

## RESPONSE H1N1

```
>
> r1<-
glm(ResponseH1N1~Group+Age+Gender+Diabetes+IL1+IL6+Monthsondialysis+HD
access+HDFvolume, family=binomial)
> summary(r1)
```

Call:

```
glm(formula = ResponseH1N1 ~ Group + Age + Gender + Diabetes +
     IL1 + IL6 + Monthsondialysis + HDaccess + HDFvolume, family =
     binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.6903	-1.1744	0.8127	1.0662	1.3594

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-3.010e+01	1.029e+03	-0.029	0.9767
GroupHD	1.581e+01	7.277e+02	0.022	0.9827
GroupHDF	7.029e-01	7.456e-01	0.943	0.3458
Age	-1.544e-02	6.892e-03	-2.240	0.0251 *
GenderM	-9.824e-02	1.999e-01	-0.492	0.6230
DiabetesY	8.929e-01	2.176e-01	4.103	4.09e-05 ***
IL1	-5.314e-02	1.192e-01	-0.446	0.6557
IL6	-1.206e-02	9.174e-03	-1.315	0.1885
Monthsondialysis	4.758e-03	1.926e-03	2.470	0.0135 *
HDaccessCVC	3.119e+01	1.029e+03	0.030	0.9758
HDaccessFistula	3.093e+01	1.029e+03	0.030	0.9760
HDaccessGraft	3.069e+01	1.029e+03	0.030	0.9762
HDFvolume	-3.090e-02	3.724e-02	-0.830	0.4067

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 778.26 on 567 degrees of freedom  
Residual deviance: 738.85 on 555 degrees of freedom  
(188 observations deleted due to missingness)  
AIC: 764.85

Number of Fisher Scoring iterations: 14

```
> anova(r1,test="Chisq")
Analysis of Deviance Table
```

Model: binomial, link: logit

Response: ResponseH1N1

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			567	778.26	
Group	2	1.3661	565	776.90	0.5050816
Age	1	2.0321	564	774.87	0.1540099
Gender	1	0.8107	563	774.05	0.3679156
Diabetes	1	12.5528	562	761.50	0.0003956 ***
IL1	1	1.2537	561	760.25	0.2628397
IL6	1	1.2259	560	759.02	0.2682062
Monthsondialysis	1	5.9940	559	753.03	0.0143545 *
HDaccess	3	13.4909	556	739.54	0.0036868 **
HDFvolume	1	0.6912	555	738.85	0.4057405

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

>

### PROTECTION H1N1

> p1<-

```
glm(ProtectionH1N1~Group+Age+Gender+Time+Diabetes+IL1+IL6+Monthsondialysis+HDaccess+HDFvolume, family=binomial)
```

Warning message:

glm.fit: fitted probabilities numerically 0 or 1 occurred

> summary(p1)

Call:

```
glm(formula = ProtectionH1N1 ~ Group + Age + Gender + Time +  
    Diabetes + IL1 + IL6 + Monthsondialysis + HDaccess + HDFvolume,  
    family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.37324	0.00000	0.00000	0.00006	1.09755

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	1.897e+00	6.029e+04	0.000	1.0000
GroupHD	1.994e+01	3.115e+04	0.001	0.9995
GroupHDF	-6.960e+00	4.167e+00	-1.670	0.0949 .
Age	-9.348e-03	1.929e-02	-0.485	0.6280
GenderM	2.576e-01	5.348e-01	0.482	0.6300
Time	1.902e+01	1.450e+03	0.013	0.9895
DiabetesY	-5.359e-01	5.484e-01	-0.977	0.3285
IL1	3.181e+00	3.436e+03	0.001	0.9993
IL6	3.983e-02	3.011e-02	1.323	0.1860

Monthsondialysis	2.181e-05	4.483e-03	0.005	0.9961
HDaccessCVC	-2.939e-01	6.029e+04	0.000	1.0000
HDaccessFistula	5.648e-01	6.029e+04	0.000	1.0000
HDaccessGraft	6.864e-01	6.029e+04	0.000	1.0000
HDFvolume	3.338e-01	2.242e-01	1.489	0.1365

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 196.73 on 543 degrees of freedom  
 Residual deviance: 117.48 on 530 degrees of freedom  
 (212 observations deleted due to missingness)  
 AIC: 145.48

Number of Fisher Scoring iterations: 22

```
> anova(p1,test="Chisq")
Analysis of Deviance Table
```

Model: binomial, link: logit

Response: ProtectionH1N1

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			543	196.73	
Group	2	1.410	541	195.32	0.49416
Age	1	0.610	540	194.71	0.43465
Gender	1	0.204	539	194.50	0.65178
Time	1	68.431	538	126.07	< 2e-16 ***
Diabetes	1	0.558	537	125.52	0.45494
IL1	1	0.463	536	125.05	0.49625
IL6	1	1.666	535	123.39	0.19685
Monthsondialysis	1	0.006	534	123.38	0.94030
HDaccess	3	2.119	531	121.26	0.54801
HDFvolume	1	3.780	530	117.48	0.05186 .

---

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

=====

ResponseH3N2

```
> r2<-
glm(ResponseH3N2~Group+Age+Gender+Diabetes+IL1+IL6+Monthsondialysis+HD
```

```
access+HDFvolume, family=binomial)
> summary(r2)
```

Call:

```
glm(formula = ResponseH3N2 ~ Group + Age + Gender + Diabetes +
     IL1 + IL6 + Monthsondialysis + HDaccess + HDFvolume, family =
     binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.4671	-0.8570	-0.6885	1.1544	2.0054

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-8.835e-01	1.697e+03	-0.001	0.999585
GroupHD	-1.678e+01	1.200e+03	-0.014	0.988842
GroupHDF	3.758e+00	1.375e+00	2.733	0.006270 **
Age	7.418e-03	7.636e-03	0.971	0.331326
GenderM	-7.205e-01	2.223e-01	-3.241	0.001192 **
DiabetesY	2.515e-01	2.321e-01	1.083	0.278641
IL1	-2.846e+00	1.237e+02	-0.023	0.981653
IL6	3.553e-02	1.011e-02	3.516	0.000439 ***
Monthsondialysis	1.655e-03	1.718e-03	0.964	0.335267
HDaccessCVC	-4.756e-01	1.697e+03	0.000	0.999776
HDaccessFistula	1.855e-01	1.697e+03	0.000	0.999913
HDaccessGraft	-6.337e-01	1.697e+03	0.000	0.999702
HDFvolume	-2.241e-01	7.273e-02	-3.081	0.002063 **

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 696.63 on 567 degrees of freedom  
 Residual deviance: 634.61 on 555 degrees of freedom  
 (188 observations deleted due to missingness)  
 AIC: 660.61

Number of Fisher Scoring iterations: 15

```
> anova(r2,test="Chisq")
Analysis of Deviance Table
```

Model: binomial, link: logit

Response: ResponseH3N2

Terms added sequentially (first to last)

Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
----	----------	-----------	------------	----------

NULL			567	696.63	
Group	2	10.3133	565	686.32	0.0057610 **
Age	1	1.2249	564	685.09	0.2684061
Gender	1	6.4694	563	678.62	0.0109747 *
Diabetes	1	0.0041	562	678.62	0.9491660
IL1	1	5.3598	561	673.26	0.0206064 *
IL6	1	11.7029	560	661.56	0.0006240 ***
Monthsondialysis	1	1.3888	559	660.17	0.2386102
HDaccess	3	11.6260	556	648.54	0.0087805 **
HDFvolume	1	13.9346	555	634.61	0.0001893 ***

---

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

>

=====

ProtectionH3N2

> p2<-

glm(ProtectionH3N2~Group+Age+Gender+Time+Diabetes+IL1+IL6+Monthsondialysis+HDaccess+HDFvolume, family=binomial)

> summary(p2)

Call:

glm(formula = ProtectionH3N2 ~ Group + Age + Gender + Time + Diabetes + IL1 + IL6 + Monthsondialysis + HDaccess + HDFvolume, family = binomial)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-3.3553	0.0551	0.1533	0.3027	0.7938

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	5.701e+00	5.484e+03	0.001	0.99917
GroupHD	1.562e+01	3.016e+03	0.005	0.99587
GroupHDF	-4.457e+00	3.980e+00	-1.120	0.26270
Age	-4.010e-02	2.226e-02	-1.802	0.07155 .
GenderM	-4.007e-02	5.973e-01	-0.067	0.94651
Time	7.601e-01	2.598e-01	2.926	0.00344 **
DiabetesY	2.618e-01	6.227e-01	0.420	0.67423
IL1	2.317e+00	3.333e+02	0.007	0.99445
IL6	-7.327e-03	2.511e-02	-0.292	0.77044
Monthsondialysis	1.705e-03	5.022e-03	0.340	0.73414
HDaccessCVC	-3.581e-01	5.484e+03	0.000	0.99995
HDaccessFistula	-6.332e-01	5.484e+03	0.000	0.99991
HDaccessGraft	4.361e-01	5.484e+03	0.000	0.99994
HDFvolume	2.094e-01	2.161e-01	0.969	0.33252

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 158.11 on 543 degrees of freedom  
Residual deviance: 131.23 on 530 degrees of freedom  
(212 observations deleted due to missingness)  
AIC: 159.23

Number of Fisher Scoring iterations: 17

```
> anova(p2, test="Chisq")  
Analysis of Deviance Table
```

Model: binomial, link: logit

Response: ProtectionH3N2

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			543	158.11	
Group	2	0.7198	541	157.39	0.69775
Age	1	4.2721	540	153.12	0.03874 *
Gender	1	0.1402	539	152.97	0.70813
Time	1	17.7107	538	135.26	2.572e-05 ***
Diabetes	1	0.5260	537	134.74	0.46830
IL1	1	0.1785	536	134.56	0.67266
IL6	1	0.0550	535	134.50	0.81466
Monthsondialysis	1	0.1184	534	134.39	0.73075
HDaccess	3	1.7046	531	132.68	0.63590
HDFvolume	1	1.4518	530	131.23	0.22824

---

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

>

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ResponseYamagata

>

> r3<-

```
glm(ResponseYamagata~Group+Age+Gender+Diabetes+IL1+IL6+Monthsondialysis+HDaccess+HDFvolume, family=binomial)
```

```
> summary(r3)
```

Call:

```
glm(formula = ResponseYamagata ~ Group + Age + Gender + Diabetes +  
      IL1 + IL6 + Monthsondialysis + HDaccess + HDFvolume, family =  
      binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.0729	-1.2336	0.6961	0.8998	1.3713

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-3.197e+01	1.029e+03	-0.031	0.975214
GroupHD	1.422e+01	7.277e+02	0.020	0.984412
GroupHDF	2.375e-01	8.906e-01	0.267	0.789747
Age	-7.628e-04	7.371e-03	-0.103	0.917572
GenderM	5.297e-01	2.116e-01	2.503	0.012329 *
DiabetesY	1.833e-01	2.291e-01	0.800	0.423597
IL1	-3.109e-01	1.353e-01	-2.298	0.021565 *
IL6	4.800e-02	1.295e-02	3.708	0.000209 ***
Monthsondialysis	2.158e-03	2.056e-03	1.049	0.293977
HDaccessCVC	3.212e+01	1.029e+03	0.031	0.975100
HDaccessFistula	3.153e+01	1.029e+03	0.031	0.975557
HDaccessGraft	3.147e+01	1.029e+03	0.031	0.975609
HDFvolume	2.814e-02	4.495e-02	0.626	0.531344

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 726.72 on 567 degrees of freedom  
Residual deviance: 667.20 on 555 degrees of freedom  
(188 observations deleted due to missingness)  
AIC: 693.2

Number of Fisher Scoring iterations: 14

```
> anova(r3,test="Chisq")
Analysis of Deviance Table
```

Model: binomial, link: logit

Response: ResponseYamagata

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			567	726.72	
Group	2	12.9466	565	713.77	0.001544 **
Age	1	1.3725	564	712.40	0.241382
Gender	1	3.0761	563	709.33	0.079450 .
Diabetes	1	1.0391	562	708.29	0.308036
IL1	1	1.2519	561	707.03	0.263188
IL6	1	19.4496	560	687.58	1.033e-05 ***
Monthsondialysis	1	0.6668	559	686.92	0.414174
HDaccess	3	19.3089	556	667.61	0.000236 ***

```
HDFvolume      1    0.4091      555      667.20  0.522420
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
>
```

```
=====
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```

### ProtectionYamagata

```
>
> p3<-
glm(ProtectionYamagata~Group+Age+Gender+Time+Diabetes+IL1+IL6+Monthson
dialysis+HDaccess+HDFvolume, family=binomial)
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
> summary(p3)
```

Call:

```
glm(formula = ProtectionYamagata ~ Group + Age + Gender + Time +
      Diabetes + IL1 + IL6 + Monthsondialysis + HDaccess + HDFvolume,
      family = binomial)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.59784	0.00000	0.00000	0.00007	1.14905

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	3.035e+00	6.062e+04	0.000	1.000
GroupHD	2.003e+01	3.162e+04	0.001	0.999
GroupHDF	-3.344e-01	2.495e+00	-0.134	0.893
Age	1.306e-02	2.431e-02	0.537	0.591
GenderM	-1.700e-01	7.735e-01	-0.220	0.826
Time	1.805e+01	1.467e+03	0.012	0.990
DiabetesY	1.153e+00	1.121e+00	1.028	0.304
IL1	3.298e+00	3.481e+03	0.001	0.999
IL6	-3.197e-02	2.669e-02	-1.198	0.231
Monthsondialysis	-1.356e-03	5.217e-03	-0.260	0.795
HDaccessCVC	-1.610e+00	6.062e+04	0.000	1.000
HDaccessFistula	-6.456e-01	6.062e+04	0.000	1.000
HDaccessGraft	-4.523e-01	6.062e+04	0.000	1.000
HDFvolume	-5.724e-03	1.229e-01	-0.047	0.963

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 99.742 on 543 degrees of freedom  
Residual deviance: 65.751 on 530 degrees of freedom  
(212 observations deleted due to missingness)



AIC: 93.751

Number of Fisher Scoring iterations: 22

```
> anova(p3,test="Chisq")
Analysis of Deviance Table
```

Model: binomial, link: logit

Response: ProtectionYamagata

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			543	99.742	
Group	2	0.7135	541	99.029	0.7000
Age	1	0.2364	540	98.792	0.6268
Gender	1	0.1276	539	98.665	0.7209
Time	1	27.5418	538	71.123	1.537e-07 ***
Diabetes	1	1.6384	537	69.485	0.2005
IL1	1	0.2169	536	69.268	0.6414
IL6	1	2.3243	535	66.943	0.1274
Monthsondialysis	1	0.0101	534	66.933	0.9198
HDaccess	3	1.1806	531	65.753	0.7577
HDFvolume	1	0.0021	530	65.751	0.9631

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

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ResponseVictolia

```
>
> r4<-
glm(ResponseVictolia~Group+Age+Gender+Diabetes+IL1+IL6+Monthsondialysi
s+HDaccess+HDFvolume, family=binomial)
> summary(r4)
```

Call:  
glm(formula = ResponseVictolia ~ Group + Age + Gender + Diabetes +  
IL1 + IL6 + Monthsondialysis + HDaccess + HDFvolume, family =  
binomial)

Deviance Residuals:

Min	1Q	Median	3Q	Max
-2.2292	-1.2554	0.6478	0.9670	1.3123

Coefficients:

	Estimate	Std. Error	z value	Pr(> z )
(Intercept)	-2.930e+01	1.029e+03	-0.028	0.97728
GroupHD	1.391e+01	7.277e+02	0.019	0.98475
GroupHDF	-1.356e+00	8.960e-01	-1.513	0.13019
Age	-4.502e-03	7.390e-03	-0.609	0.54240
GenderM	2.067e-02	2.145e-01	0.096	0.92320
DiabetesY	6.519e-01	2.405e-01	2.711	0.00671 **
IL1	-1.836e-01	1.283e-01	-1.431	0.15254
IL6	1.296e-02	1.135e-02	1.142	0.25364
Monthsondialysis	-3.830e-03	1.774e-03	-2.159	0.03087 *
HDaccessCVC	3.126e+01	1.029e+03	0.030	0.97577
HDaccessFistula	2.995e+01	1.029e+03	0.029	0.97679
HDaccessGraft	2.982e+01	1.029e+03	0.029	0.97689
HDFvolume	8.660e-02	4.575e-02	1.893	0.05839 .

---

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 726.72 on 567 degrees of freedom  
Residual deviance: 667.32 on 555 degrees of freedom  
(188 observations deleted due to missingness)  
AIC: 693.32

Number of Fisher Scoring iterations: 14

```
> anova(r4,test="Chisq")
Analysis of Deviance Table
```

Model: binomial, link: logit

Response: ResponseVictoria

Terms added sequentially (first to last)

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			567	726.72	
Group	2	1.2526	565	725.47	0.5345631
Age	1	0.4932	564	724.97	0.4824906
Gender	1	0.5441	563	724.43	0.4607591
Diabetes	1	12.1634	562	712.27	0.0004874 ***
IL1	1	1.9612	561	710.31	0.1613798
IL6	1	1.4744	560	708.83	0.2246455
Monthsondialysis	1	8.1302	559	700.70	0.0043533 **
HDaccess	3	29.2565	556	671.45	1.978e-06 ***
HDFvolume	1	4.1241	555	667.32	0.0422757 *

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

>

```
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ProtectionVictoria
```

```
>
> p4<-
glm(ProtectionVictoria~Group+Age+Gender+Time+Diabetes+IL1+IL6+Monthson
dialysis+HDaccess+HDFvolume, family=binomial)
Warning message:
glm.fit: fitted probabilities numerically 0 or 1 occurred
> summary(p4)
```

```
Call:
glm(formula = ProtectionVictoria ~ Group + Age + Gender + Time +
    Diabetes + IL1 + IL6 + Monthsondialysis + HDaccess + HDFvolume,
    family = binomial)
```

Deviance Residuals:

	Min	1Q	Median	3Q	Max
	-2.71841	0.00000	0.00000	0.00007	0.85620

Coefficients:

	Estimate	Std. Error	z	value	Pr(> z )
(Intercept)	4.493e+00	6.061e+04	0.000	0.9999	
GroupHD	1.914e+01	3.155e+04	0.001	0.9995	
GroupHDF	1.647e+00	2.123e+00	0.776	0.4380	
Age	2.253e-03	2.386e-02	0.094	0.9248	
GenderM	2.152e-01	6.985e-01	0.308	0.7580	
Time	1.822e+01	1.481e+03	0.012	0.9902	
DiabetesY	1.707e-01	7.592e-01	0.225	0.8221	
IL1	3.653e+00	3.445e+03	0.001	0.9992	
IL6	-4.626e-02	2.749e-02	-1.683	0.0924	.
Monthsondialysis	2.681e-03	6.571e-03	0.408	0.6833	
HDaccessCVC	-1.164e+00	6.061e+04	0.000	1.0000	
HDaccessFistula	-2.516e+00	6.061e+04	0.000	1.0000	
HDaccessGraft	-2.202e+00	6.061e+04	0.000	1.0000	
HDFvolume	-7.859e-02	9.997e-02	-0.786	0.4318	

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

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 115.270 on 543 degrees of freedom  
Residual deviance: 77.448 on 530 degrees of freedom  
(212 observations deleted due to missingness)  
AIC: 105.45

Number of Fisher Scoring iterations: 22

```
> anova(p4,test="Chisq")
Analysis of Deviance Table
```

```
Model: binomial, link: logit
```

```
Response: ProtectionVictoria
```

```
Terms added sequentially (first to last)
```

	Df	Deviance	Resid. Df	Resid. Dev	Pr(>Chi)
NULL			543	115.270	
Group	2	0.273	541	114.997	0.8722
Age	1	0.062	540	114.935	0.8040
Gender	1	0.000	539	114.935	0.9830
Time	1	33.094	538	81.841	8.783e-09 ***
Diabetes	1	0.039	537	81.803	0.8439
IL1	1	0.386	536	81.417	0.5345
IL6	1	1.798	535	79.619	0.1799
Monthsondialysis	1	0.101	534	79.518	0.7510
HDaccess	3	1.515	531	78.003	0.6787
HDFvolume	1	0.555	530	77.448	0.4563

```
---
```

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