.scot.Plasma.CFH.Rank.Transformed
1.00000000
phenotypes.scot.CFHnew
-0.01129447
              phenotypes.scot.CFHne
w
phenotypes.scot.Plasma.CFH.Normalised.to.VIS
-0.004374329
phenotypes.scot.cfhrl
-0.033606228

```

```

phenotypes.scot.Plasma.CFH.Rank.Transformed
-0.011294473
phenotypes.scot.CFHnew
1.000000000
>
> tapply(phenotypes.scot$CFHnew, g.scot[, 6], mean)
 0  1  2
NA NA NA
>
>
> ## compare old and new CFH
> summary(glm(phenotypes.scot$Plasma.CFH.Normalised.to.VIS ~
age.scot + sex.scot +
+           nsg.scot[, 1] + nsg.scot[, 2] + g.scot[, 6],
family="gaussian"))

Call:
glm(formula = phenotypes.scot$Plasma.CFH.Normalised.to.VIS ~
     age.scot + sex.scot + nsg.scot[, 1] + nsg.scot[, 2] + g.scot[,
     6], family = "gaussian")

Deviance Residuals:
    Min       1Q   Median       3Q      Max
-293.874  -27.207    5.211   37.318  133.191

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  405.81898    7.08701  57.262 < 2e-16 ***
age.scot     -0.09874    0.29444  -0.335  0.738
sex.scot      1.48681    5.41447   0.275  0.784
nsg.scot[, 1] -0.08000    4.13535  -0.019  0.985
nsg.scot[, 2]  0.05983    4.90236   0.012  0.990
g.scot[, 6]   35.06378    5.33930   6.567 1.44e-10 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for gaussian family taken to be 3107.032)

Null deviance: 1530056 on 447 degrees of freedom
Residual deviance: 1373308 on 442 degrees of freedom
(374 observations deleted due to missingness)
AIC: 4881.9

Number of Fisher Scoring iterations: 2

> summary(glm(phenotypes.scot$CFHnew ~ age.scot + sex.scot +
+           nsg.scot[, 1] + nsg.scot[, 2] + g.scot[, 6],
family="gaussian"))

Call:
glm(formula = phenotypes.scot$CFHnew ~ age.scot + sex.scot +
     nsg.scot[, 1] + nsg.scot[, 2] + g.scot[, 6], family =
     "gaussian")

```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-734.30	-135.16	-31.51	124.62	511.88

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	606.846	27.682	21.922	<2e-16 ***
age.scot	1.763	1.164	1.515	0.131
sex.scot	34.054	21.518	1.583	0.114
nsg.scot[, 1]	-11.189	16.347	-0.684	0.494
nsg.scot[, 2]	15.325	19.062	0.804	0.422
g.scot[, 6]	-6.557	21.403	-0.306	0.760

---

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

(Dispersion parameter for gaussian family taken to be 39758.13)

Null deviance: 14555305 on 365 degrees of freedom  
Residual deviance: 14312928 on 360 degrees of freedom  
(456 observations deleted due to missingness)  
AIC: 4922.8

Number of Fisher Scoring iterations: 2

>

>

```
> summary(glm(phenotypes.vis$cfh ~ age.vis + sex.vis +  
as.numeric(phenotypes.vis$bmi) +  
+ nsg.vis[, 1] + nsg.vis[, 2] + g.vis[, 6],  
family="gaussian"))
```

Call:

```
glm(formula = phenotypes.vis$cfh ~ age.vis + sex.vis +  
as.numeric(phenotypes.vis$bmi) +  
nsg.vis[, 1] + nsg.vis[, 2] + g.vis[, 6], family = "gaussian")
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-160.033	-31.974	-3.872	30.093	183.653

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	361.18545	11.93975	30.251	< 2e-16 ***
age.vis	0.60966	0.16869	3.614	0.000336 ***
sex.vis	-4.84431	4.90299	-0.988	0.323674
as.numeric(phenotypes.vis\$bmi)	0.05560	0.01244	4.468	0.000005 ***
nsg.vis[, 1]	0.23624	4.53330	0.052	

```

0.958463
nsg.vis[, 2]          10.58678      4.92393      2.150
0.032088 *
g.vis[, 6]           59.06239      5.15523     11.457 < 2e-
16 ***

```

---

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

(Dispersion parameter for gaussian family taken to be 2522.433)

Null deviance: 1731622 on 451 degrees of freedom

Residual deviance: 1122483 on 445 degrees of freedom

(35 observations deleted due to missingness)

AIC: 4832.2

Number of Fisher Scoring iterations: 2

```

> summary(glm(phenotypes.vis$newcfh ~ age.vis + sex.vis +
as.numeric(phenotypes.vis$bmi) +
+           nsg.vis[, 1] + nsg.vis[, 2] + g.vis[, 6],
family="gaussian"))

```

Call:

glm(formula = phenotypes.vis\$newcfh ~ age.vis + sex.vis +

as.numeric(phenotypes.vis\$bmi) +

nsg.vis[, 1] + nsg.vis[, 2] + g.vis[, 6], family = "gaussian")

Deviance Residuals:

Min	1Q	Median	3Q	Max
-695.9	-259.0	54.0	278.2	879.7

Coefficients:

	Estimate	Std. Error	t value	Pr(> t )
(Intercept)	508.80219	88.33428	5.760	1.54e-08 ***
age.vis	-0.89930	1.26017	-0.714	0.47582
sex.vis	95.32424	36.38319	2.620	0.00908 **
as.numeric(phenotypes.vis\$bmi)	0.07570	0.09318	0.812	0.41697
nsg.vis[, 1]	-51.69616	33.50679	-1.543	0.12355
nsg.vis[, 2]	-38.47824	36.17284	-1.064	0.28801
g.vis[, 6]	-14.89982	38.25771	-0.389	0.69712

---

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

(Dispersion parameter for gaussian family taken to be 143596.6)

Null deviance: 67510634 on 465 degrees of freedom  
Residual deviance: 65910836 on 459 degrees of freedom  
(21 observations deleted due to missingness)  
AIC: 6865

Number of Fisher Scoring iterations: 2

>  
>