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Environmental Monitoring
Systems Laboratory
P.O. Box 93478
Las Vegas NV 89193-3478

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Chromosomal Aberration Data Analysis and Interpretation System

User's Guide

USER'S GUIDE

CHROMOSOMAL ABERRATION DATA ANALYSIS AND INTERPRETATION SYSTEM

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Integrated Laboratory Systems
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Research Triangle Park, NC 27709

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Project Officer

Charles H. Nauman
Exposure Assessment Research Division
Environmental Monitoring Systems Laboratory
Las Vegas, Nevada 89193-3478

ENVIRONMENTAL MONITORING SYSTEMS LABORATORY
OFFICE OF RESEARCH AND DEVELOPMENT
U. S. ENVIRONMENTAL PROTECTION AGENCY
LAS VEGAS, NEVADA 89193-3478

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ABSTRACT

This user's manual provides guidance to researchers and the regulatory community for interacting with a data analysis and interpretation system, designated CA. CA is a data management and analysis system designed for chromosomal aberration and mitotic index data collected using in vivo test systems. The objective in developing this system has been to promote consistency and intercomparability of assay test results across laboratories, thus providing researchers and government decision makers with a means to assure comparable analyses of test data. The CA data analysis and interpretation system has been developed in consultation with a panel of biostatisticians and experts in the field of cytogenetics.

CONTENTS

Introduction

Structural chromosomal aberrations are broadly defined as alterations in chromosome morphology. These alterations are assessed usually in cells at metaphase, but certain kinds of chromosomal damage can be detected during anaphase (e.g., anaphase bridges) or at interphase (micronuclei). Most chromosomal aberrations are deleterious and result in cell death. However, some types (e.g., reciprocal translocations, small deletions, inversions) can lead to altered gene function(s) without an accompanying loss in cell viability. Alterations in gene function occurring as a result of interchanges between specific chromosome regions are correlated with the appearance of several different kinds of cancers[1], indicating the probable involvement of these events in carcinogenesis. Consistent with this relationship, chromosomal aberrations are induced by many known mutagens and carcinogens.[2] These findings make the analysis of chromosomal aberrations a useful indicator of genotoxic damage in proliferating cell systems.

CA is a data management and analysis system designed for chromosomal aberration and mitotic index data collected using in vivo test systems. The software consists of a set of routines for 1) entering, editing and storing experimental data and descriptive information; 2) generating statistics appropriate to the analysis of chromosomal aberrations and micronucleus index data; and 3) presenting the results of these statistics through graphs and tables. CA was developed in consultation with a panel of biostatisticians and experts in the field of cytogenetics (see Appendix 1).

This user's manual consists of two parts. The first describes the CA Installation program provided on the program disk. This description should be read carefully to ensure that installation is performed correctly. The second part describes

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[1]Schwab and Amler (1990) Genes, Chromosomes and Cancer, 1, 181.

[2]Preston, R.J., Au, W., Bender, M.A., Brewen, J.G., Carrano, A.V., Heddle, J.A., McFee, A.F., Wolff, S., and Wassom, J.S. (1983) Mutat. Res. 87:143-188.

how to use CA. The

description follows the organization of the program, describing the main menu first, followed by the individual routines corresponding to each of the menu entries.

Part 1: Installation

CA is intended to run on an IBM PC compatible with a hard disk under DOS. The hard disk is assumed to be the C drive. Throughout this manual, words bracketed by < and > signify single keystrokes of the named key.

CA is distributed on two disks. Disk 1 contains the program itself. Disk 2 contains the help files and sample data. Each disk contains an installation batch file as well. Installation is simple:

At the C:\ prompt, insert the distribution disk 1 in drive A and type

A:INSTALL1 <ENTER>

INSTALL1 will first create the directory C:\CA and will then copy the executable file CA.EXE into it. When this is done, you will be prompted to insert distribution disk 2 and type

A:INSTALL2 <ENTER>

INSTALL2 will create the C:\CA\HELP subdirectory and will then copy the help files into it.[3] The sample data can be copied to the CA directory by typing at the C:\ prompt

copy A:*.ILS C:\CA <ENTER>

To start CA, go to the CA directory by typing

CD\CA <ENTER>
CA <ENTER>

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[3]CA may be run from any directory or subdirectory. To install CA in another directory, 1) copy CA.EXE into the directory from which it is to be run, 2) make a subdirectory named HELP, and 3) copy the help files from the distribution diskette into the new HELP subdirectory.

The first command changes the directory, the second begins the program.

Initially, an introductory screen will appear noting the program's sponsor, authors and version number, and prompting for a user ID. If nothing appears on the screen, confirm 1) that the CA directory exists, and 2) that CA.EXE and the HELP subdirectory reside within it. If not, repeat the installation procedure. If the file structure appears correct but the program will not run, contact the Data Management Section at Integrated Laboratory Systems (919 - 544-4589) for assistance.

After the introductory screen appears and the user's ID has been entered, press any key to bring up the main menu (Fig. 1).

Part 2: Operation

About Menus and Forms

The main menu is a single selection menu. Select an item by using the arrow keys to move the highlight bar and then press <ENTER>. When a selection is made, the menu closes and the selected operation begins.

Some menus permit multiple selections. If multiple selections are permitted, <ENTER> will flag or unflag the highlighted item but will not close the menu. Multiple-selection menus are closed with a special menu item or the ESCAPE <ESC> key.

The form screens are data entry devices. They consist of a set of (usually labelled) fields into which text may be entered. Selecting a field is much like selecting a menu item. To enter text into a field, move the cursor to the field using the arrow keys and type in the appropriate text.

Some screens are part menu and part form. Treat the menu portion as a multiple entry menu and the form portion as a text entry screen.

CA's Data Model

Each CA session maintains two distinct datasets. The first is a multi-page fixed form containing descriptive information relating to several aspects of the experiment. The second is a spreadsheet for the experimental data, where the rows represent observations and the columns represent fields. This spreadsheet has a number of fixed fields and a number of optional fields that may be selected to tailor a session to the nature of the experiment. Help screens are available within each menu selection through the F1 key.

Entering Data and Other Information

CA employs two line editors. The first is a very simple editor used for the spreadsheet (except for the remarks field)

and various parameter entry fields on some control screens. These are short fields and their values are simply replaced. Entering new text into these fields clears the field and the new text appears as entered. <BACKSPACE> removes characters in the order they were entered.

Longer fields like DOS path prompts, the fields comprising the experiment description section, and the remarks fields of the spreadsheet and the experiment description section employ a more complete line editor. The control keys supported are <INSERT>, <DELETE>, <BACKSPACE>, <HOME>, <END>, and the left and right arrow keys.

<INSERT> toggles between insert and overtype modes. In insert mode, new text shifts existing text to the right. In overtype mode, new text simply replaces the old.

<DELETE> removes the character under the cursor and shifts the remaining text to the left.

<BACKSPACE> is similar to DELETE except that it removes the character to the left of the cursor.

<HOME> moves the cursor to the beginning of the field.

<END> moves the cursor to the end of the field.

The left and right arrow keys move the cursor one character. If the cursor is positioned under the first character, the left arrow key will close the window and move to the field to the left. Similarly, if the cursor is positioned at the end of the text, the right arrow key will close the window and move to the field on the right.

Remarks fields are found at the bottom of each page of the experiment description forms and on the end of each row of the data entry spreadsheet. Moving the cursor into a remarks fields opens a broad single line window. If the field is not empty, the cursor moves to the end of the existing text. Any new text will

be appended. Moving out of the window[4] closes the window, displaying as much of the text as the standard form field width will allow. The hidden text is not lost and will become visible again when the window is reopened.

The Main Menu

All but one ('Leave CA') of the sixteen items of the main menu (Fig. 1) are grouped into six classes: Set Up, Data Entry, Disk I/O, Analysis, Utility, and Miscellaneous (Misc.)

0. Leave CA

This is a special item outside the six functional categories to be described. Selecting this item will first prompt for disposition of any unsaved changes and then return to DOS.

1. Set Up

The setup routines (Endpoints and Optional Fields) determine which of the non-default fields will appear on the spreadsheet. 'Endpoint' allows the selection of either or both the chromosomal aberration and the mitotic index endpoints. 'Optional Fields' provides a way to define up to fifteen additional data fields.

1.1 Select Endpoints

This routine consists of a single screen (Fig. 2A) presenting the two types of endpoints CA supports: Chromosomal Aberrations and Mitotic Index. You may select either or both. Endpoints are selected and deselected by moving the cursor between 'Yes' and 'No'. It is not necessary to press <ENTER> here. To lock in the selection and return to the main menu, move the cursor to the 'Go' button and press <ENTER>. To ignore any changes and return to the main menu, move to the 'Cancel' button

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[4]The left and right arrow keys usually move the cursor within the text field of the remark, but if the cursor is at either edge of the text, the corresponding arrow key can be used to leave the field. Note that in all cases, using an arrow key to leave a field assumes that there is another field in the indicated direction to move to.

and press <ENTER>.

Selecting 'Chromosomal Aberrations' will activate twenty-one columns. These include nine columns for general categories of various types of chromosomal aberrations and twelve columns for the distribution of aberrations among cells. Selecting 'Mitotic Index' will activate three columns.

1.2 Optional Fields

This selection presents a subscreen consisting of four columns and fifteen lines (Fig. 3a) with which the user may name, describe, and type up to fifteen additional fields. A new field is created (and subsequently appears in the spreadsheet) simply by naming it. The only restriction on the field names is that they may not be duplicated. 'Name 1' will appear on the first title line of the spreadsheet, 'Name 2' will appear on the second. There is no restriction on the description field; this is for the user's convenience and may be omitted. The fields are assumed to contain integers unless otherwise defined. To change the default field types, go to the Type Field and make a selection from the menu that appears when the field is entered (Fig. 3b). Currently, optional fields are not used in the statistical analysis or in the graphs. However, one category of optional fields 'aberration' can be used to insert specific categories of chromosomal aberrations, not previously defined, into that portion of the spreadsheet where such data are entered. Data in these columns are used to calculate the locked field 'CA/cell'. Note that the 'aberration' field type will not appear in the field type menu unless the 'chromosomal aberration' end point has been previously selected. <ESCAPE> returns to the main menu.

2. Data Entry

The data entry selections (Experiment Description and Spreadsheet) are the means by which data are entered into CA sessions by keyboard. 'Experiment Description' consists of a six page form with which to enter descriptive information pertaining to the experiment, test article, solvent, positive control, test system, and treatment. The 'Spreadsheet' allows access to the

actual data.

2.1 Experiment Description

This routine consists of a six page form presented in a double window format (Figs. 4a-4f). The left window contains the current page of the form. To enter the descriptions, use the arrow keys to move between fields. The right window contains an index listing the six pages, highlighting the current page. The form opens displaying the experiment page. Pages are changed using the
PAGE-UP and PAGE-DOWN keys. There are no entries among these forms that are explicitly required before statistical analysis can be conducted, but the contents of the test agent and dose fields are used in labelling the statistics report. If these fields are blank, "?" will appear in their place.

2.2 Spreadsheet

The spreadsheet consists of one thousand rows, eight permanent columns (including a remarks field), and whatever fields were defined by the setup routines. Fifteen rows and seven columns are visible onscreen at any one time. The arrow keys move the cursor a single row or column at a time, adjusting the display when an attempt is made to move outside the current 7x15 window. <PAGE-UP> and <PAGE-DOWN> shift the display up and down a page (fifteen lines). <CTRL LEFT-ARROW> and <CTRL RIGHT-ARROW> shift the display left and right a page (seven columns). <CTRL PAGE-UP> and <CTRL PAGE-DOWN> move to the first and last pages of the spreadsheet. <HOME> and <END> move to the first and last columns of the current row. <ENTER> moves the cursor to the first column of the next line.

CA assumes that the three fields ANIMAL, SLIDE, and SCORER will be the basic key fields and provides a small window in the lower left corner of the spreadsheet where the values of these fields for the current line are displayed. This is for the convenience of the user since whenever the window is shifted to the right, at least one of the key fields is lost from view.

Fields are limited to nine characters except for the remarks field which will accept eighty. Entering text into the remarks field opens a subwindow and activates the text editor. On closing the subwindow, only the first nine characters of the remarks text will be displayed in the spreadsheet. Each field also has a fixed data type that is reflected in a small tag in the lower right corner of the screen. Edits to check for illegal values are currently installed for the integer (whole number), real (decimal), flag (yes/no), sex (male/female), and treatment type (treatment, control, positive-control) so attempts to enter illegal values in these fields will be rejected. The one exception to this is a single period, which may be entered into any numeric field to denote a missing value.

The Sample Time field may be left blank but, if so, it must be blank for every observation. To CA, blank sample times imply that time is not a factor and the analyses will be conducted accordingly. If only some Sample Time fields are blank, CA will not know how to interpret them.

Treatment Code may be left blank. The accepted treatment codes are 't' for treatment group, 'p' for positive control and 'c' for solvent or negative control. Records with blank treatment codes are assumed to belong to the treatment group.

Sex initially defaults to 'm' (male), but this may be changed with the F2 setup option described below.

As stated in section 1.1, selecting 'Chromosomal Aberrations' while in 'Select Endpoints' will activate twenty-one columns in the spreadsheet. The first nine columns (plus any additional optional columns specified for chromosomal aberrations) are provided for entries on specific types of chromosomal aberrations. The ninth column of this set contains the number of aberrations per cell (excluding gaps), including any user defined aberration column(s). Data in these columns are **not used** in any of the subsequent statistical analyses conducted on chromosomal aberration data, but are provided for the convenience of the user. The next eleven columns of this set are used to indicate the number of cells with 0,1,2,3...9,10 or more aberrations. The last column contains the percentage of cells

with at least one aberration. The user has the option of entering data which excludes or includes information on "gaps". Data in these columns are used in the statistical analysis to determine if the treatment increased significantly either the frequency of damaged cells (i.e., the number of cells with at least one chromosomal aberration, excluding or including gaps) or increased significantly the number of aberrations among cells (excluding or including gaps).

When 'Mitotic Index' has been selected, three columns are activated in the spreadsheet. These include two columns for data entry, one for the total number of cells scored and one for the number of cells at metaphase. The third column contains the mitotic index (cells at metaphase/total cells), presented as a percentage.

The ditto character (initially the double quote "), if entered as the first character of a field, copies into the current field the contents of the field immediately above it, and then moves one space down. The designated ditto character may be toggled between the double quote and the single quote with the F2 setup option. This option can also be used to toggle the cursor movement between down and right.

<ESC> returns to the main menu.

F1 accesses the Help screens for data entry.

F2 opens a spreadsheet setup menu with nine selections (Fig. 5a).

ASSIGN CURRENT COLUMN [fieldname] (Fig. 5b) allows you to assign a constant value to all or part of the current column (Fig. 5c, note the default value of SEX). The screen consists of three lines. The first line accepts the value to be assigned. The second specifies the range through which the value is to be set. The default range is from the current row to the last non-empty row. The third line allows you to either GO or CANCEL.

SET DEFAULT FOR SEX TO {other-sex} toggles the default sex. If the current default is male, {other-sex} will be "female", and vice-versa.

CHANGE THE DISPLAY opens a screen (Fig. 5d) that allows you to select a subset of the defined fields for display and to modify the order in which they appear. The defined fields are listed on the left of the screen. Select (or deselect) fields for display with the arrow keys and <ENTER>. They will appear or disappear from a list on the right. Only the selected fields will appear in the spreadsheet and they will appear in the order they were selected (Fig. 5e). To reset the default display, deselect all fields. <DELETE> will do this.

MOVE {direction} AFTER DITTO allows you to toggle the direction of cursor movement after dittoing between down and right. {direction} is "right" if the cursor currently moves down, and vice-versa. <ENTER> will implement the change and close the setup screen. <ESC> will just close the screen.

CHANGE THE DITTO CHARACTER TO {other-character} toggles the ditto character between single and double quote. The double quote is default, but it requires the shift key. If the ditto function is to be used frequently, it may be more convenient to substitute the single quote.

MOVE TO LINE (Fig. 5f) allows immediate movement to any line in the spreadsheet. Selecting it opens a small screen into which you enter a line number between 1 and 1000. You are then returned to the spreadsheet with the cursor positioned on the indicated line at the same column. (The pound sign # is a quick way to do this directly from the spreadsheet).

IMPORT DATA AS ASCII FILE opens a control screen (Fig. 5g)

from which you can name the file to be imported and the range of lines within the spreadsheet into which the imported data will be entered. The file to be imported must contain data in ASCII format (simple text files) with fields separated by one or more blanks. (Blanks within fields are not permitted.) The fields themselves are assumed to correspond directly to the spreadsheet the way it is currently configured (see CHANGE THE DISPLAY above). When 'Select source file' is selected, CA will prompt you for a search path (Fig. 5h), and then open a screen depicting all files within the indicated path (Fig. 5i). This screen is nearly identical to the screens that open when 'Recall' is selected from the main menu (Fig. 6). The only difference is that only CA data files will be listed when recalling, but every file within the search path will be listed when importing. To select a file from the list, highlight its name (with the arrow keys) and <ENTER>. For an explanation of how to change the search path, see Recall (Section 3.1).

When a file is selected, CA will read the data into the corresponding columns of the spreadsheet, beginning at the 'From' line and stopping at either the 'To' line or the end of the input file, whichever comes first. If the file is locked (see Section 3.2), CA will note overwritten fields in the log but will perform no edits. Therefore it is critical that you make sure the data are legal and the spreadsheet is set up correctly.

EXPORT DATA AS ASCII FILE is the inverse of IMPORT DATA. You are again prompted for a filename and two line numbers (Fig. 5j), but this time CA will transfer the data in the fields defined by the spreadsheet's current configuration to the named file.

IMPORT and EXPORT provide a convenient means to move data between CA and other applications.

3. Disk I/O

'Recall' reads an CA file from disk and makes it the current file. 'Save' writes the current CA file to disk. 'Import' and

'Export', being multi-step operations, are too complicated to execute as a single menu selection. When selected as main menu items, 'Import' and 'Export' display text screens describing the procedures.

3.1 Recall

'Recall' is the means by which existing (previously saved) CA files are brought back into an active session. To do this, 'Recall' first identifies the CA files in the current search path and then presents the resulting list in the main recall screen.

When 'Recall' is selected, it first offers the option of changing the current search path (Fig. 5h). When the search path has been defined (that is, when the default has been either changed or confirmed), 'Recall' conducts the search and opens the main screen (Fig 6).

The main screen consists of five subwindows. The first and by far the largest is the list of files in the current directory presented alphabetically from left to right in four columns and as many rows as necessary. In a column to the right of the file window are 1) the drive menu, 2) the 'parent directory' button (a button is just a one item menu), 3) the subdirectory menu, and 4) the 'cancel' button.

The subwindow containing the highlight bar is always the currently active subwindow. To move between the subwindows, use 1) CTRL LEFT-ARROW, CTRL RIGHT-ARROW, CTRL PAGE-UP, and CTRL PAGE-DOWN, or 2) TAB to cycle clockwise.

When the file list is active, the bar responds to the arrow keys, and if the list is too long to fit in the window, PAGE-UP and PAGE-DOWN to scroll. ENTER will select the currently highlighted filename and close the window, returning to the point of call.

Of the remaining subwindows, all but 'cancel' modify the

search path. Selecting one of the drives redefines the search path to the root directory of the disk residing on the indicated drive.

The 'parent' button modifies the search path by removing the last directory level from it.

Selecting one of the subdirectories modifies the search path by appending the selected subdirectory to it.

If the current search path is the root directory, there will be no parent. In this case, the highlight bar will skip the button. Likewise, there may be no subdirectories within the current directory. Again, in this case, the bar will skip the appropriate button.

'Cancel' closes the screen and performs no action.

3.2 Save

CA incorporates two file attributes, 'locking' and 'password protection'. These attributes can be modified only when files are saved.

New files are initially neither locked nor protected. If such a file is to be saved, the first menu (Fig. 7a) offers the options LEAVE UNPROTECTED, PROTECT and CANCEL. If you select PROTECT, you will be prompted for the password (Fig. 7b). Anyone wishing to recall this file will have to give the password exactly as entered here (including capitalization). If the file to be saved is already password protected, the first menu (Fig. 7c) will offer related options: KEEP PASSWORD, CHANGE PASSWORD, REMOVE PASSWORD, and CANCEL.

The second menu (Fig. 7d) consists of four items:

UPDATE THE CURRENT FILE can be selected only if the current session was read from disk. If so, this option rewrites the source file, saving any changes made during the current session.

CREATE A NEW FILE allows you to save the data under a new name. If this item is selected, CA assumes the target file does not exist. If it finds a file with the given name, it will prompt you to OVERWRITE or CANCEL.

OVERWRITE AN EXISTING FILE calls a screen identical to RECALL SAVED SESSION, except that the selected file will be overwritten by the current session. To save disk space, files are compressed before saving.

CANCEL returns to the main menu.

Finally, if the current file is not locked, the last menu (Fig. 7e) will consist of the items: WRITE UNLOCKED, LOCK AND WRITE, and CANCEL. If the file is locked, any future additions or changes will be recorded in its GLP log. Once a file is locked, it cannot be unlocked.

3.3 Import and 3.4 Export

'Import' and 'Export', being multi-step operations, are too complicated to execute as single menu selections. When selected as main menu items (as opposed to spreadsheet / F2 menu items), 'Import' and 'Export' open text screens describing the respective procedures. Leaving 'Import' and 'Export' as main menu items, even though they cannot be executed from the main menu, appropriately reflects their status as high-level operations.

4. Analysis

'Statistics' conducts specialized statistical analyses on selected endpoints and presents the results via the screen with an option to print as well. The CA software is designed to analyze an *in vivo* experiment involving either one or both sexes, from 1 to 5 scorers, and a maximum of 8 dose groups and 6 sample times. 'Graph' plots the means of selected response variables.

4.1 Statistics

When 'Statistics' is chosen from the main menu, CA looks for

defined fields representing cell counts suitable for analysis. If it finds none, CA prints a warning and returns to the main menu. If it finds entries for only a single endpoint (e.g., mitotic index), CA assumes analysis is to be done on this endpoint and opens the control screen. If it finds either the chromosomal aberration endpoint or the chromosomal aberration and the mitotic index endpoints selected, it opens an analysis selection menu (Fig 8a). Chromosomal aberration data can be analyzed either as the percentage of cells containing at least one aberration or as the total number of aberrations.

The control screen for either of the two chromosomal aberration statistical tests (Fig. 8b) allows the user to set certain test parameters and listing options. The screen consists of 6 lines: (1) allows you to select the treatment or positive control data for analysis; (2) sets the significance or alpha level (default = 0.05); (3) allows you to select one of three options for including or excluding the high dose from the test (more on this below). Because the analysis of the mitotic index is based on an ANOVA, dropping the high dose is not relevant and this option is excluded from the control screen (Fig. 8c); (4) gives you the option of evaluating scorer differences in addition to time and sex (this option is not possible for positive control data); (5) determines whether the output is to be printed as well as listed to the screen; and (6) either initiates the statistical analysis (GO + <ENTER>) or returns to the main menu (CANCEL + <ENTER>)[5]. The current selections for these parameters are highlighted.

When the analysis begins, each exposure group (defined by sex, treatment and dose) is analyzed for outlier data based on intragroup standardized residuals. If any outliers are identified among the control, treated, or positive control groups, a screen is opened (Fig. 8d) listing the outliers and related information[6]. This screen gives you the options of printing the outliers, omitting the outliers, retaining them, or

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[5] Entering 'g' at any point is equivalent to GO + <ENTER>. Entering 'c' is equivalent to CANCEL + <ENTER>.

[6] The outliers listed here were created to demonstrate the window. They are not part of the analysis reported in the figures.

aborting the analysis.

After the outliers, if any, have been considered, CA presents (Fig. 8e) the variance inflation factor (a method for taking into consideration the extent of interanimal variability present among treatment groups), the alpha level set by the user, the results of the initial analysis to determine whether the data can be pooled across sexes and/or across sample times and, if selected, the results of the scorer analysis. In the lower box, the most appropriate model is highlighted, indicating whether the data should be pooled across sexes, sample time, both or neither. The user can override the initial selection or return to the main menu.

CA uses a statistical approach appropriate to the type of endpoint selected (i.e., for chromosomal aberration data or for mitotic index data). Two statistical procedures for evaluating the ability of chemicals to induce chromosomal aberrations are available to the user. In the first analysis, called chromosomal aberration (pct. damaged cells), for each animal tested, the number of cells with at least one aberration (excluding or including gaps depending on data input by the user) along with the total number of cells scored are treated as binomial observations. Extrabinomial variability is looked for and quantified. Then, for control and treatment group data, ANOVA procedures are used to test for scorer, sex and sample time effects while a trend test is used to evaluate treatment effects. The second analysis, called chromosomal aberration (total aberrations), treats the total number of aberrations per animal as Poisson observations (assuming that approximately (i.e. within 10%) the same number of cells are scored for all animals) and performs the Poisson counterpart to the binomial analysis discussed above. For data on the mitotic index, an ANOVA analysis is used to evaluate for agent-induced differences in the frequency of cells in mitosis. If the statistical analysis is continued, the next screens (Fig. 8f) present: (i) the sample time and sex, the calculated probability value (p) and the preset alpha level; and (ii) summary information on the endpoint selected, including the group mean and the standard error of the mean for observations (Note: In this calculation, each row of data is treated as a single observation). The results of a

comparison of the data at each dose versus the data in the control group (pairwise significance) is presented, with significant values indicated by a '*'. Pressing any key allows the user to page through each analysis, eventually being returned to the main menu.

For a detailed description of the statistical approach used in these analyses, see Appendix 2 of the Micronucleus Data Management and Statistical Analysis Software[7]. Generally, since the purpose of a chromosomal aberration assay is to determine whether an agent is capable of inducing a significant increase in either the frequency of damaged cells or in the total number of aberrations, the resulting data should be analyzed by a one-tailed trend test. One of the assumptions implicit to a statistical analysis based on a trend test is that the dependent response increases monotonically with increasing dose. However, in a number of biological systems (including in vivo chromosomal aberration studies), an initial increase in response, followed by a significant downturn at higher doses, has been detected for a small number of chemicals. To avoid the possibility that such data would result in the improper classification of a test chemical as being without clastogenic activity, the ability to formally exclude data at the highest dose only from the trend test analysis has been included in the statistical package. Of course, the user can informally conduct the same type of analysis by excluding data at specific doses during data entry. However, in this case, the analysis for scorer, sex and sample time effects would not contain the complete data set and may result in false conclusions about the appropriateness of pooling various data sets. If the user decides to formally incorporate the possibility of excluding from the trend test analysis, at any future point in time, data at the highest dose, then the preset alpha level will be adjusted to retain the same overall beta error rate. To accomplish this goal, the alpha level set by the user (default level of 0.05) will be reapportioned between a primary analysis, which would include all dose data, and a second analysis, which would exclude data at the highest dose. The

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[7]Micronucleus Assay Data Management and Analysis System, Data Management Systems in Genetic Toxicology, Integrated Laboratory Systems, version 1.4, October, 1990.

alpha for the primary analysis has been set at 80% alpha (default of 0.04), while that for the second test has been set at 20% alpha (default of 0.01). It would be statistically inappropriate for the user to first analyze the data set at 100% alpha, and then decide to exclude the data at the highest dose from the statistical analysis. The exclusion of the highest dose from the trend test analysis will have no effect on the analysis for scorer, sex and sample time effects, which will utilize the total data set.

Two methods of statistical analysis are offered for evaluating chromosomal aberration data, one based on the frequency of damaged cells and one based on the total number of chromosomal aberrations among cells. The former method is the statistical approach used most commonly. However, since the method is insensitive for detecting agents which, for one reason or another, selectively induce a very small number of heavily damaged cells only, the latter method was included also in CA.

For mitotic index data, an ANOVA is used since the frequency of cells at metaphase, depending on the duration of the treatment, may be decreased or increased at a particular sample time, and because the dose response often does not change monotonically.

4.2 Graph

This selection instructs CA to plot the means of a response variable against a classification variable with the option of stratifying by a third variable (Fig. 9a). There is also an option to present this information in the form of a table (Fig. 9b), either along with or instead of the graph. The response values are assumed to be the percentage of cells with aberrations, the frequency of aberrations per cell and the mitotic index. The default is the first variable in this list that is defined for the current session. The classification variables are assumed to be 'Dose' and 'Sample Time'. The default is 'Dose'.

The third 'by' variables are limited to 'Sex' and 'Sample Time'. If a 'by' variable is selected (Sex is the default), the

data will be stratified accordingly and presented. Stratification means two separate means are computed and plotted for each value of the classification variable, one for each value of the 'by' variable.

The control screen consists of four individual submenus (Fig. 9c). Three of these present lists of the defined fields in the spreadsheet and are used to select the independent, the dependent, and the classification variables respectively. The fourth selects the type of output. The up and down arrow keys are used to move within a submenu and the left and right arrow keys to move between them. As with the statistics setup menus, <ENTER> is not necessary except to select the 'GO' options. The graph presents all data listed, regardless of whether the data at the high dose are excluded from the trend test analysis or whether any outliers have been detected and excluded from the statistical analysis. By manually removing selected data from the spreadsheet, the user can exclude these data from the graph.

Use <PRINT SCREEN> to make hard copies of the graphs and tables.

5. Utility

'List' produces a hard copy listing through a printer connected to the serial port. There are a number of parameters with which the user can determine the form of the report. 'Sort' reorders the lines of the spreadsheet (and optionally subsequent listings) according to the values of any combination of key fields, either ascending or descending. 'Clear Session' deletes all data and removes all Set Up fields, in effect starting over.

5.1 List

CA can generate a hard copy listing of either the experiment description, the data or both. A preliminary menu (not shown) presents this choice. A control screen (Fig. 10a) governs several aspects of the list:

a) The first three lines allow the user to indicate

whether the list is to be sorted and, if so, in what order. See the Section 5.3 below on sorting the data for more information.

b) The next group consists of two lines that control the range of lines to be printed. The default is 'print to the last non-empty line', but this can be overridden on the second line by typing a range of lines into the fields.

c) Similarly, CA will by default print all fields. To change this, select the second of the next group of lines 'Select Subset'. This will open a window (Fig. 10b) in which all the defined fields are listed on the left and a blank list to be printed is displayed on the right. Select (or deselect) fields for printing with the arrow keys and <ENTER> (they will appear or disappear from the list on the right). The list on the left does not change except for small arrows that appear beside the names of the currently selected fields. Press <ESCAPE> to return to the control page.

d) The next two lines, 'Lines per page' and 'Columns per page' govern page length and width. These should be adjusted only if the printer text is set to a smaller size.

e) The last line contains the commands PRINT which begins the printing sequence and CANCEL which returns to the main menu. There is currently no way to stop printing short of restarting the equipment.

5.2 Clear Session

This is an easy way of starting over. All data and session configurations are erased. There is no screen associated with the selection. To prevent accidental erasure of unsaved changes, the user will be prompted by "Are you sure? Yes or No".

5.3 Sort

CA can order the rows of the data spreadsheet based on the values of certain key fields. The user must specify what the key fields are, what their priority is to be, and whether the records should be sorted by ascending or descending values. The sort screen (Fig. 11) lists the fields defined for the current session in a box on the left and the currently defined key fields in a box on the right. Initially, the second list is empty.

Key fields are selected and deselected with the arrow keys and <ENTER>. If the records are to be sorted by descending values (from largest to smallest) use the '-' key instead of <ENTER>. Descending keys are marked with a downward pointing arrow to their left. To change a currently selected key from ascending to descending, highlight its name and type '-'. To change it from descending to ascending, type '+'.

The order in which the keys appear in the 'selected keys' list on the right reflects their priority. The records will be sorted on the first key field and ties will be resolved on the second and so on. Any ties remaining when the keys have all been used will remain, but not necessarily in their original order. The order in which the key fields are defined is critical since there is no way to change the order of keys once they are selected. To insert a key anywhere other than at the end of the list, it is necessary to deselect then reselect the existing keys. Sometimes it is easiest to clear the list and begin again. <DELETE> does this.

When the key fields have been selected, use <ESCAPE> to begin the sort. In sorting, CA does not physically reorder the records but rather builds an index that determines a records apparent location. To remove the index, select SORT and <DELETE> the key fields.

6. Miscellaneous (Misc.)

'Key Field Search' produces a report listing either 1) the values of selected fields for all CA files in the indicated search path, or 2) the names of all CA files in the indicated

search path whose values for selected fields match key values entered here. 'GLP Log' presents by screen or printer a record of all accesses to the file and, after locking, all new entries or changes to existing entries, who made them and when.

6.1 Key Field Search

A key field file search will either a) list selected experiment description fields for all CA files in a given search path, or b) list all files in the current search path whose values for the selected fields match user defined target values.

The initial screen (not shown) allows you to select one of these options. If you elect to simply list key fields, a screen will open identical to that used to select fields for listing or reconfiguring the spreadsheet. When the fields to list have been selected, you will be given the chance to redefine the searchpath. When the search has been completed, you may elect to list the results or view them onscreen as with the GLP log report.

If, on the other hand, you elect to list the names of files with matching key field values, selecting a field opens a subwindow (Fig. 12a) into which you enter the target string. When the target string is defined, a subwindow opens (Fig. 12b) prompting you for a match criteria (e.g. whether the field is to exactly match the target string or is only to contain the target string). The third option, a partial match, is not yet implemented.

6.2 GLP Log

To further compliance with good laboratory practices, CA maintains a log as part of each file recording the time and date of each access and the ID entered at the beginning of the current ses-sion. If a file has been 'locked' (see Section 3.2), then this log will record all additional entries and changes to existing entries.

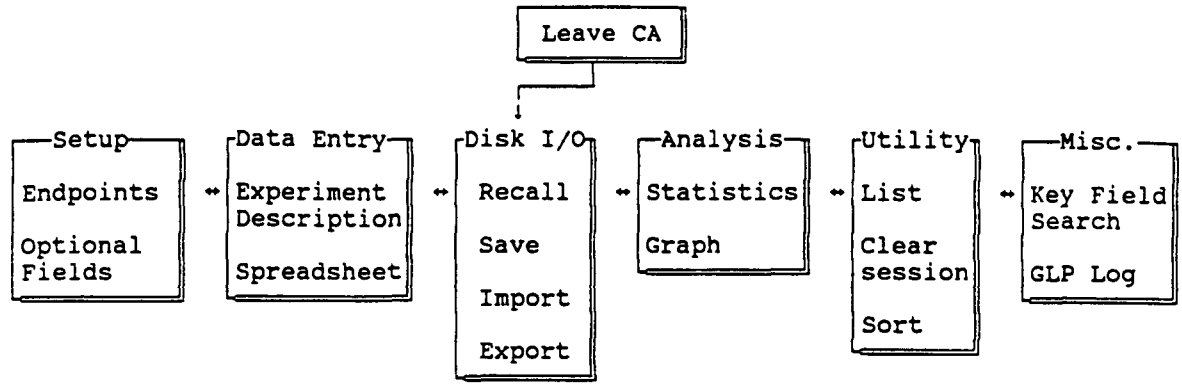
The log may be viewed onscreen or printed.

Sample Data Sets

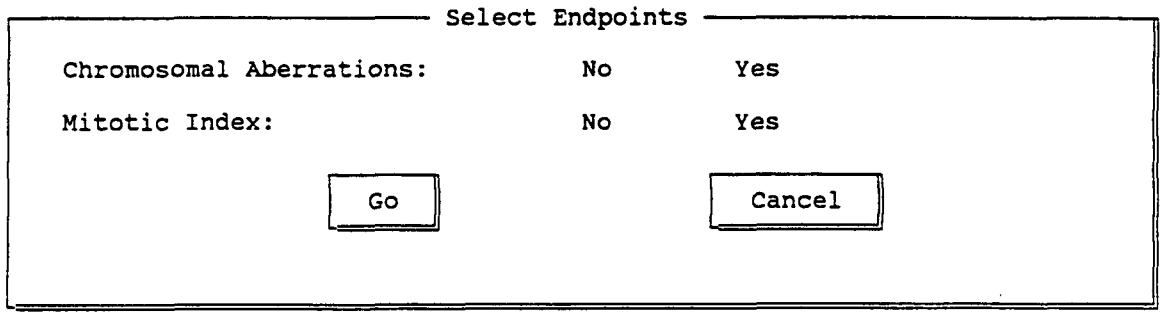
To assist the user in becoming familiar with CA, data from two sample experiments (CATEST01.ILS and CATEST02.ILS) have been included (Appendix 2). Both experiments present data in which male and female mice were treated once with a test chemical, bone marrow samples collected at 24, 48 and 72 hours after treatment and the frequency and distribution of chromosomal aberrations and the mitotic index were determined by two scorers. In CATEST01, the chromosomal aberration data includes cells containing 0, 1 or 2 aberrations. In CATEST02, cells containing multiple aberrations were detected among the treated mice. The same outlier data are included in both data sets. The statistical analyses of the chromosomal aberration data are based on the assumption that excluding the data at the highest dose would always be considered and that scorer differences would be evaluated. Finally, the trend test analysis was conducted (i) without pooling data obtained on males and females or at the three sample times, and (ii) pooling data, where appropriate, across sexes and sample times. The corresponding hard copies of the experimental information, the chromosomal aberration and mitotic index data and the results of the various statistical analyses are provided in Appendix 2. It is suggested that the user recall the sample test data files, page through the various screens and invoke each of the subroutines. It may also be useful to modify the entries and rerun the menu options.

We sincerely hope that you will find this program both useful and friendly. We welcome any suggestions or comments you might have. Please write, call, or FAX to:

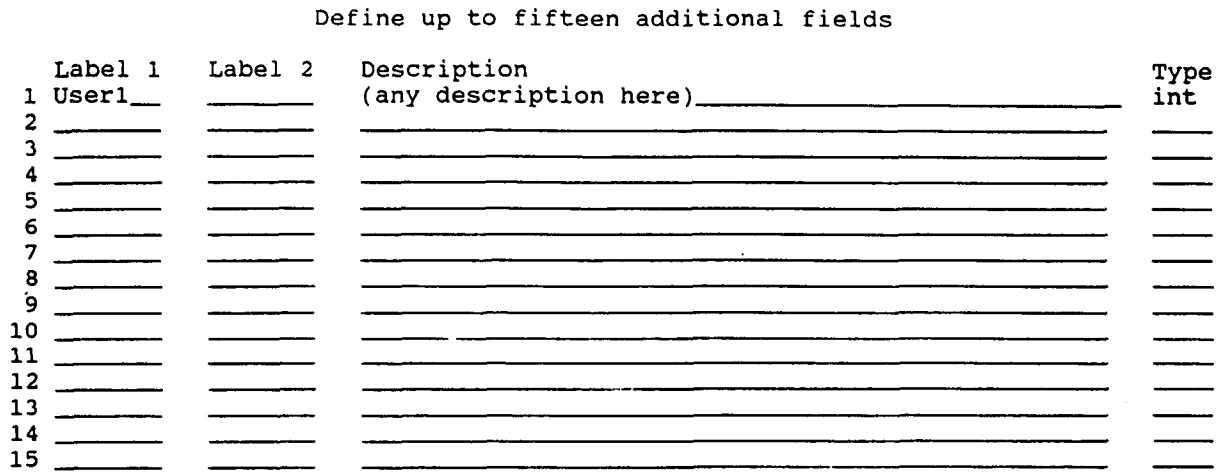
EPA Software Development Project
Integrated Laboratory Systems
Genetic Toxicology Program
P.O. Box 13501
Research Triangle Park, NC 27709
(919) 544-4589

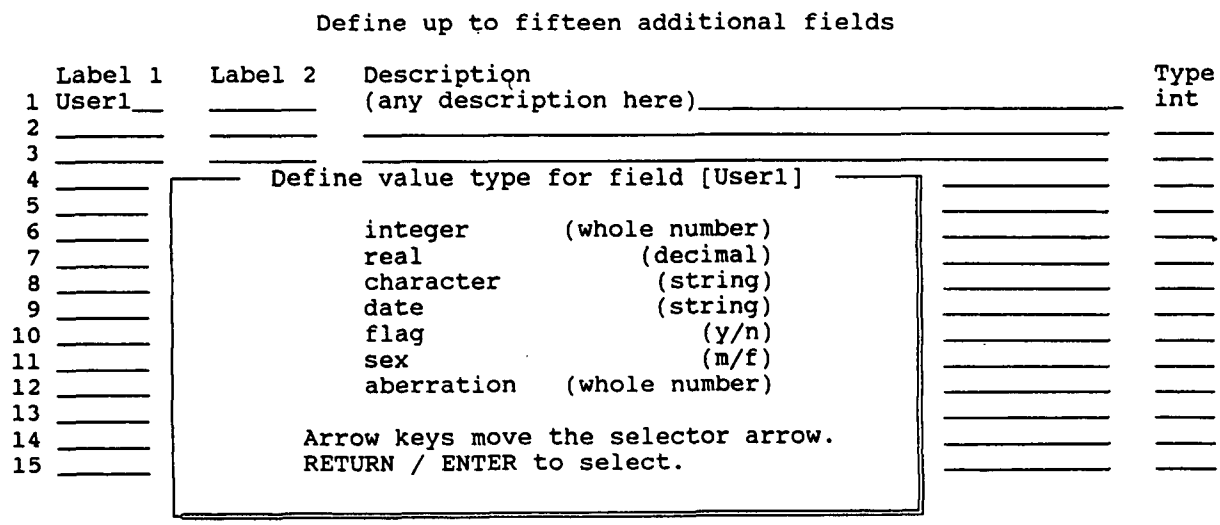


Return to DOS.

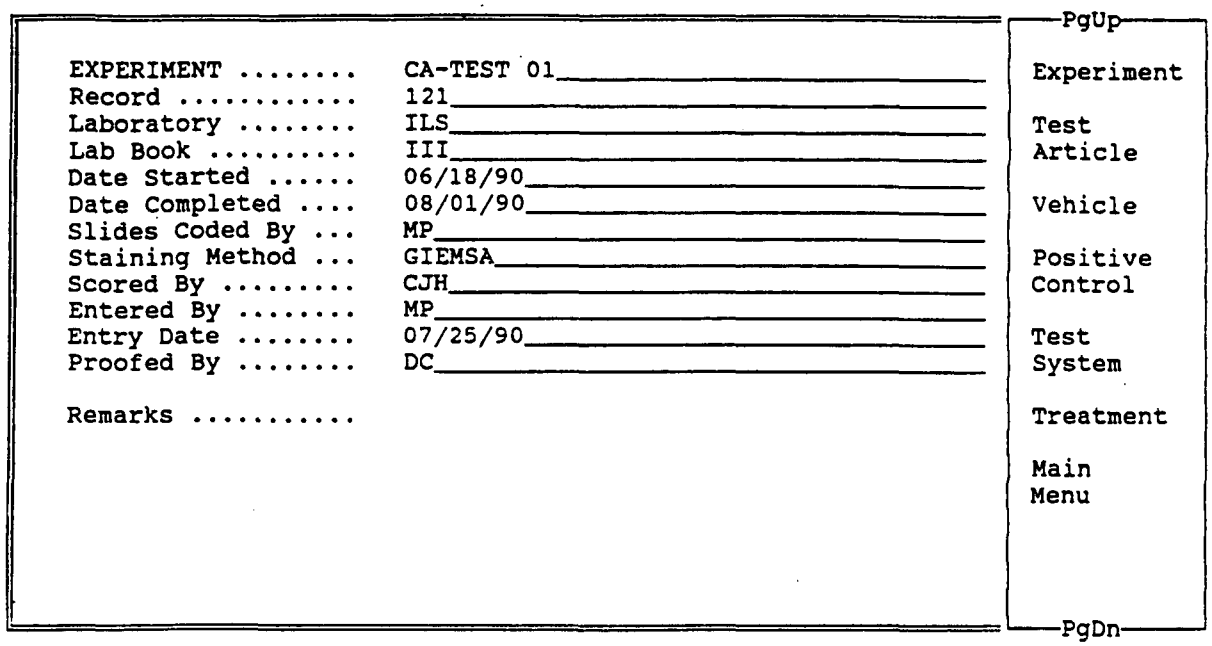


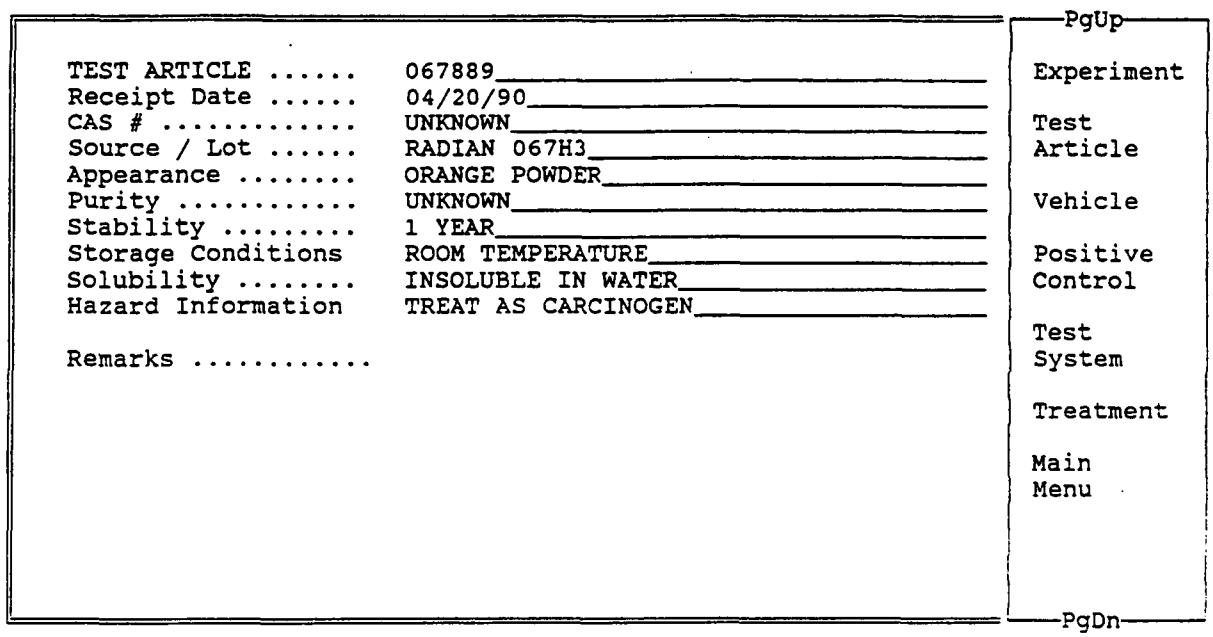
Figures 1 & 2



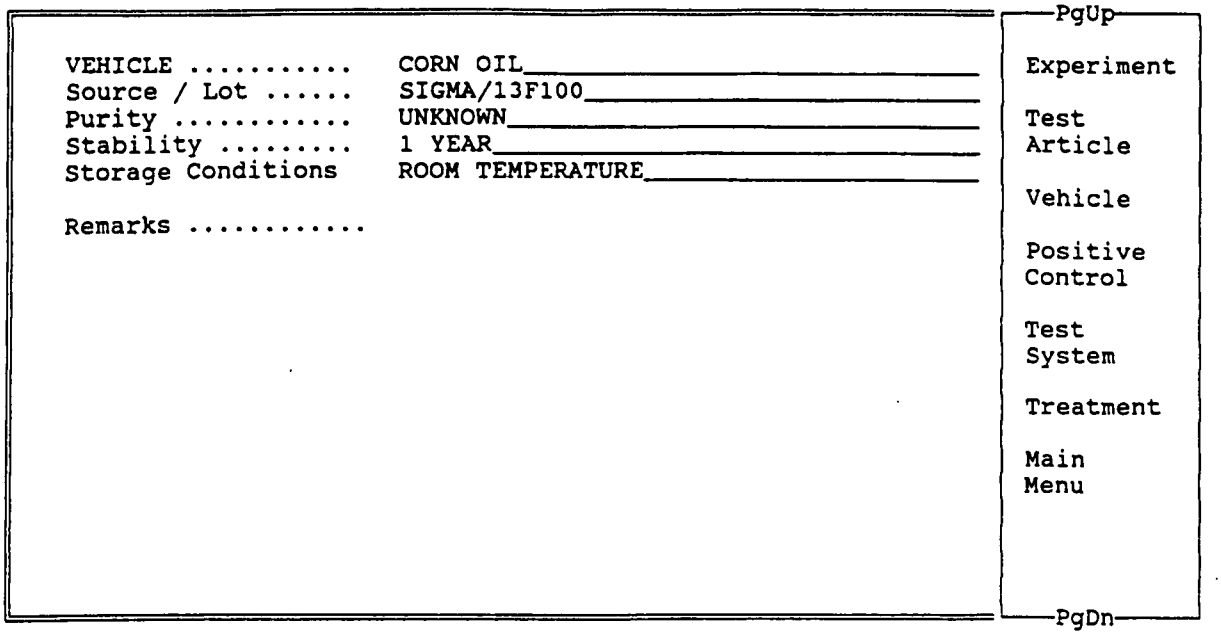


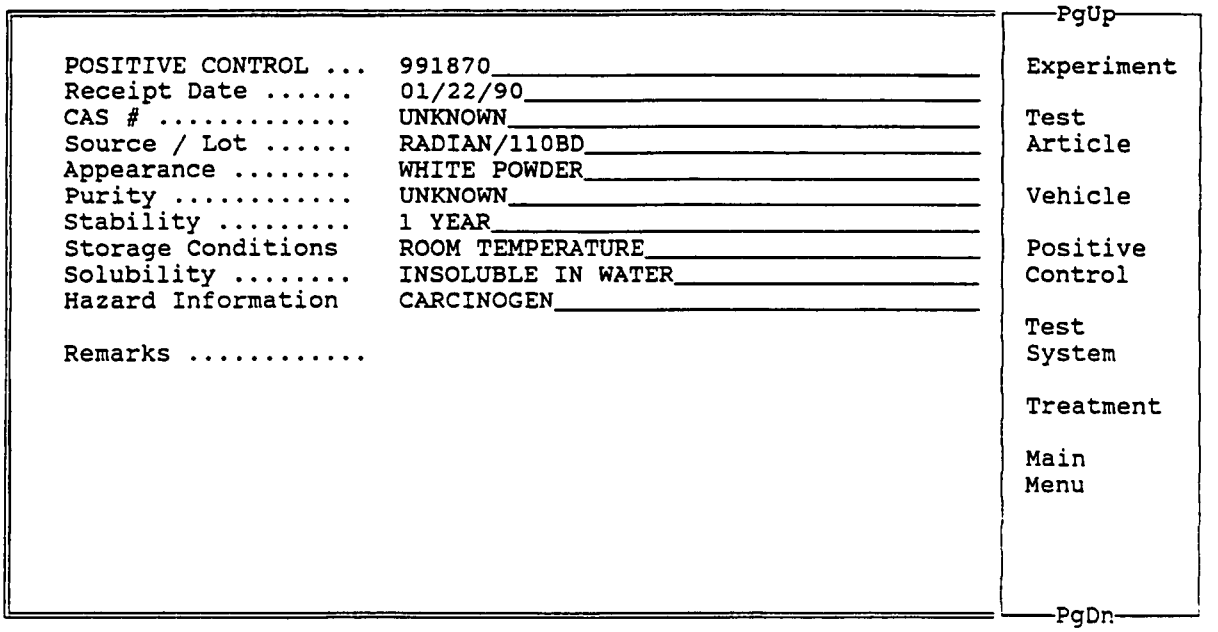
Figures 3a & 3b



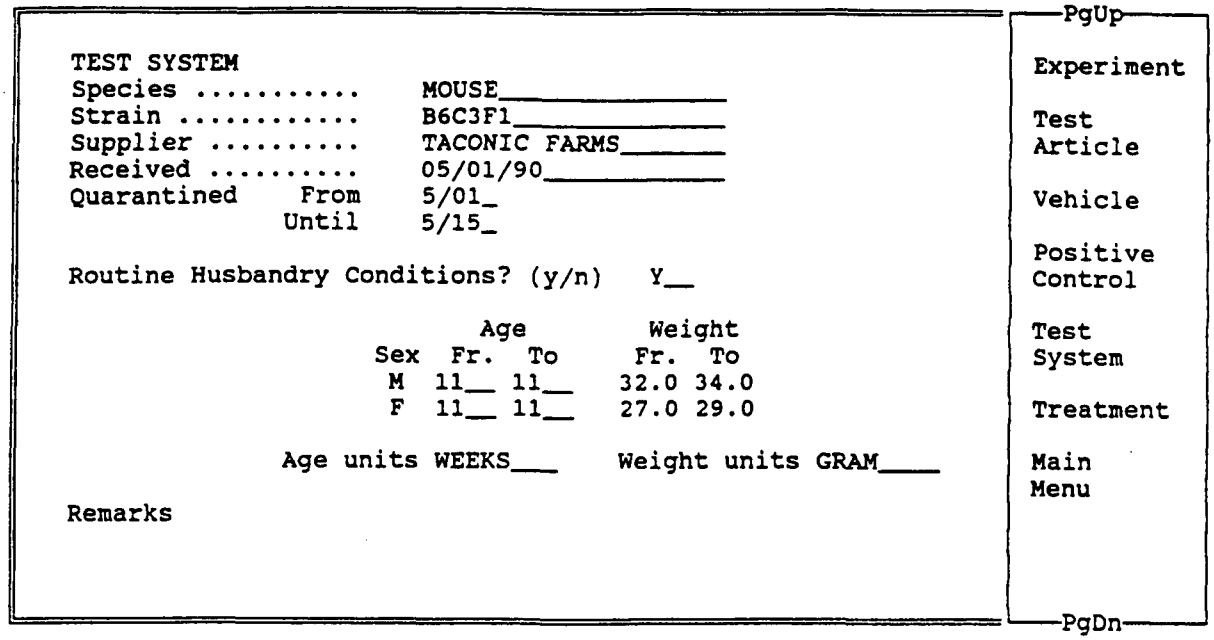


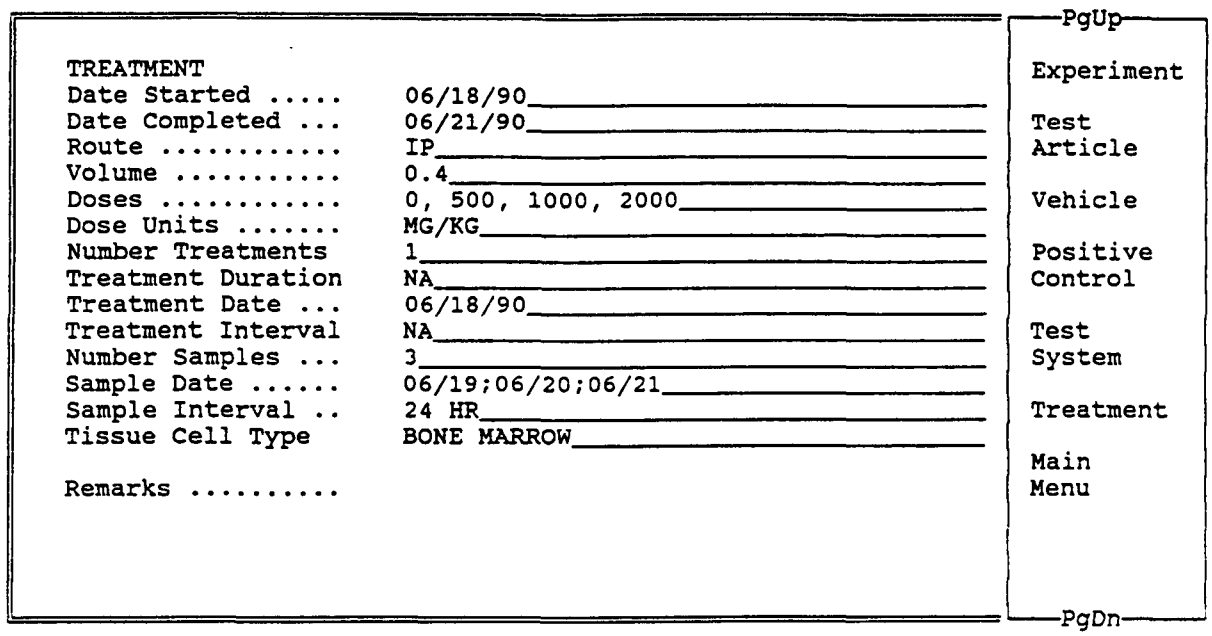
Figures 4a & 4b



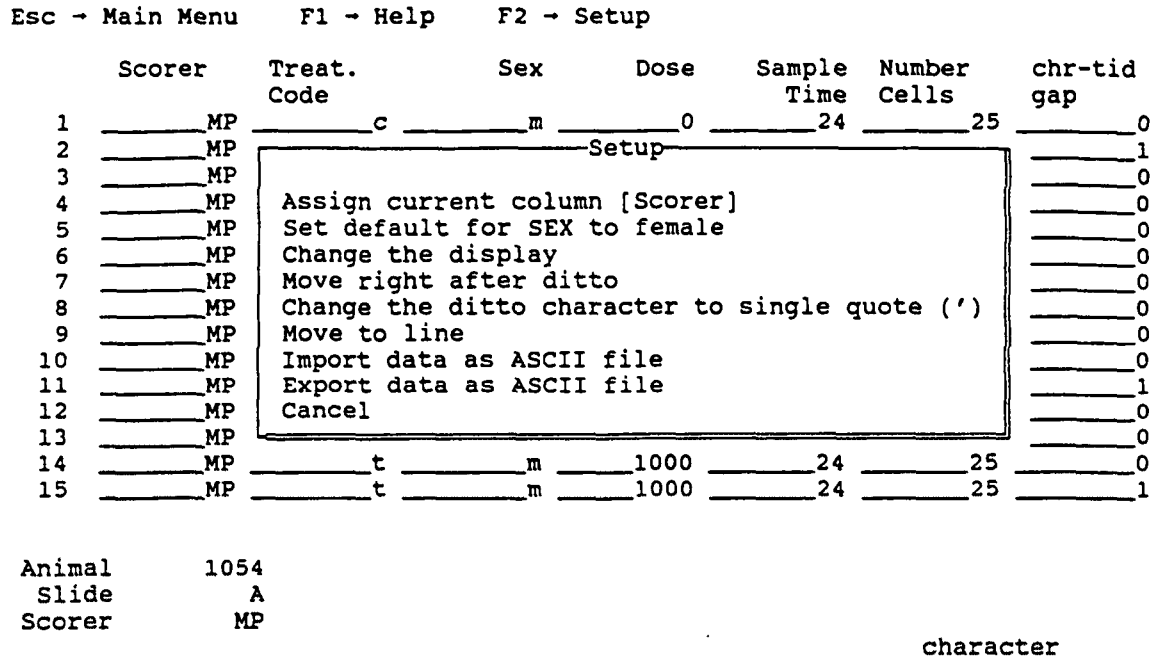


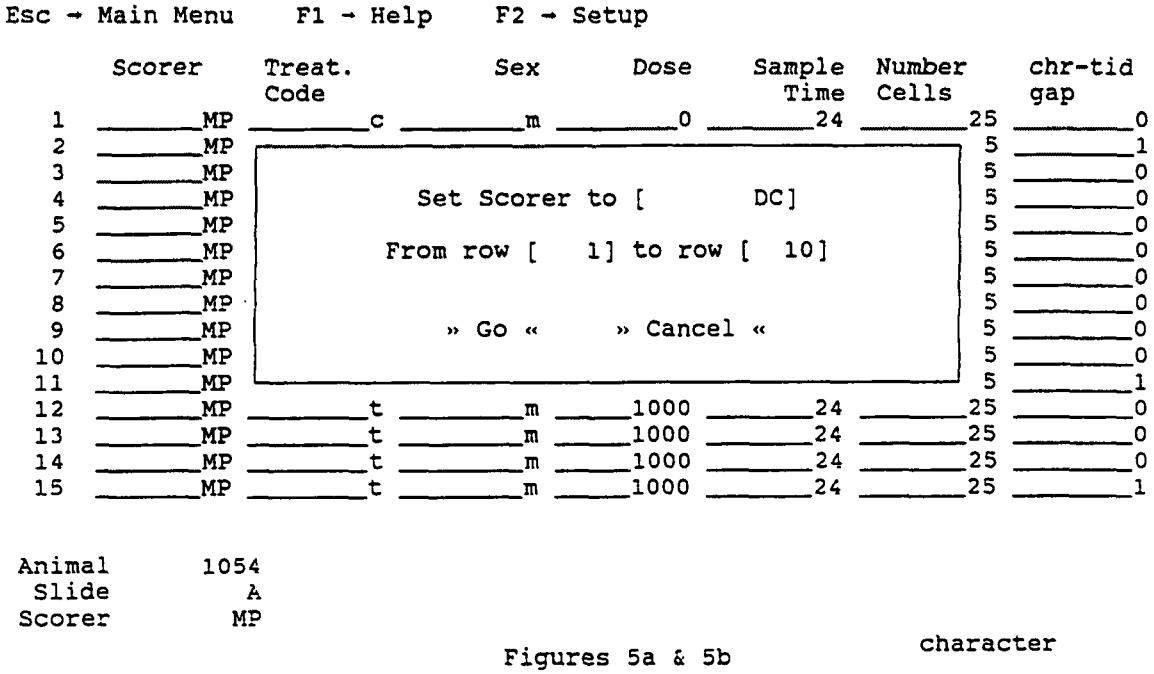
Figures 4c & 4d





Figures 4e & 4f





Figures 5a & 5b

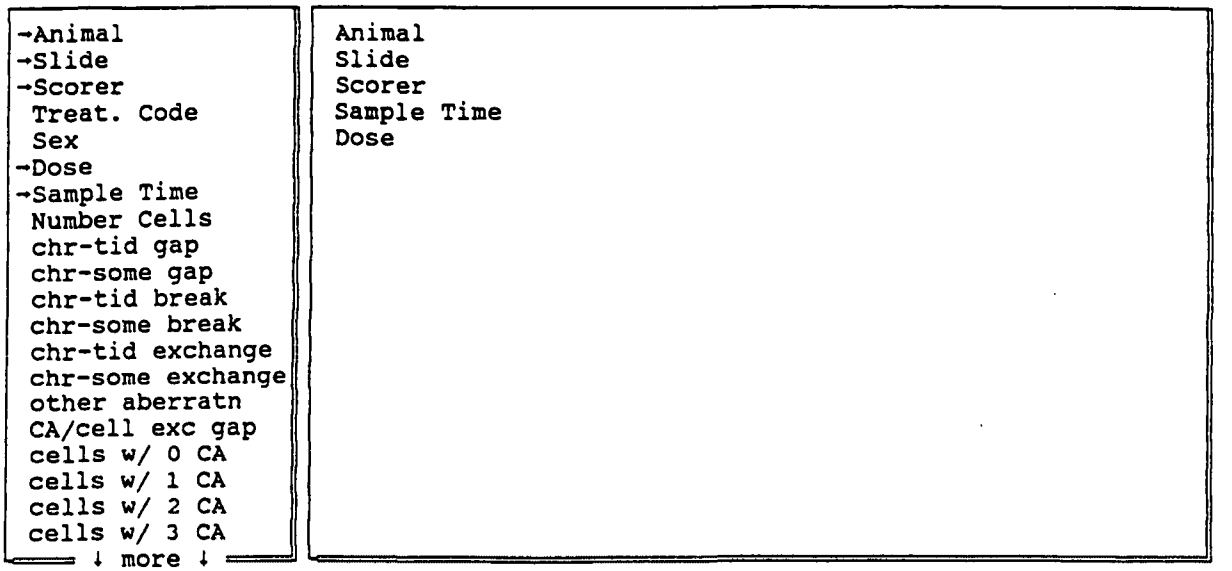
Esc → Main Menu F1 → Help F2 → Setup

	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap
1	DC	c	m	0	24	25	0
2	DC	c	m	0	24	25	1
3	DC	c	m	0	24	25	0
4	DC	c	m	0	24	25	0
5	DC	c	m	0	24	25	0
6	DC	t	m	500	24	25	0
7	DC	t	m	500	24	25	0
8	DC	t	m	500	24	25	0
9	DC	t	m	500	24	25	0
10	DC	t	m	500	24	25	0
11	MP	t	m	1000	24	25	1
12	MP	t	m	1000	24	25	0
13	MP	t	m	1000	24	25	0
14	MP	t	m	1000	24	25	0
15	MP	t	m	1000	24	25	1

Animal 1054
Slide A
Scorer DC

character

Figure 5c



Figures 5d & 5e

character

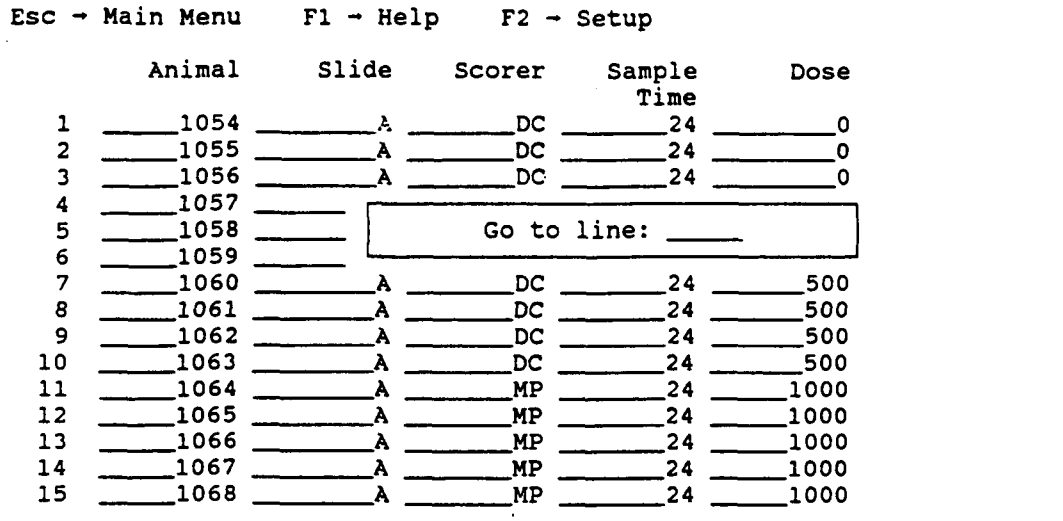
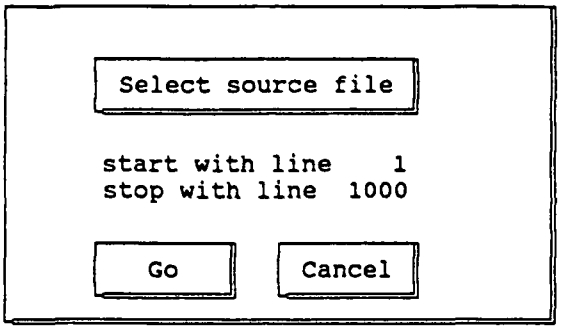
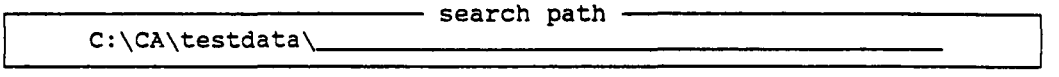
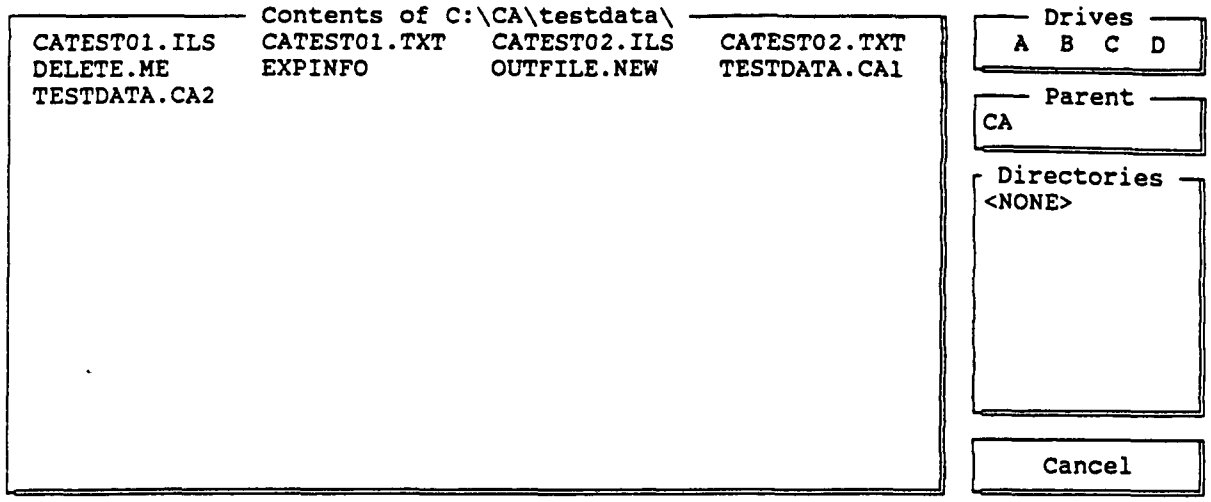

Esc → Main Menu
F1 → Help
F2 → Setup
Animal
Slide
Scorer
Sample Time
Dose
1 1054 A DC 24 0
2 1055 A DC 24 0
3 1056 A DC 24 0
4 1057
5 1058
6 1059
Go to line:
7 1060 A DC 24 500
8 1061 A DC 24 500
9 1062 A DC 24 500
10 1063 A DC 24 500
11 1064 A MP 24 1000
12 1065 A MP 24 1000
13 1066 A MP 24 1000
14 1067 A MP 24 1000
15 1068 A MP 24 1000
Animal 1054
Slide A
Scorer DC
character

Figure 5f

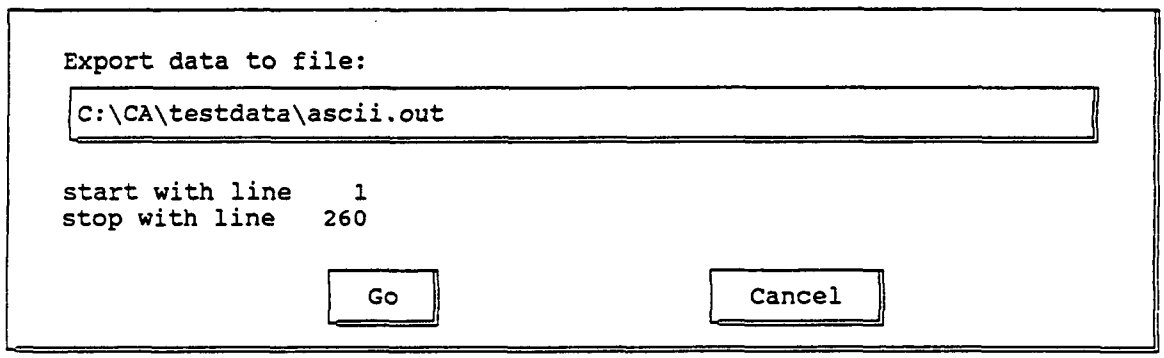




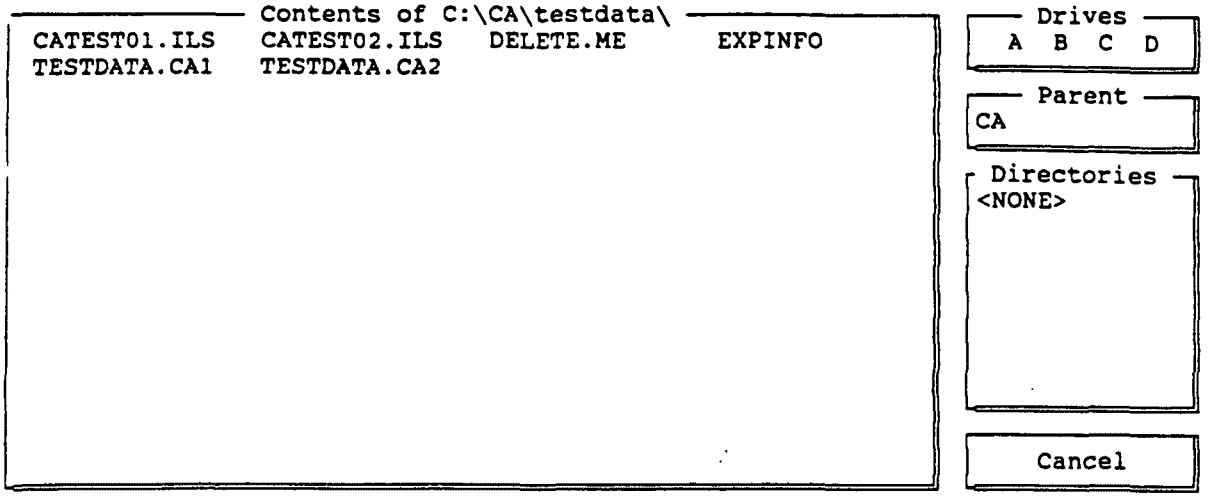
Figures 5g & 5h



Import C:\CA\testdata\ CATEST01.ILS

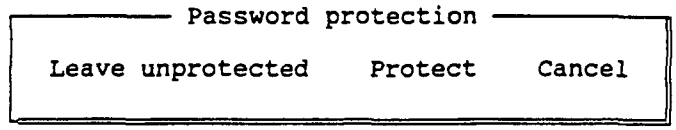


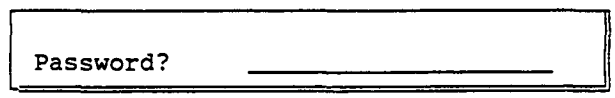
Figures 5i & 5j



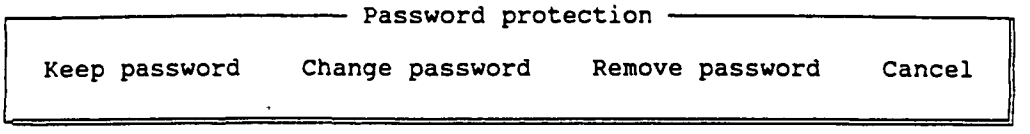
Recall C:\CA\testdata\ CATEST01.ILS

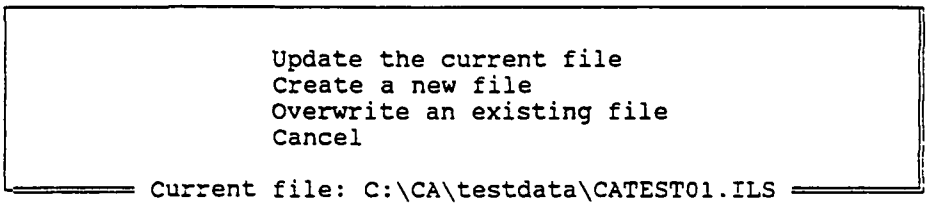
Figure 6





Figures 7a & 7b





Figures 7c & 7d

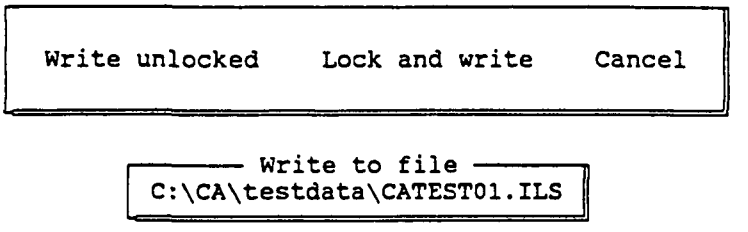

Write unlocked
Lock and write
Cancel
Write to file
C:\CA\testdata\CATEST01.ILS

Figure 7e

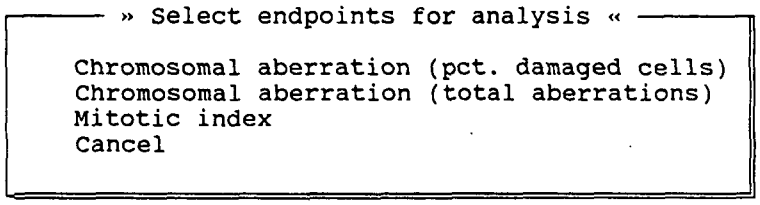
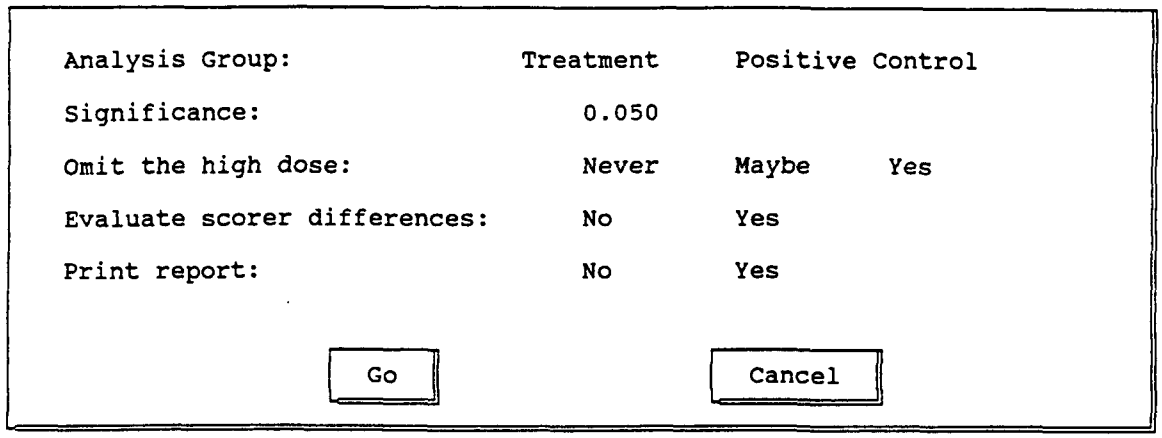
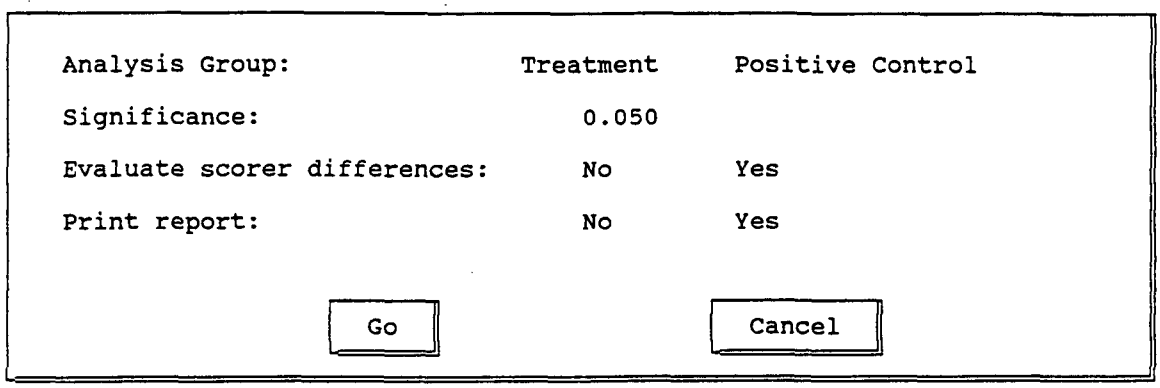

» Select endpoints for analysis «
Chromosomal aberration (pct. damaged cells)
Chromosomal aberration (total aberrations)
Mitotic index
Cancel

Figure 8a





Figures 8b & 8c

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Pct.	Mean Pct.
1	3	0.0	24.0	m	60.000	13.600
2	133	0.0	24.0	m	80.000	17.600

Omit outliers Keep outliers Print outliers Cancel

Endpoint: Chromosomal aberration (pct. damaged cells)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	30.014	24	0.1843
Sex	8.226	12	0.7673
Time	30.904	8	0.0001

Select trends option

Collapse on Sex Time Both Neither Cancel

Best choice: SEX

Figures 8d & 8e

Time = 24.00 (Both sexes) for 067889

p = 0.000
alpha = 0.050

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	7	450	1.5556	0.5729		
500.00	15	500	3.0000	0.6407	0.0697	
1000.00	28	500	5.6000	0.8897	0.0005	*
2000.00	56	500	11.2000	1.1462	0.0000	*

Hit any key ..

Time = 48.00 (Both sexes) for 067889

p = 0.000
alpha = 0.050

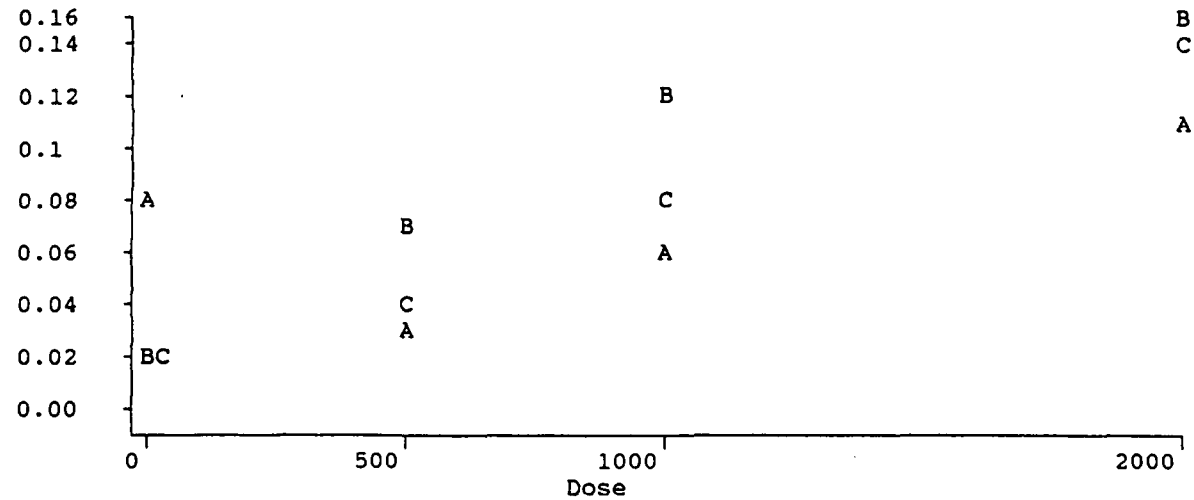
One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	6	500	1.2000	0.5109		
500.00	37	500	7.4000	1.3067	0.0000	*
1000.00	61	500	12.2000	1.5755	0.0000	*
2000.00	81	500	16.2000	2.1418	0.0000	*

Hit any key ..

Figure 8f

Average number of aberrations per cell



Stratified by Sample Time A = 24.00 B = 48.00 C = 72.00

ENTER → continue

Average number of aberrations per cell

For sample time =		24.00	48.00	72.00
Dose	0.00	0.084	0.012	0.012
	500.00	0.030	0.074	0.040
	1000.00	0.056	0.122	0.086
	2000.00	0.112	0.162	0.148

Figures 9a & 9b

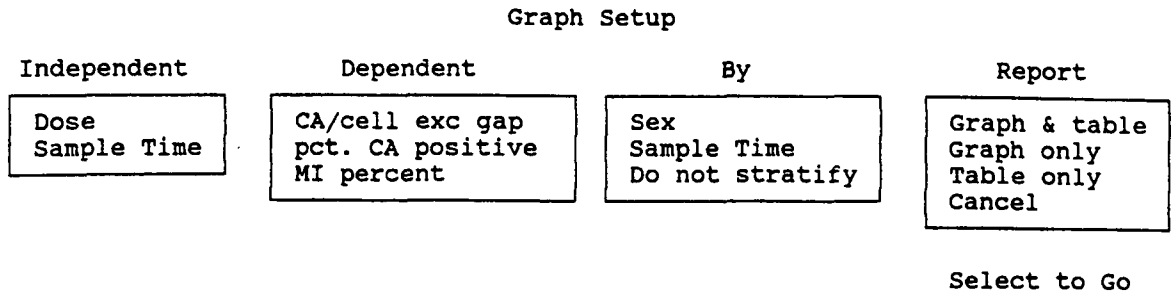
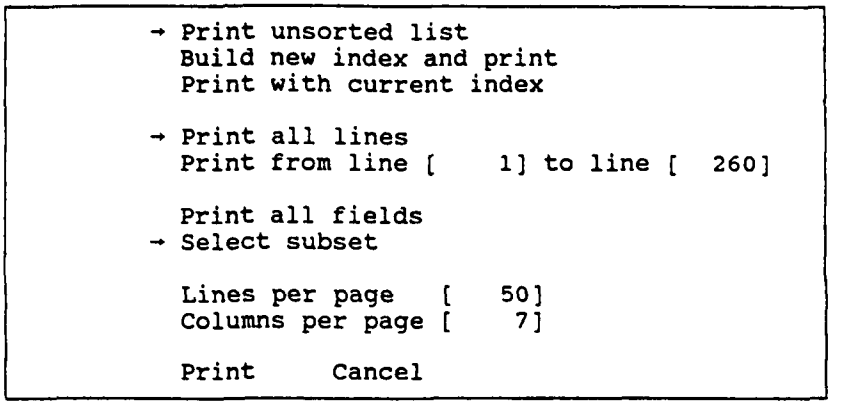
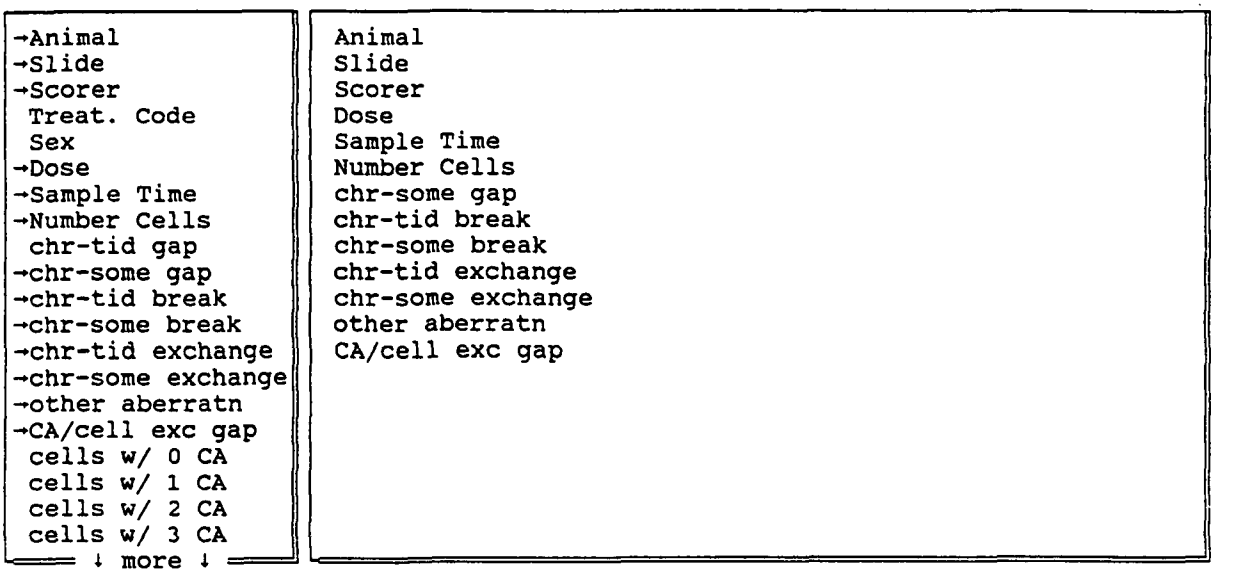

Graph Setup
Independent
Dose
Sample Time
Dependent
CA/cell exc gap
pct. CA positive
MI percent
By
Sex
Sample Time
Do not stratify
Report
Graph & table
Graph only
Table only
Cancel
Select to Go

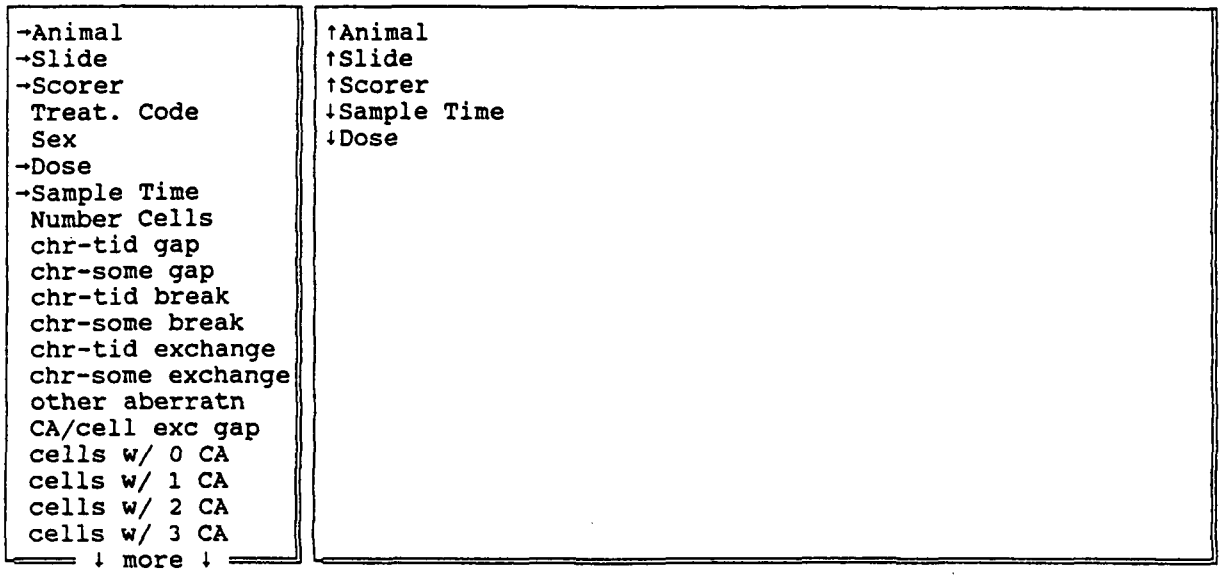
Figure 9c





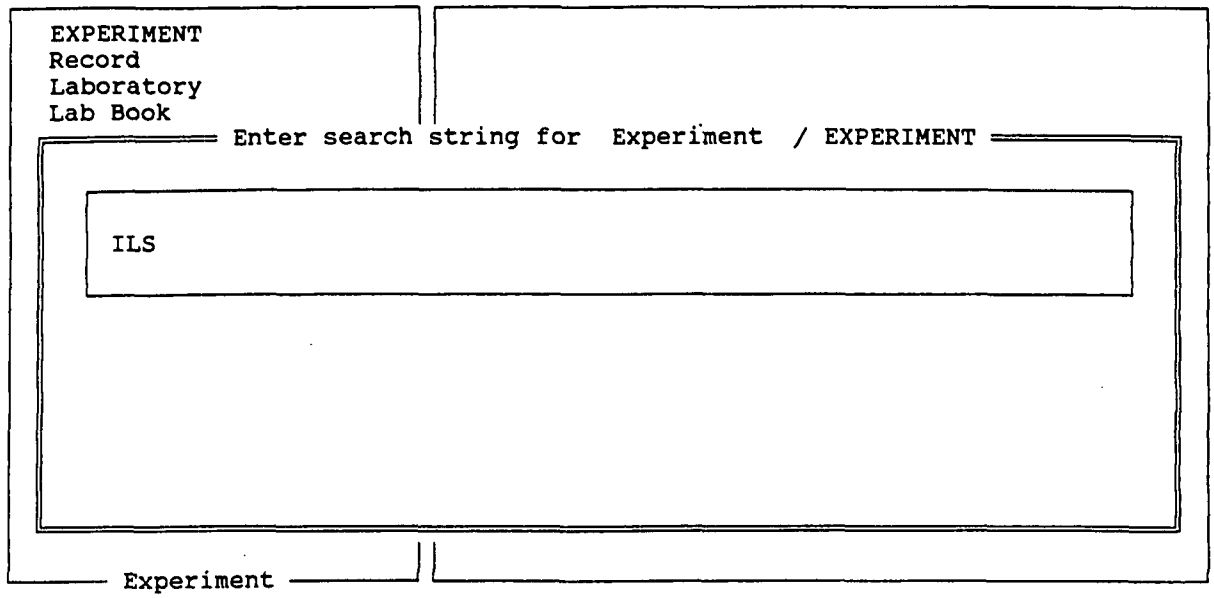
[↑] [↓] [PAGE UP] [PAGE DOWN] [ENTER] [DELETE] [ESCAPE] [F1 = help]

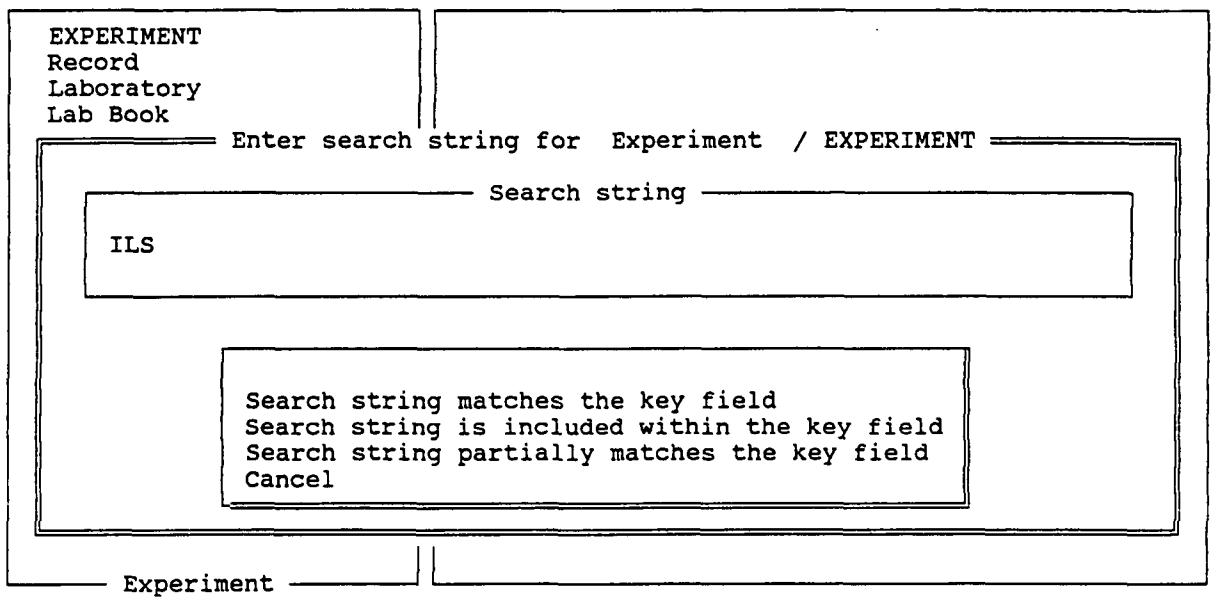
Figures 10 a & 10b



[↑] [↓] [PAGE UP] [PAGE DOWN] [ENTER] [+] [-] [DELETE] [ESCAPE] [F1 = help]

Figure 11





Figures 12a & 12b

APPENDIX 1

CHROMOSOMAL ABERRATION ASSAY SOFTWARE DEVELOPMENT PANEL MEMBERS

-Dr. James Allen
U.S. Environmental Protection Agency

-Dr. David H. Blakey
Health and Welfare Canada

-Dr. Michael Cimino
U.S. Environmental Protection Agency

-Dr. Russell J. DuFrain
Bristol-Myers Co.

-Dr. Ed Frome
Oak Ridge National Laboratories

-Dr. Osamu Hirai
Fujisawa Pharmaceutical Co. Ltd.

-Dr. Hank E. Holden
Pfizer Inc.

-Dr. Graham Hook
UT-Oak Ridge National Laboratories

-Dr. Andrew Kligerman
U.S. Environmental Protection Agency

-Dr. James MacGregor
Toxicology Consultants Services, Inc.

-Dr. Barry H. Margolin
University of North Carolina

-Dr. Al F. McFee
Oak Ridge National Laboratories

-Dr. Robert Naismith
Biofor, Inc.

-Dr. Charles H. Nauman
U.S. Environmental Protection Agency

-Dr. R. Julian Preston
Oak Ridge National Laboratories

-Dr. Michael F. Salamone
Ministry of the Environment, Canada

-Dr. Juan San Sebastian
Parmakon Research International

-Dr. Elizabeth S. Von Halle
Oak Ridge National Laboratories

-Dr. Deiter Wild
University of Wuerzburg

-Dr. Llewellyn R. Williams
U.S. Environmental Protection Agency

APPENDIX 2

SAMPLE TEST DATA

SAMPLE TEST DATA

CATESTO1

C:\CA\CATEST01.ILS listed at on

EXPERIMENT	CA-TEST 01
Record	121
Laboratory	ILS
Lab Book	III
Date Started	06/18/90
Date Completed	08/01/90
Slides Coded By ...	MP
Staining Method ...	GIEMSA
Scored By	CJH
Entered By	MP
Entry Date	07/25/90
Proofed By	DC

Remarks ..... _____

TEST ARTICLE	067889
Receipt Date	04/20/90
CAS #	UNKNOWN
Source / Lot	RADIAN 067H3
Appearance	ORANGE POWDER
Purity	UNKNOWN
Stability	1 YEAR
Storage Conditions	ROOM TEMPERATURE
Solubility	INSOLUBLE IN WATER
Hazard Information	TREAT AS CARCINOGEN

Remarks ..... _____

VEHICLE	CORN OIL
Source / Lot	SIGMA/13F100
Purity	UNKNOWN
Stability	1 YEAR
Storage Conditions	ROOM TEMPERATURE

Remarks ..... _____

POSITIVE CONTROL ...	991870
Receipt Date	01/22/90
CAS #	UNKNOWN
Source / Lot	RADIAN/110BD
Appearance	WHITE POWDER
Purity	UNKNOWN
Stability	1 YEAR
Storage Conditions	ROOM TEMPERATURE
Solubility	INSOLUBLE IN WATER
Hazard Information	CARCINOGEN

Remarks ..... _____

TEST SYSTEM

Species	MOUSE
Strain	B6C3F1
Supplier	TACONIC FARMS
Received	05/01/90
Quarantined From	5/01
Until	5/15

Routine Husbandry Conditions? (y/n) Y

	Age		Weight	
Sex	Fr.	To	Fr.	To
M	11	11	32.0	34.0
F	11	11	27.0	29.0

Age units WEEKS Weight units GRAM

Remarks _____

TREATMENT

Date Started	06/18/90
Date Completed ...	06/21/90
Route	IP
Volume	0.4
Doses	0, 500, 1000, 2000
Dose Units	MG/KG
Number Treatments	1
Treatment Duration	NA
Treatment Date ...	06/18/90
Treatment Interval	NA
Number Samples ...	3
Sample Date	06/19;06/20;06/21
Sample Interval ..	24 HR
Tissue Cell Type	_____
Remarks	_____

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
1	1054	A	MP	c	m	0	24	25	0	0	0
2	1055	A	MP	c	m	0	24	25	1	0	0
3	1056	A	MP	c	m	0	24	25	0	0	15
4	1057	A	MP	c	m	0	24	25	0	0	1
5	1058	A	MP	c	m	0	24	25	0	0	1
6	1059	A	MP	t	m	500	24	25	0	0	0
7	1060	A	MP	t	m	500	24	25	0	0	0
8	1061	A	MP	t	m	500	24	25	0	0	0
9	1062	A	MP	t	m	500	24	25	0	0	1
10	1063	A	MP	t	m	500	24	25	0	0	1
11	1064	A	MP	t	m	1000	24	25	1	0	1
12	1065	A	MP	t	m	1000	24	25	0	0	2
13	1066	A	MP	t	m	1000	24	25	0	0	1
14	1067	A	MP	t	m	1000	24	25	0	0	0
15	1068	A	MP	t	m	1000	24	25	1	0	1
16	1069	A	MP	t	m	2000	24	25	1	0	3
17	1070	A	MP	t	m	2000	24	25	1	0	4
18	1071	A	MP	t	m	2000	24	25	0	0	3
19	1072	A	MP	t	m	2000	24	25	0	0	2
20	1073	A	MP	t	m	2000	24	25	1	0	1
21	1074	A	MP	c	m	0	48	25	0	0	0
22	1075	A	MP	c	m	0	48	25	0	0	1
23	1076	A	MP	c	m	0	48	25	0	0	0
24	1077	A	MP	c	m	0	48	25	0	0	0
25	1078	A	MP	c	m	0	48	25	0	0	1
26	1079	A	MP	t	m	500	48	25	0	0	1
27	1080	A	MP	t	m	500	48	25	1	0	2
28	1081	A	MP	t	m	500	48	25	0	0	0
29	1082	A	MP	t	m	500	48	25	0	0	1
30	1083	A	MP	t	m	500	48	25	0	0	1
31	1084	A	MP	t	m	1000	48	25	3	0	3
32	1085	A	MP	t	m	1000	48	25	0	0	3
33	1086	A	MP	t	m	1000	48	25	0	0	2
34	1087	A	MP	t	m	1000	48	25	1	0	5
35	1088	A	MP	t	m	1000	48	25	0	0	0
36	1089	A	MP	t	m	2000	48	25	3	0	6
37	1090	A	MP	t	m	2000	48	25	0	0	3
38	1091	A	MP	t	m	2000	48	25	0	0	2
39	1092	A	MP	t	m	2000	48	25	0	0	7
40	1093	A	MP	t	m	2000	48	25	2	0	5
41	1094	A	MP	c	m	0	72	25	1	0	0
42	1095	A	MP	c	m	0	72	25	1	0	0
43	1096	A	MP	c	m	0	72	25	0	0	0
44	1097	A	MP	c	m	0	72	25	0	0	1
45	1098	A	MP	c	m	0	72	25	0	0	0
46	1099	A	MP	t	m	500	72	25	0	0	1
47	1100	A	MP	t	m	500	72	25	0	0	0
48	1101	A	MP	t	m	500	72	25	0	0	0
49	1102	A	MP	t	m	500	72	25	0	0	1
50	1103	A	MP	t	m	500	72	25	1	0	1

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
1	0	0	0	0	0	25	0	0	0	0	0
2	0	0	0	0	0	25	0	0	0	0	0
3	0	0	0	0	0.600	10	15	0	0	0	0
4	0	0	0	0	0.040	24	1	0	0	0	0
5	0	0	0	0	0.040	24	1	0	0	0	0
6	0	0	0	0	0	25	0	0	0	0	0
7	0	0	0	0	0	25	0	0	0	0	0
8	0	0	0	0	0	25	0	0	0	0	0
9	0	0	0	0	0.040	24	1	0	0	0	0
10	0	0	0	0	0.040	24	1	0	0	0	0
11	0	0	0	0	0.040	24	1	0	0	0	0
12	0	0	0	0	0.080	23	2	0	0	0	0
13	0	0	0	0	0.040	24	1	0	0	0	0
14	0	0	0	0	0	25	0	0	0	0	0
15	0	0	0	0	0.040	24	1	0	0	0	0
16	0	0	0	0	0.120	22	3	0	0	0	0
17	0	0	0	0	0.160	21	4	0	0	0	0
18	0	0	0	0	0.120	22	3	0	0	0	0
19	0	0	0	0	0.080	23	2	0	0	0	0
20	0	0	0	0	0.040	24	1	0	0	0	0
21	0	0	0	0	0	25	0	0	0	0	0
22	0	0	0	0	0.040	24	1	0	0	0	0
23	0	0	0	0	0	25	0	0	0	0	0
24	0	0	0	0	0	25	0	0	0	0	0
25	0	0	0	0	0.040	24	1	0	0	0	0
26	0	0	0	0	0.040	24	1	0	0	0	0
27	0	0	0	0	0.080	23	2	0	0	0	0
28	0	0	0	0	0	25	0	0	0	0	0
29	0	0	0	0	0.040	24	1	0	0	0	0
30	0	0	0	0	0.040	24	1	0	0	0	0
31	0	0	0	0	0.120	22	3	0	0	0	0
32	0	0	0	0	0.120	23	2	0	0	0	0
33	0	0	0	0	0.080	22	3	0	0	0	0
34	0	0	0	0	0.200	20	5	0	0	0	0
35	0	0	0	0	0	25	0	0	0	0	0
36	0	0	0	0	0.240	19	6	0	0	0	0
37	0	0	0	0	0.120	22	3	0	0	0	0
38	0	0	0	0	0.080	23	2	0	0	0	0
39	0	0	0	0	0.280	19	5	1	0	0	0
40	0	0	0	0	0.200	20	5	0	0	0	0
41	0	0	0	0	0	25	0	0	0	0	0
42	0	0	0	0	0	25	0	0	0	0	0
43	0	0	0	0	0	25	0	0	0	0	0
44	0	0	0	0	0.040	24	1	0	0	0	0
45	0	0	0	0	0	25	0	0	0	0	0
46	0	0	0	0	0.040	24	1	0	0	0	0
47	0	0	0	0	0	25	0	0	0	0	0
48	0	0	0	0	0	25	0	0	0	0	0
49	0	0	0	0	0.040	24	1	0	0	0	0
50	0	0	0	0	0.040	24	1	0	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # mets	MI percent
1	0	0	0	0	0	0.0	500	15	3.00
2	0	0	0	0	0	0.0	500	12	2.40
3	0	0	0	0	0	60.0	500	21	4.20
4	0	0	0	0	0	4.0	500	10	2.00
5	0	0	0	0	0	4.0	500	9	1.80
6	0	0	0	0	0	0.0	500	25	5.00
7	0	0	0	0	0	0.0	500	33	6.60
8	0	0	0	0	0	0.0	500	14	2.80
9	0	0	0	0	0	4.0	500	18	3.60
10	0	0	0	0	0	4.0	500	15	3.00
11	0	0	0	0	0	4.0	500	16	3.20
12	0	0	0	0	0	8.0	500	25	5.00
13	0	0	0	0	0	4.0	500	24	4.80
14	0	0	0	0	0	0.0	500	21	4.20
15	0	0	0	0	0	4.0	500	15	3.00
16	0	0	0	0	0	12.0	500	16	3.20
17	0	0	0	0	0	16.0	500	25	5.00
18	0	0	0	0	0	12.0	500	14	2.80
19	0	0	0	0	0	8.0	500	25	5.00
20	0	0	0	0	0	4.0	500	24	4.80
21	0	0	0	0	0	0.0	500	25	5.00
22	0	0	0	0	0	4.0	500	28	5.60
23	0	0	0	0	0	0.0	500	32	6.40
24	0	0	0	0	0	0.0	500	18	3.60
25	0	0	0	0	0	4.0	500	19	3.80
26	0	0	0	0	0	4.0	500	21	4.20
27	0	0	0	0	0	8.0	500	24	4.80
28	0	0	0	0	0	0.0	500	18	3.60
29	0	0	0	0	0	4.0	500	17	3.40
30	0	0	0	0	0	4.0	500	19	3.80
31	0	0	0	0	0	12.0	500	15	3.00
32	0	0	0	0	0	8.0	500	14	2.80
33	0	0	0	0	0	12.0	500	13	2.60
34	0	0	0	0	0	20.0	500	15	3.00
35	0	0	0	0	0	0.0	500	18	3.60
36	0	0	0	0	0	24.0	500	10	2.00
37	0	0	0	0	0	12.0	500	9	1.80
38	0	0	0	0	0	8.0	500	5	1.00
39	0	0	0	0	0	24.0	500	8	1.60
40	0	0	0	0	0	20.0	500	7	1.40
41	0	0	0	0	0	0.0	500	25	5.00
42	0	0	0	0	0	0.0	500	32	6.40
43	0	0	0	0	0	0.0	500	18	3.60
44	0	0	0	0	0	4.0	500	12	2.40
45	0	0	0	0	0	0.0	500	15	3.00
46	0	0	0	0	0	4.0	500	18	3.60
47	0	0	0	0	0	0.0	500	19	3.80
48	0	0	0	0	0	0.0	500	21	4.20
49	0	0	0	0	0	4.0	500	22	4.40
50	0	0	0	0	0	4.0	500	15	3.00

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
51	1104	A	MP	t	m	1000	72	25	2	0	3
52	1105	A	MP	t	m	1000	72	25	0	0	1
53	1106	A	MP	t	m	1000	72	25	0	0	0
54	1107	A	MP	t	m	1000	72	25	0	0	4
55	1108	A	MP	t	m	1000	72	25	0	0	3
56	1109	A	MP	t	m	2000	72	25	3	0	6
57	1110	A	MP	t	m	2000	72	25	3	0	2
58	1111	A	MP	t	m	2000	72	25	0	0	6
59	1112	A	MP	t	m	2000	72	25	0	0	3
60	1113	A	MP	t	m	2000	72	25	3	0	1
61	1114	A	MP	c	f	0	24	25	0	0	0
62	1115	A	MP	c	f	0	24	25	0	0	0
63	1116	A	MP	c	f	0	24	25	0	0	0
64	1117	A	MP	c	f	0	24	25	0	0	0
65	1118	A	MP	c	f	0	24	25	0	0	0
66	1119	A	MP	t	f	500	24	25	0	0	1
67	1120	A	MP	t	f	500	24	25	0	0	1
68	1121	A	MP	t	f	500	24	25	0	0	0
69	1122	A	MP	t	f	500	24	25	0	0	1
70	1123	A	MP	t	f	500	24	25	0	0	0
71	1124	A	MP	t	f	1000	24	25	0	0	1
72	1125	A	MP	t	f	1000	24	25	1	0	1
73	1126	A	MP	t	f	1000	24	25	0	0	2
74	1127	A	MP	t	f	1000	24	25	1	0	1
75	1128	A	MP	t	f	1000	24	25	0	0	0
76	1129	A	MP	t	f	2000	24	25	0	0	2
77	1130	A	MP	t	f	2000	24	25	1	0	2
78	1131	A	MP	t	f	2000	24	25	0	0	1
79	1132	A	MP	t	f	2000	24	25	3	0	3
80	1133	A	MP	t	f	2000	24	25	0	0	2
81	1134	A	MP	c	f	0	48	25	0	0	1
82	1135	A	MP	c	f	0	48	25	0	0	2
83	1136	A	MP	c	f	0	48	25	0	0	0
84	1137	A	MP	c	f	0	48	25	0	0	0
85	1138	A	MP	c	f	0	48	25	0	0	0
86	1139	A	MP	t	f	500	48	25	0	0	1
87	1140	A	MP	t	f	500	48	25	0	0	2
88	1141	A	MP	t	f	500	48	25	0	0	2
89	1142	A	MP	t	f	500	48	25	0	0	3
90	1143	A	MP	t	f	500	48	25	0	0	3
91	1144	A	MP	t	f	1000	48	25	0	0	3
92	1145	A	MP	t	f	1000	48	25	2	0	3
93	1146	A	MP	t	f	1000	48	25	0	0	2
94	1147	A	MP	t	f	1000	48	25	2	0	4
95	1148	A	MP	t	f	1000	48	25	0	0	1
96	1149	A	MP	t	f	2000	48	25	0	0	1
97	1150	A	MP	t	f	2000	48	25	0	0	3
98	1151	A	MP	t	f	2000	48	25	2	0	0
99	1152	A	MP	t	f	2000	48	25	0	0	6
100	1153	A	MP	t	f	2000	48	25	2	0	3

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
51	0	0	0	0	0.120	22	3	0	0	0	0
52	0	0	0	0	0.040	24	1	0	0	0	0
53	0	0	0	0	0	25	0	0	0	0	0
54	0	0	0	0	0.160	21	4	0	0	0	0
55	0	0	0	0	0.120	22	3	0	0	0	0
56	0	0	0	0	0.240	19	6	0	0	0	0
57	0	0	0	0	0.080	23	2	0	0	0	0
58	1	0	0	0	0.280	18	5	2	0	0	0
59	0	0	0	0	0.120	22	3	0	0	0	0
60	0	0	0	0	0.040	24	1	0	0	0	0
61	0	0	0	0	0	25	0	0	0	0	0
62	0	0	0	0	0	25	0	0	0	0	0
63	0	0	0	0	0	25	0	0	0	0	0
64	0	0	0	0	0	25	0	0	0	0	0
65	0	0	0	0	0	25	0	0	0	0	0
66	0	0	0	0	0.040	24	1	0	0	0	0
67	0	0	0	0	0.040	24	1	0	0	0	0
68	0	0	0	0	0	25	0	0	0	0	0
69	0	0	0	0	0.040	24	1	0	0	0	0
70	0	0	0	0	0	25	0	0	0	0	0
71	0	0	0	0	0.040	24	1	0	0	0	0
72	0	0	0	0	0.040	24	1	0	0	0	0
73	0	0	0	0	0.080	23	2	0	0	0	0
74	0	0	0	0	0.040	24	1	0	0	0	0
75	0	0	0	0	0	25	0	0	0	0	0
76	0	0	0	0	0.080	23	2	0	0	0	0
77	0	0	0	0	0.080	23	2	0	0	0	0
78	0	0	0	0	0.040	24	1	0	0	0	0
79	1	0	0	0	0.160	21	4	0	0	0	0
80	0	0	0	0	0.080	23	2	0	0	0	0
81	0	0	0	0	0.040	24	1	0	0	0	0
82	0	0	0	0	0.080	23	2	0	0	0	0
83	0	0	0	0	0	25	0	0	0	0	0
84	0	0	0	0	0	25	0	0	0	0	0
85	0	0	0	0	0	25	0	0	0	0	0
86	0	0	0	0	0.040	24	1	0	0	0	0
87	0	0	0	0	0.080	23	2	0	0	0	0
88	0	0	0	0	0.080	23	2	0	0	0	0
89	0	0	0	0	0.120	22	3	0	0	0	0
90	0	0	0	0	0.120	22	3	0	0	0	0
91	0	0	0	0	0.120	22	3	0	0	0	0
92	0	0	0	0	0.120	22	3	0	0	0	0
93	0	0	0	0	0.080	23	2	0	0	0	0
94	1	0	0	0	0.200	20	5	0	0	0	0
95	0	0	0	0	0.040	24	1	0	0	0	0
96	0	0	0	0	0.040	24	1	0	0	0	0
97	0	0	0	0	0.120	22	3	0	0	0	0
98	0	0	0	0	0	25	0	0	0	0	0
99	0	0	0	0	0.240	19	6	0	0	0	0
100	0	0	0	0	0.120	22	3	0	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
51	0	0	0	0	0	12.0	500	15	3.00
52	0	0	0	0	0	4.0	500	12	2.40
53	0	0	0	0	0	0.0	500	11	2.20
54	0	0	0	0	0	16.0	500	14	2.80
55	0	0	0	0	0	12.0	500	19	3.80
56	0	0	0	0	0	24.0	500	2	0.40
57	0	0	0	0	0	8.0	500	5	1.00
58	0	0	0	0	0	28.0	500	4	0.80
59	0	0	0	0	0	12.0	500	8	1.60
60	0	0	0	0	0	4.0	500	9	1.80
61	0	0	0	0	0	0.0	500	25	5.00
62	0	0	0	0	0	0.0	500	24	4.80
63	0	0	0	0	0	0.0	500	23	4.60
64	0	0	0	0	0	0.0	500	26	5.20
65	0	0	0	0	0	0.0	500	32	6.40
66	0	0	0	0	0	4.0	500	25	5.00
67	0	0	0	0	0	4.0	500	24	4.80
68	0	0	0	0	0	0.0	500	26	5.20
69	0	0	0	0	0	4.0	500	25	5.00
70	0	0	0	0	0	0.0	500	21	4.20
71	0	0	0	0	0	4.0	500	24	4.80
72	0	0	0	0	0	4.0	500	23	4.60
73	0	0	0	0	0	8.0	500	23	4.60
74	0	0	0	0	0	4.0	500	24	4.80
75	0	0	0	0	0	0.0	500	25	5.00
76	0	0	0	0	0	8.0	500	32	6.40
77	0	0	0	0	0	8.0	500	25	5.00
78	0	0	0	0	0	4.0	500	21	4.20
79	0	0	0	0	0	16.0	500	22	4.40
80	0	0	0	0	0	8.0	500	19	3.80
81	0	0	0	0	0	4.0	500	25	5.00
82	0	0	0	0	0	8.0	500	18	3.60
83	0	0	0	0	0	0.0	500	17	3.40
84	0	0	0	0	0	0.0	500	25	5.00
85	0	0	0	0	0	0.0	500	32	6.40
86	0	0	0	0	0	4.0	500	31	6.20
87	0	0	0	0	0	8.0	500	30	6.00
88	0	0	0	0	0	8.0	500	18	3.60
89	0	0	0	0	0	12.0	500	19	3.80
90	0	0	0	0	0	12.0	500	25	5.00
91	0	0	0	0	0	12.0	500	15	3.00
92	0	0	0	0	0	12.0	500	18	3.60
93	0	0	0	0	0	8.0	500	20	4.00
94	0	0	0	0	0	20.0	500	30	6.00
95	0	0	0	0	0	4.0	500	14	2.80
96	0	0	0	0	0	4.0	500	18	3.60
97	0	0	0	0	0	12.0	500	19	3.80
98	0	0	0	0	0	0.0	500	25	5.00
99	0	0	0	0	0	24.0	500	14	2.80
100	0	0	0	0	0	12.0	500	15	3.00

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
101	1154	A	MP	c	f	0	72	25	0	0	1
102	1155	A	MP	c	f	0	72	25	0	0	0
103	1156	A	MP	c	f	0	72	25	2	0	0
104	1157	A	MP	c	f	0	72	25	0	0	1
105	1158	A	MP	c	f	0	72	25	0	0	0
106	1159	A	MP	t	f	500	72	25	0	0	1
107	1160	A	MP	t	f	500	72	25	0	0	1
108	1161	A	MP	t	f	500	72	25	0	0	0
109	1162	A	MP	t	f	500	72	25	0	0	2
110	1163	A	MP	t	f	500	72	25	0	0	2
111	1164	A	MP	t	f	1000	72	25	1	0	3
112	1165	A	MP	t	f	1000	72	25	0	0	2
113	1166	A	MP	t	f	1000	72	25	2	0	1
114	1167	A	MP	t	f	1000	72	25	0	0	2
115	1168	A	MP	t	f	1000	72	25	0	0	1
116	1169	A	MP	t	f	2000	72	25	0	0	5
117	1170	A	MP	t	f	2000	72	25	0	0	1
118	1171	A	MP	t	f	2000	72	25	2	0	3
119	1172	A	MP	t	f	2000	72	25	0	0	1
120	1173	A	MP	t	f	2000	72	25	2	0	5
121	1174	A	MP	p	m	12.5	48	25	3	0	7
122	1175	A	MP	p	m	12.5	48	25	0	0	6
123	1176	A	MP	p	m	12.5	48	25	0	0	4
124	1177	A	MP	p	m	12.5	48	25	3	0	10
125	1178	A	MP	p	m	12.5	48	25	0	0	10
126	1179	A	MP	p	f	12.5	48	25	1	0	9
127	1180	A	MP	p	f	12.5	48	25	0	0	3
128	1181	A	MP	p	f	12.5	48	25	2	0	4
129	1182	A	MP	p	f	12.5	48	25	0	0	4
130	1183	A	MP	p	f	12.5	48	25	4	0	6
131	1054	B	BN	c	m	0	24	25	0	0	0
132	1055	B	BN	c	m	0	24	25	0	0	0
133	1056	B	BN	c	m	0	24	25	0	0	20
134	1057	B	BN	c	m	0	24	25	0	0	2
135	1058	B	BN	c	m	0	24	25	0	0	0
136	1059	B	BN	t	m	500	24	25	0	0	1
137	1060	B	BN	t	m	500	24	25	0	0	1
138	1061	B	BN	t	m	500	24	25	0	0	0
139	1062	B	BN	t	m	500	24	25	0	0	2
140	1063	B	BN	t	m	500	24	25	0	0	2
141	1064	B	BN	t	m	1000	24	25	0	0	2
142	1065	B	BN	t	m	1000	24	25	0	0	2
143	1066	B	BN	t	m	1000	24	25	2	0	0
144	1067	B	BN	t	m	1000	24	25	0	0	4
145	1068	B	BN	t	m	1000	24	25	0	0	2
146	1069	B	BN	t	m	2000	24	25	0	0	5
147	1070	B	BN	t	m	2000	24	25	0	0	3
148	1071	B	BN	t	m	2000	24	25	0	0	2
149	1072	B	BN	t	m	2000	24	25	0	0	4
150	1073	B	BN	t	m	2000	24	25	0	0	2

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
101	0	0	0	0	0.040	24	1	0	0	0	0
102	0	0	0	0	0	25	0	0	0	0	0
103	0	0	0	0	0	25	0	0	0	0	0
104	0	0	0	0	0.040	24	1	0	0	0	0
105	0	0	0	0	0	25	0	0	0	0	0
106	0	0	0	0	0.040	24	1	0	0	0	0
107	0	0	0	0	0.040	24	1	0	0	0	0
108	0	0	0	0	0	25	0	0	0	0	0
109	0	0	0	0	0.080	23	2	0	0	0	0
110	0	0	0	0	0.080	23	2	0	0	0	0
111	0	0	0	0	0.120	22	3	0	0	0	0
112	0	0	0	0	0.080	23	2	0	0	0	0
113	0	0	0	0	0.040	24	1	0	0	0	0
114	0	0	0	0	0.080	23	2	0	0	0	0
115	0	0	0	0	0.040	24	1	0	0	0	0
116	0	0	0	0	0.200	20	5	0	0	0	0
117	0	0	0	0	0.040	24	1	0	0	0	0
118	0	0	0	0	0.120	22	3	0	0	0	0
119	1	0	0	0	0.080	23	2	0	0	0	0
120	0	0	0	0	0.200	20	5	0	0	0	0
121	1	0	0	0	0.320	17	8	0	0	0	0
122	0	0	0	0	0.240	19	6	0	0	0	0
123	0	0	0	0	0.160	21	4	0	0	0	0
124	1	0	0	0	0.440	15	9	1	0	0	0
125	0	0	0	0	0.400	17	7	0	1	0	0
126	0	1	0	0	0.400	16	8	1	0	0	0
127	0	4	0	0	0.280	18	7	0	0	0	0
128	0	0	0	0	0.160	21	4	0	0	0	0
129	0	2	0	0	0.240	19	6	0	0	0	0
130	1	0	0	0	0.280	19	5	1	0	0	0
131	0	0	0	0	0	25	0	0	0	0	0
132	0	0	0	0	0	25	0	0	0	0	0
133	0	0	0	0	0.800	5	20	0	0	0	0
134	0	0	0	0	0.080	23	2	0	0	0	0
135	0	0	0	0	0	25	0	0	0	0	0
136	0	0	0	0	0.040	24	1	0	0	0	0
137	0	0	0	0	0.040	24	1	0	0	0	0
138	0	0	0	0	0	25	0	0	0	0	0
139	0	0	0	0	0.080	23	2	0	0	0	0
140	0	0	0	0	0.080	23	2	0	0	0	0
141	0	0	0	0	0.080	23	2	0	0	0	0
142	0	0	0	0	0.080	23	2	0	0	0	0
143	0	0	0	0	0	25	0	0	0	0	0
144	0	0	0	0	0.160	21	4	0	0	0	0
145	0	0	0	0	0.080	23	2	0	0	0	0
146	1	1	0	0	0.280	19	5	1	0	0	0
147	0	0	0	0	0.120	22	3	0	0	0	0
148	0	0	0	0	0.080	23	2	0	0	0	0
149	1	0	0	0	0.200	20	5	0	0	0	0
150	0	0	0	0	0.080	23	2	0	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
101	0	0	0	0	0	4.0	500	12	2.40
102	0	0	0	0	0	0.0	500	15	3.00
103	0	0	0	0	0	0.0	500	14	2.80
104	0	0	0	0	0	4.0	500	25	5.00
105	0	0	0	0	0	0.0	500	24	4.80
106	0	0	0	0	0	4.0	500	21	4.20
107	0	0	0	0	0	4.0	500	25	5.00
108	0	0	0	0	0	0.0	500	15	3.00
109	0	0	0	0	0	8.0	500	16	3.20
110	0	0	0	0	0	8.0	500	25	5.00
111	0	0	0	0	0	12.0	500	28	5.60
112	0	0	0	0	0	8.0	500	24	4.80
113	0	0	0	0	0	4.0	500	25	5.00
114	0	0	0	0	0	8.0	500	26	5.20
115	0	0	0	0	0	4.0	500	28	5.60
116	0	0	0	0	0	20.0	500	24	4.80
117	0	0	0	0	0	4.0	500	25	5.00
118	0	0	0	0	0	12.0	500	26	5.20
119	0	0	0	0	0	8.0	500	32	6.40
120	0	0	0	0	0	20.0	500	19	3.80
121	0	0	0	0	0	32.0	500	15	3.00
122	0	0	0	0	0	24.0	500	32	6.40
123	0	0	0	0	0	16.0	500	15	3.00
124	0	0	0	0	0	40.0	500	28	5.60
125	0	0	0	0	0	32.0	500	24	4.80
126	0	0	0	0	0	36.0	500	23	4.60
127	0	0	0	0	0	28.0	500	25	5.00
128	0	0	0	0	0	16.0	500	25	5.00
129	0	0	0	0	0	24.0	500	21	4.20
130	0	0	0	0	0	24.0	500	25	5.00
131	0	0	0	0	0	0.0	500	25	5.00
132	0	0	0	0	0	0.0	500	24	4.80
133	0	0	0	0	0	80.0	500	32	6.40
134	0	0	0	0	0	8.0	500	33	6.60
135	0	0	0	0	0	0.0	500	15	3.00
136	0	0	0	0	0	4.0	500	15	3.00
137	0	0	0	0	0	4.0	500	25	5.00
138	0	0	0	0	0	0.0	500	24	4.80
139	0	0	0	0	0	8.0	500	26	5.20
140	0	0	0	0	0	8.0	500	23	4.60
141	0	0	0	0	0	8.0	500	25	5.00
142	0	0	0	0	0	8.0	500	14	2.80
143	0	0	0	0	0	0.0	500	25	5.00
144	0	0	0	0	0	16.0	500	23	4.60
145	0	0	0	0	0	8.0	500	25	5.00
146	0	0	0	0	0	24.0	500	32	6.40
147	0	0	0	0	0	12.0	500	18	3.60
148	0	0	0	0	0	8.0	500	17	3.40
149	0	0	0	0	0	20.0	500	16	3.20
150	0	0	0	0	0	8.0	500	15	3.00

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
151	1074	B	BN	c	m	0	48	25	0	0	0
152	1075	B	BN	c	m	0	48	25	0	0	0
153	1076	B	BN	c	m	0	48	25	0	0	1
154	1077	B	BN	c	m	0	48	25	1	0	0
155	1078	B	BN	c	m	0	48	25	0	0	0
156	1079	B	BN	t	m	500	48	25	0	0	3
157	1080	B	BN	t	m	500	48	25	0	0	4
158	1081	B	BN	t	m	500	48	25	0	0	5
159	1082	B	BN	t	m	500	48	25	3	0	0
160	1083	B	BN	t	m	500	48	25	0	0	2
161	1084	B	BN	t	m	1000	48	25	0	0	4
162	1085	B	BN	t	m	1000	48	25	4	0	4
163	1086	B	BN	t	m	1000	48	25	0	0	8
164	1087	B	BN	t	m	1000	48	25	0	0	3
165	1088	B	BN	t	m	1000	48	25	3	0	0
166	1089	B	BN	t	m	2000	48	25	0	0	8
167	1090	B	BN	t	m	2000	48	25	3	0	2
168	1091	B	BN	t	m	2000	48	25	0	0	7
169	1092	B	BN	t	m	2000	48	25	0	0	3
170	1093	B	BN	t	m	2000	48	25	4	0	3
171	1094	B	BN	c	m	0	72	25	0	0	0
172	1095	B	BN	c	m	0	72	25	0	0	0
173	1096	B	BN	c	m	0	72	25	0	0	0
174	1097	B	BN	c	m	0	72	25	0	0	1
175	1098	B	BN	c	m	0	72	25	3	0	0
176	1099	B	BN	t	m	500	72	25	0	0	1
177	1100	B	BN	t	m	500	72	25	0	0	1
178	1101	B	BN	t	m	500	72	25	0	0	2
179	1102	B	BN	t	m	500	72	25	0	0	0
180	1103	B	BN	t	m	500	72	25	0	0	2
181	1104	B	BN	t	m	1000	72	25	0	0	2
182	1105	B	BN	t	m	1000	72	25	0	0	3
183	1106	B	BN	t	m	1000	72	25	0	0	4
184	1107	B	BN	t	m	1000	72	25	0	0	0
185	1108	B	BN	t	m	1000	72	25	2	0	2
186	1109	B	BN	t	m	2000	72	25	0	0	1
187	1110	B	BN	t	m	2000	72	25	0	0	3
188	1111	B	BN	t	m	2000	72	25	0	0	8
189	1112	B	BN	t	m	2000	72	25	0	0	5
190	1113	B	BN	t	m	2000	72	25	0	0	5
191	1114	B	BN	c	f	0	24	25	2	0	0
192	1115	B	BN	c	f	0	24	25	0	0	0
193	1116	B	BN	c	f	0	24	25	0	0	1
194	1117	B	BN	c	f	0	24	25	0	0	1
195	1118	B	BN	c	f	0	24	25	0	0	1
196	1119	B	BN	t	f	500	24	25	0	0	0
197	1120	B	BN	t	f	500	24	25	0	0	0
198	1121	B	BN	t	f	500	24	25	0	0	1
199	1122	B	BN	t	f	500	24	25	0	0	2
200	1123	B	BN	t	f	500	24	25	3	0	1

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
151	0	0	0	0	0	25	0	0	0	0	0
152	0	0	0	0	0	25	0	0	0	0	0
153	0	0	0	0	0.040	24	1	0	0	0	0
154	0	0	0	0	0	25	0	0	0	0	0
155	0	0	0	0	0	25	0	0	0	0	0
156	0	0	0	0	0.120	22	3	0	0	0	0
157	0	0	0	0	0.160	21	4	0	0	0	0
158	0	1	0	0	0.240	19	6	0	0	0	0
159	0	0	0	0	0	25	0	0	0	0	0
160	0	0	0	0	0.080	23	2	0	0	0	0
161	0	0	0	0	0.160	21	4	0	0	0	0
162	1	0	0	0	0.200	20	4	1	0	0	0
163	1	1	0	0	0.400	17	7	0	1	0	0
164	0	0	0	0	0.120	22	3	0	0	0	0
165	0	3	0	0	0.120	22	3	0	0	0	0
166	1	0	0	0	0.360	16	9	0	0	0	0
167	0	0	0	0	0.080	23	2	0	0	0	0
168	0	1	0	0	0.320	18	6	1	0	0	0
169	0	3	0	0	0.240	21	3	0	1	0	0
170	0	0	0	0	0.120	22	3	0	0	0	0
171	0	0	0	0	0	25	0	0	0	0	0
172	0	0	0	0	0	25	0	0	0	0	0
173	0	0	0	0	0	25	0	0	0	0	0
174	0	0	0	0	0.040	24	1	0	0	0	0
175	0	0	0	0	0	25	0	0	0	0	0
176	0	0	0	0	0.040	24	1	0	0	0	0
177	0	0	0	0	0.040	24	1	0	0	0	0
178	0	0	0	0	0.080	23	2	0	0	0	0
179	0	0	0	0	0	25	0	0	0	0	0
180	0	0	0	0	0.080	23	2	0	0	0	0
181	0	0	0	0	0.080	23	2	0	0	0	0
182	0	0	0	0	0.120	22	3	0	0	0	0
183	2	1	0	0	0.280	19	5	1	0	0	0
184	0	0	0	0	0	25	0	0	0	0	0
185	0	0	0	0	0.080	23	2	0	0	0	0
186	0	0	0	0	0.040	24	1	0	0	0	0
187	0	0	0	0	0.120	22	3	0	0	0	0
188	0	0	0	0	0.320	18	6	1	0	0	0
189	1	0	0	0	0.240	21	2	2	0	0	0
190	0	0	0	0	0.200	20	5	0	0	0	0
191	0	0	0	0	0	25	0	0	0	0	0
192	0	0	0	0	0	25	0	0	0	0	0
193	0	0	0	0	0.040	24	1	0	0	0	0
194	0	0	0	0	0.040	24	1	0	0	0	0
195	0	0	0	0	0.040	24	1	0	0	0	0
196	0	0	0	0	0	25	0	0	0	0	0
197	0	0	0	0	0	25	0	0	0	0	0
198	0	0	0	0	0.040	24	1	0	0	0	0
199	0	0	0	0	0.080	23	2	0	0	0	0
200	0	0	0	0	0.040	24	1	0	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
151	0	0	0	0	0	0.0	500	25	5.00
152	0	0	0	0	0	0.0	500	35	7.00
153	0	0	0	0	0	4.0	500	32	6.40
154	0	0	0	0	0	0.0	500	24	4.80
155	0	0	0	0	0	0.0	500	26	5.20
156	0	0	0	0	0	12.0	500	15	3.00
157	0	0	0	0	0	16.0	500	18	3.60
158	0	0	0	0	0	24.0	500	17	3.40
159	0	0	0	0	0	0.0	500	16	3.20
160	0	0	0	0	0	8.0	500	14	2.80
161	0	0	0	0	0	16.0	500	12	2.40
162	0	0	0	0	0	20.0	500	10	2.00
163	0	0	0	0	0	32.0	500	15	3.00
164	0	0	0	0	0	12.0	500	18	3.60
165	0	0	0	0	0	12.0	500	10	2.00
166	0	0	0	0	0	36.0	500	9	1.80
167	0	0	0	0	0	8.0	500	5	1.00
168	0	0	0	0	0	28.0	500	2	0.40
169	0	0	0	0	0	16.0	500	1	0.20
170	0	0	0	0	0	12.0	500	8	1.60
171	0	0	0	0	0	0.0	500	25	5.00
172	0	0	0	0	0	0.0	500	26	5.20
173	0	0	0	0	0	0.0	500	24	4.80
174	0	0	0	0	0	4.0	500	25	5.00
175	0	0	0	0	0	0.0	500	28	5.60
176	0	0	0	0	0	4.0	500	32	6.40
177	0	0	0	0	0	4.0	500	15	3.00
178	0	0	0	0	0	8.0	500	24	4.80
179	0	0	0	0	0	0.0	500	25	5.00
180	0	0	0	0	0	8.0	500	15	3.00
181	0	0	0	0	0	8.0	500	25	5.00
182	0	0	0	0	0	12.0	500	15	3.00
183	0	0	0	0	0	24.0	500	14	2.80
184	0	0	0	0	0	0.0	500	15	3.00
185	0	0	0	0	0	8.0	500	12	2.40
186	0	0	0	0	0	4.0	500	11	2.20
187	0	0	0	0	0	12.0	500	12	2.40
188	0	0	0	0	0	28.0	500	13	2.60
189	0	0	0	0	0	16.0	500	10	2.00
190	0	0	0	0	0	20.0	500	2	0.40
191	0	0	0	0	0	0.0	500	25	5.00
192	0	0	0	0	0	0.0	500	32	6.40
193	0	0	0	0	0	4.0	500	25	5.00
194	0	0	0	0	0	4.0	500	23	4.60
195	0	0	0	0	0	4.0	500	21	4.20
196	0	0	0	0	0	0.0	500	24	4.80
197	0	0	0	0	0	0.0	500	25	5.00
198	0	0	0	0	0	4.0	500	25	5.00
199	0	0	0	0	0	8.0	500	25	5.00
200	0	0	0	0	0	4.0	500	21	4.20

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
201	1124	B	BN	t	f	1000	24	25	0	0	1
202	1125	B	BN	t	f	1000	24	25	0	0	1
203	1126	B	BN	t	f	1000	24	25	0	0	2
204	1127	B	BN	t	f	1000	24	25	0	0	3
205	1128	B	BN	t	f	1000	24	25	0	0	1
206	1129	B	BN	t	f	2000	24	25	0	0	1
207	1130	B	BN	t	f	2000	24	25	3	0	3
208	1131	B	BN	t	f	2000	24	25	0	0	4
209	1132	B	BN	t	f	2000	24	25	1	0	3
210	1133	B	BN	t	f	2000	24	25	1	0	1
211	1134	B	BN	c	f	0	48	25	0	0	0
212	1135	B	BN	c	f	0	48	25	0	0	0
213	1136	B	BN	c	f	0	48	25	0	0	0
214	1137	B	BN	c	f	0	48	25	0	0	0
215	1138	B	BN	c	f	0	48	25	1	0	0
216	1139	B	BN	t	f	500	48	25	0	0	2
217	1140	B	BN	t	f	500	48	25	0	0	1
218	1141	B	BN	t	f	500	48	25	1	0	0
219	1142	B	BN	t	f	500	48	25	1	0	2
220	1143	B	BN	t	f	500	48	25	0	0	1
221	1144	B	BN	t	f	1000	48	25	0	0	1
222	1145	B	BN	t	f	1000	48	25	0	0	1
223	1146	B	BN	t	f	1000	48	25	1	0	2
224	1147	B	BN	t	f	1000	48	25	0	0	3
225	1148	B	BN	t	f	1000	48	25	1	0	1
226	1149	B	BN	t	f	2000	48	25	0	0	5
227	1150	B	BN	t	f	2000	48	25	0	0	4
228	1151	B	BN	t	f	2000	48	25	1	0	5
229	1152	B	BN	t	f	2000	48	25	1	0	0
230	1153	B	BN	t	f	2000	48	25	0	0	5
231	1154	B	BN	c	f	0	72	25	0	0	0
232	1155	B	BN	c	f	0	72	25	0	0	0
233	1156	B	BN	c	f	0	72	25	0	0	0
234	1157	B	BN	c	f	0	72	25	2	0	2
235	1158	B	BN	c	f	0	72	25	0	0	0
236	1159	B	BN	t	f	500	72	25	0	0	1
237	1160	B	BN	t	f	500	72	25	1	0	1
238	1161	B	BN	t	f	500	72	25	0	0	1
239	1162	B	BN	t	f	500	72	25	0	0	2
240	1163	B	BN	t	f	500	72	25	0	0	0
241	1164	B	BN	t	f	1000	72	25	0	0	2
242	1165	B	BN	t	f	1000	72	25	0	0	3
243	1166	B	BN	t	f	1000	72	25	0	0	3
244	1167	B	BN	t	f	1000	72	25	0	0	1
245	1168	B	BN	t	f	1000	72	25	0	0	0
246	1169	B	BN	t	f	2000	72	25	1	0	5
247	1170	B	BN	t	f	2000	72	25	0	0	3
248	1171	B	BN	t	f	2000	72	25	1	0	1
249	1172	B	BN	t	f	2000	72	25	0	0	4
250	1173	B	BN	t	f	2000	72	25	3	0	3

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
201	0	0	0	0	0.040	24	1	0	0	0	0
202	0	0	0	0	0.040	24	1	0	0	0	0
203	0	0	0	0	0.080	23	2	0	0	0	0
204	0	0	0	0	0.120	22	3	0	0	0	0
205	0	0	0	0	0.040	24	1	0	0	0	0
206	1	0	0	0	0.080	23	2	0	0	0	0
207	0	0	0	0	0.120	22	3	0	0	0	0
208	0	0	0	0	0.160	21	4	0	0	0	0
209	0	0	0	0	0.120	22	3	0	0	0	0
210	0	1	0	0	0.080	23	2	0	0	0	0
211	0	0	0	0	0	25	0	0	0	0	0
212	0	0	0	0	0	25	0	0	0	0	0
213	0	0	0	0	0	25	0	0	0	0	0
214	0	0	0	0	0	25	0	0	0	0	0
215	0	0	0	0	0	25	0	0	0	0	0
216	0	0	0	0	0.080	23	2	0	0	0	0
217	0	0	0	0	0.040	24	1	0	0	0	0
218	0	0	0	0	0	25	0	0	0	0	0
219	0	0	0	0	0.080	23	2	0	0	0	0
220	0	0	0	0	0.040	24	1	0	0	0	0
221	1	0	0	0	0.080	23	2	0	0	0	0
222	0	0	0	0	0.040	24	1	0	0	0	0
223	0	0	0	0	0.080	23	2	0	0	0	0
224	0	0	0	0	0.120	22	3	0	0	0	0
225	1	1	0	0	0.120	22	3	0	0	0	0
226	1	0	0	0	0.240	19	6	0	0	0	0
227	0	0	0	0	0.160	21	4	0	0	0	0
228	0	0	0	0	0.200	20	5	0	0	0	0
229	0	0	0	0	0	25	0	0	0	0	0
230	1	0	0	0	0.240	19	6	0	0	0	0
231	0	0	0	0	0	25	0	0	0	0	0
232	0	0	0	0	0	25	0	0	0	0	0
233	0	0	0	0	0	25	0	0	0	0	0
234	0	0	0	0	0.080	23	2	0	0	0	0
235	0	0	0	0	0	25	0	0	0	0	0
236	0	0	0	0	0.040	24	1	0	0	0	0
237	0	0	0	0	0.040	24	1	0	0	0	0
238	0	0	0	0	0.040	24	1	0	0	0	0
239	0	0	0	0	0.080	23	2	0	0	0	0
240	0	0	0	0	0	25	0	0	0	0	0
241	1	0	0	0	0.120	22	3	0	0	0	0
242	0	0	0	0	0.120	22	3	0	0	0	0
243	0	0	0	0	0.120	22	3	0	0	0	0
244	0	0	0	0	0.040	24	1	0	0	0	0
245	0	0	0	0	0	25	0	0	0	0	0
246	1	0	0	0	0.240	19	6	0	0	0	0
247	0	0	0	0	0.120	22	3	0	0	0	0
248	0	0	0	0	0.040	24	1	0	0	0	0
249	0	0	0	0	0.160	21	4	0	0	0	0
250	0	2	0	0	0.200	20	5	0	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
201	0	0	0	0	0	4.0	500	20	4.00
202	0	0	0	0	0	4.0	500	30	6.00
203	0	0	0	0	0	8.0	500	21	4.20
204	0	0	0	0	0	12.0	500	25	5.00
205	0	0	0	0	0	4.0	500	21	4.20
206	0	0	0	0	0	8.0	500	25	5.00
207	0	0	0	0	0	12.0	500	32	6.40
208	0	0	0	0	0	16.0	500	14	2.80
209	0	0	0	0	0	12.0	500	18	3.60
210	0	0	0	0	0	8.0	500	19	3.80
211	0	0	0	0	0	0.0	500	15	3.00
212	0	0	0	0	0	0.0	500	19	3.80
213	0	0	0	0	0	0.0	500	32	6.40
214	0	0	0	0	0	0.0	500	35	7.00
215	0	0	0	0	0	0.0	500	35	7.00
216	0	0	0	0	0	8.0	500	15	3.00
217	0	0	0	0	0	4.0	500	25	5.00
218	0	0	0	0	0	0.0	500	24	4.80
219	0	0	0	0	0	8.0	500	28	5.60
220	0	0	0	0	0	4.0	500	24	4.80
221	0	0	0	0	0	8.0	500	26	5.20
222	0	0	0	0	0	4.0	500	27	5.40
223	0	0	0	0	0	8.0	500	42	8.40
224	0	0	0	0	0	12.0	500	15	3.00
225	0	0	0	0	0	12.0	500	25	5.00
226	0	0	0	0	0	24.0	500	32	6.40
227	0	0	0	0	0	16.0	500	25	5.00
228	0	0	0	0	0	20.0	500	32	6.40
229	0	0	0	0	0	0.0	500	15	3.00
230	0	0	0	0	0	24.0	500	24	4.80
231	0	0	0	0	0	0.0	500	25	5.00
232	0	0	0	0	0	0.0	500	26	5.20
233	0	0	0	0	0	0.0	500	24	4.80
234	0	0	0	0	0	8.0	500	25	5.00
235	0	0	0	0	0	0.0	500	32	6.40
236	0	0	0	0	0	4.0	500	32	6.40
237	0	0	0	0	0	4.0	500	21	4.20
238	0	0	0	0	0	4.0	500	20	4.00
239	0	0	0	0	0	8.0	500	19	3.80
240	0	0	0	0	0	0.0	500	18	3.60
241	0	0	0	0	0	12.0	500	20	4.00
242	0	0	0	0	0	12.0	500	25	5.00
243	0	0	0	0	0	12.0	500	21	4.20
244	0	0	0	0	0	4.0	500	24	4.80
245	0	0	0	0	0	0.0	500	19	3.80
246	0	0	0	0	0	24.0	500	18	3.60
247	0	0	0	0	0	12.0	500	25	5.00
248	0	0	0	0	0	4.0	500	26	5.20
249	0	0	0	0	0	16.0	500	15	3.00
250	0	0	0	0	0	20.0	500	14	2.80

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
251	1174	B	BN	p	m	12.5	48	25	0	0	9
252	1175	B	BN	p	m	12.5	48	25	3	0	7
253	1176	B	BN	p	m	12.5	48	25	0	0	5
254	1177	B	BN	p	m	12.5	48	25	1	0	0
255	1178	B	BN	p	m	12.5	48	25	0	0	4
256	1179	B	BN	p	f	12.5	48	25	0	0	4
257	1180	B	BN	p	f	12.5	48	25	5	0	3
258	1181	B	BN	p	f	12.5	48	25	0	0	7
259	1182	B	BN	p	f	12.5	48	25	0	0	4
260	1183	B	BN	p	f	12.5	48	25	4	0	5

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
251	2	3	0	0	0.560	14	8	3	0	0	0
252	3	1	0	0	0.440	15	9	1	0	0	0
253	1	0	0	0	0.240	19	6	0	0	0	0
254	0	0	0	0	0	25	0	0	0	0	0
255	0	0	0	0	0.160	21	4	0	0	0	0
256	1	0	0	0	0.200	20	5	0	0	0	0
257	0	0	0	0	0.120	22	3	0	0	0	0
258	0	0	0	0	0.280	18	7	0	0	0	0
259	0	0	0	0	0.160	21	4	0	0	0	0
260	0	0	0	0	0.200	20	5	0	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
251	0	0	0	0	0	44.0	500	15	3.00
252	0	0	0	0	0	40.0	500	25	5.00
253	0	0	0	0	0	24.0	500	32	6.40
254	0	0	0	0	0	0.0	500	32	6.40
255	0	0	0	0	0	16.0	500	25	5.00
256	0	0	0	0	0	20.0	500	24	4.80
257	0	0	0	0	0	12.0	500	26	5.20
258	0	0	0	0	0	28.0	500	28	5.60
259	0	0	0	0	0	16.0	500	29	5.80
260	0	0	0	0	0	20.0	500	27	5.40

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Pct.	Mean Pct.
1	3	0.0	24.0	m	60.000	13.600
2	133	0.0	24.0	m	80.000	17.600

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	30.014	24	0.1843
Sex	8.226	12	0.7673
Time	30.904	8	0.0001

filename: C:\CA\CATEST01.ILS date: time:

Time = 24.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	4	200	2.0000	1.0690		
500.00	8	250	3.2000	0.9978	0.2162	
1000.00	15	250	6.0000	1.4907	0.0180	*
2000.00	31	250	12.4000	1.9276	0.0000	*

Time = 48.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	3	250	1.2000	0.6110		
500.00	20	250	8.0000	2.3851	0.0001	*
1000.00	36	250	14.4000	2.6800	0.0000	*
2000.00	47	250	18.8000	2.9242	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Time = 72.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	2	250	0.8000	0.5333		
500.00	9	250	3.6000	0.9333	0.0164	*
1000.00	24	250	9.6000	2.3247	0.0000	*
2000.00	39	250	15.6000	2.8875	0.0000	*

Time = 24.00 (Females) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	3	250	1.2000	0.6110		
500.00	7	250	2.8000	0.8537	0.1007	
1000.00	13	250	5.2000	1.0414	0.0055	*
2000.00	25	250	10.0000	1.2293	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Time = 48.00 (Females) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	3	250	1.2000	0.8537		
500.00	17	250	6.8000	1.2000	0.0007	*
1000.00	25	250	10.0000	1.4907	0.0000	*
2000.00	34	250	13.6000	3.0521	0.0000	*

Time = 72.00 (Females) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	4	250	1.6000	0.8844		
500.00	11	250	4.4000	0.9333	0.0332	*
1000.00	19	250	7.6000	1.3920	0.0007	*
2000.00	35	250	14.0000	2.2509	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Pct.	Mean Pct.
1	3	0.0	24.0	m	60.000	13.600
2	133	0.0	24.0	m	80.000	17.600

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	30.014	24	0.1843
Sex	8.226	12	0.7673
Time	30.904	8	0.0001

filename: C:\CA\CATEST01.ILS date: time:

Time = 24.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	7	450	1.5556	0.5729		
500.00	15	500	3.0000	0.6407	0.0697	
1000.00	28	500	5.6000	0.8897	0.0005	*
2000.00	56	500	11.2000	1.1462	0.0000	*

Time = 48.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	6	500	1.2000	0.5109		
500.00	37	500	7.4000	1.3067	0.0000	*
1000.00	61	500	12.2000	1.5755	0.0000	*
2000.00	81	500	16.2000	2.1418	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Time = 72.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	6	500	1.2000	0.5109		
500.00	20	500	4.0000	0.6489	0.0027	*
1000.00	43	500	8.6000	1.3385	0.0000	*
2000.00	74	500	14.8000	1.7912	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Pct.	Mean Pct.
1	3	0.0	24.0	m	60.000	13.600
2	133	0.0	24.0	m	80.000	17.600

filename: C:\CA\CATEST01.ILS date: time:

Time = 48.00 (Males) for 067889

alpha = 0.050

One tailed test (binomial) for chromosomal aberration (pct. damaged cells) (with positive controls)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	3	250	1.2000	0.6110		
12.50	67	250	26.8000	4.3019	0.0000	*

Time = 48.00 (Females) for 067889

alpha = 0.050

One tailed test (binomial) for chromosomal aberration (pct. damaged cells) (with positive controls)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance	
0.00	3	250	1.2000	0.8537		
12.50	56	250	22.4000	2.2470	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	27.057	24	0.3018
Sex	4.281	12	0.9778
Time	21.975	8	0.0050

filename: C:\CA\CATEST01.ILS date: time:

Time = 24.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	4	200	0.0200	0.0107		
500.00	8	250	0.0320	0.010	0.2193	
1000.00	15	250	0.0600	0.0149	0.0201	*
2000.00	32	250	0.1280	0.0222	0.0000	*

Time = 48.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	3	250	0.0120	0.0061		
500.00	20	250	0.0800	0.0239	0.0002	*
1000.00	39	250	0.1560	0.0340	0.0000	*
2000.00	51	250	0.2040	0.0318	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Time = 72.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	2	250	0.0080	0.0053		
500.00	9	250	0.0360	0.0093	0.0174	*
1000.00	25	250	0.1000	0.0262	0.0000	*
2000.00	44	250	0.1760	0.0359	0.0000	*

Time = 24.00 (Females) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	3	250	0.0120	0.0061		
500.00	7	250	0.0280	0.0085	0.1030	
1000.00	13	250	0.0520	0.0104	0.0062	*
2000.00	25	250	0.1000	0.0123	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Time = 48.00 (Females) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	3	250	0.0120	0.0085		
500.00	17	250	0.0680	0.0120	0.0009	*
1000.00	25	250	0.1000	0.0149	0.0000	*
2000.00	34	250	0.1360	0.0305	0.0000	*

Time = 72.00 (Females) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	4	250	0.0160	0.0088		
500.00	11	250	0.0440	0.0093	0.0354	*
1000.00	19	250	0.0760	0.0139	0.0009	*
2000.00	35	250	0.1400	0.0225	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Abs/Cell	Av Abs/Cell
1	3	0.0	24.0	m	0.600	0.136
2	133	0.0	24.0	m	0.800	0.176

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	27.057	24	0.3018
Sex	4.281	12	0.9778
Time	21.975	8	0.0050

filename: C:\CA\CATEST01.ILS date: time:

Time = 24.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	7	450	0.0156	0.0057		
500.00	15	500	0.0300	0.0064	0.0720	
1000.00	28	500	0.0560	0.0089	0.0006	*
2000.00	57	500	0.1140	0.0127	0.0000	*

Time = 48.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	6	500	0.0120	0.0051		
500.00	37	500	0.0740	0.0131	0.0000	*
1000.00	64	500	0.1280	0.0192	0.0000	*
2000.00	85	500	0.1700	0.0228	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Abs/Cell	Av Abs/Cell
1	3	0.0	24.0	m	0.600	0.136
2	133	0.0	24.0	m	0.800	0.176

filename: C:\CA\CATEST01.ILS date: time:

Time = 48.00 (Males) for 067889

alpha = 0.050

One tailed test (Poisson) for chromosomal aberration (total aberrations) (with positive controls)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	3	250	0.0120	0.0061		
12.50	74	250	0.2960	0.0531	0.0000	*

Time = 48.00 (Females) for 067889

alpha = 0.050

One tailed test (Poisson) for chromosomal aberration (total aberrations) (with positive controls)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	3	250	0.0120	0.0085		
12.50	58	250	0.2320	0.0259	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Time = 72.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	6	500	0.0120	0.0051		
500.00	20	500	0.0400	0.0065	0.0030	*
1000.00	44	500	0.0880	0.0147	0.0000	*
2000.00	79	500	0.1580	0.0210	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Endpoint: Mitotic Index

Variance inflation factor: 1.341
Alpha: 0.050

Factor	Deviance	df	p
Scorer	52.058	24	0.0008
Sex	206.145	24	0.0000
Time	136.872	32	0.0000

filename: C:\CA\CATEST01.ILS date: time:

Time = 24.00 (Males) for 067889

p = 0.768
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance	
0.00	196	5000	3.9200	0.5531		
500.00	218	5000	4.3600	0.3874	0.8298	
1000.00	213	5000	4.2600	0.2876	0.7707	
2000.00	202	5000	4.0400	0.3745	0.6045	

Time = 48.00 (Males) for 067889

p = 0.000
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance	
0.00	264	5000	5.2800	0.3492		
500.00	179	5000	3.5800	0.1849	0.0002	*
1000.00	140	5000	2.8000	0.1789	0.0000	*
2000.00	64	5000	1.2800	0.1937	0.0000	*

filename: C:\CA\CATEST01.ILS date: time:

Time = 72.00 (Males) for 067889

p = 0.000
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance	
0.00	230	5000	4.6000	0.3876		
500.00	206	5000	4.1200	0.3441	0.1551	
1000.00	152	5000	3.0400	0.2596	0.0002	*
2000.00	76	5000	1.5200	0.2585	0.0000	*

Time = 24.00 (Females) for 067889

p = 0.697
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	256	5000	5.1200	0.2313	
500.00	241	5000	4.8200	0.1093	0.2756
1000.00	236	5000	4.7200	0.1794	0.2123
2000.00	227	5000	4.5400	0.3724	0.1214

filename: C:\CA\CATEST01.ILS date: time:

Time = 48.00 (Females) for 067889

p = 0.572
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	253	5000	5.0600	0.4927	
500.00	239	5000	4.7800	0.3299	0.2881
1000.00	232	5000	4.6400	0.5504	0.1993
2000.00	219	5000	4.3800	0.4263	0.0831

Time = 72.00 (Females) for 067889

p = 0.707
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	222	5000	4.4400	0.4020	
500.00	212	5000	4.2400	0.3180	0.3359
1000.00	240	5000	4.8000	0.1978	0.7705
2000.00	224	5000	4.4800	0.3593	0.5333

filename: C:\CA\CATEST01.ILS date: time:

Time = 48.00 (Males) for 067889

alpha = 0.050

Likelihood ratio for mitotic index (with positive controls)

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	264	5000	5.2800	0.3492	
12.50	243	5000	4.8600	0.4483	0.1692

Time = 48.00 (Females) for 067889

alpha = 0.050

Likelihood ratio for mitotic index (with positive controls)

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	253	5000	5.0600	0.4927	
12.50	253	5000	5.0600	0.1492	0.5000

SAMPLE TEST DATA

CATESTO2

C:\CA\CATEST02.ILS listed at on

EXPERIMENT	CA-TEST 02
Record	121
Laboratory	ILS
Lab Book	III
Date Started	06/18/90
Date Completed	08/01/90
Slides Coded By ...	MP
Staining Method ...	GIEMSA
Scored By	CJH
Entered By	MP
Entry Date	07/25/90
Proofed By	DC

Remarks .....

TEST ARTICLE	067889
Receipt Date	04/20/90
CAS #	UNKNOWN
Source / Lot	RADIAN 067H3
Appearance	ORANGE POWDER
Purity	UNKNOWN
Stability	1 YEAR
Storage Conditions	ROOM TEMPERATURE
Solubility	INSOLUBLE IN WATER
Hazard Information	TREAT AS CARCINOGEN

Remarks .....

VEHICLE	CORN OIL
Source / Lot	SIGMA/13F100
Purity	UNKNOWN
Stability	1 YEAR
Storage Conditions	ROOM TEMPERATURE

Remarks ..... _____

POSITIVE CONTROL ...	991870
Receipt Date	01/22/90
CAS #	UNKNOWN
Source / Lot	RADIAN/110BD
Appearance	WHITE POWDER
Purity	UNKNOWN
Stability	1 YEAR
Storage Conditions	ROOM TEMPERATURE
Solubility	INSOLUBLE IN WATER
Hazard Information	CARCINOGEN

Remarks ..... _____

TEST SYSTEM

Species		MOUSE
Strain		B6C3F1
Supplier		TACONIC FARMS
Received		05/01/90
Quarantined	From	05/01
	Until	05/15

Routine Husbandry Conditions? (y/n) Y

	Age		Weight	
Sex	Fr.	To	Fr.	To
M	11	11	32.0	34.0
F	11	11	27.0	29.0

Age units WEEKS Weight units GRAM

Remarks _____

TREATMENT

Date Started	06/18/90
Date Completed ...	06/21/90
Route	IP
Volume	0.4
Doses	0, 500, 1000, 2000
Dose Units	MG/KG
Number Treatments	1
Treatment Duration	NA
Treatment Date ...	06/18/90
Treatment Interval	NA
Number Samples ...	3
Sample Date	06/19;06/20;06/21
Sample Interval ..	24 HR
Tissue Cell Type	_____
Remarks	_____

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
1	1054	A	MP	c	m	0	24	25	0	0	2
2	1055	A	MP	c	m	0	24	25	1	0	2
3	1056	A	MP	c	m	0	24	25	0	0	15
4	1057	A	MP	c	m	0	24	25	0	0	2
5	1058	A	MP	c	m	0	24	25	0	0	2
6	1059	A	MP	t	m	500	24	25	0	0	0
7	1060	A	MP	t	m	500	24	25	0	0	0
8	1061	A	MP	t	m	500	24	25	0	0	0
9	1062	A	MP	t	m	500	24	25	0	0	1
10	1063	A	MP	t	m	500	24	25	0	0	1
11	1064	A	MP	t	m	1000	24	25	1	0	1
12	1065	A	MP	t	m	1000	24	25	0	0	2
13	1066	A	MP	t	m	1000	24	25	0	0	1
14	1067	A	MP	t	m	1000	24	25	0	0	0
15	1068	A	MP	t	m	1000	24	25	1	0	1
16	1069	A	MP	t	m	2000	24	25	1	0	1
17	1070	A	MP	t	m	2000	24	25	1	0	4
18	1071	A	MP	t	m	2000	24	25	0	0	3
19	1072	A	MP	t	m	2000	24	25	0	0	2
20	1073	A	MP	t	m	2000	24	25	1	0	1
21	1074	A	MP	c	m	0	48	25	0	0	1
22	1075	A	MP	c	m	0	48	25	0	0	3
23	1076	A	MP	c	m	0	48	25	0	0	2
24	1077	A	MP	c	m	0	48	25	0	0	2
25	1078	A	MP	c	m	0	48	25	0	0	1
26	1079	A	MP	t	m	500	48	25	0	0	1
27	1080	A	MP	t	m	500	48	25	1	0	2
28	1081	A	MP	t	m	500	48	25	0	0	0
29	1082	A	MP	t	m	500	48	25	0	0	1
30	1083	A	MP	t	m	500	48	25	0	0	1
31	1084	A	MP	t	m	1000	48	25	3	0	1
32	1085	A	MP	t	m	1000	48	25	0	0	2
33	1086	A	MP	t	m	1000	48	25	0	0	3
34	1087	A	MP	t	m	1000	48	25	1	0	5
35	1088	A	MP	t	m	1000	48	25	0	0	0
36	1089	A	MP	t	m	2000	48	25	3	0	6
37	1090	A	MP	t	m	2000	48	25	0	0	3
38	1091	A	MP	t	m	2000	48	25	0	0	2
39	1092	A	MP	t	m	2000	48	25	0	0	7
40	1093	A	MP	t	m	2000	48	25	2	0	5
41	1094	A	MP	c	m	0	72	25	1	0	2
42	1095	A	MP	c	m	0	72	25	1	0	1
43	1096	A	MP	c	m	0	72	25	0	0	3
44	1097	A	MP	c	m	0	72	25	0	0	1
45	1098	A	MP	c	m	0	72	25	0	0	1
46	1099	A	MP	t	m	500	72	25	0	0	1
47	1100	A	MP	t	m	500	72	25	0	0	0
48	1101	A	MP	t	m	500	72	25	0	0	0
49	1102	A	MP	t	m	500	72	25	0	0	1
50	1103	A	MP	t	m	500	72	25	1	0	1

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
1	0	0	0	0	0.080	23	2	0	0	0	0
2	0	0	0	0	0.080	23	2	0	0	0	0
3	0	0	0	0	0.600	10	15	0	0	0	0
4	0	0	0	0	0.080	23	2	0	0	0	0
5	0	0	0	0	0.080	23	2	0	0	0	0
6	0	0	0	0	0	25	0	0	0	0	0
7	0	0	0	0	0	25	0	0	0	0	0
8	0	0	0	0	0	25	0	0	0	0	0
9	0	0	0	0	0.040	24	1	0	0	0	0
10	0	0	0	0	0.040	24	1	0	0	0	0
11	0	0	0	0	0.040	24	1	0	0	0	0
12	0	0	0	0	0.080	24	0	1	0	0	0
13	0	0	0	0	0.040	24	1	0	0	0	0
14	0	0	0	0	0	25	0	0	0	0	0
15	0	0	0	0	0.040	24	1	0	0	0	0
16	0	0	0	0	0.040	24	1	0	0	0	0
17	0	0	0	0	0.160	24	0	0	0	1	0
18	0	0	0	0	0.120	22	0	0	3	0	0
19	0	0	0	0	0.080	24	0	1	0	0	0
20	0	0	0	0	0.040	24	1	0	0	0	0
21	0	0	0	0	0.040	24	1	0	0	0	0
22	0	0	0	0	0.120	24	0	0	1	0	0
23	0	0	0	0	0.080	23	2	0	0	0	0
24	0	0	0	0	0.080	23	2	0	0	0	0
25	0	0	0	0	0.040	24	1	0	0	0	0
26	0	0	0	0	0.040	24	1	0	0	0	0
27	0	0	0	0	0.080	24	0	1	0	0	0
28	0	0	0	0	0	25	0	0	0	0	0
29	0	0	0	0	0.040	24	1	0	0	0	0
30	0	0	0	0	0.040	24	1	0	0	0	0
31	0	0	0	0	0.040	24	1	0	0	0	0
32	0	0	0	0	0.080	24	0	1	0	0	0
33	0	0	0	0	0.120	24	0	0	1	0	0
34	0	0	0	0	0.200	24	0	0	0	0	1
35	0	0	0	0	0	25	0	0	0	0	0
36	0	0	0	0	0.240	24	0	0	0	0	0
37	0	0	0	0	0.120	24	0	0	1	0	0
38	0	0	0	0	0.080	24	0	1	0	0	0
39	0	0	0	0	0.280	23	0	1	0	0	1
40	0	0	0	0	0.200	24	0	0	0	0	1
41	0	0	0	0	0.080	23	2	0	0	0	0
42	0	0	0	0	0.040	24	1	0	0	0	0
43	0	0	0	0	0.120	24	0	0	1	0	0
44	0	0	0	0	0.040	24	1	0	0	0	0
45	0	0	0	0	0.040	24	1	0	0	0	0
46	0	0	0	0	0.040	24	1	0	0	0	0
47	0	0	0	0	0	25	0	0	0	0	0
48	0	0	0	0	0	25	0	0	0	0	0
49	0	0	0	0	0.040	24	1	0	0	0	0
50	0	0	0	0	0.040	24	1	0	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
1	0	0	0	0	0	8.0	500	15	3.00
2	0	0	0	0	0	8.0	500	12	2.40
3	0	0	0	0	0	60.0	500	21	4.20
4	0	0	0	0	0	8.0	500	10	2.00
5	0	0	0	0	0	8.0	500	9	1.80
6	0	0	0	0	0	0.0	500	25	5.00
7	0	0	0	0	0	0.0	500	33	6.60
8	0	0	0	0	0	0.0	500	14	2.80
9	0	0	0	0	0	4.0	500	18	3.60
10	0	0	0	0	0	4.0	500	15	3.00
11	0	0	0	0	0	4.0	500	16	3.20
12	0	0	0	0	0	4.0	500	25	5.00
13	0	0	0	0	0	4.0	500	24	4.80
14	0	0	0	0	0	0.0	500	21	4.20
15	0	0	0	0	0	4.0	500	15	3.00
16	0	0	0	0	0	4.0	500	16	3.20
17	0	0	0	0	0	4.0	500	25	5.00
18	0	0	0	0	0	12.0	500	14	2.80
19	0	0	0	0	0	4.0	500	25	5.00
20	0	0	0	0	0	4.0	500	24	4.80
21	0	0	0	0	0	4.0	500	25	5.00
22	0	0	0	0	0	4.0	500	28	5.60
23	0	0	0	0	0	8.0	500	32	6.40
24	0	0	0	0	0	8.0	500	18	3.60
25	0	0	0	0	0	4.0	500	19	3.80
26	0	0	0	0	0	4.0	500	21	4.20
27	0	0	0	0	0	4.0	500	24	4.80
28	0	0	0	0	0	0.0	500	18	3.60
29	0	0	0	0	0	4.0	500	17	3.40
30	0	0	0	0	0	4.0	500	19	3.80
31	0	0	0	0	0	4.0	500	15	3.00
32	0	0	0	0	0	4.0	500	14	2.80
33	0	0	0	0	0	4.0	500	13	2.60
34	0	0	0	0	0	4.0	500	15	3.00
35	0	0	0	0	0	0.0	500	18	3.60
36	1	0	0	0	0	4.0	500	10	2.00
37	0	0	0	0	0	4.0	500	9	1.80
38	0	0	0	0	0	4.0	500	5	1.00
39	0	0	0	0	0	8.0	500	8	1.60
40	0	0	0	0	0	4.0	500	7	1.40
41	0	0	0	0	0	8.0	500	25	5.00
42	0	0	0	0	0	4.0	500	32	6.40
43	0	0	0	0	0	4.0	500	18	3.60
44	0	0	0	0	0	4.0	500	12	2.40
45	0	0	0	0	0	4.0	500	15	3.00
46	0	0	0	0	0	4.0	500	18	3.60
47	0	0	0	0	0	0.0	500	19	3.80
48	0	0	0	0	0	0.0	500	21	4.20
49	0	0	0	0	0	4.0	500	22	4.40
50	0	0	0	0	0	4.0	500	15	3.00

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
51	1104	A	MP	t	m	1000	72	25	2	0	3
52	1105	A	MP	t	m	1000	72	25	0	0	1
53	1106	A	MP	t	m	1000	72	25	0	0	0
54	1107	A	MP	t	m	1000	72	25	0	0	1
55	1108	A	MP	t	m	1000	72	25	0	0	3
56	1109	A	MP	t	m	2000	72	25	3	0	6
57	1110	A	MP	t	m	2000	72	25	3	0	2
58	1111	A	MP	t	m	2000	72	25	0	0	1
59	1112	A	MP	t	m	2000	72	25	0	0	3
60	1113	A	MP	t	m	2000	72	25	3	0	1
61	1114	A	MP	c	f	0	24	25	0	0	1
62	1115	A	MP	c	f	0	24	25	0	0	1
63	1116	A	MP	c	f	0	24	25	0	0	1
64	1117	A	MP	c	f	0	24	25	0	0	1
65	1118	A	MP	c	f	0	24	25	0	0	1
66	1119	A	MP	t	f	500	24	25	0	0	1
67	1120	A	MP	t	f	500	24	25	0	0	1
68	1121	A	MP	t	f	500	24	25	0	0	0
69	1122	A	MP	t	f	500	24	25	0	0	1
70	1123	A	MP	t	f	500	24	25	0	0	0
71	1124	A	MP	t	f	1000	24	25	0	0	1
72	1125	A	MP	t	f	1000	24	25	1	0	1
73	1126	A	MP	t	f	1000	24	25	0	0	2
74	1127	A	MP	t	f	1000	24	25	1	0	1
75	1128	A	MP	t	f	1000	24	25	0	0	0
76	1129	A	MP	t	f	2000	24	25	0	0	2
77	1130	A	MP	t	f	2000	24	25	1	0	2
78	1131	A	MP	t	f	2000	24	25	0	0	1
79	1132	A	MP	t	f	2000	24	25	3	0	3
80	1133	A	MP	t	f	2000	24	25	0	0	3
81	1134	A	MP	c	f	0	48	25	0	0	1
82	1135	A	MP	c	f	0	48	25	0	0	2
83	1136	A	MP	c	f	0	48	25	0	0	0
84	1137	A	MP	c	f	0	48	25	0	0	0
85	1138	A	MP	c	f	0	48	25	0	0	0
86	1139	A	MP	t	f	500	48	25	0	0	1
87	1140	A	MP	t	f	500	48	25	0	0	2
88	1141	A	MP	t	f	500	48	25	0	0	2
89	1142	A	MP	t	f	500	48	25	0	0	3
90	1143	A	MP	t	f	500	48	25	0	0	3
91	1144	A	MP	t	f	1000	48	25	0	0	4
92	1145	A	MP	t	f	1000	48	25	2	0	3
93	1146	A	MP	t	f	1000	48	25	0	0	2
94	1147	A	MP	t	f	1000	48	25	2	0	4
95	1148	A	MP	t	f	1000	48	25	0	0	1
96	1149	A	MP	t	f	2000	48	25	0	0	1
97	1150	A	MP	t	f	2000	48	25	0	0	3
98	1151	A	MP	t	f	2000	48	25	2	0	0
99	1152	A	MP	t	f	2000	48	25	0	0	6
100	1153	A	MP	t	f	2000	48	25	2	0	3

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
51	0	0	0	0	0.120	24	0	0	1	0	0
52	0	0	0	0	0.040	24	1	0	0	0	0
53	0	0	0	0	0	25	0	0	0	0	0
54	0	0	0	0	0.040	24	1	0	0	0	0
55	0	0	0	0	0.120	24	0	0	1	0	0
56	0	0	0	0	0.240	24	0	0	0	0	0
57	0	0	0	0	0.080	24	0	1	0	0	0
58	0	0	0	0	0.040	24	1	0	0	0	0
59	0	0	0	0	0.120	24	0	0	1	0	0
60	0	0	0	0	0.040	24	1	0	0	0	0
61	0	0	0	0	0.040	24	1	0	0	0	0
62	0	0	0	0	0.040	24	1	0	0	0	0
63	0	0	0	0	0.040	24	1	0	0	0	0
64	0	0	0	0	0.040	24	1	0	0	0	0
65	0	0	0	0	0.040	24	1	0	0	0	0
66	0	0	0	0	0.040	24	1	0	0	0	0
67	0	0	0	0	0.040	24	1	0	0	0	0
68	0	0	0	0	0	25	0	0	0	0	0
69	0	0	0	0	0.040	24	1	0	0	0	0
70	0	0	0	0	0	25	0	0	0	0	0
71	0	0	0	0	0.040	24	1	0	0	0	0
72	0	0	0	0	0.040	24	1	0	0	0	0
73	2	0	0	0	0.160	23	0	2	0	0	0
74	0	0	0	0	0.040	24	1	0	0	0	0
75	0	0	0	0	0	25	0	0	0	0	0
76	0	0	0	0	0.080	24	0	1	0	0	0
77	0	0	0	0	0.080	24	0	1	0	0	0
78	0	0	0	0	0.040	24	1	0	0	0	0
79	1	0	0	0	0.160	24	0	0	0	1	0
80	0	0	0	0	0.120	24	0	1	0	0	0
81	0	0	0	0	0.040	24	1	0	0	0	0
82	0	0	0	0	0.080	23	2	0	0	0	0
83	0	0	0	0	0	25	0	0	0	0	0
84	0	0	0	0	0	25	0	0	0	0	0
85	0	0	0	0	0	25	0	0	0	0	0
86	0	0	0	0	0.040	24	1	0	0	0	0
87	0	0	0	0	0.080	24	0	1	0	0	0
88	0	0	0	0	0.080	24	0	1	0	0	0
89	0	0	0	0	0.120	24	0	0	1	0	0
90	0	0	0	0	0.120	24	0	0	1	0	0
91	1	0	0	0	0.200	22	1	2	0	0	0
92	0	0	0	0	0.120	24	0	0	1	0	0
93	0	0	0	0	0.080	24	0	1	0	0	0
94	1	0	0	0	0.200	24	0	0	0	0	1
95	0	0	0	0	0.040	24	1	0	0	0	0
96	0	0	0	0	0.040	24	1	0	0	0	0
97	0	0	0	0	0.120	24	0	0	1	0	0
98	0	0	0	0	0	25	0	0	0	0	0
99	0	0	0	0	0.240	24	0	0	0	0	0
100	0	0	0	0	0.120	24	0	0	1	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
51	0	0	0	0	0	4.0	500	15	3.00
52	0	0	0	0	0	4.0	500	12	2.40
53	0	0	0	0	0	0.0	500	11	2.20
54	0	0	0	0	0	4.0	500	14	2.80
55	0	0	0	0	0	4.0	500	19	3.80
56	1	0	0	0	0	4.0	500	2	0.40
57	0	0	0	0	0	4.0	500	5	1.00
58	0	0	0	0	0	4.0	500	4	0.80
59	0	0	0	0	0	4.0	500	8	1.60
60	0	0	0	0	0	4.0	500	9	1.80
61	0	0	0	0	0	4.0	500	25	5.00
62	0	0	0	0	0	4.0	500	24	4.80
63	0	0	0	0	0	4.0	500	23	4.60
64	0	0	0	0	0	4.0	500	26	5.20
65	0	0	0	0	0	4.0	500	32	6.40
66	0	0	0	0	0	4.0	500	25	5.00
67	0	0	0	0	0	4.0	500	24	4.80
68	0	0	0	0	0	0.0	500	26	5.20
69	0	0	0	0	0	4.0	500	25	5.00
70	0	0	0	0	0	0.0	500	21	4.20
71	0	0	0	0	0	4.0	500	24	4.80
72	0	0	0	0	0	4.0	500	23	4.60
73	0	0	0	0	0	8.0	500	23	4.60
74	0	0	0	0	0	4.0	500	24	4.80
75	0	0	0	0	0	0.0	500	25	5.00
76	0	0	0	0	0	4.0	500	32	6.40
77	0	0	0	0	0	4.0	500	25	5.00
78	0	0	0	0	0	4.0	500	21	4.20
79	0	0	0	0	0	4.0	500	22	4.40
80	0	0	0	0	0	4.0	500	19	3.80
81	0	0	0	0	0	4.0	500	25	5.00
82	0	0	0	0	0	8.0	500	18	3.60
83	0	0	0	0	0	0.0	500	17	3.40
84	0	0	0	0	0	0.0	500	25	5.00
85	0	0	0	0	0	0.0	500	32	6.40
86	0	0	0	0	0	4.0	500	31	6.20
87	0	0	0	0	0	4.0	500	30	6.00
88	0	0	0	0	0	4.0	500	18	3.60
89	0	0	0	0	0	4.0	500	19	3.80
90	0	0	0	0	0	4.0	500	25	5.00
91	0	0	0	0	0	12.0	500	15	3.00
92	0	0	0	0	0	4.0	500	18	3.60
93	0	0	0	0	0	4.0	500	20	4.00
94	0	0	0	0	0	4.0	500	30	6.00
95	0	0	0	0	0	4.0	500	14	2.80
96	0	0	0	0	0	4.0	500	18	3.60
97	0	0	0	0	0	4.0	500	19	3.80
98	0	0	0	0	0	0.0	500	25	5.00
99	1	0	0	0	0	4.0	500	14	2.80
100	0	0	0	0	0	4.0	500	15	3.00

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
101	1154	A	MP	c	f	0	72	25	0	0	1
102	1155	A	MP	c	f	0	72	25	0	0	0
103	1156	A	MP	c	f	0	72	25	2	0	3
104	1157	A	MP	c	f	0	72	25	0	0	1
105	1158	A	MP	c	f	0	72	25	0	0	0
106	1159	A	MP	t	f	500	72	25	0	0	1
107	1160	A	MP	t	f	500	72	25	0	0	1
108	1161	A	MP	t	f	500	72	25	0	0	0
109	1162	A	MP	t	f	500	72	25	0	0	2
110	1163	A	MP	t	f	500	72	25	0	0	2
111	1164	A	MP	t	f	1000	72	25	1	0	3
112	1165	A	MP	t	f	1000	72	25	0	0	2
113	1166	A	MP	t	f	1000	72	25	2	0	1
114	1167	A	MP	t	f	1000	72	25	0	0	2
115	1168	A	MP	t	f	1000	72	25	0	0	1
116	1169	A	MP	t	f	2000	72	25	0	0	5
117	1170	A	MP	t	f	2000	72	25	0	0	1
118	1171	A	MP	t	f	2000	72	25	2	0	3
119	1172	A	MP	t	f	2000	72	25	0	0	1
120	1173	A	MP	t	f	2000	72	25	2	0	5
121	1174	A	MP	p	m	12.5	48	25	3	0	7
122	1175	A	MP	p	m	12.5	48	25	0	0	6
123	1176	A	MP	p	m	12.5	48	25	0	0	4
124	1177	A	MP	p	m	12.5	48	25	3	0	11
125	1178	A	MP	p	m	12.5	48	25	0	0	10
126	1179	A	MP	p	f	12.5	48	25	1	0	9
127	1180	A	MP	p	f	12.5	48	25	0	0	3
128	1181	A	MP	p	f	12.5	48	25	2	0	4
129	1182	A	MP	p	f	12.5	48	25	0	0	4
130	1183	A	MP	p	f	12.5	48	25	4	0	6
131	1054	B	BN	c	m	0	24	25	0	0	2
132	1055	B	BN	c	m	0	24	25	0	0	1
133	1056	B	BN	c	m	0	24	25	0	0	20
134	1057	B	BN	c	m	0	24	25	0	0	2
135	1058	B	BN	c	m	0	24	25	0	0	0
136	1059	B	BN	t	m	500	24	25	0	0	1
137	1060	B	BN	t	m	500	24	25	0	0	1
138	1061	B	BN	t	m	500	24	25	0	0	0
139	1062	B	BN	t	m	500	24	25	0	0	2
140	1063	B	BN	t	m	500	24	25	0	0	2
141	1064	B	BN	t	m	1000	24	25	0	0	2
142	1065	B	BN	t	m	1000	24	25	0	0	2
143	1066	B	BN	t	m	1000	24	25	2	0	0
144	1067	B	BN	t	m	1000	24	25	0	0	4
145	1068	B	BN	t	m	1000	24	25	0	0	2
146	1069	B	BN	t	m	2000	24	25	0	0	5
147	1070	B	BN	t	m	2000	24	25	0	0	4
148	1071	B	BN	t	m	2000	24	25	0	0	2
149	1072	B	BN	t	m	2000	24	25	0	0	4
150	1073	B	BN	t	m	2000	24	25	0	0	2

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
101	0	0	0	0	0.040	24	1	0	0	0	0
102	0	0	0	0	0	25	0	0	0	0	0
103	0	0	0	0	0.120	22	3	0	0	0	0
104	0	0	0	0	0.040	24	1	0	0	0	0
105	0	0	0	0	0	25	0	0	0	0	0
106	0	0	0	0	0.040	24	1	0	0	0	0
107	0	0	0	0	0.040	24	1	0	0	0	0
108	0	0	0	0	0	25	0	0	0	0	0
109	0	0	0	0	0.080	24	0	1	0	0	0
110	0	0	0	0	0.080	24	0	1	0	0	0
111	0	0	0	0	0.120	24	0	0	1	0	0
112	0	0	0	0	0.080	24	0	1	0	0	0
113	0	0	0	0	0.040	24	1	0	0	0	0
114	0	0	0	0	0.080	24	0	1	0	0	0
115	0	0	0	0	0.040	24	1	0	0	0	0
116	0	0	0	0	0.200	24	0	0	0	0	1
117	0	0	0	0	0.040	24	1	0	0	0	0
118	0	0	0	0	0.120	24	0	0	1	0	0
119	1	0	0	0	0.080	24	0	1	0	0	0
120	0	0	0	0	0.200	24	0	0	0	0	1
121	1	0	0	0	0.320	24	0	0	0	0	0
122	0	0	0	0	0.240	24	0	0	0	0	0
123	0	0	0	0	0.160	24	0	0	0	1	0
124	1	1	0	0	0.520	22	1	1	0	0	0
125	0	0	0	0	0.400	23	0	0	1	0	0
126	0	1	0	0	0.400	23	0	1	0	0	0
127	0	4	0	0	0.280	24	0	0	0	0	0
128	0	0	0	0	0.160	24	0	0	0	1	0
129	0	2	0	0	0.240	24	0	0	0	0	0
130	1	0	0	0	0.280	23	0	1	0	0	1
131	0	0	0	0	0.080	23	2	0	0	0	0
132	0	0	0	0	0.040	24	1	0	0	0	0
133	0	0	0	0	0.800	5	20	0	0	0	0
134	0	0	0	0	0.080	23	2	0	0	0	0
135	0	0	0	0	0	25	0	0	0	0	0
136	0	0	0	0	0.040	24	1	0	0	0	0
137	0	0	0	0	0.040	24	1	0	0	0	0
138	0	0	0	0	0	25	0	0	0	0	0
139	0	0	0	0	0.080	24	0	1	0	0	0
140	0	0	0	0	0.080	24	0	1	0	0	0
141	0	0	0	0	0.080	24	0	1	0	0	0
142	0	0	0	0	0.080	24	0	1	0	0	0
143	0	0	0	0	0	25	0	0	0	0	0
144	0	0	0	0	0.160	24	0	0	0	1	0
145	0	0	0	0	0.080	24	0	1	0	0	0
146	1	1	0	0	0.280	23	0	1	0	0	1
147	0	0	0	0	0.160	24	0	0	0	1	0
148	0	0	0	0	0.080	24	0	1	0	0	0
149	1	0	0	0	0.200	24	0	0	0	0	1
150	0	0	0	0	0.080	24	0	1	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
101	0	0	0	0	0	4.0	500	12	2.40
102	0	0	0	0	0	0.0	500	15	3.00
103	0	0	0	0	0	12.0	500	14	2.80
104	0	0	0	0	0	4.0	500	25	5.00
105	0	0	0	0	0	0.0	500	24	4.80
106	0	0	0	0	0	4.0	500	21	4.20
107	0	0	0	0	0	4.0	500	25	5.00
108	0	0	0	0	0	0.0	500	15	3.00
109	0	0	0	0	0	4.0	500	16	3.20
110	0	0	0	0	0	4.0	500	25	5.00
111	0	0	0	0	0	4.0	500	28	5.60
112	0	0	0	0	0	4.0	500	24	4.80
113	0	0	0	0	0	4.0	500	25	5.00
114	0	0	0	0	0	4.0	500	26	5.20
115	0	0	0	0	0	4.0	500	28	5.60
116	0	0	0	0	0	4.0	500	24	4.80
117	0	0	0	0	0	4.0	500	25	5.00
118	0	0	0	0	0	4.0	500	26	5.20
119	0	0	0	0	0	4.0	500	32	6.40
120	0	0	0	0	0	4.0	500	19	3.80
121	0	0	1	0	0	4.0	500	15	3.00
122	1	0	0	0	0	4.0	500	32	6.40
123	0	0	0	0	0	4.0	500	15	3.00
124	0	0	0	0	1	12.0	500	28	5.60
125	0	1	0	0	0	8.0	500	24	4.80
126	0	0	1	0	0	8.0	500	23	4.60
127	0	1	0	0	0	4.0	500	25	5.00
128	0	0	0	0	0	4.0	500	25	5.00
129	1	0	0	0	0	4.0	500	21	4.20
130	0	0	0	0	0	8.0	500	25	5.00
131	0	0	0	0	0	8.0	500	25	5.00
132	0	0	0	0	0	4.0	500	24	4.80
133	0	0	0	0	0	80.0	500	32	6.40
134	0	0	0	0	0	8.0	500	33	6.60
135	0	0	0	0	0	0.0	500	15	3.00
136	0	0	0	0	0	4.0	500	15	3.00
137	0	0	0	0	0	4.0	500	25	5.00
138	0	0	0	0	0	0.0	500	24	4.80
139	0	0	0	0	0	4.0	500	26	5.20
140	0	0	0	0	0	4.0	500	23	4.60
141	0	0	0	0	0	4.0	500	25	5.00
142	0	0	0	0	0	4.0	500	14	2.80
143	0	0	0	0	0	0.0	500	25	5.00
144	0	0	0	0	0	4.0	500	23	4.60
145	0	0	0	0	0	4.0	500	25	5.00
146	0	0	0	0	0	8.0	500	32	6.40
147	0	0	0	0	0	4.0	500	18	3.60
148	0	0	0	0	0	4.0	500	17	3.40
149	0	0	0	0	0	4.0	500	16	3.20
150	0	0	0	0	0	4.0	500	15	3.00

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
151	1074	B	BN	c	m	0	48	25	0	0	2
152	1075	B	BN	c	m	0	48	25	0	0	0
153	1076	B	BN	c	m	0	48	25	0	0	1
154	1077	B	BN	c	m	0	48	25	1	0	1
155	1078	B	BN	c	m	0	48	25	0	0	1
156	1079	B	BN	t	m	500	48	25	0	0	3
157	1080	B	BN	t	m	500	48	25	0	0	4
158	1081	B	BN	t	m	500	48	25	0	0	5
159	1082	B	BN	t	m	500	48	25	3	0	0
160	1083	B	BN	t	m	500	48	25	0	0	2
161	1084	B	BN	t	m	1000	48	25	0	0	4
162	1085	B	BN	t	m	1000	48	25	4	0	5
163	1086	B	BN	t	m	1000	48	25	0	0	8
164	1087	B	BN	t	m	1000	48	25	0	0	3
165	1088	B	BN	t	m	1000	48	25	3	0	0
166	1089	B	BN	t	m	2000	48	25	0	0	10
167	1090	B	BN	t	m	2000	48	25	3	0	2
168	1091	B	BN	t	m	2000	48	25	0	0	7
169	1092	B	BN	t	m	2000	48	25	0	0	3
170	1093	B	BN	t	m	2000	48	25	4	0	7
171	1094	B	BN	c	m	0	72	25	0	0	1
172	1095	B	BN	c	m	0	72	25	0	0	2
173	1096	B	BN	c	m	0	72	25	0	0	0
174	1097	B	BN	c	m	0	72	25	0	0	1
175	1098	B	BN	c	m	0	72	25	3	0	1
176	1099	B	BN	t	m	500	72	25	0	0	1
177	1100	B	BN	t	m	500	72	25	0	0	1
178	1101	B	BN	t	m	500	72	25	0	0	2
179	1102	B	BN	t	m	500	72	25	0	0	0
180	1103	B	BN	t	m	500	72	25	0	0	2
181	1104	B	BN	t	m	1000	72	25	0	0	2
182	1105	B	BN	t	m	1000	72	25	0	0	3
183	1106	B	BN	t	m	1000	72	25	0	0	4
184	1107	B	BN	t	m	1000	72	25	0	0	0
185	1108	B	BN	t	m	1000	72	25	2	0	2
186	1109	B	BN	t	m	2000	72	25	0	0	1
187	1110	B	BN	t	m	2000	72	25	0	0	6
188	1111	B	BN	t	m	2000	72	25	0	0	2
189	1112	B	BN	t	m	2000	72	25	0	0	5
190	1113	B	BN	t	m	2000	72	25	0	0	5
191	1114	B	BN	c	f	0	24	25	2	0	2
192	1115	B	BN	c	f	0	24	25	0	0	0
193	1116	B	BN	c	f	0	24	25	0	0	1
194	1117	B	BN	c	f	0	24	25	0	0	1
195	1118	B	BN	c	f	0	24	25	0	0	1
196	1119	B	BN	t	f	500	24	25	0	0	0
197	1120	B	BN	t	f	500	24	25	0	0	0
198	1121	B	BN	t	f	500	24	25	0	0	1
199	1122	B	BN	t	f	500	24	25	0	0	4
200	1123	B	BN	t	f	500	24	25	3	0	1

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
151	0	0	0	0	0.080	23	2	0	0	0	0
152	0	0	0	0	0	25	0	0	0	0	0
153	0	0	0	0	0.040	24	1	0	0	0	0
154	0	0	0	0	0.040	24	1	0	0	0	0
155	0	0	0	0	0.040	24	1	0	0	0	0
156	0	0	0	0	0.120	24	0	0	1	0	0
157	0	0	0	0	0.160	24	0	0	0	1	0
158	0	1	0	0	0.240	23	0	1	0	1	0
159	0	0	0	0	0	25	0	0	0	0	0
160	0	0	0	0	0.080	24	0	1	0	0	0
161	0	0	0	0	0.160	24	0	0	0	1	0
162	1	0	0	0	0.240	23	0	1	0	1	0
163	1	1	0	0	0.400	23	0	0	1	0	0
164	0	0	0	0	0.120	24	0	0	1	0	0
165	0	3	0	0	0.120	24	0	0	1	0	0
166	1	1	0	0	0.480	22	0	0	1	1	1
167	0	0	0	0	0.080	24	0	1	0	0	0
168	0	1	0	0	0.320	23	0	1	0	0	0
169	0	3	0	0	0.240	23	0	0	2	0	0
170	0	2	0	0	0.360	22	0	0	3	0	0
171	0	0	0	0	0.040	24	1	0	0	0	0
172	0	0	0	0	0.080	23	2	0	0	0	0
173	0	0	0	0	0	25	0	0	0	0	0
174	0	0	0	0	0.040	24	1	0	0	0	0
175	0	0	0	0	0.040	24	1	0	0	0	0
176	0	0	0	0	0.040	24	1	0	0	0	0
177	0	0	0	0	0.040	24	1	0	0	0	0
178	0	0	0	0	0.080	24	0	1	0	0	0
179	0	0	0	0	0	25	0	0	0	0	0
180	0	0	0	0	0.080	24	0	1	0	0	0
181	0	0	0	0	0.080	24	0	1	0	0	0
182	0	0	0	0	0.120	24	0	0	1	0	0
183	2	1	0	0	0.280	23	0	1	0	0	1
184	0	0	0	0	0	25	0	0	0	0	0
185	0	0	0	0	0.080	24	0	1	0	0	0
186	0	0	0	0	0.040	24	1	0	0	0	0
187	1	0	0	0	0.280	22	0	1	2	0	0
188	0	0	0	0	0.080	24	0	1	0	0	0
189	1	0	0	0	0.240	21	2	2	0	0	0
190	0	0	0	0	0.200	24	0	0	0	0	1
191	0	0	0	0	0.080	23	2	0	0	0	0
192	0	0	0	0	0	25	0	0	0	0	0
193	0	0	0	0	0.040	24	1	0	0	0	0
194	0	0	0	0	0.040	24	1	0	0	0	0
195	0	0	0	0	0.040	24	1	0	0	0	0
196	0	0	0	0	0	25	0	0	0	0	0
197	0	0	0	0	0	25	0	0	0	0	0
198	0	0	0	0	0.040	24	1	0	0	0	0
199	0	0	0	0	0.160	23	0	2	0	0	0
200	0	0	0	0	0.040	24	1	0	0	0	0

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
151	0	0	0	0	0	8.0	500	25	5.00
152	0	0	0	0	0	0.0	500	35	7.00
153	0	0	0	0	0	4.0	500	32	6.40
154	0	0	0	0	0	4.0	500	24	4.80
155	0	0	0	0	0	4.0	500	26	5.20
156	0	0	0	0	0	4.0	500	15	3.00
157	0	0	0	0	0	4.0	500	18	3.60
158	0	0	0	0	0	8.0	500	17	3.40
159	0	0	0	0	0	0.0	500	16	3.20
160	0	0	0	0	0	4.0	500	14	2.80
161	0	0	0	0	0	4.0	500	12	2.40
162	0	0	0	0	0	8.0	500	10	2.00
163	0	1	0	0	0	8.0	500	15	3.00
164	0	0	0	0	0	4.0	500	18	3.60
165	0	0	0	0	0	4.0	500	10	2.00
166	0	0	0	0	0	12.0	500	9	1.80
167	0	0	0	0	0	4.0	500	5	1.00
168	1	0	0	0	0	8.0	500	2	0.40
169	0	0	0	0	0	8.0	500	1	0.20
170	0	0	0	0	0	12.0	500	8	1.60
171	0	0	0	0	0	4.0	500	25	5.00
172	0	0	0	0	0	8.0	500	26	5.20
173	0	0	0	0	0	0.0	500	24	4.80
174	0	0	0	0	0	4.0	500	25	5.00
175	0	0	0	0	0	4.0	500	28	5.60
176	0	0	0	0	0	4.0	500	32	6.40
177	0	0	0	0	0	4.0	500	15	3.00
178	0	0	0	0	0	4.0	500	24	4.80
179	0	0	0	0	0	0.0	500	25	5.00
180	0	0	0	0	0	4.0	500	15	3.00
181	0	0	0	0	0	4.0	500	25	5.00
182	0	0	0	0	0	4.0	500	15	3.00
183	0	0	0	0	0	8.0	500	14	2.80
184	0	0	0	0	0	0.0	500	15	3.00
185	0	0	0	0	0	4.0	500	12	2.40
186	0	0	0	0	0	4.0	500	11	2.20
187	0	0	0	0	0	12.0	500	12	2.40
188	0	0	0	0	0	4.0	500	13	2.60
189	0	0	0	0	0	16.0	500	10	2.00
190	0	0	0	0	0	4.0	500	2	0.40
191	0	0	0	0	0	8.0	500	25	5.00
192	0	0	0	0	0	8.0	500	32	6.40
193	0	0	0	0	0	4.0	500	25	5.00
194	0	0	0	0	0	4.0	500	23	4.60
195	0	0	0	0	0	4.0	500	21	4.20
196	0	0	0	0	0	0.0	500	24	4.80
197	0	0	0	0	0	0.0	500	25	5.00
198	0	0	0	0	0	4.0	500	25	5.00
199	0	0	0	0	0	8.0	500	25	5.00
200	0	0	0	0	0	4.0	500	21	4.20

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
201	1124	B	BN	t	f	1000	24	25	0	0	1
202	1125	B	BN	t	f	1000	24	25	0	0	1
203	1126	B	BN	t	f	1000	24	25	0	0	2
204	1127	B	BN	t	f	1000	24	25	0	0	8
205	1128	B	BN	t	f	1000	24	25	0	0	1
206	1129	B	BN	t	f	2000	24	25	0	0	1
207	1130	B	BN	t	f	2000	24	25	3	0	3
208	1131	B	BN	t	f	2000	24	25	0	0	4
209	1132	B	BN	t	f	2000	24	25	1	0	3
210	1133	B	BN	t	f	2000	24	25	1	0	1
211	1134	B	BN	c	f	0	48	25	0	0	3
212	1135	B	BN	c	f	0	48	25	0	0	0
213	1136	B	BN	c	f	0	48	25	0	0	0
214	1137	B	BN	c	f	0	48	25	0	0	1
215	1138	B	BN	c	f	0	48	25	1	0	0
216	1139	B	BN	t	f	500	48	25	0	0	2
217	1140	B	BN	t	f	500	48	25	0	0	1
218	1141	B	BN	t	f	500	48	25	1	0	0
219	1142	B	BN	t	f	500	48	25	1	0	2
220	1143	B	BN	t	f	500	48	25	0	0	1
221	1144	B	BN	t	f	1000	48	25	0	0	1
222	1145	B	BN	t	f	1000	48	25	0	0	1
223	1146	B	BN	t	f	1000	48	25	1	0	2
224	1147	B	BN	t	f	1000	48	25	0	0	3
225	1148	B	BN	t	f	1000	48	25	1	0	1
226	1149	B	BN	t	f	2000	48	25	0	0	5
227	1150	B	BN	t	f	2000	48	25	0	0	4
228	1151	B	BN	t	f	2000	48	25	1	0	5
229	1152	B	BN	t	f	2000	48	25	1	0	0
230	1153	B	BN	t	f	2000	48	25	0	0	5
231	1154	B	BN	c	f	0	72	25	0	0	0
232	1155	B	BN	c	f	0	72	25	0	0	2
233	1156	B	BN	c	f	0	72	25	0	0	0
234	1157	B	BN	c	f	0	72	25	2	0	2
235	1158	B	BN	c	f	0	72	25	0	0	1
236	1159	B	BN	t	f	500	72	25	0	0	1
237	1160	B	BN	t	f	500	72	25	1	0	1
238	1161	B	BN	t	f	500	72	25	0	0	1
239	1162	B	BN	t	f	500	72	25	0	0	2
240	1163	B	BN	t	f	500	72	25	0	0	0
241	1164	B	BN	t	f	1000	72	25	0	0	2
242	1165	B	BN	t	f	1000	72	25	0	0	3
243	1166	B	BN	t	f	1000	72	25	0	0	3
244	1167	B	BN	t	f	1000	72	25	0	0	1
245	1168	B	BN	t	f	1000	72	25	0	0	0
246	1169	B	BN	t	f	2000	72	25	1	0	5
247	1170	B	BN	t	f	2000	72	25	0	0	3
248	1171	B	BN	t	f	2000	72	25	1	0	1
249	1172	B	BN	t	f	2000	72	25	0	0	4
250	1173	B	BN	t	f	2000	72	25	3	0	3

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
201	0	0	0	0	0.040	24	1	0	0	0	0
202	0	0	0	0	0.040	24	1	0	0	0	0
203	0	0	0	0	0.080	24	0	1	0	0	0
204	0	1	0	0	0.360	22	0	0	3	0	0
205	0	0	0	0	0.040	24	1	0	0	0	0
206	1	0	0	0	0.080	24	0	1	0	0	0
207	0	0	0	0	0.120	24	0	0	1	0	0
208	0	0	0	0	0.160	24	0	0	0	1	0
209	0	0	0	0	0.120	24	0	0	1	0	0
210	0	1	0	0	0.080	24	0	1	0	0	0
211	0	0	0	0	0.120	22	3	0	0	0	0
212	0	0	0	0	0	25	0	0	0	0	0
213	0	0	0	0	0	25	0	0	0	0	0
214	0	0	0	0	0.040	24	1	0	0	0	0
215	0	0	0	0	0	25	0	0	0	0	0
216	0	0	0	0	0.080	23	2	0	0	0	0
217	0	0	0	0	0.040	24	1	0	0	0	0
218	0	0	0	0	0	25	0	0	0	0	0
219	0	0	0	0	0.080	24	0	1	0	0	0
220	0	0	0	0	0.040	24	1	0	0	0	0
221	1	0	0	0	0.080	24	0	1	0	0	0
222	0	0	0	0	0.040	24	1	0	0	0	0
223	0	0	0	0	0.080	24	0	1	0	0	0
224	0	0	0	0	0.120	24	0	0	1	0	0
225	1	1	0	0	0.120	24	0	0	1	0	0
226	1	0	0	0	0.240	23	0	0	2	0	0
227	0	0	0	0	0.160	24	0	0	0	1	0
228	0	0	0	0	0.200	24	0	0	0	0	1
229	0	0	0	0	0	25	0	0	0	0	0
230	1	0	0	0	0.240	24	0	0	0	0	0
231	0	0	0	0	0	25	0	0	0	0	0
232	0	0	0	0	0.080	23	2	0	0	0	0
233	0	0	0	0	0	25	0	0	0	0	0
234	0	0	0	0	0.080	23	2	0	0	0	0
235	0	0	0	0	0.040	24	1	0	0	0	0
236	0	0	0	0	0.040	24	1	0	0	0	0
237	0	0	0	0	0.040	24	1	0	0	0	0
238	0	0	0	0	0.040	24	1	0	0	0	0
239	0	0	0	0	0.080	24	0	1	0	0	0
240	0	0	0	0	0	25	0	0	0	0	0
241	1	0	0	0	0.120	24	0	0	1	0	0
242	0	0	0	0	0.120	24	0	0	1	0	0
243	0	0	0	0	0.120	24	0	0	1	0	0
244	0	0	0	0	0.040	24	1	0	0	0	0
245	0	0	0	0	0	25	0	0	0	0	0
246	1	0	0	0	0.240	24	0	0	0	0	0
247	0	0	0	0	0.120	24	0	0	1	0	0
248	0	0	0	0	0.040	24	1	0	0	0	0
249	0	0	0	0	0.160	23	1	0	1	0	0
250	0	2	0	0	0.200	24	0	0	0	0	1

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
201	0	0	0	0	0	4.0	500	20	4.00
202	0	0	0	0	0	4.0	500	30	6.00
203	0	0	0	0	0	4.0	500	21	4.20
204	0	0	0	0	0	12.0	500	25	5.00
205	0	0	0	0	0	4.0	500	21	4.20
206	0	0	0	0	0	4.0	500	25	5.00
207	0	0	0	0	0	4.0	500	32	6.40
208	0	0	0	0	0	4.0	500	14	2.80
209	0	0	0	0	0	4.0	500	18	3.60
210	0	0	0	0	0	4.0	500	19	3.80
211	0	0	0	0	0	12.0	500	15	3.00
212	0	0	0	0	0	0.0	500	19	3.80
213	0	0	0	0	0	0.0	500	32	6.40
214	0	0	0	0	0	4.0	500	35	7.00
215	0	0	0	0	0	0.0	500	35	7.00
216	0	0	0	0	0	8.0	500	15	3.00
217	0	0	0	0	0	4.0	500	25	5.00
218	0	0	0	0	0	0.0	500	24	4.80
219	0	0	0	0	0	4.0	500	28	5.60
220	0	0	0	0	0	4.0	500	24	4.80
221	0	0	0	0	0	4.0	500	26	5.20
222	0	0	0	0	0	4.0	500	27	5.40
223	0	0	0	0	0	4.0	500	42	8.40
224	0	0	0	0	0	4.0	500	15	3.00
225	0	0	0	0	0	4.0	500	25	5.00
226	0	0	0	0	0	8.0	500	32	6.40
227	0	0	0	0	0	4.0	500	25	5.00
228	0	0	0	0	0	4.0	500	32	6.40
229	0	0	0	0	0	0.0	500	15	3.00
230	1	0	0	0	0	4.0	500	24	4.80
231	0	0	0	0	0	0.0	500	25	5.00
232	0	0	0	0	0	8.0	500	26	5.20
233	0	0	0	0	0	0.0	500	24	4.80
234	0	0	0	0	0	8.0	500	25	5.00
235	0	0	0	0	0	4.0	500	32	6.40
236	0	0	0	0	0	4.0	500	32	6.40
237	0	0	0	0	0	4.0	500	21	4.20
238	0	0	0	0	0	4.0	500	20	4.00
239	0	0	0	0	0	4.0	500	19	3.80
240	0	0	0	0	0	0.0	500	18	3.60
241	0	0	0	0	0	4.0	500	20	4.00
242	0	0	0	0	0	4.0	500	25	5.00
243	0	0	0	0	0	4.0	500	21	4.20
244	0	0	0	0	0	4.0	500	24	4.80
245	0	0	0	0	0	0.0	500	19	3.80
246	1	0	0	0	0	4.0	500	18	3.60
247	0	0	0	0	0	4.0	500	25	5.00
248	0	0	0	0	0	4.0	500	26	5.20
249	0	0	0	0	0	8.0	500	15	3.00
250	0	0	0	0	0	4.0	500	14	2.80

	Animal	Slide	Scorer	Treat. Code	Sex	Dose	Sample Time	Number Cells	chr-tid gap	chr-some gap	chr-tid break
251	1174	B	BN	p	m	12.5	48	25	0	0	9
252	1175	B	BN	p	m	12.5	48	25	3	0	7
253	1176	B	BN	p	m	12.5	48	25	0	0	5
254	1177	B	BN	p	m	12.5	48	25	1	0	0
255	1178	B	BN	p	m	12.5	48	25	0	0	4
256	1179	B	BN	p	f	12.5	48	25	0	0	4
257	1180	B	BN	p	f	12.5	48	25	5	0	3
258	1181	B	BN	p	f	12.5	48	25	0	0	7
259	1182	B	BN	p	f	12.5	48	25	0	0	5
260	1183	B	BN	p	f	12.5	48	25	4	0	5

	chr-some break	chr-tid exchange	chr-some exchange	other aberratn	CA/cell exc gap	cells w/ 0 CA	cells w/ 1 CA	cells w/ 2 CA	cells w/ 3 CA	cells w/ 4 CA	cells w/ 5 CA
251	2	3	0	0	0.560	20	0	3	0	2	0
252	3	1	0	0	0.440	22	0	1	0	1	1
253	1	0	0	0	0.240	24	0	0	0	0	0
254	0	0	0	0	0	25	0	0	0	0	0
255	0	0	0	0	0.160	24	0	0	0	1	0
256	1	0	0	0	0.200	24	0	0	0	0	1
257	0	0	0	0	0.120	24	0	0	1	0	0
258	0	0	0	0	0.280	23	0	0	1	1	0
259	0	0	0	0	0.200	24	0	0	0	1	0
260	0	0	0	0	0.200	24	0	0	0	0	1

	cells w/ 6 CA	cells w/ 7 CA	cells w/ 8 CA	cells w/ 9 CA	cells w/ 10+ CA	pct. CA positive	MI # cells	MI # meta	MI percent
251	0	0	0	0	0	20.0	500	15	3.00
252	0	0	0	0	0	12.0	500	25	5.00
253	1	0	0	0	0	4.0	500	32	6.40
254	0	0	0	0	0	0.0	500	32	6.40
255	0	0	0	0	0	4.0	500	25	5.00
256	0	0	0	0	0	4.0	500	24	4.80
257	0	0	0	0	0	4.0	500	26	5.20
258	0	0	0	0	0	8.0	500	28	5.60
259	0	0	0	0	0	4.0	500	29	5.80
260	0	0	0	0	0	4.0	500	27	5.40

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Pct.	Mean Pct.
1	3	0.0	24.0	m	60.000	18.400
2	133	0.0	24.0	m	80.000	20.000

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	7.945	24	0.9991
Sex	7.641	12	0.8125
Time	3.116	8	0.9269

filename: C:\CA\CATEST02.ILS date: time:

Time = 24.00 (Males) for 067889

p = 0.486
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	13	200	6.5000	1.0522	
500.00	6	250	2.4000	0.6532	0.9842
1000.00	8	250	3.2000	0.5333	0.9504
2000.00	13	250	5.2000	0.8537	0.7215

Time = 48.00 (Males) for 067889

p = 0.095
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	12	250	4.8000	0.8000	
500.00	9	250	3.6000	0.7180	0.7482
1000.00	11	250	4.4000	0.7180	0.5845
2000.00	17	250	6.8000	1.0414	0.1694

filename: C:\CA\CATEST02.ILS date: time:

Time = 72.00 (Males) for 067889

p = 0.110
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	11	250	4.4000	0.7180	
500.00	7	250	2.8000	0.6110	0.8315
1000.00	9	250	3.6000	0.7180	0.6760
2000.00	15	250	6.0000	1.3663	0.2102

Time = 24.00 (Females) for 067889

p = 0.381
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	10	250	4.0000	0.5963	
500.00	7	250	2.8000	0.8537	0.7704
1000.00	12	250	4.8000	0.9978	0.3314
2000.00	10	250	4.0000	0.0000	0.5000

filename: C:\CA\CATEST02.ILS date: time:

Time = 48.00 (Females) for 067889

p = 0.348
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	7	250	2.8000	1.3400	
500.00	10	250	4.0000	0.5963	0.2296
1000.00	12	250	4.8000	0.8000	0.1211
2000.00	9	250	3.6000	0.7180	0.3057

Time = 72.00 (Females) for 067889

p = 0.348
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	10	250	4.0000	1.3333	
500.00	8	250	3.2000	0.5333	0.6844
1000.00	9	250	3.6000	0.4000	0.5925
2000.00	11	250	4.4000	0.4000	0.4118

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Pct.	Mean Pct.
1	3	0.0	24.0	m	60.000	18.400
2	133	0.0	24.0	m	80.000	20.000

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	7.945	24	0.9991
Sex	7.641	12	0.8125
Time	3.116	8	0.9269

filename: C:\CA\CATEST02.ILS date: time:

Both sexes (All times) for 067889

p = 0.062
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (binomial) for chromosomal aberration (pct. damaged cells)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	63	1450	4.3448	0.4207	
500.00	47	1500	3.1333	0.2705	0.9587
1000.00	61	1500	4.0667	0.2929	0.6467
2000.00	75	1500	5.0000	0.3636	0.1998

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (pct. damaged cells)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Pct.	Mean Pct.
1	3	0.0	24.0	m	60.000	18.400
2	133	0.0	24.0	m	80.000	20.000

filename: C:\CA\CATEST02.ILS date: time:

Time = 48.00 (Males) for 067889

alpha = 0.050

One tailed test (binomial) for chromosomal aberration (pct. damaged cells) (with positive controls)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	12	250	4.8000	0.8000	
12.50	18	250	7.2000	1.8667	0.1293

Time = 48.00 (Females) for 067889

alpha = 0.050

One tailed test (binomial) for chromosomal aberration (pct. damaged cells) (with positive controls)

MG/KG	Aberrant Cells	Cells Scored	Percent Aberrant	SEM (for Obs)	Pairwise Significance
0.00	7	250	2.8000	1.3400	
12.50	13	250	5.2000	0.6110	0.0855

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Abs/Cell	Av Abs/Cell
1	3	0.0	24.0	m	0.600	0.184
2	133	0.0	24.0	m	0.800	0.200

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	26.414	24	0.3325
Sex	7.181	12	0.8454
Time	17.934	8	0.0217

filename: C:\CA\CATEST02.ILS date: time:

Time = 24.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	13	200	0.0650	0.0105		
500.00	8	250	0.0320	0.010	0.9463	
1000.00	15	250	0.0600	0.0149	0.5837	
2000.00	37	250	0.1480	0.0338	0.0043	*

Time = 48.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	14	250	0.0560	0.0107		
500.00	20	250	0.0800	0.0239	0.1517	
1000.00	37	250	0.1480	0.0358	0.0006	*
2000.00	60	250	0.2400	0.0404	0.0000	*

filename: C:\CA\CATEST02.ILS date: time:

Time = 72.00 (Males) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	13	250	0.0520	0.0104		
500.00	9	250	0.0360	0.0093	0.8031	
1000.00	22	250	0.0880	0.0259	0.0641	
2000.00	35	250	0.1400	0.0322	0.0007	*

Time = 24.00 (Females) for 067889

p = 0.001
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	10	250	0.0400	0.0060		
500.00	9	250	0.0360	0.0151	0.5907	
1000.00	21	250	0.0840	0.0334	0.0241	*
2000.00	25	250	0.1000	0.0123	0.0056	*

filename: C:\CA\CATEST02.ILS date: time:

Time = 48.00 (Females) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	7	250	0.0280	0.0134		
500.00	17	250	0.0680	0.0120	0.0206	*
1000.00	27	250	0.1080	0.0179	0.0003	*
2000.00	34	250	0.1360	0.0305	0.0000	*

Time = 72.00 (Females) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	10	250	0.0400	0.0133		
500.00	11	250	0.0440	0.0093	0.4136	
1000.00	19	250	0.0760	0.0139	0.0473	*
2000.00	35	250	0.1400	0.0225	0.0001	*

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Abs/Cell	Av Abs/Cell
1	3	0.0	24.0	m	0.600	0.184
2	133	0.0	24.0	m	0.800	0.200

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

Variance inflation factor: 1.000
Alpha: 0.050

Factor	Deviance	df	p
Scorer	26.414	24	0.3325
Sex	7.181	12	0.8454
Time	17.934	8	0.0217

filename: C:\CA\CATEST02.ILS date: time:

Time = 24.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	23	450	0.0511	0.0063		
500.00	17	500	0.0340	0.0088	0.9003	
1000.00	36	500	0.0720	0.0180	0.0985	
2000.00	62	500	0.1240	0.0183	0.0001	*

Time = 48.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	21	500	0.0420	0.0089		
500.00	37	500	0.0740	0.0131	0.0178	*
1000.00	64	500	0.1280	0.0200	0.0000	*
2000.00	94	500	0.1880	0.0274	0.0000	*

filename: C:\CA\CATEST02.ILS date: time:

Time = 72.00 (Both sexes) for 067889

p = 0.000
alpha = 0.040 (scaled by .8, assuming next run to exclude high dose)

One tailed test (Poisson) for chromosomal aberration (total aberrations)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	23	500	0.0460	0.0083		
500.00	20	500	0.0400	0.0065	0.6763	
1000.00	41	500	0.0820	0.0144	0.0122	*
2000.00	70	500	0.1400	0.0191	0.0000	*

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Chromosomal aberration (total aberrations)

There are 2 outliers at the .05 significance level.

	Line	Dose	Time	Sex	Abs/Cell	Av Abs/Cell
1	3	0.0	24.0	m	0.600	0.184
2	133	0.0	24.0	m	0.800	0.200

filename: C:\CA\CATEST02.ILS date: time:

Time = 48.00 (Males) for 067889

alpha = 0.050

One tailed test (Poisson) for chromosomal aberration (total aberrations) (with positive controls)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	14	250	0.0560	0.0107		
12.50	76	250	0.3040	0.0560	0.0000	*

Time = 48.00 (Females) for 067889

alpha = 0.050

One tailed test (Poisson) for chromosomal aberration (total aberrations) (with positive controls)

MG/KG	Total Aberrat'ns	Cells Scored	Aberrat'ns / Cell	SEM (for Obs)	Pairwise Significance	
0.00	7	250	0.0280	0.0134		
12.50	58	250	0.2320	0.0259	0.0000	*

filename: C:\CA\CATEST02.ILS date: time:

Endpoint: Mitotic Index

Variance inflation factor: 1.341
Alpha: 0.050

Factor	Deviance	df	p
Scorer	52.058	24	0.0008
Sex	206.145	24	0.0000
Time	136.872	32	0.0000

filename: C:\CA\CATEST02.ILS date: time:

Time = 24.00 (Males) for 067889

p = 0.768
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance	
0.00	196	5000	3.9200	0.5531		
500.00	218	5000	4.3600	0.3874	0.8298	
1000.00	213	5000	4.2600	0.2876	0.7707	
2000.00	202	5000	4.0400	0.3745	0.6045	

Time = 48.00 (Males) for 067889

p = 0.000
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance	
0.00	264	5000	5.2800	0.3492		
500.00	179	5000	3.5800	0.1849	0.0002	*
1000.00	140	5000	2.8000	0.1789	0.0000	*
2000.00	64	5000	1.2800	0.1937	0.0000	*

filename: C:\CA\CATEST02.ILS date: time:

Time = 72.00 (Males) for 067889

p = 0.000
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance	
0.00	230	5000	4.6000	0.3876		
500.00	206	5000	4.1200	0.3441	0.1551	
1000.00	152	5000	3.0400	0.2596	0.0002	*
2000.00	76	5000	1.5200	0.2585	0.0000	*

Time = 24.00 (Females) for 067889

p = 0.697
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	256	5000	5.1200	0.2313	
500.00	241	5000	4.8200	0.1093	0.2756
1000.00	236	5000	4.7200	0.1794	0.2123
2000.00	227	5000	4.5400	0.3724	0.1214

filename: C:\CA\CATEST02.ILS date: time:

Time = 48.00 (Females) for 067889

p = 0.572
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	253	5000	5.0600	0.4927	
500.00	239	5000	4.7800	0.3299	0.2881
1000.00	232	5000	4.6400	0.5504	0.1993
2000.00	219	5000	4.3800	0.4263	0.0831

Time = 72.00 (Females) for 067889

p = 0.707
alpha = 0.050

Likelihood ratio for mitotic index

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	222	5000	4.4400	0.4020	
500.00	212	5000	4.2400	0.3180	0.3359
1000.00	240	5000	4.8000	0.1978	0.7705
2000.00	224	5000	4.4800	0.3593	0.5333

filename: C:\CA\CATEST02.ILS date: time:

Time = 48.00 (Males) for 067889

alpha = 0.050

Likelihood ratio for mitotic index (with positive controls)

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	264	5000	5.2800	0.3492	
12.50	243	5000	4.8600	0.4483	0.1692

Time = 48.00 (Females) for 067889

alpha = 0.050

Likelihood ratio for mitotic index (with positive controls)

MG/KG	Cells in Mitosis	Cells Scored	Mitotic Index (%)	SEM (for Obs)	Pairwise Significance
0.00	253	5000	5.0600	0.4927	
12.50	253	5000	5.0600	0.1492	0.5000