

## **Dataset Integrity Check for the Study of Viral Resistance to Antiviral Therapy for Chronic Hepatitis C (Virahep-C) Baseline Files**

**Note.** This current version, dated 01/08/08, replaces the previously released DSIC dated 12/17/07.

The Virahep-C multicenter treatment trial was designed to assess the rates of response to peginterferon combination therapy for hepatitis C among African-American (AA) and Caucasian-American (CA) treatment-naïve patients. The goal of the study was to elucidate the mechanisms of antiviral resistance among patients who fail to respond to peginterferon combination therapy. As a partial check of the integrity of the Virahep-C main study datasets archived in the NIDDK data repository, a dataset integrity check (DSIC) was performed to verify that selected published results from the main study can be reproduced using the archived datasets. The DSIC consists of a small number of analyses performed to duplicate published results reported by the Virahep-C Study Group [1] in *Gastroenterology* in August, 2006. Results of the DSIC are described below.

The intent of this DSIC is to provide confidence that the data distributed by the NIDDK repository is a true copy of the study data. Our intent is *not* to assess the integrity of the statistical analyses reported by study investigators. As with all statistical analyses of complex datasets, complete replication of a set of statistical results should not be expected on a first (or second) exercise in secondary analysis. This occurs for a number of reasons including differences in the handling of missing data, restrictions on cases included in samples for a particular analysis, software coding used to define complex variables, etc. Experience suggests that most discrepancies can ordinarily be resolved by consultation with the study data coordinating center (DCC), however this process is labor-intensive for both DCC and Repository staff. It is thus not our policy to resolve every discrepancy that is observed in an integrity check. Specifically, we do not attempt to resolve minor or inconsequential discrepancies with published results or discrepancies that involve complex analyses, *unless staff of the NIDDK Repository suspect that the observed discrepancy suggests that the dataset may have been corrupted in storage, transmission, or processing by repository staff.* We do, however, document in footnotes to the integrity check those instances in which our secondary analyses produced results that were not fully consistent with those reported in the target publication.

**Dataset Integrity Check.** The DCC submitted 34 data files representing the raw data collected for the Virahep-C main protocol, together with corresponding data collection forms, brief dataset descriptions, variable labels, and SAS formats (value labels). Contents of the archived raw datasets exactly matched the dataset descriptions provided by the DCC. Missing data values were qualified, using SAS formats, as “Unknown”, “N/A”, “Refused”, or “Missing”. Analysis datasets used for results published by the Virahep-C Study Group were not provided at the time of this DSIC. A representative of the DCC was available for general questions regarding study and data protocols; however, reconstruction of the analysis dataset was left primarily to Repository analysts. For purposes of the DSIC, an analysis dataset was recreated by Repository staff from portions of the 34 raw data files. Results of analyses on the reconstructed analysis dataset were compared to published results. A percentage of published results were replicated, selected to assure the quality of the archived datasets.

**Analysis Methods.** As indicated in the publication, baseline demographic and clinical characteristics among racial groups (AA and CA) were compared using the  $\chi^2$  test of association with continuity correction or exact tests. The nonparametric Wilcoxon rank-sum test was used to test for racial

differences in the distributions of continuous variables. The primary end point, sustained virologic response (SVR), was defined as the absence of detectable HCV RNA in serum 24 weeks after therapy was stopped<sup>1</sup>. Accordingly, an outcome indicator denoting presence or absence of SVR was constructed. The DCC provided the following protocol for the calculation of SVR:

### **Definition of Sustained Viral Response (SVR)<sup>2</sup>**

Qualitative tests were completed in duplicate. SVR was defined by qualitative test results at 24 weeks post treatment with a minimum time of 20 weeks post treatment. If both qualitative tests were positive, then participant was considered to be a non-responder (NR) for SVR.

If qualitative results were not available at 24 weeks post treatment:

- 1.) If no further tests were available, the participant was considered to be a non-responder (NR)
- 2.) If subsequent qualitative tests were available then these results were used to determine SVR status.

Associations between measures of interest and SVR were reported as relative risks with 95% confidence intervals. Estimates of relative risk were assessed using generalized estimating equations<sup>3</sup>. Statistical analyses were performed using *PC-SAS v.9.1 (Cary, NC)*<sup>4</sup>.

**Analysis Cohort.** The study publication reports that of the 401 patients who met the entry criteria and subsequently enrolled, 196 were AA and 205 were CA. Upon examination of the raw datasets, Repository analysts constructed an analysis dataset as follows:

- 1.) Patients with baseline lab or viral load data were identified (N=403)
- 2.) Patients who withdrew consent at baseline visit (N=1)
- 3.) Patients who were found to be ineligible during the course of the study were removed (N=1)<sup>5</sup>
- 4.) The analysis dataset was limited to the 401 remaining patients, 196 AA and 205 CA.

**Baseline Comparisons.** The following results, reported in the study publication (text, p.472 and table, p.473), were replicated by analyses of archived data for the 401 patients. AA and CA did not differ significantly in regards to sex and age. Education greater than high school level was less common among AA patients. AA patients were heavier and more likely to have a history of diabetes and hypertension. AA patients were more likely to be currently smoking than CA patients, but the difference is not significant. AA patients had lower levels of serum ALT, albumin, total bilirubin, and hemoglobin, compared to CA patients. AA patients also had borderline lower levels of serum AST and WBC compared to CA. HCV-RNA levels were similar between the two racial groups<sup>6</sup>. Actual medians and proportions for these baseline characteristics differed slightly when comparing archived data results to published results (DSIC Table 1).

---

<sup>1</sup> Per study publication, p. 471.

<sup>2</sup> Per E-Mail communication with the DCC, 8/13/07.

<sup>3</sup> For purposes of the DSIC, generalized estimating equations (GEE) were used to estimate relative risk of univariable associations with SVR. (The study publication does not explicitly state the statistical methods used to assess univariable associations.)

<sup>4</sup> The study publication states that *SAS v.8.02* and the R language and environment were used in analyses.

<sup>5</sup> Patient #295076 was found to be ineligible, even though the patient collected data for baseline and treatment visits.

<sup>6</sup> Communication with the DCC verified that published baseline viral load levels were in units of **log<sub>10</sub>**. These units are not stated anywhere in Table 1 of the publication (p.473). By assessing log<sub>10</sub> of the archived intent-to-treat viral load variable <vload\_itt>, we succeeded in replicating published baseline values.

**DSIC Table 1. Selected<sup>†</sup> Baseline Characteristics of Virahep-C Participants.**

<sup>†</sup>analyses selected from publication Table 1, p. 473.

Characteristic	Source* Dataset / variable	African Americans						Caucasian Americans						P-value	
		Archived (n=196)		Published (n=196)		Difference (0)		Archived (n=205)		Published (n=205)		Difference (0)		Arch- ived	Pub- lished
Male, n (%)	SE / sex	127	(64.8)	127	(64.8)	0	(0)	134	(65.4)	134	(65.4)	0	(0)	0.99	0.99
Age, y	SE / (various)	49.2	(45.3, 53.0)	49.0	(45.0, 52.5)	-0.2	(-0.3, -0.5)	48.2	(42.9, 52.4)	48.0	(43.0, 52.0)	-0.2	(-0.1, -0.4)	0.07	0.08
Education	SQ / educ	(n=192)		(n=191)		(-1)		(n=204)		(n=202)		(2)			
>High School		104	(54.2)	104	(54.5)	0	(0.3)	132	(65.0)	132	(65.4)	0	(0.4)	0.04	0.04
≤High School		88	(45.8)	87	(45.6)	-1	(-0.2)	71	(35.0)	70	(34.7)	-1	(-0.3)		
Weight (kg)	SE / wgtlb	(n=193)		(n=194)		(1)								0.001	0.001
		87.3	(78.2, 100.9)	87.5	(78.6, 100.9)	0.2	(0.4, 0)	82.3	(72.7, 95.9)	82.3	(72.7, 95.5)	0.0	(0, -0.4)		
Body mass index, kg/m <sup>2</sup>	SE / (various)	(n=191)		(n=193)		(2)		(n=203)		(n=203)		(0)		0.0003	0.0003
		29.5	(26.3, 34.2)	29.3	(26.4, 34.0)	-0.2	(0.1, -0.2)	27.6	(24.4, 31.5)	27.6	(24.4, 31.5)	0.0	(0, 0)		
History of diabetes, n(%)	SE / mxdiab	30	(15.3)	30	(15.3)	0	(0)	9	(4.4)	9	(4.4)	0	(0)	0.0004	0.0004
History of hypertension	SE / mxbp	85	(43.4)	84	(42.9)	-1	(-0.5)	43	(21.0)	43	(21.0)	0	(0)	<0.0001	<0.0001
Currently smoking, n(%)	SQ / cursmk, evsmk	78	(41.1)	78	(41.3)	0	(0.2)	70	(34.5)	70	(34.5)	0	(0)	0.22	0.20
Alanine transaminase level, IU/L	LE / ALT	59.0	(40.0, 90.0)	59.0	(40.0, 88.0)	0	(0, -2)	74.0	(51.0, 138.0)	74.0	(51.0, 138.0)	0.0	(0, 0)	<0.0001	<0.0001
Aspartate transaminase level, IU/L	LE / AST	51.0	(33.0, 69.0)	51.0	(33.5, 69.0)	0	(0.5, 0)	52.0	(37.0, 87.0)	52.0	(37.0, 87.0)	0	(0, 0)	0.06	0.06
Albumin level	LE / ALB	4.0	(3.7, 4.2)	4.1	(3.8, 4.3)	0.1	(0.1, 0.1)	4.2	(4.0, 4.4)	4.2	(4.0, 4.4)	0	(0, 0)	<0.0001	<0.0001
Total bilirubin level, mg/dL	LE / TBILI	0.6	(0.4, 0.8)	0.6	(0.4, 0.8)	0	(0, 0)	0.7	(0.5, 0.9)	0.7	(0.5, 0.9)	0	(0, 0)	0.0008	0.0007
Hemoglobin level, g/dL	LE / HGB	14.3	(13.5, 15.1)	14.3	(13.5, 15.1)	0	(0, 0)	15.1	(13.9, 15.9)	15.0	(13.9, 15.9)	-0.1	(0, 0)	<0.0001	<0.0001
White blood cell count, 10 <sup>3</sup> cells/mm <sup>3</sup>	LE / WBC	5.8	(4.7, 7.4)	5.8	(4.7, 7.5)	0	(0, 0.1)	6.2	(4.9, 7.4)	6.2	(4.9, 7.4)	0	(0, 0)	0.09	0.08
HCV RNA level, x10 <sup>6</sup> IU/mL **	VLOAD / vload_itt	6.4	(5.6, 6.7)	6.4	(5.6, 6.7)	0	(0, 0)	6.5	(5.7, 6.8)	6.5	(5.7, 6.8)	0	(0, 0)	0.09	0.08

NOTE: Continuous variables are represented by median (25<sup>th</sup> percentile, 75<sup>th</sup> percentile). The Wilcoxon rank-sum test was used to compare distributions for continuous variables, Pearson's  $\chi^2$  test was used to compare percentages.

\* archived data

\*\* HCV RNA level reported as log<sub>10</sub>, per E-Mail communication with DCC, 8/13/2007

**Primary Outcome.** The study publication reported that the primary end point, sustained virologic response (SVR), was achieved in 28% of AA compared with 52% of CA patients ( $P < 0.0001$ ). Similarly, analyses of archived data indicated that SVR was achieved in 27% of AA compared with 52% of CA patients ( $P < 0.0001$ ). Selected univariable associations with SVR were analyzed for purposes of this DSIC. Results are presented in DSIC Table 2. Analyses of archived data indicated the following factors were associated with higher SVR: CA race, female sex, more than high school education, and lower weight. A history of diabetes was associated with lower response rates. Some laboratory measures were found to be possibly associated with lower response rates, including serum AST and WBC. Relative risks, 95% confidence intervals, and  $P$ -values for these selected univariable associations were very similar to those published by the study group (DSIC Table 2).

**DSIC Table 2<sup>†</sup>. Relationship between SVR and variables of interest: Selected Univariable Analyses<sup>7</sup>**

<sup>†</sup> analyses selected from publication Table 3, p. 475.

Variable	Univariable Analysis					P -value	
	Archived		Published		RR: Percent difference	Archived	Published
	Relative Risk	(95% CI)	Relative Risk	(95% CI)			
CA race	1.93	(1.48 - 2.51)	1.89	(1.46 - 2.46)	-2.1%	<0.0001	<0.0001
Male sex	0.74	(0.59 - 0.94)	0.73	(0.58 - 0.93)	-1.4%	0.02	0.01
Age, per 5 years	0.96	(0.89 - 1.03)	0.97	(0.89 - 1.03)	1.0%	0.23	0.24
Education (<high school)	0.71	(0.55 - 0.93)	0.72	(0.55 - 0.94)	1.4%	0.01	0.02
Weight (kg) per 5 kg	0.94	(0.91 - 0.97)	0.94	(0.91 - 0.97)	0.0%	0.0003	0.0004
BMI, kg/m <sup>2</sup>	0.98	(0.96 - 0.9995)	0.98	(0.96 - 1.00)	0.0%	0.046	0.07
History of diabetes	0.49	(0.26 - 0.92)	0.49	(0.26 - 0.91)	0.0%	0.03	0.02
History of hypertension	0.73	(0.55 - 0.98)	0.76	(0.57 - 1.01)	3.9%	0.03	0.06
Current smoking	1.14	(0.89 - 1.45)	1.13	(0.89 - 1.45)	-0.9%	0.30	0.31
Alanine transaminase level (IU) per 100 IU	1.05	(0.91 - 1.22)	1.05	(0.90 - 1.22)	0.0%	0.49	0.53
Asparate transaminase level (IU) per 100 IU	0.75	(0.55 - 1.03)	0.75	(0.55 - 1.02)	0.0%	0.07	0.06
Hemoglobin, g/DL	0.95	(0.87 - 1.04)	0.95	(0.87 - 1.04)	0.0%	0.30	0.26
White blood cells, per 10 <sup>3</sup> cells/mm <sup>3</sup>	1.05	(0.993 - 1.10)	1.05	(0.996 - 1.11)	0.0%	0.09	0.07
Baseline viral level, log <sub>10</sub> IU/mL	0.78	(0.71 - 0.86)	0.76	(0.66 - 0.88)	-2.6%	<0.0001	0.0002

<sup>7</sup> For purposes of the DSIC, generalized estimating equations (GEE) (*PC-SAS: Proc Genmod*, where *dist=binomial*, *link=log*) were used to estimate relative risk of univariable associations with SVR. The study publication does not explicitly state the statistical methods used to assess univariable associations. Small differences between archived and published results may be expected, due to differences in methods of estimation.

**Notes**

- (1) Eight of 34 raw datasets were used for the current analysis. Additional datasets will be analyzed as part of dataset integrity checks for other main publications.

**References**

[1] Virahep-C Study Group (Hari S. Conjeevaram et al). Peginterferon and Ribavirin Treatment in African American and Caucasian American Patients With Hepatitis C Genotype 1. **Gastroenterology** 2006;131:470–477.

# Attachment 1

**“The full text of the article referenced will be provided to approved data requestors along with the data archived.”**

Hari S. Conjeevaram, Michael W. Fried, Lennox J. Jeffers, Norah A. Terrault, Thelma E. Wiley-Lucas, Nezam Afdhal, Robert S. Brown, Steven H. Belle, Jay H. Hoofnagle, David E. Kleiner, and Charles D. Howell, for the Virahep-C Study Group. **Peginterferon and Ribavirin Treatment in African American and Caucasian American Patients With Hepatitis C Genotype 1.**  
*Gastroenterology* 2006;131:470–477

## **Attachment 2**

**SAS 9.1 Log for programming code submitted  
for the replication of results in Table 1  
“Baseline Characteristics of Virahep-C Participants”  
Conjeevaram et.al. 2006**

1

## The SAS System

NOTE: Copyright (c) 2002-2003 by SAS Institute Inc., Cary, NC, USA.

NOTE: SAS (r) 9.1 (TS1M3)

Licensed to RESEARCH TRIANGLE INSTITUTE, Site 0047670011.

NOTE: This session is executing on the XP\_PRO platform.

NOTE: SAS 9.1.3 Service Pack 3

NOTE: SAS initialization used:

real time 2.30 seconds

cpu time 0.32 seconds

```
1          options ps=55 ls=78 nonumber formchar='|----|+\----+=| -^<>*' mprint
orientation=portrait
```

```
1          ! ;
```

```
2
```

```
3          libname main 'Z:\05_Users\Sylvia\Virahep-C\main_study\mainstudy';
```

NOTE: Libref MAIN was successfully assigned as follows:

Engine: V9

Physical Name: Z:\05\_Users\Sylvia\Virahep-C\main\_study\mainstudy

```
4          %include 'Z:\05_Users\Sylvia\Virahep-C\vhpefmt.sas';
```

NOTE: Format ACTION has been output.

NOTE: Format AEVENT has been output.

NOTE: Format ALC has been output.

NOTE: Format ALL5NO has been output.

NOTE: Format ALL6NO has been output.

NOTE: Format ALWNEV has been output.

NOTE: Format BDYPN has been output.

NOTE: Format BETTER has been output.

NOTE: Format BIN has been output.

NOTE: Format BXSC has been output.

NOTE: Format CESD has been output.

NOTE: Format COMPBY has been output.

NOTE: Format DCHRS has been output.

NOTE: Format DIAB has been output.

NOTE: Format DISCD has been output.

NOTE: Format DRUGDS has been output.

NOTE: Format DRUGRL has been output.

NOTE: Format EDUC has been output.

NOTE: Format EVTYPE has been output.

NOTE: Format EXCPOR has been output.

NOTE: Format GFBC has been output.

NOTE: Format GRF has been output.

NOTE: Format GI has been output.

NOTE: Format HCVRES has been output.

NOTE: Format HERBCAT has been output.

NOTE: Format HISP has been output.

NOTE: Format HL1YR has been output.

NOTE: Format INCDEC has been output.

NOTE: Format INS has been output.

NOTE: Format LIMIT has been output.

NOTE: Format MARST has been output.

NOTE: Format MEDDC has been output.



The SAS System

NOTE: Format MISINT has been output.  
NOTE: Format MISSM has been output.  
NOTE: Format MISRIB has been output.  
NOTE: Format NEVALL has been output.  
NOTE: Format NEVER has been output.  
NOTE: Format NEVOFT has been output.  
NOTE: Format NEVWK has been output.  
NOTE: Format NONALL has been output.  
NOTE: Format NOTEXT has been output.  
NOTE: Format POSNEG has been output.  
NOTE: Format REMEM has been output.  
NOTE: Format RESLV has been output.  
NOTE: Format RISK has been output.  
NOTE: Format SATDIS has been output.  
NOTE: Format SATISF has been output.  
NOTE: Format SEVER has been output.  
NOTE: Format SEX has been output.  
NOTE: Format SEXFUNC has been output.  
NOTE: Format SMOKE has been output.  
NOTE: Format SOC has been output.  
NOTE: Format SOURCE has been output.  
NOTE: Format STATIN has been output.  
NOTE: Format STDYDC has been output.  
NOTE: Format TIMEOP has been output.  
NOTE: Format TMDC has been output.  
NOTE: Format TMPT has been output.  
NOTE: Format TMPTT has been output.  
NOTE: Format TMPTDW has been output.  
NOTE: Format TRFAL has been output.  
NOTE: Format TTPT has been output.  
NOTE: Format USA has been output.  
NOTE: Format VISIT has been output.  
NOTE: Format VQUALDET has been output.  
NOTE: Format WORK has been output.  
NOTE: Format YESNO has been output.

NOTE: PROCEDURE FORMAT used (Total process time):  
real time 0.16 seconds  
cpu time 0.03 seconds

830 libname analysis 'Z:\05\_Users\Sylvia\Virahep-C\main\_study\analysis';  
NOTE: Libref ANALYSIS was successfully assigned as follows:  
Engine: V9  
Physical Name: Z:\05\_Users\Sylvia\Virahep-C\main\_study\analysis

831  
832 \* define sample of 401 and perform bsln analyses \*;  
833 data sc; set main.sc;

NOTE: There were 546 observations read from the data set MAIN.SC.  
NOTE: The data set WORK.SC has 546 observations and 52 variables.  
NOTE: DATA statement used (Total process time):  
real time 0.50 seconds

The SAS System

cpu time 0.02 seconds

```
834      proc sort; by vhcid rsc;
```

NOTE: There were 546 observations read from the data set WORK.SC.

NOTE: The data set WORK.SC has 546 observations and 52 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.01 seconds  
cpu time 0.01 seconds

```
835      data sc; set sc; by vhcid rsc; if last.vhcid;  
836      keep vhcid rsc cons; *cons = gave informed consent *;  
837
```

NOTE: There were 546 observations read from the data set WORK.SC.

NOTE: The data set WORK.SC has 536 observations and 3 variables.

NOTE: DATA statement used (Total process time):

real time 0.00 seconds  
cpu time 0.01 seconds

```
838      data demo; set main.se; keep vhcid rsc male racew--raceos wgtkg mxdiab mxlla  
mxbp dob  
838      ! doe age hgtin hgtcm bmi;  
839      wgtkg=wgtlb/2.2;  
840      if sex=1 then male=1;  
841      else if sex=2 then male=0;  
842      dob=mdy(dobm,dobd,doby);  
843      doe=mdy(doem,doed,doey);  
844      format dob doe MMDDYY10.;  
845      age=round((doe-dob)/365.25,0.1);  
846      hgtcm=round((hgtin*2.54),0.1);  
847      bmi=wgtkg/(hgtcm*hgtcm/10000); ***weight kg / ht2 in m***;
```

NOTE: Missing values were generated as a result of performing an operation on missing values.

Each place is given by: (Number of times) at (Line):(Column).

17 at 839:14 30 at 846:9 30 at 846:21 5 at 847:12 30 at 847:19

NOTE: There were 552 observations read from the data set MAIN.SE.

NOTE: The data set WORK.DEMO has 552 observations and 20 variables.

NOTE: DATA statement used (Total process time):

real time 1.34 seconds  
cpu time 0.02 seconds

```
848      proc sort; by vhcid rsc; * rsc = rescreen *;
```

NOTE: There were 552 observations read from the data set WORK.DEMO.

NOTE: The data set WORK.DEMO has 552 observations and 20 variables.

NOTE: PROCEDURE SORT used (Total process time):

real time 0.00 seconds  
cpu time 0.01 seconds

The SAS System

```
849      data demo; set demo; by vhcid rsc;
850          if first.vhcid;
851
```

NOTE: There were 552 observations read from the data set WORK.DEMO.  
NOTE: The data set WORK.DEMO has 536 observations and 20 variables.  
NOTE: DATA statement used (Total process time):  
real time 0.00 seconds  
cpu time 0.01 seconds

```
852      data screen; set main.sq; keep vhcid educ evsmk cursmk alc alcbe alcwi alclq;
```

NOTE: There were 430 observations read from the data set MAIN.SQ.  
NOTE: The data set WORK.SCREEN has 430 observations and 8 variables.  
NOTE: DATA statement used (Total process time):  
real time 0.40 seconds  
cpu time 0.02 seconds

```
853      proc sort; by vhcid;
854
```

NOTE: There were 430 observations read from the data set WORK.SCREEN.  
NOTE: The data set WORK.SCREEN has 430 observations and 8 variables.  
NOTE: PROCEDURE SORT used (Total process time):  
real time 0.01 seconds  
cpu time 0.02 seconds

```
855      data labbase; set main.le; if tmpt=3;
```

NOTE: There were 7345 observations read from the data set MAIN.LE.  
NOTE: The data set WORK.LABBASE has 401 observations and 80 variables.  
NOTE: DATA statement used (Total process time):  
real time 6.91 seconds  
cpu time 0.06 seconds

```
856      proc sort; by vhcid;
```

NOTE: There were 401 observations read from the data set WORK.LABBASE.  
NOTE: The data set WORK.LABBASE has 401 observations and 80 variables.  
NOTE: PROCEDURE SORT used (Total process time):  
real time 0.00 seconds  
cpu time 0.00 seconds

```
857      data hcv_base; set main.vload;
858          if tmpt=3;
```

NOTE: There were 5247 observations read from the data set MAIN.VLOAD.

The SAS System

NOTE: The data set WORK.HCV\_BASE has 401 observations and 13 variables.

NOTE: DATA statement used (Total process time):

```
real time      1.11 seconds
cpu time       0.00 seconds
```

```
859      proc sort; by vhcid;
860
861      * hepatic steatosis / fibrosis measures *;
```

NOTE: There were 401 observations read from the data set WORK.HCV\_BASE.

NOTE: The data set WORK.HCV\_BASE has 401 observations and 13 variables.

NOTE: PROCEDURE SORT used (Total process time):

```
real time      0.00 seconds
cpu time       0.00 seconds
```

```
862      data hepa; set main.pe;
```

NOTE: There were 429 observations read from the data set MAIN.PE.

NOTE: The data set WORK.HEPA has 429 observations and 50 variables.

NOTE: DATA statement used (Total process time):

```
real time      0.43 seconds
cpu time       0.01 seconds
```

```
863      proc sort; by vhcid;
864
```

NOTE: There were 429 observations read from the data set WORK.HEPA.

NOTE: The data set WORK.HEPA has 429 observations and 50 variables.

NOTE: PROCEDURE SORT used (Total process time):

```
real time      0.01 seconds
cpu time       0.00 seconds
```

```
865      data demobase; merge sc demo screen labbase(in=in1) hcv_base(in=in2) hepa;
866      by vhcid; if in1 or in2; * anyone with bsln lab or viral load data, n=403 *;
867      if vhcid^=295076; * found to be ineligible during course of study, even
though has bsln and f/up data (DCC email 8/13/07) *;
868      if cons=1; * 292043 withdrew consent at bsln(cons=0), has bsln vload data,
869      but has no bsln lab or followup data ;
870      * THIS GIVES US FINAL N OF 401 ELIGIBLE (PRESUMABLY -- SINCE HAVE BSLN DATA
871      AND CONSENTED TO STUDY) *;
872      if educ>4 then hсорless=0; * high school or less *;
873      else if .<educ<=4 then hсорless=1;
874      log10vload=log10(vload_itt);
875      currentsmk=cursmk;
876      if evsmk in (0,.B) then currentsmk=0; *cursmk was set to n/a when evsmk=0 *;
877
878      run;
```

NOTE: Missing values were generated as a result of performing an operation on missing values.

Each place is given by: (Number of times) at (Line):(Column).

The SAS System

2 at 874:14

NOTE: There were 536 observations read from the data set WORK.SC.  
NOTE: There were 536 observations read from the data set WORK.DEMO.  
NOTE: There were 430 observations read from the data set WORK.SCREEN.  
NOTE: There were 401 observations read from the data set WORK.LABBASE.  
NOTE: There were 401 observations read from the data set WORK.HCV\_BASE.  
NOTE: There were 429 observations read from the data set WORK.HEPA.  
NOTE: The data set WORK.DEMOBASE has 401 observations and 167 variables.  
NOTE: DATA statement used (Total process time):  
real time 0.03 seconds  
cpu time 0.03 seconds

879  
880 DATA ANALYSIS.DEMOBASE; SET DEMOBASE; RUN;

NOTE: There were 401 observations read from the data set WORK.DEMOBASE.  
NOTE: The data set ANALYSIS.DEMOBASE has 401 observations and 167 variables.  
NOTE: DATA statement used (Total process time):  
real time 1.51 seconds  
cpu time 0.04 seconds

881  
882 \*\*\*\*\*;  
883 \* for table 1 (analysis of baseline factors) \*;  
884 \* use continuity adjusted chisq test for proportions \*;  
885 \* wilcoxon 2-group z-test for medians \*;  
886 \*\*\*\*\*;  
887 proc printto print='Z:\05\_Users\Sylvia\Virahep-C\main\_study\vhepc\_demo.out'  
new;  
888 title table 1: analysis of baseline factors;

NOTE: PROCEDURE PRINTTO used (Total process time):  
real time 0.14 seconds  
cpu time 0.00 seconds

889 proc freq data=demobase; tables racew\*raceb/missing; run;

NOTE: There were 401 observations read from the data set WORK.DEMOBASE.  
NOTE: The PROCEDURE FREQ printed page 1.  
NOTE: PROCEDURE FREQ used (Total process time):  
real time 0.07 seconds  
cpu time 0.01 seconds

890 proc freq data=demobase; tables (male hsorless mxdiab mxbp  
currentsmk)\*racew/chisq  
890 ! exact; run;

NOTE: There were 401 observations read from the data set WORK.DEMOBASE.  
NOTE: The PROCEDURE FREQ printed pages 2-7.  
NOTE: PROCEDURE FREQ used (Total process time):  
real time 0.05 seconds

The SAS System

cpu time 0.03 seconds

```
891      proc univariate data=demobase plot normal; class racew; var age wgtkg bmi
alt ast alb
891      !  tbili hgb wbc log10vload; run;
```

NOTE: The PROCEDURE UNIVARIATE printed pages 8-77.

NOTE: PROCEDURE UNIVARIATE used (Total process time):

real time	0.28 seconds
cpu time	0.05 seconds

```
892      proc npar1way wilcoxon data=demobase; class racew; var age wgtkg bmi alt ast
alb
892      !  tbili hgb wbc log10vload; run;
```

NOTE: There were 401 observations read from the data set WORK.DEMOBASE.

NOTE: The PROCEDURE NPAR1WAY printed pages 78-87.

NOTE: PROCEDURE NPAR1WAY used (Total process time):

real time	0.04 seconds
cpu time	0.03 seconds

```
893      proc printto; run;
```

NOTE: PROCEDURE PRINTTO used (Total process time):

real time	0.08 seconds
cpu time	0.00 seconds

```
894      *****;
```

NOTE: SAS Institute Inc., SAS Campus Drive, Cary, NC USA 27513-2414

NOTE: The SAS System used:

real time	16.70 seconds
cpu time	0.82 seconds

## **Attachment 3**

**SAS 9.1 Log for programming code submitted  
for the replication of selected results in Table 3  
“Relationship Between SVR and Each Variable of Interest  
in Univariable and Multivariable Analysis”  
Conjeevaram et.al. 2006**

1

## The SAS System

NOTE: Copyright (c) 2002-2003 by SAS Institute Inc., Cary, NC, USA.

NOTE: SAS (r) 9.1 (TS1M3)

Licensed to RESEARCH TRIANGLE INSTITUTE, Site 0047670011.

NOTE: This session is executing on the XP\_PRO platform.

NOTE: SAS 9.1.3 Service Pack 3

NOTE: SAS initialization used:

real time 3.93 seconds

cpu time 0.32 seconds

```
1          options ps=55 ls=78 nonumber formchar='|----|+\---+=|^-<>*' mprint
orientation=portrait
```

```
1          ! ;
```

2

```
3          libname main 'Z:\05_Users\Sylvia\Virahep-C\main_study\mainstudy';
```

NOTE: Libref MAIN was successfully assigned as follows:

Engine: V9

Physical Name: Z:\05\_Users\Sylvia\Virahep-C\main\_study\mainstudy

```
4          libname library 'Z:\05_Users\Sylvia\Virahep-C\main_study';
```

NOTE: Libref LIBRARY was successfully assigned as follows:

Engine: V9

Physical Name: Z:\05\_Users\Sylvia\Virahep-C\main\_study

```
5          libname analysis 'Z:\05_Users\Sylvia\Virahep-C\main_study\analysis';
```

NOTE: Libref ANALYSIS was successfully assigned as follows:

Engine: V9

Physical Name: Z:\05\_Users\Sylvia\Virahep-C\main\_study\analysis

6

```
7          DATA DEMOBASE; SET ANALYSIS.DEMOBASE; RUN;
```

NOTE: There were 401 observations read from the data set ANALYSIS.DEMOBASE.

NOTE: The data set WORK.DEMOBASE has 401 observations and 167 variables.

NOTE: DATA statement used (Total process time):

real time 4.76 seconds

cpu time 0.06 seconds

8

```
9          * construct SVR outcome *;
```

```
10         data hcv_fuwk24; set main.vload;
```

```
11         if tmpt=25; *f-up wk 24 *;
```

NOTE: There were 5247 observations read from the data set MAIN.VLOAD.

NOTE: The data set WORK.HCV\_FUWK24 has 326 observations and 13 variables.

NOTE: DATA statement used (Total process time):

real time 3.34 seconds

cpu time 0.03 seconds

```
12         proc sort; by vhcid;
```

```
13         *note: DATASET VLOAD contains both qualitative and quantitative results *;
```

14



The SAS System

NOTE: There were 326 observations read from the data set WORK.HCV\_FUWK24.

NOTE: The data set WORK.HCV\_FUWK24 has 326 observations and 13 variables.

NOTE: PROCEDURE SORT used (Total process time):

```
real time      0.01 seconds
cpu time       0.01 seconds
```

```
15      data all24_fu; merge demobase(in=in1 keep=vhcid age bmi male racew raceb
16                                hsrless mxdiab mxbp currentsmk
17                                wgtkg wbc alt ast hgb log10vload vload vload_itt
18                                gluf insf fatsc2
19                                rename=(log10vload=blog10vload vload=bvload
20                                        vload_itt=bvload_itt))
21                                hcv_fuwk24(in=in2);
22      by vhcid;
23      * Defn of primary endpoint:  an SVR defined as the absence of detectable
24      HCV RNA in serum 24 weeks after therapy was stopped... At week 24 and
25      time points thereafter, missing HCV RNA data were considered a
26      nonresponse (Conjeevaram 2006, p. 471);
27
28      *initially set SVR to VQUAL=0 at f-up wk 24 *;
29      svr=1-vqual;
30
31      if in1 and not in2 then do; svr=0; flag1=1; end;
32      *no data at fuwk 24 -- set to non-response *;
33      if in2 and vqual in (.,.C) then do;
34          if vload_itt>599 then svr=0; *detectable viral load
35                                using quantitative tests *;
36          else do; svr=0; flag2=1; end;
37      * vload_itt=599 is an unknown response, so set to non-response*;
38      end;
39
40      if in1; * keep all eligible in dataset *;
41      if racew=1 then race='W'; else if racew=0 then race='B';
42      age_5=age/5;
43      wgtkg_5=wgtkg/5;
44      alt_100=alt/100;
45      ast_100=ast/100;
46      * steatosis outcome (based on FATSC2, in main.pe ) *;
47      steat=fatsc2;
48      if fatsc2 in (2,3,4) then steat=2;
49      homa=(insf*gluf/18)/22.5;
50
51      * per email DCC (8/13/07): if HCV data not available at fuwk24,
52      then glean from later visits *;
```

NOTE: Missing values were generated as a result of performing an operation on missing values.

Each place is given by: (Number of times) at (Line):(Column).

186 at 29:10 3 at 43:16 2 at 44:14 2 at 45:14 59 at 49:13

NOTE: There were 401 observations read from the data set WORK.DEMOBASE.

NOTE: There were 326 observations read from the data set WORK.HCV\_FUWK24.

NOTE: The data set WORK.ALL24\_FU has 401 observations and 43 variables.

The SAS System

NOTE: DATA statement used (Total process time):  
real time 0.95 seconds  
cpu time 0.01 seconds

```
53 data postfu_wk24; set main.vload;  
54 if tmpt in (26,27,33);  
55
```

NOTE: There were 5247 observations read from the data set MAIN.VLOAD.  
NOTE: The data set WORK.POSTFU\_WK24 has 220 observations and 13 variables.  
NOTE: DATA statement used (Total process time):  
real time 3.37 seconds  
cpu time 0.03 seconds

```
55 ! proc sort; by vhcid tmpt;  
56
```

NOTE: There were 220 observations read from the data set WORK.POSTFU\_WK24.  
NOTE: The data set WORK.POSTFU\_WK24 has 220 observations and 13 variables.  
NOTE: PROCEDURE SORT used (Total process time):  
real time 0.01 seconds  
cpu time 0.00 seconds

```
57 proc freq data=all24_fu; where flag1=1; tables vhcid/out=nohcv_fu24;
```

NOTE: There were 75 observations read from the data set WORK.ALL24\_FU.  
WHERE flag1=1;  
NOTE: The data set WORK.NOHCV\_FU24 has 75 observations and 3 variables.  
NOTE: The PROCEDURE FREQ printed pages 1-2.  
NOTE: PROCEDURE FREQ used (Total process time):  
real time 0.12 seconds  
cpu time 0.03 seconds

```
58 proc freq data=all24_fu; where flag2=1; tables vhcid/out=misshcv_fu24;  
59 run;
```

NOTE: There were 3 observations read from the data set WORK.ALL24\_FU.  
WHERE flag2=1;  
NOTE: The data set WORK.MISSHCV\_FU24 has 3 observations and 3 variables.  
NOTE: The PROCEDURE FREQ printed page 3.  
NOTE: PROCEDURE FREQ used (Total process time):  
real time 0.01 seconds  
cpu time 0.00 seconds

```
60 * pick up later data for those with no data at fuwk24 *;  
61 data nohcv_fu24_post; merge nohcv_fu24(in=in1) postfu_wk24(in=in2);  
62 by vhcid; if in1 and in2;  
63 svr=1-vqual;
```

The SAS System

```
64          if vqual=. then do; if vload_itt>599 then svr=0; end; run;
```

NOTE: Missing values were generated as a result of performing an operation on missing values.

Each place is given by: (Number of times) at (Line):(Column).  
2 at 63:10

NOTE: There were 75 observations read from the data set WORK.NOHCV\_FU24.

NOTE: There were 220 observations read from the data set WORK.POSTFU\_WK24.

NOTE: The data set WORK.NOHCV\_FU24\_POST has 5 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time	0.67 seconds
cpu time	0.01 seconds

```
65          /* * check results: ;
66          proc print; by vhcid; id vhcid; var tmpt vqual--vload_itt svr;
67          run; */
68          * pick up later data for those missing data at fuwk24 *;
69          data misshcv_fu24_post; merge misshcv_fu24(in=in1) postfu_wk24(in=in2);
70          by vhcid; if in1 and in2;
71          svr=1-vqual;
72          if vqual=. then do; if vload_itt>599 then svr=0; end; run;
```

NOTE: There were 3 observations read from the data set WORK.MISSHCV\_FU24.

NOTE: There were 220 observations read from the data set WORK.POSTFU\_WK24.

NOTE: The data set WORK.MISSHCV\_FU24\_POST has 3 observations and 16 variables.

NOTE: DATA statement used (Total process time):

real time	0.64 seconds
cpu time	0.00 seconds

```
73          /* * check results: ;
74          proc print data=misshcv_fu24_post; by vhcid;
75          id vhcid; var tmpt vqual--vload_itt svr; run; */
76
77          data all24_fu2; merge all24_fu nohcv_fu24_post(keep=vhcid svr)
78          misshcv_fu24_post(keep=vhcid svr);
79          by vhcid;
80          run;
```

NOTE: There were 401 observations read from the data set WORK.ALL24\_FU.

NOTE: There were 5 observations read from the data set WORK.NOHCV\_FU24\_POST.

NOTE: There were 3 observations read from the data set WORK.MISSHCV\_FU24\_POST.

NOTE: The data set WORK.ALL24\_FU2 has 401 observations and 43 variables.

NOTE: DATA statement used (Total process time):

real time	0.63 seconds
cpu time	0.00 seconds

```
81
82          * final analysis of race by SVR *;
83          proc freq data=all24_fu2; tables race*svr/chisq exact; run;
```

NOTE: There were 401 observations read from the data set WORK.ALL24\_FU2.

The SAS System

NOTE: The PROCEDURE FREQ printed page 4.

NOTE: PROCEDURE FREQ used (Total process time):

```
real time      0.01 seconds
cpu time       0.00 seconds
```

```
84
85      ** use log-binomial for all continuous to get RR **;
86      * for replication of table 2 *;
87      %macro relrisks(covar);
88      proc genmod data=all124_fu2 descending;
89      model svr=&covar/dist = binomial link=log type3;
90      estimate "Beta &covar" &covar 1 -1/ exp;
91      run;
92      %mend;
93
94      * the warning " more coefficients specified than levels" pops up when an
95      estimate of the beta coefficient (RR) -- with contrast levels 1 -1 --
96      is requested for a trend test, this does not seem to affect estimates *;
97      proc printto
98      print='Z:\05_Users\Sylvia\Virahep-C\main_study\vhepc_svr.out' new;
99      title replication of selected results in table 3: SVR<=>variables of interest;
100     %relrisks(racew);
```

NOTE: PROCEDURE PRINTTO used (Total process time):

```
real time      0.15 seconds
cpu time       0.00 seconds
```

```
MPRINT(RELRISKS):  proc genmod data=all124_fu2 descending;
MPRINT(RELRISKS):  model svr=racew/dist = binomial link=log type3;
MPRINT(RELRISKS):  estimate "Beta racew" racew 1 -1/ exp;
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect RACEW. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 5-6.

NOTE: PROCEDURE GENMOD used (Total process time):

```
real time      0.03 seconds
cpu time       0.03 seconds
```

```
101     %relrisks(male);
MPRINT(RELRISKS):  proc genmod data=all124_fu2 descending;
MPRINT(RELRISKS):  model svr=male/dist = binomial link=log type3;
MPRINT(RELRISKS):  estimate "Beta male" male 1 -1/ exp;
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

The SAS System

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect male. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 7-8.

NOTE: PROCEDURE GENMOD used (Total process time):

real time	0.03 seconds
cpu time	0.03 seconds

102           %relrisks(age\_5);

```
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):  model svr=age_5/dist = binomial link=log type3;
MPRINT(RELRISKS):  estimate "Beta age_5" age_5 1 -1/ exp;
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect age\_5. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 9-10.

NOTE: PROCEDURE GENMOD used (Total process time):

real time	0.03 seconds
cpu time	0.01 seconds

103           %relrisks(hsorless);

```
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):  model svr=hsorless/dist = binomial link=log type3;
MPRINT(RELRISKS):  estimate "Beta hsorless" hsorless 1 -1/ exp;
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect hsorless. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 11-12.

NOTE: PROCEDURE GENMOD used (Total process time):

real time	0.01 seconds
cpu time	0.01 seconds

104           %relrisks(wgtk\_5);

```
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):  model svr=wgtk_5/dist = binomial link=log type3;
MPRINT(RELRISKS):  estimate "Beta wgtk_5" wgtk_5 1 -1/ exp;
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect wgtk\_5. Some coefficients will be

The SAS System

ignored.

NOTE: The PROCEDURE GENMOD printed pages 13-14.

NOTE: PROCEDURE GENMOD used (Total process time):

real time	0.01 seconds
cpu time	0.01 seconds

105           %relrisks(bmi);

```
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):  model svr=bmi/dist = binomial link=log type3;
MPRINT(RELRISKS):  estimate "Beta bmi" bmi 1 -1/ exp;
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect bmi. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 15-16.

NOTE: PROCEDURE GENMOD used (Total process time):

real time	0.01 seconds
cpu time	0.01 seconds

106           %relrisks(mxdiab);

```
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):  model svr=mxdiab/dist = binomial link=log type3;
MPRINT(RELRISKS):  estimate "Beta mxdiab" mxdiab 1 -1/ exp;
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect MXDIAB. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 17-18.

NOTE: PROCEDURE GENMOD used (Total process time):

real time	0.01 seconds
cpu time	0.01 seconds

107           %relrisks(mxbp);

```
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):  model svr=mxbp/dist = binomial link=log type3;
MPRINT(RELRISKS):  estimate "Beta mxbp" mxbp 1 -1/ exp;
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect MXBP. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 19-20.

The SAS System

NOTE: PROCEDURE GENMOD used (Total process time):  
real time 0.03 seconds  
cpu time 0.01 seconds

```
108      %relrisks(currentsmk);  
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;  
MPRINT(RELRISKS):  model svr=currentsmk/dist = binomial link=log type3;  
MPRINT(RELRISKS):  estimate "Beta currentsmk" currentsmk 1 -1/ exp;  
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.  
NOTE: Algorithm converged.  
NOTE: The scale parameter was held fixed.  
WARNING: More coefficients than levels specified for effect currentsmk. Some coefficients will be ignored.  
NOTE: The PROCEDURE GENMOD printed pages 21-22.  
NOTE: PROCEDURE GENMOD used (Total process time):  
real time 0.01 seconds  
cpu time 0.01 seconds

```
109      %relrisks(alt_100);  
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;  
MPRINT(RELRISKS):  model svr=alt_100/dist = binomial link=log type3;  
MPRINT(RELRISKS):  estimate "Beta alt_100" alt_100 1 -1/ exp;  
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.  
NOTE: Algorithm converged.  
NOTE: The scale parameter was held fixed.  
WARNING: More coefficients than levels specified for effect alt\_100. Some coefficients will be ignored.  
NOTE: The PROCEDURE GENMOD printed pages 23-24.  
NOTE: PROCEDURE GENMOD used (Total process time):  
real time 0.03 seconds  
cpu time 0.01 seconds

```
110      %relrisks(ast_100);  
MPRINT(RELRISKS):  proc genmod data=all24_fu2 descending;  
MPRINT(RELRISKS):  model svr=ast_100/dist = binomial link=log type3;  
MPRINT(RELRISKS):  estimate "Beta ast_100" ast_100 1 -1/ exp;  
MPRINT(RELRISKS):  run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.  
NOTE: Algorithm converged.  
NOTE: The scale parameter was held fixed.  
WARNING: More coefficients than levels specified for effect ast\_100. Some coefficients will be ignored.  
NOTE: The PROCEDURE GENMOD printed pages 25-26.  
NOTE: PROCEDURE GENMOD used (Total process time):  
real time 0.01 seconds

The SAS System

cpu time                    0.01 seconds

```
111            %relrisks(hgb);
MPRINT(RELRISKS):    proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):    model svr=hgb/dist = binomial link=log type3;
MPRINT(RELRISKS):    estimate "Beta hgb" hgb 1 -1/ exp;
MPRINT(RELRISKS):    run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect HGB. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 27-28.

NOTE: PROCEDURE GENMOD used (Total process time):

```
real time                0.01 seconds
cpu time                 0.01 seconds
```

```
112            %relrisks(wbc);
MPRINT(RELRISKS):    proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):    model svr=wbc/dist = binomial link=log type3;
MPRINT(RELRISKS):    estimate "Beta wbc" wbc 1 -1/ exp;
MPRINT(RELRISKS):    run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect WBC. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 29-30.

NOTE: PROCEDURE GENMOD used (Total process time):

```
real time                0.03 seconds
cpu time                 0.03 seconds
```

```
113            %relrisks(blog10vload);
MPRINT(RELRISKS):    proc genmod data=all24_fu2 descending;
MPRINT(RELRISKS):    model svr=blog10vload/dist = binomial link=log type3;
MPRINT(RELRISKS):    estimate "Beta blog10vload" blog10vload 1 -1/ exp;
MPRINT(RELRISKS):    run;
```

NOTE: PROC GENMOD is modeling the probability that svr='1'.

NOTE: Algorithm converged.

NOTE: The scale parameter was held fixed.

WARNING: More coefficients than levels specified for effect blog10vload. Some coefficients will be ignored.

NOTE: The PROCEDURE GENMOD printed pages 31-32.

NOTE: PROCEDURE GENMOD used (Total process time):

```
real time                0.01 seconds
cpu time                 0.01 seconds
```



The SAS System

```
114      proc printto; run;
```

NOTE: PROCEDURE PRINTTO used (Total process time):

real time	0.07 seconds
cpu time	0.00 seconds

NOTE: SAS Institute Inc., SAS Campus Drive, Cary, NC USA 27513-2414

NOTE: The SAS System used:

real time	21.46 seconds
cpu time	0.93 seconds

# **Attachment 4**

**SAS 9.1 Output for programming code submitted  
for the replication of results in Table 1  
“Baseline Characteristics of Virahep-C Participants”  
Conjeevaram et.al. 2006**

table 1: analysis of baseline factors

The FREQ Procedure

Table of RACEW by RACEB

RACEW(White or Caucasian)		RACEB(Black or African American)		
Frequency				
Percent				
Row Pct				
Col Pct	No	Yes		Total
No	0	196		196
	0.00	48.88		48.88
	0.00	100.00		
	0.00	100.00		
Yes	205	0		205
	51.12	0.00		51.12
	100.00	0.00		
	100.00	0.00		
Total	205	196		401
	51.12	48.88		100.00

table 1: analysis of baseline factors

The FREQ Procedure

Table of male by RACEW

male	RACEW(White or Caucasian)		Total
	No	Yes	
Frequency			
Percent			
Row Pct			
Col Pct			
0	69	71	140
	17.21	17.71	34.91
	49.29	50.71	
	35.20	34.63	
1	127	134	261
	31.67	33.42	65.09
	48.66	51.34	
	64.80	65.37	
Total	196	205	401
	48.88	51.12	100.00

Statistics for Table of male by RACEW

Statistic	DF	Value	Prob
Chi-Square	1	0.0143	0.9047
Likelihood Ratio Chi-Square	1	0.0143	0.9047
Continuity Adj. Chi-Square	1	0.0002	0.9881
Mantel-Haenszel Chi-Square	1	0.0143	0.9049
Phi Coefficient		0.0060	
Contingency Coefficient		0.0060	
Cramer's V		0.0060	

Fisher's Exact Test

Cell (1,1) Frequency (F)	69
Left-sided Pr <= F	0.5889
Right-sided Pr >= F	0.4940
Table Probability (P)	0.0828
Two-sided Pr <= P	0.9169

Sample Size = 401

table 1: analysis of baseline factors

The FREQ Procedure

Table of hsorless by RACEW

hsorless      RACEW(White or Caucasian)

Frequency			
Percent			
Row Pct			
Col Pct	No	Yes	Total
0	104	132	236
	26.33	33.42	59.75
	44.07	55.93	
	54.17	65.02	
1	88	71	159
	22.28	17.97	40.25
	55.35	44.65	
	45.83	34.98	
Total	192	203	395
	48.61	51.39	100.00

Frequency Missing = 6

table 1: analysis of baseline factors

The FREQ Procedure

Statistics for Table of hsorless by RACEW

Statistic	DF	Value	Prob
Chi-Square	1	4.8371	0.0279
Likelihood Ratio Chi-Square	1	4.8446	0.0277
Continuity Adj. Chi-Square	1	4.3961	0.0360
Mantel-Haenszel Chi-Square	1	4.8248	0.0281
Phi Coefficient		-0.1107	
Contingency Coefficient		0.1100	
Cramer's V		-0.1107	

Fisher's Exact Test

Cell (1,1) Frequency (F)	104
Left-sided Pr <= F	0.0180
Right-sided Pr >= F	0.9894
Table Probability (P)	0.0073
Two-sided Pr <= P	0.0313

Effective Sample Size = 395  
 Frequency Missing = 6

Table of MXDIAB by RACEW

MXDIAB(Med history diabetes)		RACEW(White or Caucasian)		
Frequency	Percent	Row Pct	Col Pct	Total
			No	Yes
No	166	41.40	196	362
	45.86	54.14		90.27
	84.69	95.61		
Yes	30	7.48	9	39
	76.92	23.08		9.73
	15.31	4.39		
Total	196	48.88	205	401
			51.12	100.00

table 1: analysis of baseline factors

The FREQ Procedure

Statistics for Table of MXDIAB by RACEW

Statistic	DF	Value	Prob
Chi-Square	1	13.5987	0.0002
Likelihood Ratio Chi-Square	1	14.2166	0.0002
Continuity Adj. Chi-Square	1	12.3839	0.0004
Mantel-Haenszel Chi-Square	1	13.5648	0.0002
Phi Coefficient		-0.1842	
Contingency Coefficient		0.1811	
Cramer's V		-0.1842	

Fisher's Exact Test

Cell (1,1) Frequency (F)	166
Left-sided Pr <= F	1.694E-04
Right-sided Pr >= F	1.0000
Table Probability (P)	1.297E-04
Two-sided Pr <= P	2.969E-04

Sample Size = 401

Table of MXBP by RACEW

		RACEW(White or Caucasian)		
MXBP(Med hx hypertension)		No	Yes	Total
Frequency	Percent			
Row Pct	Col Pct			
No		111	162	273
		27.68	40.40	68.08
		40.66	59.34	
		56.63	79.02	
Yes		85	43	128
		21.20	10.72	31.92
		66.41	33.59	
		43.37	20.98	
Total		196	205	401
		48.88	51.12	100.00

table 1: analysis of baseline factors

The FREQ Procedure

Statistics for Table of MXBP by RACEW

Statistic	DF	Value	Prob
Chi-Square	1	23.1184	<.0001
Likelihood Ratio Chi-Square	1	23.4215	<.0001
Continuity Adj. Chi-Square	1	22.0995	<.0001
Mantel-Haenszel Chi-Square	1	23.0607	<.0001
Phi Coefficient		-0.2401	
Contingency Coefficient		0.2335	
Cramer's V		-0.2401	

Fisher's Exact Test

Cell (1,1) Frequency (F)	111
Left-sided Pr <= F	1.129E-06
Right-sided Pr >= F	1.0000
Table Probability (P)	7.536E-07
Two-sided Pr <= P	2.050E-06

Sample Size = 401

Table of currentsmk by RACEW

currentsmk RACEW(White or Caucasian)

Frequency Percent Row Pct Col Pct	No	Yes	Total
0	112 28.50 45.71 58.95	133 33.84 54.29 65.52	245 62.34
1	78 19.85 52.70 41.05	70 17.81 47.30 34.48	148 37.66
Total	190 48.35	203 51.65	393 100.00

Frequency Missing = 8



table 1: analysis of baseline factors

The FREQ Procedure

Statistics for Table of currentsmk by RACEW

Statistic	DF	Value	Prob
Chi-Square	1	1.8044	0.1792
Likelihood Ratio Chi-Square	1	1.8047	0.1791
Continuity Adj. Chi-Square	1	1.5354	0.2153
Mantel-Haenszel Chi-Square	1	1.7998	0.1797
Phi Coefficient		-0.0678	
Contingency Coefficient		0.0676	
Cramer's V		-0.0678	

Fisher's Exact Test

Cell (1,1) Frequency (F)	112
Left-sided Pr <= F	0.1076
Right-sided Pr >= F	0.9261
Table Probability (P)	0.0338
Two-sided Pr <= P	0.2113

Effective Sample Size = 393

Frequency Missing = 8

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: age  
 RACEW = No

Moments

N	196	Sum Weights	196
Mean	49.0673469	Sum Observations	9617.2
Std Deviation	7.19345537	Variance	51.7458001
Skewness	0.19652272	Kurtosis	0.98649779
Uncorrected SS	481980.92	Corrected SS	10090.431
Coeff Variation	14.6603715	Std Error Mean	0.51381824

Basic Statistical Measures

Location		Variability	
Mean	49.06735	Std Deviation	7.19346
Median	49.15000	Variance	51.74580
Mode	49.20000	Range	42.80000
		Interquartile Range	7.70000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----	
Student's t	t 95.49553	Pr >  t	<.0001
Sign	M 98	Pr >=  M	<.0001
Signed Rank	S 9653	Pr >=  S	<.0001

Quantiles (Definition 5)

Quantile	Estimate
10 0% Max	70.40
99%	69.50
95%	61.70
90%	57.90
75% Q3	53.00
50% Median	49.15
25% Q1	45.30
10%	39.80
5%	35.90
1%	31.50
0% Min	27.60

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
Variable: age  
RACEW = No

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
27.6	86	67.4	135
31.5	145	68.7	147
32.7	157	68.9	312
33.9	49	69.5	78
34.1	205	70.4	151

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: age  
 RACEW = Yes

Moments

N	205	Sum Weights	205
Mean	47.3253659	Sum Observations	9701.7
Std Deviation	8.50517377	Variance	72.3379809
Skewness	-0.3471691	Kurtosis	0.97855102
Uncorrected SS	473893.45	Corrected SS	14756.9481
Coeff Variation	17.9717021	Std Error Mean	0.5940271

Basic Statistical Measures

Location		Variability	
Mean	47.32537	Std Deviation	8.50517
Median	48.20000	Variance	72.33798
Mode	56.70000	Range	48.20000
		Interquartile Range	9.50000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 79.6687	Pr >  t  <.0001
Sign	M 102.5	Pr >=  M  <.0001
Signed Rank	S 10557.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	70.7
99%	69.6
95%	59.2
90%	56.7
75% Q3	52.4
50% Median	48.2
25% Q1	42.9
10%	37.3
5%	31.8
1%	24.1
0% Min	22.5

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
Variable: age  
RACEW = Yes

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
22.5	369	64.3	111
23.1	367	68.6	196
24.1	164	69.6	113
24.4	326	70.4	234
25.4	56	70.7	21

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: wgtkg  
 RACEW = No

Moments

N	193	Sum Weights	193
Mean	91.0174282	Sum Observations	17566.3636
Std Deviation	19.628771	Variance	385.28865
Skewness	0.83374019	Kurtosis	0.84820102
Uncorrected SS	1672820.66	Corrected SS	73975.4207
Coeff Variation	21.5659477	Std Error Mean	1.41290985

Basic Statistical Measures

Location		Variability	
Mean	91.01743	Std Deviation	19.62877
Median	87.27273	Variance	385.28865
Mode	74.54545	Range	102.27273
		Interquartile Range	22.72727

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----	
Student's t	t 64.41843	Pr >  t	<.0001
Sign	M 96.5	Pr >=  M	<.0001
Si gned Rank	S 9360.5	Pr >=  S	<.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	157.2727
99%	156.8182
95%	133.6364
90%	114.5455
75% Q3	100.9091
50% Median	87.2727
25% Q1	78.1818
10%	70.0000
5%	62.7273
1%	55.9091
0% Min	55.0000

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: wgtkg  
 RACEW = No

Extreme Observations

-----Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
55.0000	49	138.182	341
55.9091	392	139.091	368
55.9091	315	148.182	82
57.2727	33	156.818	18
59.0909	172	157.273	202

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	3	1.53	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: wgtkg  
 RACEW = Yes

Moments

N	205	Sum Weights	205
Mean	84.3104213	Sum Observations	17283.6364
Std Deviation	17.7016357	Variance	313.347908
Skewness	0.48340341	Kurtosis	0.22263762
Uncorrected SS	1521113.64	Corrected SS	63922.9732
Coeff Variation	20.9957861	Std Error Mean	1.23633587

Basic Statistical Measures

Location		Variability	
Mean	84.31042	Std Deviation	17.70164
Median	82.27273	Variance	313.34791
Mode	72.72727	Range	97.72727
		Interquartile Range	23.18182

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----	
Student's t	t 68.19378	Pr >  t	<.0001
Sign	M 102.5	Pr >=  M	<.0001
Signed Rank	S 10557.5	Pr >=  S	<.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	148.6364
99%	126.8182
95%	115.9091
90%	106.8182
75% Q3	95.9091
50% Median	82.2727
25% Q1	72.7273
10%	60.4545
5%	56.3636
1%	52.2727
0% Min	50.9091



table 1: analysis of baseline factors

The UNIVARIATE Procedure  
Variable: wgtkg  
RACEW = Yes

Extreme Observations

-----Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
50.9091	70	125.000	12
52.2727	348	125.000	271
52.2727	23	126.818	388
53.1818	190	127.273	154
53.6364	313	148.636	239

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: bmi  
 RACEW = No

Moments

N	191	Sum Weights	191
Mean	30.6467432	Sum Observations	5853.52795
Std Deviation	6.27370547	Variance	39.3593803
Skewness	0.99454186	Kurtosis	1.36646596
Uncorrected SS	186869.85	Corrected SS	7478.28226
Coeff Variation	20.4710348	Std Error Mean	0.4539494

Basic Statistical Measures

Location		Variability	
Mean	30.64674	Std Deviation	6.27371
Median	29.49960	Variance	39.35938
Mode	22.28403	Range	36.69399
		Interquartile Range	7.85278

NOTE: The mode displayed is the smallest of 4 modes with a count of 2.

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 67.51136	Pr >  t  <.0001
Sign	M 95.5	Pr >=  M  <.0001
Signed Rank	S 9168	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	56.0709
99%	49.7853
95%	41.2045
90%	38.8627
75% Q3	34.1851
50% Median	29.4996
25% Q1	26.3323
10%	23.6648
5%	22.2322
1%	19.9680
0% Min	19.3769

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: bmi  
 RACEW = No

Extreme Observations

-----Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
19.3769	81	47.5516	18
19.9680	377	48.3796	202
21.0914	206	48.5581	105
21.3410	172	49.7853	341
21.6010	322	56.0709	368

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	5	2.55	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: bmi  
 RACEW = Yes

Moments

N	203	Sum Weights	203
Mean	28.4650559	Sum Observations	5778.40635
Std Deviation	5.64308585	Variance	31.8444179
Skewness	1.13609849	Kurtosis	2.24236009
Uncorrected SS	170915.232	Corrected SS	6432.57241
Coeff Variation	19.8246083	Std Error Mean	0.39606698

Basic Statistical Measures

Location		Variability	
Mean	28.46506	Std Deviation	5.64309
Median	27.59877	Variance	31.84442
Mode	29.08367	Range	34.27125
		Interquartile Range	7.12627

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----	
Student's t	t 71.8693	Pr >  t	<.0001
Sign	M 101.5	Pr >=  M	<.0001
Signed Rank	S 10353	Pr >=  S	<.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	53.2041
99%	45.8581
95%	37.8656
90%	35.4053
75% Q3	31.5395
50% Median	27.5988
25% Q1	24.4132
10%	21.8951
5%	21.0316
1%	19.4572
0% Min	18.9328

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: bmi  
 RACEW = Yes

Extreme Observations

-----Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
18.9328	190	44.6683	42
19.0708	103	45.7229	239
19.4572	168	45.8581	12
19.9037	237	47.8252	129
20.1880	70	53.2041	329

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	2	0.98	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: ALT (ALT result lab)  
 RACEW = No

Moments

N	194	Sum Weights	194
Mean	71.0309278	Sum Observations	13780
Std Deviation	45.5106783	Variance	2071.22184
Skewness	2.37506199	Kurtosis	9.59007239
Uncorrected SS	1378552	Corrected SS	399745.814
Coeff Variation	64.071637	Std Error Mean	3.26747628

Basic Statistical Measures

Location		Variability	
Mean	71.03093	Std Deviation	45.51068
Median	59.00000	Variance	2071
Mode	40.00000	Range	347.00000
		Interquartile Range	50.00000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 21.73877	Pr >  t  <.0001
Sign	M 97	Pr >=  M  <.0001
Signed Rank	S 9457.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	363
99%	238
95%	146
90%	126
75% Q3	90
50% Median	59
25% Q1	40
10%	31
5%	24
1%	16
0% Min	16

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: ALT (ALT result lab)  
 RACEW = No

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
16	201	198	156
16	39	210	345
18	215	230	80
19	283	238	366
20	79	363	101

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	1	0.51	50.00
B	1	0.51	50.00
Total	2	1.02	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: ALT (ALT result lab)  
 RACEW = Yes

Moments

N	205	Sum Weights	205
Mean	107.517073	Sum Observations	22041
Std Deviation	90.6526226	Variance	8217.89799
Skewness	2.08974237	Kurtosis	5.02759921
Uncorrected SS	4046235	Corrected SS	1676451.19
Coeff Variation	84.3146302	Std Error Mean	6.3314538

Basic Statistical Measures

Location		Variability	
Mean	107.5171	Std Deviation	90.65262
Median	74.0000	Variance	8218
Mode	54.0000	Range	494.00000
		Interquartile Range	87.00000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 16.98142	Pr >  t  <.0001
Sign	M 102.5	Pr >=  M  <.0001
Signed Rank	S 10557.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	508
99%	478
95%	281
90%	221
75% Q3	138
50% Median	74
25% Q1	51
10%	36
5%	28
1%	21
0% Min	14



table 1: analysis of baseline factors

The UNIVARIATE Procedure  
Variable: ALT (ALT result lab)  
RACEW = Yes

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
14	263	409	238
20	129	428	299
21	70	478	302
23	281	505	35
23	164	508	378

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: AST (AST result lab)  
 RACEW = No

Moments

N	194	Sum Weights	194
Mean	59.0360825	Sum Observations	11453
Std Deviation	41.079775	Variance	1687.54791
Skewness	3.46092158	Kurtosis	18.1765964
Uncorrected SS	1001837	Corrected SS	325696.747
Coeff Variation	69.5841819	Std Error Mean	2.94935596

Basic Statistical Measures

Location		Variability	
Mean	59.03608	Std Deviation	41.07978
Median	51.00000	Variance	1688
Mode	24.00000	Range	345.00000
		Interquartile Range	36.00000

NOTE: The mode displayed is the smallest of 3 modes with a count of 6.

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 20.0166	Pr >  t  <.0001
Sign	M 97	Pr >=  M  <.0001
Signed Rank	S 9457.5	Pr >=  S  <.0001

Qu antiles (Definition 5)

Quantile	Estimate
100% Max	363
99%	234
95%	126
90%	95
75% Q3	69
50% Median	51
25% Q1	33
10%	25
5%	24
1%	19
0% Min	18

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: AST (AST result lab)  
 RACEW = No

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
18	39	195	197
19	283	203	80
20	195	208	360
21	277	234	345
23	398	363	101

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	1	0.51	50.00
B	1	0.51	50.00
Total	2	1.02	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: AST (AST result lab)  
 RACEW = Yes

Moments

N	205	Sum Weights	205
Mean	72.9609756	Sum Observations	14957
Std Deviation	59.382595	Variance	3526.29259
Skewness	2.66525749	Kurtosis	9.97105001
Uncorrected SS	1810641	Corrected SS	719363.688
Coeff Variation	81.3895298	Std Error Mean	4.14746034

Basic Statistical Measures

Location		Variability	
Mean	72.96098	Std Deviation	59.38259
Median	52.00000	Variance	3526
Mode	36.00000	Range	439.00000
		Interquartile Range	50.00000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----	
Student's t	t 17.59172	Pr >  t	<.0001
Sign	M 102.5	Pr >=  M	<.0001
Signed Rank	S 10557.5	Pr >=  S	<.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	455
99%	275
95%	207
90%	142
75% Q3	87
50% Median	52
25% Q1	37
10%	27
5%	24
1%	18
0% Min	16

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
Variable: AST (AST result lab)  
RACEW = Yes

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
16	70	263	378
17	251	269	238
18	263	275	68
18	129	283	192
20	177	455	326

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: ALB (Albumin result lab)  
 RACEW = No

Moments

N	139	Sum Weights	139
Mean	3.99208633	Sum Observations	554.9
Std Deviation	0.38861791	Variance	0.15102388
Skewness	-0.5865309	Kurtosis	2.12718791
Uncorrected SS	2236.05	Corrected SS	20.841295
Coeff Variation	9.73470695	Std Error Mean	0.03296214

Basic Statistical Measures

Location		Variability	
Mean	3.992086	Std Deviation	0.38862
Median	4.000000	Variance	0.15102
Mode	4.000000	Range	2.70000
		Interquartile Range	0.50000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----	
Student's t	t 121.1113	Pr >  t	<.0001
Sign	M 69.5	Pr >=  M	<.0001
Signed Rank	S 4865	Pr >=  S	<.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	5.0
99%	4.8
95%	4.6
90%	4.4
75% Q3	4.2
50% Median	4.0
25% Q1	3.7
10%	3.5
5%	3.4
1%	2.9
0% Min	2.3

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: ALB (Albumin result lab)  
 RACEW = No

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
2.3	83	4.7	77
2.9	340	4.7	81
3.1	396	4.7	180
3.1	314	4.8	291
3.4	394	5.0	182

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	1	0.51	1.75
B	56	28.57	98.25
Total	57	29.08	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: ALB (Albumin result lab)  
 RACEW = Yes

Moments

N	143	Sum Weights	143
Mean	4.17342657	Sum Observations	596.8
Std Deviation	0.32565234	Variance	0.10604944
Skewness	-0.18588	Kurtosis	-0.1270047
Uncorrected SS	2505.76	Corrected SS	15.059021
Coeff Variation	7.80299664	Std Error Mean	0.02723242

Basic Statistical Measures

Location		Variability	
Mean	4.173427	Std Deviation	0.32565
Median	4.200000	Variance	0.10605
Mode	4.100000	Range	1.70000
		Interquartile Range	0.40000

NOTE: The mode displayed is the smallest of 2 modes with a count of 19.

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 153.2522	Pr >  t  <.0001
Sign	M 71.5	Pr >=  M  <.0001
Signed Rank	S 5148	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	5.0
99%	4.9
95%	4.6
90%	4.6
75% Q3	4.4
50% Median	4.2
25% Q1	4.0
10%	3.8
5%	3.7
1%	3.3
0% Min	3.3



table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: ALB (Albumin result lab)  
 RACEW = Yes

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
3.3	303	4.7	388
3.3	142	4.8	114
3.5	168	4.8	347
3.5	159	4.9	335
3.5	129	5.0	331

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
B	62	30.24	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: TBILI (Total bilirubin lab result)  
 RACEW = No

Moments

N	194	Sum Weights	194
Mean	0.6314433	Sum Observations	122.5
Std Deviation	0.31042505	Variance	0.09636371
Skewness	1.72084376	Kurtosis	5.67232557
Uncorrected SS	95.95	Corrected SS	18.5981959
Coeff Variation	49.161191	Std Error Mean	0.02228722

Basic Statistical Measures

Location		Variability	
Mean	0.631443	Std Deviation	0.31043
Median	0.600000	Variance	0.09636
Mode	0.400000	Range	2.30000
		Interquartile Range	0.40000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 28.33208	Pr >  t  <.0001
Sign	M 97	Pr >=  M  <.0001
Signed Rank	S 9457.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	2.4
99%	1.7
95%	1.2
90%	0.9
75% Q3	0.8
50% Median	0.6
25% Q1	0.4
10%	0.3
5%	0.3
1%	0.2
0% Min	0.1

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: TBILI (Total bilirubin lab result)  
 RACEW = No

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
0.1	323	1.4	280
0.2	399	1.5	51
0.2	398	1.5	125
0.2	362	1.7	345
0.2	205	2.4	314

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	1	0.51	50.00
B	1	0.51	50.00
Total	2	1.02	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: TBILI (Total bilirubin lab result)  
 RACEW = Yes

Moments

N	204	Sum Weights	204
Mean	0.74264706	Sum Observations	151.5
Std Deviation	0.38146058	Variance	0.14551217
Skewness	2.27308677	Kurtosis	9.31999064
Uncorrected SS	142.05	Corrected SS	29.5389706
Coeff Variation	51.3649883	Std Error Mean	0.02670758

Basic Statistical Measures

Location		Variability	
Mean	0.742647	Std Deviation	0.38146
Median	0.700000	Variance	0.14551
Mode	0.700000	Range	2.80000
		Interquartile Range	0.40000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 27.8066	Pr >  t  <.0001
Sign	M 102	Pr >=  M  <.0001
Signed Rank	S 10455	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	2.9
99%	1.9
95%	1.4
90%	1.2
75% Q3	0.9
50% Median	0.7
25% Q1	0.5
10%	0.4
5%	0.3
1%	0.2
0% Min	0.1

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: TBILI (Total bilirubin lab result)  
 RACEW = Yes

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
0.1	210	1.7	66
0.2	348	1.9	32
0.2	320	1.9	378
0.2	306	2.9	68
0.2	303	2.9	395

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
B	1	0.49	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: HGB (Hemoglobin lab)  
 RACEW = No

Moments

N	193	Sum Weights	193
Mean	14.3165803	Sum Observations	2763.1
Std Deviation	1.31934118	Variance	1.74066116
Skewness	0.00938519	Kurtosis	0.32578536
Uncorrected SS	39892.35	Corrected SS	334.206943
Coeff Variation	9.21547713	Std Error Mean	0.09496826

Basic Statistical Measures

Location		Variability	
Mean	14.31658	Std Deviation	1.31934
Median	14.30000	Variance	1.74066
Mode	13.70000	Range	7.30000
		Interquartile Range	1.60000

NOTE: The mode displayed is the smallest of 2 modes with a count of 11.

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 150.7512	Pr >  t  <.0001
Sign	M 96.5	Pr >=  M  <.0001
Signed Rank	S 9360.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	18.0
99%	17.8
95%	16.5
90%	16.0
75% Q3	15.1
50% Median	14.3
25% Q1	13.5
10%	12.7
5%	11.9
1%	10.8
0% Min	10.7

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: HGB (Hemoglobin lab)  
 RACEW = No

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
10.7	83	17.1	393
10.8	340	17.2	2
11.3	195	17.6	246
11.4	205	17.8	145
11.6	197	18.0	182

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	1	0.51	33.33
B	2	1.02	66.67
Total	3	1.53	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: HGB (Hemoglobin lab)  
 RACEW = Yes

Moments

N	202	Sum Weights	202
Mean	14.9386139	Sum Observations	3017.6
Std Deviation	1.29967239	Variance	1.68914832
Skewness	-0.0400601	Kurtosis	-0.4356941
Uncorrected SS	45418.28	Corrected SS	339.518812
Coeff Variation	8.70008691	Std Error Mean	0.09144463

Basic Statistical Measures

Location		Variability	
Mean	14.93861	Std Deviation	1.29967
Median	15.05000	Variance	1.68915
Mode	15.50000	Range	5.90000
		Interquartile Range	2.00000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 163.3624	Pr >  t  <.0001
Sign	M 101	Pr >=  M  <.0001
Signed Rank	S 10251.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	17.70
99%	17.60
95%	17.20
90%	16.60
75% Q3	15.90
50% Median	15.05
25% Q1	13.90
10%	13.30
5%	12.80
1%	11.90
0% Min	11.80



table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: HGB (Hemoglobin lab)  
 RACEW = Yes

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
11.8	303	17.5	311
11.9	198	17.5	387
11.9	168	17.6	335
12.1	113	17.7	124
12.4	329	17.7	236

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
B	2	0.98	66.67
F	1	0.49	33.33
Total	3	1.46	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: WBC (White blood cells lab)  
 RACEW = No

Moments

N	193	Sum Weights	193
Mean	6.13782383	Sum Observations	1184.6
Std Deviation	2.09790804	Variance	4.40121816
Skewness	0.79840598	Kurtosis	0.1966282
Uncorrected SS	8115.9	Corrected SS	845.033886
Coeff Variation	34.1799977	Std Error Mean	0.15101073

Basic Statistical Measures

Location		Variability	
Mean	6.137824	Std Deviation	2.09791
Median	5.800000	Variance	4.40122
Mode	4.800000	Range	10.00000
		Interquartile Range	2.70000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 40.64495	Pr >  t  <.0001
Sign	M 96.5	Pr >=  M  <.0001
Signed Rank	S 9360.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	12.7
99%	12.1
95%	10.5
90%	9.4
75% Q3	7.4
50% Median	5.8
25% Q1	4.7
10%	3.7
5%	3.3
1%	2.7
0% Min	2.7

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: WBC (White blood cells lab)  
 RACEW = No

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
2.7	314	11.0	141
2.7	293	11.3	80
2.7	206	11.3	183
2.8	349	12.1	362
2.9	280	12.7	96

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	1	0.51	33.33
B	2	1.02	66.67
Total	3	1.53	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: WBC (White blood cells lab)  
 RACEW = Yes

Moments

N	202	Sum Weights	202
Mean	6.41237624	Sum Observations	1295.3
Std Deviation	2.00784414	Variance	4.03143811
Skewness	1.22975499	Kurtosis	2.42528399
Uncorrected SS	9116.27	Corrected SS	810.319059
Coeff Variation	31.312014	Std Error Mean	0.14127142

Basic Statistical Measures

Location		Variability	
Mean	6.412376	Std Deviation	2.00784
Median	6.200000	Variance	4.03144
Mode	4.900000	Range	12.50000
		Interquartile Range	2.50000

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 45.39047	Pr >  t  <.0001
Sign	M 101	Pr >=  M  <.0001
Signed Rank	S 10251.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	14.5
99%	13.6
95%	10.2
90%	8.7
75% Q3	7.4
50% Median	6.2
25% Q1	4.9
10%	4.4
5%	3.9
1%	3.3
0% Min	2.0

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: WBC (White blood cells lab)  
 RACEW = Yes

Extreme Observations

----Lowest----		----Highest---	
Value	Obs	Value	Obs
2.0	149	11.9	200
3.0	88	12.5	194
3.3	119	13.6	306
3.5	208	13.9	387
3.6	237	14.5	342

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
B	2	0.98	66.67
F	1	0.49	33.33
Total	3	1.46	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: log10vload  
 RACEW = No

Moments

N	194	Sum Weights	194
Mean	6.23473169	Sum Observations	1209.53795
Std Deviation	0.66978945	Variance	0.44861791
Skewness	-0.7136958	Kurtosis	0.84701483
Uncorrected SS	7627.72783	Corrected SS	86.5832567
Coeff Variation	10.7428753	Std Error Mean	0.04808808

Basic Statistical Measures

Location		Variability	
Mean	6.234732	Std Deviation	0.66979
Median	6.393574	Variance	0.44862
Mode	6.563481	Range	4.23946
		Interquartile Range	1.07918

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 129.6523	Pr >  t  <.0001
Sign	M 97	Pr >=  M  <.0001
Signed Rank	S 9457.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	7.48001
99%	7.38917
95%	7.15229
90%	7.01284
75% Q3	6.72754
50% Median	6.39357
25% Q1	5.64836
10%	5.32428
5%	5.11394
1%	4.76790
0% Min	3.24055

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: log10vload  
 RACEW = No

Extreme Observations

-----Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
3.24055	229	7.26717	332
4.76790	172	7.29003	257
4.85552	86	7.34830	272
4.88480	52	7.38917	397
4.98722	375	7.48001	144

Missing Values

Missing Value	Count	-----Percent Of-----	
		All Obs	Missing Obs
.	2	1.02	100.00

table 1: analysis of baseline factors

The UNIVARIATE Procedure  
 Variable: log10vload  
 RACEW = Yes

Moments

N	205	Sum Weights	205
Mean	6.29757466	Sum Observations	1291.00281
Std Deviation	0.75959726	Variance	0.576988
Skewness	-1.1676952	Kurtosis	1.63028543
Uncorrected SS	8247.89211	Corrected SS	117.705552
Coeff Variation	12.0617428	Std Error Mean	0.05305257

Basic Statistical Measures

Location		Variability	
Mean	6.297575	Std Deviation	0.75960
Median	6.542825	Variance	0.57699
Mode	5.432969	Range	4.53630
		Interquartile Range	1.14972

NOTE: The mode displayed is the smallest of 12 modes with a count of 2.

Tests for Location: Mu0=0

Test	-Statistic-	-----p Value-----
Student's t	t 118.7044	Pr >  t  <.0001
Sign	M 102.5	Pr >=  M  <.0001
Signed Rank	S 10557.5	Pr >=  S  <.0001

Quantiles (Definition 5)

Quantile	Estimate
100% Max	7.67302
99%	7.46240
95%	7.19312
90%	7.07188
75% Q3	6.80003
50% Median	6.54283
25% Q1	5.65031
10%	5.32222
5%	4.99167
1%	3.95617
0% Min	3.13672



table 1: analysis of baseline factors

The UNIVARIATE Procedure  
Variable: log10vload  
RACEW = Yes

Extreme Observations

-----Lowest-----		-----Highest-----	
Value	Obs	Value	Obs
3.13672	163	7.32015	369
3.58771	308	7.35984	278
3.95617	186	7.46240	167
4.10380	129	7.56703	347
4.35793	164	7.67302	21

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable age  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	205	39091.0	41205.0	1160.15899	190.687805
No	196	41510.0	39396.0	1160.15899	211.785714

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 41510.0000

Normal Approximation

Z 1.8217  
One-Sided Pr > Z 0.0342  
Two-Sided Pr > |Z| 0.0685

t Approximation

One-Sided Pr > Z 0.0346  
Two-Sided Pr > |Z| 0.0692

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 3.3203  
DF 1  
Pr > Chi-Square 0.0684

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable wgtkg  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	205	37201.0	40897.50	1146.89657	181.468293
No	193	42200.0	38503.50	1146.89657	218.652850

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 42200.0000

Normal Approximation

Z 3.2226

One-Sided Pr > Z 0.0006

Two-Sided Pr > |Z| 0.0013

t Approximation

One-Sided Pr > Z 0.0007

Two-Sided Pr > |Z| 0.0014

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 10.3880

DF 1

Pr > Chi-Square 0.0013

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable bmi  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	203	35995.0	40092.50	1129.72327	177.315271
No	191	41820.0	37722.50	1129.72327	218.952880

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 41820.0000

Normal Approximation

Z 3.6266

One-Sided Pr > Z 0.0001

Two-Sided Pr > |Z| 0.0003

t Approximation

One-Sided Pr > Z 0.0002

Two-Sided Pr > |Z| 0.0003

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 13.1551

DF 1

Pr > Chi-Square 0.0003

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable ALT  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	205	45846.50	41000.0	1151.28180	223.641463
No	194	33953.50	38800.0	1151.28180	175.018041

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 33953.5000

Normal Approximation

Z -4.2092  
 One-Sided Pr < Z <.0001  
 Two-Sided Pr > |Z| <.0001

t Approximation

One-Sided Pr < Z <.0001  
 Two-Sided Pr > |Z| <.0001

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 17.7212  
 DF 1  
 Pr > Chi-Square <.0001

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable AST  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	205	43197.50	41000.0	1151.25407	210.719512
No	194	36602.50	38800.0	1151.25407	188.672680

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 36602.5000

Normal Approximation

Z -1.9084  
 One-Sided Pr < Z 0.0282  
 Two-Sided Pr > |Z| 0.0563

t Approximation

One-Sided Pr < Z 0.0285  
 Two-Sided Pr > |Z| 0.0571

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 3.6435  
 DF 1  
 Pr > Chi-Square 0.0563

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable ALB  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	143	23040.50	20234.50	681.850460	161.122378
No	139	16862.50	19668.50	681.850460	121.312950

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 16862.5000

Normal Approximation

Z -4.1145  
One-Sided Pr < Z <.0001  
Two-Sided Pr > |Z| <.0001

t Approximation

One-Sided Pr < Z <.0001  
Two-Sided Pr > |Z| <.0001

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 16.9355  
DF 1  
Pr > Chi-Square <.0001

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable TBILI  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	204	44525.50	40698.0	1139.24138	218.262255
No	194	34875.50	38703.0	1139.24138	179.770619

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 34875.5000

Normal Approximation

Z -3.3593  
One-Sided Pr < Z 0.0004  
Two-Sided Pr > |Z| 0.0008

t Approximation

One-Sided Pr < Z 0.0004  
Two-Sided Pr > |Z| 0.0009

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 11.2875  
DF 1  
Pr > Chi-Square 0.0008



table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable HGB  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	202	45168.0	39996.0	1133.85268	223.603960
No	193	33042.0	38214.0	1133.85268	171.202073

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 33042.0000

Normal Approximation

Z -4.5610

One-Sided Pr < Z <.0001

Two-Sided Pr > |Z| <.0001

t Approximation

One-Sided Pr < Z <.0001

Two-Sided Pr > |Z| <.0001

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 20.8067

DF 1

Pr > Chi-Square <.0001

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable WBC  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	202	41913.50	39996.0	1134.03057	207.492574
No	193	36296.50	38214.0	1134.03057	188.064767

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 36296.5000

Normal Approximation

Z -1.6904  
 One-Sided Pr < Z 0.0455  
 Two-Sided Pr > |Z| 0.0909

t Approximation

One-Sided Pr < Z 0.0459  
 Two-Sided Pr > |Z| 0.0917

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 2.8590  
 DF 1  
 Pr > Chi-Square 0.0909

table 1: analysis of baseline factors

The NPAR1WAY Procedure

Wilcoxon Scores (Rank Sums) for Variable log10vload  
Classified by Variable RACEW

RACEW	N	Sum of Scores	Expected Under H0	Std Dev Under H0	Mean Score
Yes	205	42924.0	41000.0	1151.37262	209.385366
No	194	36876.0	38800.0	1151.37262	190.082474

Average scores were used for ties.

Wilcoxon Two-Sample Test

Statistic 36876.0000

Normal Approximation

Z -1.6706

One-Sided Pr < Z 0.0474

Two-Sided Pr > |Z| 0.0948

t Approximation

One-Sided Pr < Z 0.0478

Two-Sided Pr > |Z| 0.0956

Z includes a continuity correction of 0.5.

Kruskal-Wallis Test

Chi-Square 2.7924

DF 1

Pr > Chi-Square 0.0947

# **Attachment 5**

**SAS 9.1 Output for programming code submitted  
for the replication of selected results in Table 3  
“Relationship Between SVR and Each Variable of Interest  
in Univariable and Multivariable Analysis”  
Conjeevaram et.al. 2006**

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	401
Number of Events	160
Number of Trials	401

Response Profile

Ordered Value	svr	Total Frequency
1	1	160
2	0	241

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	RACEW

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	399	512.5915	1.2847
Scaled Deviance	399	512.5915	1.2847
Pearson Chi-Square	399	401.0000	1.0050
Scaled Pearson X2	399	401.0000	1.0050
Log Likelihood		-256.2958	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-1.3078	0.1173	-1.5378	-1.0779	124.25	<.0001
RACEW	1	0.6576	0.1350	0.3930	0.9223	23.72	<.0001
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
RACEW	1	26.84	<.0001

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi-Square	Pr > ChiSq
Beta racew	0.6576	0.1350	0.05	0.3930 0.9223	23.72	<.0001
Exp(Beta racew)	1.9302	0.2606	0.05	1.4814 2.5151		

replication of selected results in table 3: SVR=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	401
Number of Events	160
Number of Trials	401

Response Profile

Ordered Value	svr	Total Frequency
1	1	160
2	0	241

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	male

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	399	533.7882	1.3378
Scaled Deviance	399	533.7882	1.3378
Pearson Chi-Square	399	401.0000	1.0050
Scaled Pearson X2	399	401.0000	1.0050
Log Likelihood		-266.8941	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-0.7369	0.0882	-0.9099	-0.5640	69.78	<.0001
male	1	-0.2950	0.1213	-0.5326	-0.0573	5.92	0.0150
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
male	1	5.64	0.0175

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi-Square	Pr > ChiSq
Beta male	-0.2950	0.1213	0.05	-0.5326 -0.0573	5.92	0.0150
Exp(Beta male)	0.7446	0.0903	0.05	0.5871 0.9443		



replication of selected results in table 3: SVR=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	401
Number of Events	160
Number of Trials	401

Response Profile

Ordered Value	svr	Total Frequency
1	1	160
2	0	241

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	age_5

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	399	538.0465	1.3485
Scaled Deviance	399	538.0465	1.3485
Pearson Chi-Square	399	400.9357	1.0049
Scaled Pearson X2	399	400.9357	1.0049
Log Likelihood		-269.0233	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-0.4962	0.3525	-1.1872	0.1947	1.98	0.1593
age_5	1	-0.0441	0.0368	-0.1162	0.0280	1.44	0.2305
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
age_5	1	1.38	0.2396

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi-Square	Pr > ChiSq
Beta age_5	-0.0441	0.0368	0.05	-0.1162 0.0280	1.44	0.2305
Exp(Beta age_5)	0.9568	0.0352	0.05	0.8903 1.0284		

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	395
Number of Events	157
Number of Trials	395
Missing Values	6

Response Profile

Ordered Value	svr	Total Frequency
1	1	157
2	0	238

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	hsorless

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	393	524.2455	1.3340
Scaled Deviance	393	524.2455	1.3340
Pearson Chi-Square	393	395.0000	1.0051
Scaled Pearson X2	393	395.0000	1.0051
Log Likelihood		-262.1228	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-0.8004	0.0721	-0.9417	-0.6591	123.28	<.0001
hsorless	1	-0.3367	0.1361	-0.6034	-0.0700	6.12	0.0133
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
hsorless	1	6.61	0.0101

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi - Square	Pr > ChiSq
Beta hsorless	-0.3367	0.1361	0.05	-0.6034 -0.0700	6.12	0.0133
Exp(Beta hsorless)	0.7141	0.0972	0.05	0.5470 0.9324		

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	398
Number of Events	158
Number of Trials	398
Missing Values	3

Response Profile

Ordered Value	svr	Total Frequency
1	1	158
2	0	240

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	wgtk_5

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	396	521.3397	1.3165
Scaled Deviance	396	521.3397	1.3165
Pearson Chi-Square	396	398.2294	1.0056
Scaled Pearson X2	396	398.2294	1.0056
Log Likelihood		-260.6699	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	0.1589	0.2919	-0.4131	0.7309	0.30	0.5862
wgtk <sub>5</sub>	1	-0.0634	0.0177	-0.0980	-0.0287	12.87	0.0003
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
wgtk <sub>5</sub>	1	13.39	0.0003

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits		Chi - Square	Pr > ChiSq
Beta wgtk <sub>5</sub>	-0.0634	0.0177	0.05	-0.0980	-0.0287	12.87	0.0003
Exp(Beta wgtk <sub>5</sub> )	0.9386	0.0166	0.05	0.9066	0.9717		

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	394
Number of Events	155
Number of Trials	394
Missing Values	7

Response Profile

Ordered Value	svr	Total Frequency
1	1	155
2	0	239

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	bmi

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	392	523.8940	1.3365
Scaled Deviance	392	523.8940	1.3365
Pearson Chi-Square	392	394.7328	1.0070
Scaled Pearson X2	392	394.7328	1.0070
Log Likelihood		-261.9470	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-0.2558	0.3353	-0.9131	0.4014	0.58	0.4455
bmi	1	-0.0232	0.0116	-0.0460	-0.0005	4.00	0.0456
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
bmi	1	4.26	0.0390

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi - Square	Pr > ChiSq
Beta bmi	-0.0232	0.0116	0.05	-0.0460 -0.0005	4.00	0.0456
Exp(Beta bmi)	0.9770	0.0114	0.05	0.9550 0.9995		



replication of selected results in table 3: SVR=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	401
Number of Events	160
Number of Trials	401

Response Profile

Ordered Value	svr	Total Frequency
1	1	160
2	0	241

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	MXDIAB

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	399	532.0851	1.3335
Scaled Deviance	399	532.0851	1.3335
Pearson Chi-Square	399	401.0000	1.0050
Scaled Pearson X2	399	401.0000	1.0050
Log Likelihood		-266.0426	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-0.8678	0.0618	-0.9888	-0.7467	197.30	<.0001
MXDIAB	1	-0.7164	0.3212	-1.3459	-0.0868	4.97	0.0257
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
MXDIAB	1	7.34	0.0067

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi - Square	Pr >
Beta mxdiab	-0.7164	0.3212	0.05	-1.3459 -0.0868	4.97	
ChiSq						0.0257
exp(Beta mxdiab)	0.4885	0.1569	0.05	0.2603 0.9169		

replication of selected results in table 3: SVR=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	401
Number of Events	160
Number of Trials	401

Response Profile

Ordered Value	svr	Total Frequency
1	1	160
2	0	241

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	MXBP

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	399	534.4976	1.3396
Scaled Deviance	399	534.4976	1.3396
Pearson Chi-Square	399	401.0000	1.0050
Scaled Pearson X2	399	401.0000	1.0050
Log Likelihood		-267.2488	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-0.8303	0.0689	-0.9653	-0.6954	145.45	<.0001
MXBP	1	-0.3081	0.1460	-0.5943	-0.0219	4.45	0.0348
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
MXBP	1	4.93	0.0264

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits		Chi - Square	Pr > ChiSq
Beta mxbp	-0.3081	0.1460	0.05	-0.5943	-0.0219	4.45	0.0348
Exp(Beta mxbp)	0.7348	0.1073	0.05	0.5520	0.9783		

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	393
Number of Events	157
Number of Trials	393
Missing Values	8

Response Profile

Ordered Value	svr	Total Frequency
1	1	157
2	0	236

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	currentsmk

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	391	527.7539	1.3498
Scaled Deviance	391	527.7539	1.3498
Pearson Chi-Square	391	392.9999	1.0051
Scaled Pearson X2	391	392.9999	1.0051
Log Likelihood		-263.8770	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-0.9687	0.0817	-1.1287	-0.8086	140.65	<.0001
currentsmk	1	0.1303	0.1247	-0.1140	0.3747	1.09	0.2958
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi-Square	Pr > ChiSq
currentsmk	1	1.07	0.3008

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi-Square	Pr > ChiSq
Beta currentsmk	0.1303	0.1247	0.05	-0.1140 0.3747	1.09	0.2958
Exp(Beta currentsmk)	1.1392	0.1420	0.05	0.8923 1.4545		

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	399
Number of Events	160
Number of Trials	399
Missing Values	2

Response Profile

Ordered Value	svr	Total Frequency
1	1	160
2	0	239

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	alt_100

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	397	536.9490	1.3525
Scaled Deviance	397	536.9490	1.3525
Pearson Chi-Square	397	399.0127	1.0051
Scaled Pearson X2	397	399.0127	1.0051
Log Likelihood		-268.4745	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-0.9614	0.0942	-1.1461	-0.7768	104.13	<.0001
alt_100	1	0.0522	0.0753	-0.0954	0.1998	0.48	0.4881
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
alt_100	1	0.44	0.5086

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits		Chi - Square	Pr > ChiSq
Beta alt_100	0.0522	0.0753	0.05	-0.0954	0.1998	0.48	0.4881
Exp(Beta alt_100)	1.0536	0.0793	0.05	0.9090	1.2211		



replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	399
Number of Events	160
Number of Trials	399
Missing Values	2

Response Profile

Ordered Value	svr	Total Frequency
1	1	160
2	0	239

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	ast_100

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	397	533.3470	1.3434
Scaled Deviance	397	533.3470	1.3434
Pearson Chi-Square	397	399.0699	1.0052
Scaled Pearson X2	397	399.0699	1.0052
Log Likelihood		-266.6735	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald 95% Confidence Limits		Chi-Square	Pr > ChiSq
Intercept	1	-0.7342	0.1099	-0.9496	-0.5188	44.64	<.0001
ast_100	1	-0.2853	0.1588	-0.5966	0.0259	3.23	0.0724
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
ast_100	1	4.04	0.0445

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits		Chi - Square	Pr > ChiSq
Beta ast_100	-0.2853	0.1588	0.05	-0.5966	0.0259	3.23	0.0724
Exp(Beta ast_100)	0.7518	0.1194	0.05	0.5507	1.0263		

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	395
Number of Events	158
Number of Trials	395
Missing Values	6

Response Profile

Ordered Value	svr	Total Frequency
1	1	158
2	0	237

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	HGB

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	393	530.5994	1.3501
Scaled Deviance	393	530.5994	1.3501
Pearson Chi-Square	393	395.1132	1.0054
Scaled Pearson X2	393	395.1132	1.0054
Log Likelihood		-265.2997	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-0.1984	0.6885	-1.5479	1.1511	0.08	0.7732
HGB	1	-0.0492	0.0473	-0.1419	0.0435	1.08	0.2984
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
HGB	1	1.08	0.2987

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi - Square	Pr > ChiSq
Beta hgb	-0.0492	0.0473	0.05	-0.1419 0.0435	1.08	0.2984
Exp(Beta hgb)	0.9520	0.0450	0.05	0.8677 1.0445		

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	395
Number of Events	158
Number of Trials	395
Missing Values	6

Response Profile

Ordered Value	svr	Total Frequency
1	1	158
2	0	237

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	WBC

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	393	529.0558	1.3462
Scaled Deviance	393	529.0558	1.3462
Pearson Chi-Square	393	394.5044	1.0038
Scaled Pearson X2	393	394.5044	1.0038
Log Likelihood		-264.5279	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	-1.1977	0.1840	-1.5583	-0.8370	42.36	<.0001
WBC	1	0.0441	0.0260	-0.0069	0.0951	2.87	0.0903
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi-Square	Pr > ChiSq
WBC	1	2.62	0.1053

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi-Square	Pr > ChiSq
Beta wbc	0.0441	0.0260	0.05	-0.0069 0.0951	2.87	0.0903
Exp(Beta wbc)	1.0451	0.0272	0.05	0.9931 1.0997		

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Model Information

Data Set	WORK.ALL24_FU2
Distribution	Binomial
Link Function	Log
Dependent Variable	svr

Number of Observations Read	401
Number of Observations Used	399
Number of Events	160
Number of Trials	399
Missing Values	2

Response Profile

Ordered Value	svr	Total Frequency
1	1	160
2	0	239

PROC GENMOD is modeling the probability that svr='1'.

Parameter Information

Parameter	Effect
Prm1	Intercept
Prm2	blog10vload

Criteria For Assessing Goodness Of Fit

Criterion	DF	Value	Value/DF
Deviance	397	524.7746	1.3219
Scaled Deviance	397	524.7746	1.3219
Pearson Chi-Square	397	398.7280	1.0044
Scaled Pearson X2	397	398.7280	1.0044
Log Likelihood		-262.3873	

Algorithm converged.

replication of selected results in table 3: SVR<=>variables of interest

The GENMOD Procedure

Analysis Of Parameter Estimates

Parameter	DF	Estimate	Standard Error	Wald	95% Confidence Limits	Chi-Square	Pr > ChiSq
Intercept	1	0.6195	0.2814	0.0681	1.1709	4.85	0.0277
blog10vload	1	-0.2476	0.0480	-0.3416	-0.1536	26.64	<.0001
Scale	0	1.0000	0.0000	1.0000	1.0000		

NOTE: The scale parameter was held fixed.

LR Statistics For Type 3 Analysis

Source	DF	Chi - Square	Pr > ChiSq
blog10vload	1	12.61	0.0004

Contrast Estimate Results

Label	Estimate	Standard Error	Alpha	Confidence Limits	Chi - Square	Pr > ChiSq
Beta blog10vload	-0.2476	0.0480	0.05	-0.3416 -0.1536	26.64	<.0001
Exp(Beta blog10vload)	0.7807	0.0374	0.05	0.7106 0.8576		