Standard Operation Procedures for

Varian Gas Chromatograph 3900

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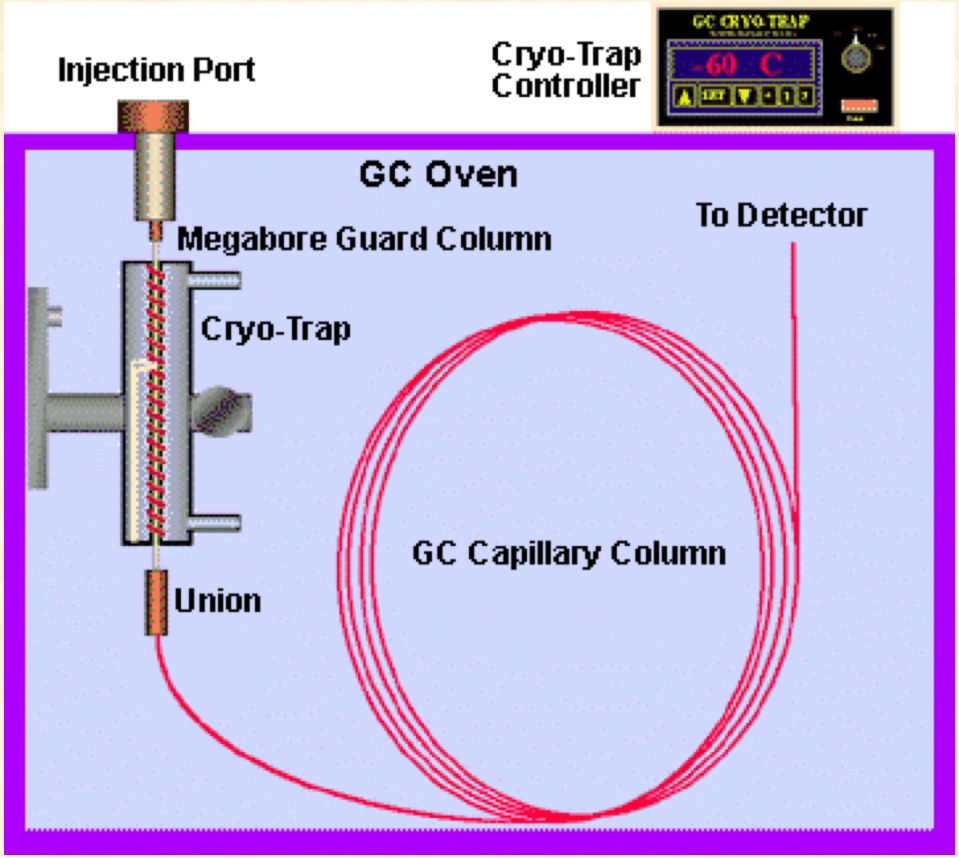
Using the Varian GC 3900 Gas Chromatography

Varian GC 3900 Operations

http://www.foodtechsource.com/emag/018/hot.htm



Precautions

- Sign log book.
- Remove gloves when operating the computer keyboard and mouse
- Do not change any of the gas settings, all gas pressure has been set.
- Do not change any of the setting on the GC through the GC console, all parameter changes should be completed through the "Star" software via the computers.
- Clean up your mess after using the instrument. After you have completed your project, take your sample vial and empty chemical in the waste refuge container.
  Clean up your work area.

Quick Overview

I. Check gas regulator and gas setting, Turn on Instrument

II. Load auto sampler

III. Setup Method

IV. Acquire chromatogram

V. Working up and Analyze data

VI Instrument shut down and clean up

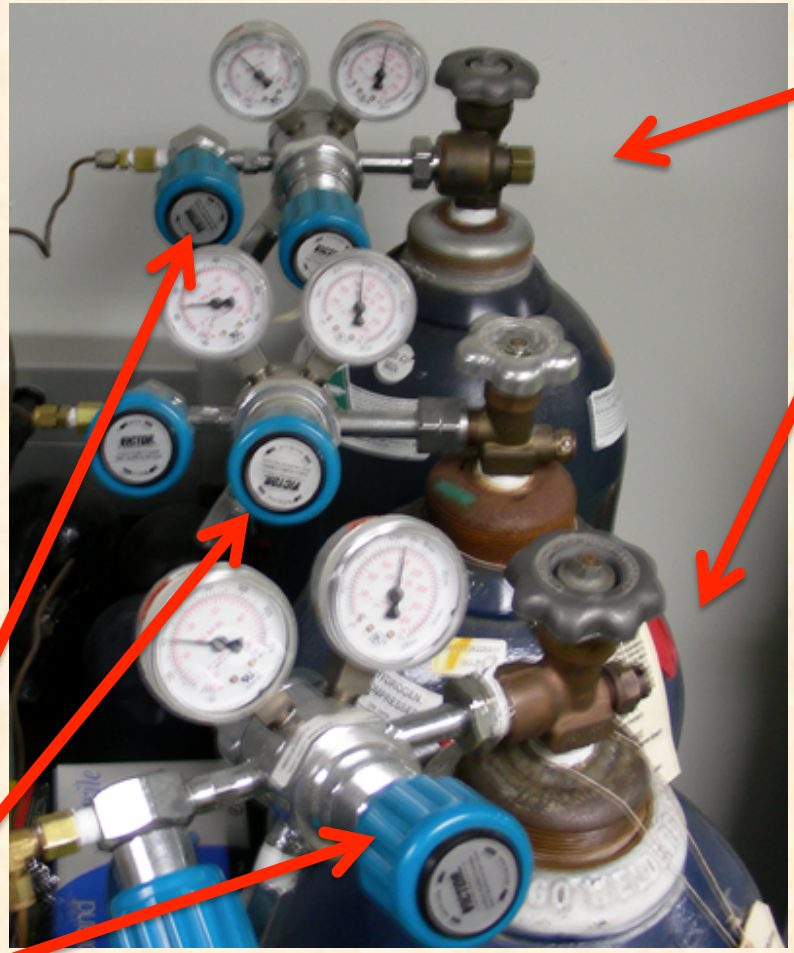
I. Check Gas Pressure

1. Sign log book
2. Check gas pressure

Check to make sure the gas cylinder have the proper pressure setting.

Air, Hydrogen and Helium gas are set to:

Air pressure 80 psi
Hydrogen 80 psi
Helium pressure 80 psi

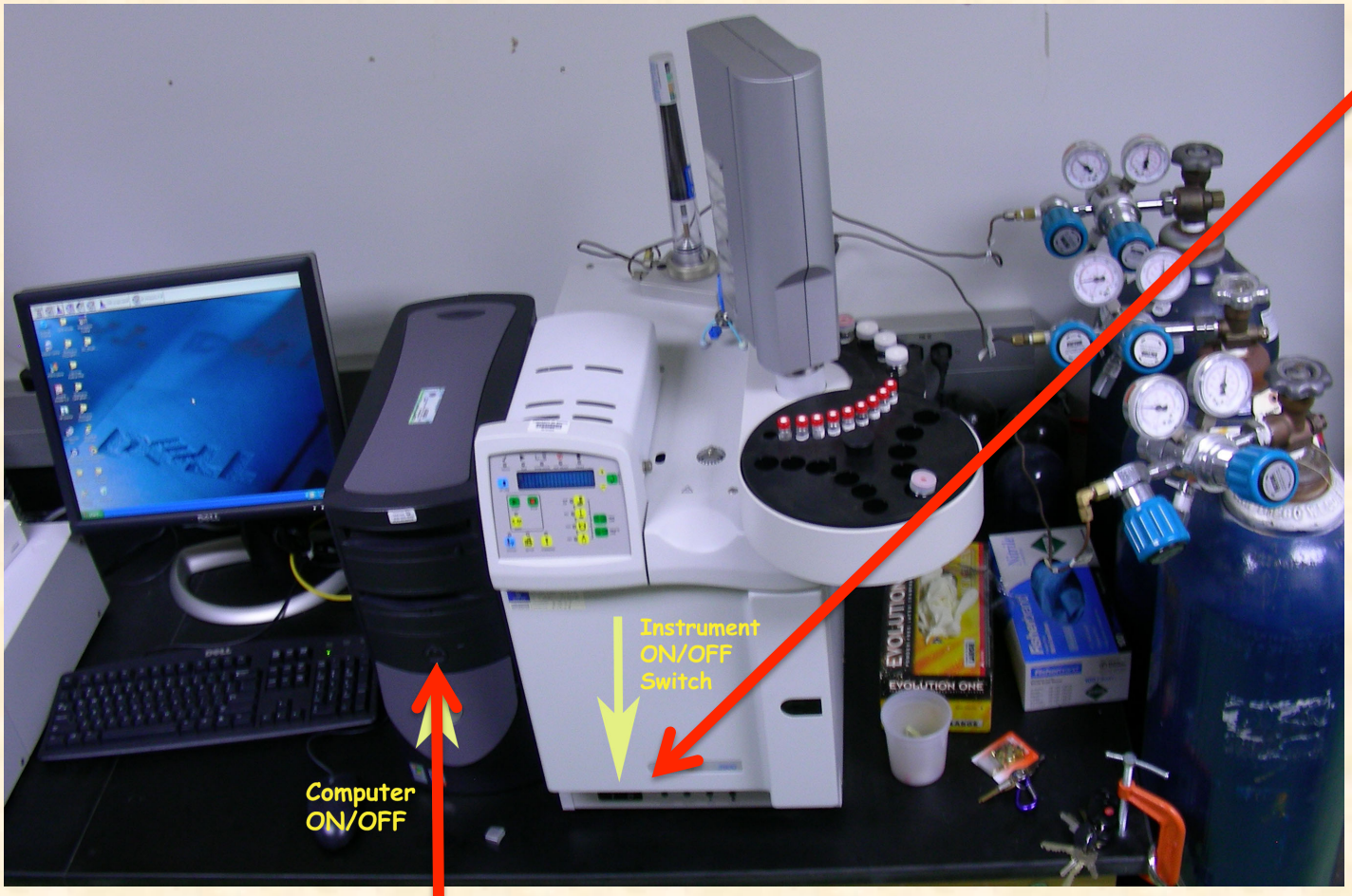


Open gas regulator here.

Do not adjust primary and secondary value of regulator.

I. Turn on GC and Computer

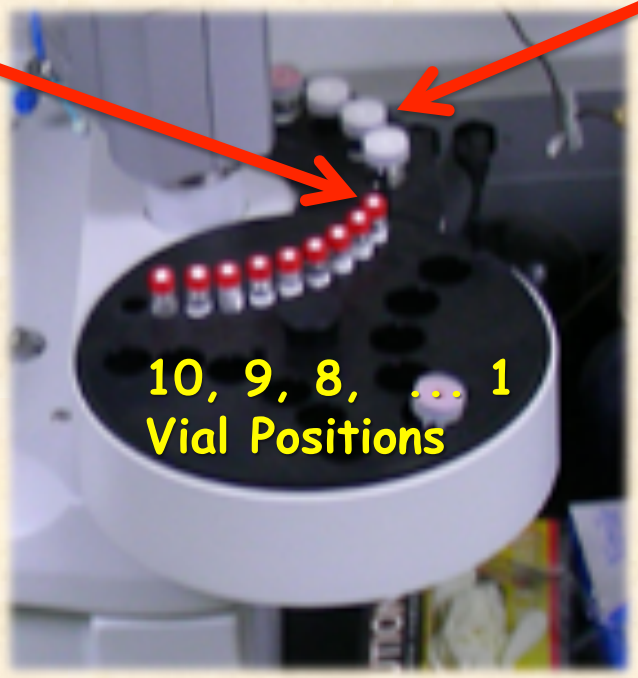
3. Flip the switch to the GC Chromatography to on the instrument
4. Turn on computer if it is not already on.



II. Load Auto Sampler

5. Load Auto Sampler
6. Check that the wash solvent and waste

Load samples in vial in carousel. Position 1 starts at the right goes to position 10.



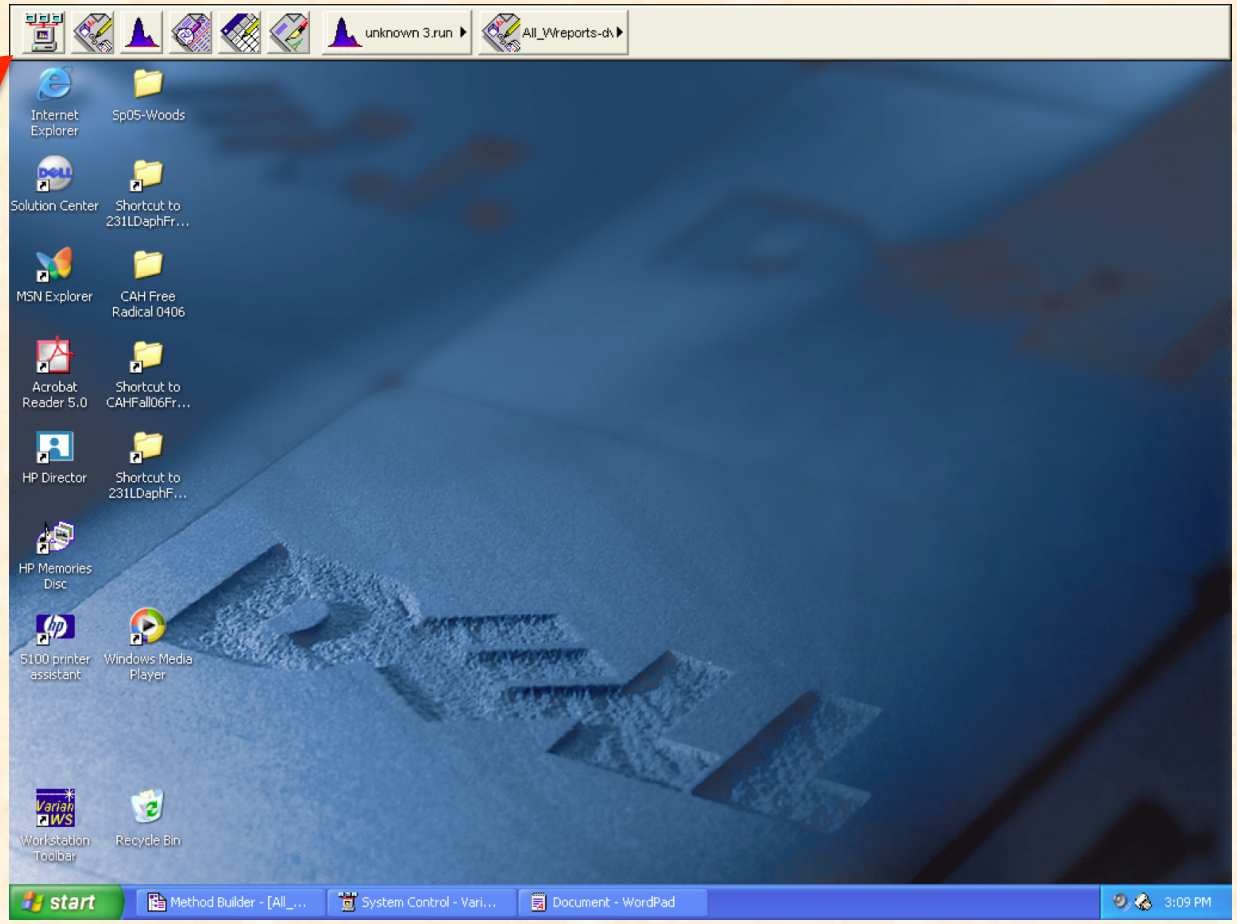
Check that wash solvent reservoir is full and that waste reservoir is empty.

III. Setup Experiment and Method

Opening screen in Windows XP

7. Click on System Control Icon.

Click on the System Control Icon to initiate "**Star**" Program (Operating system for GC).

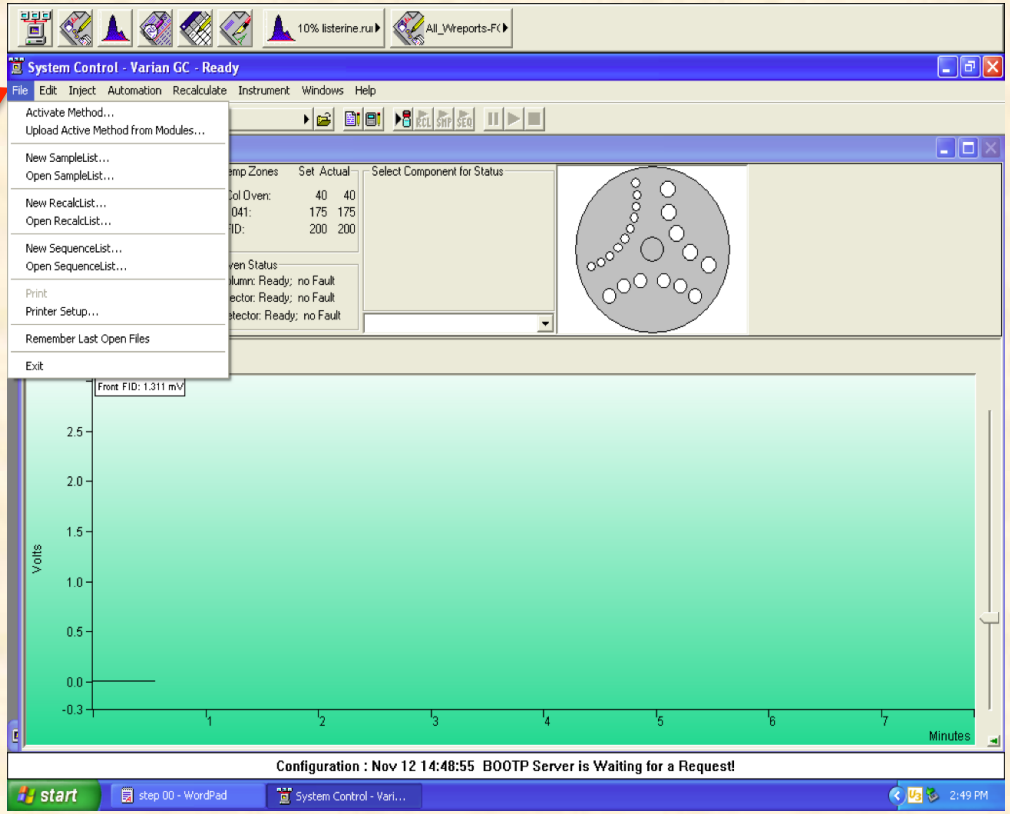


III. Setup Experiment and Method

8. Verify that the menu is for the GC and not the HPLC
9. Opening menu for GC setup menu.
10. Create new Sample list by clicking on File menu.

File → New Sample List

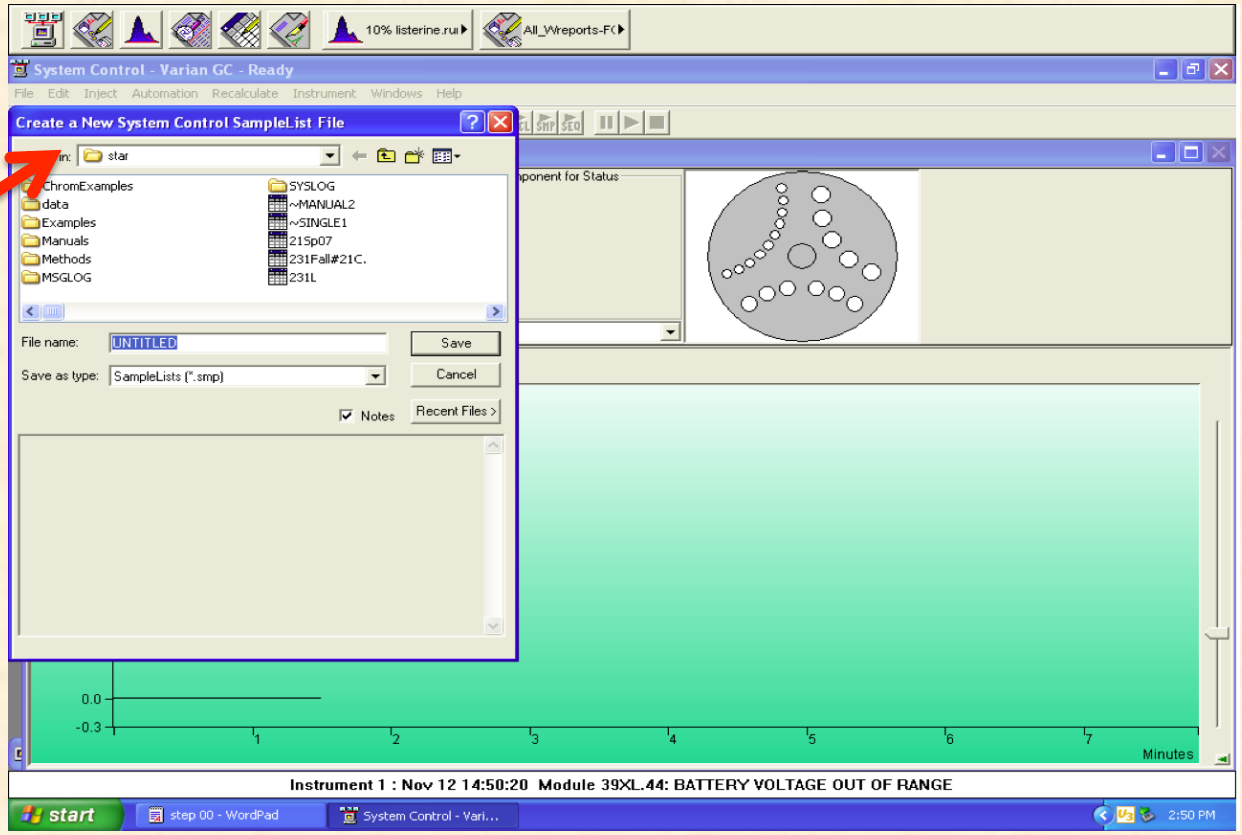
Create new Sample List by clicking on **File** and dropping down to "**New SampleList**"



III. Setup Experiment and Method

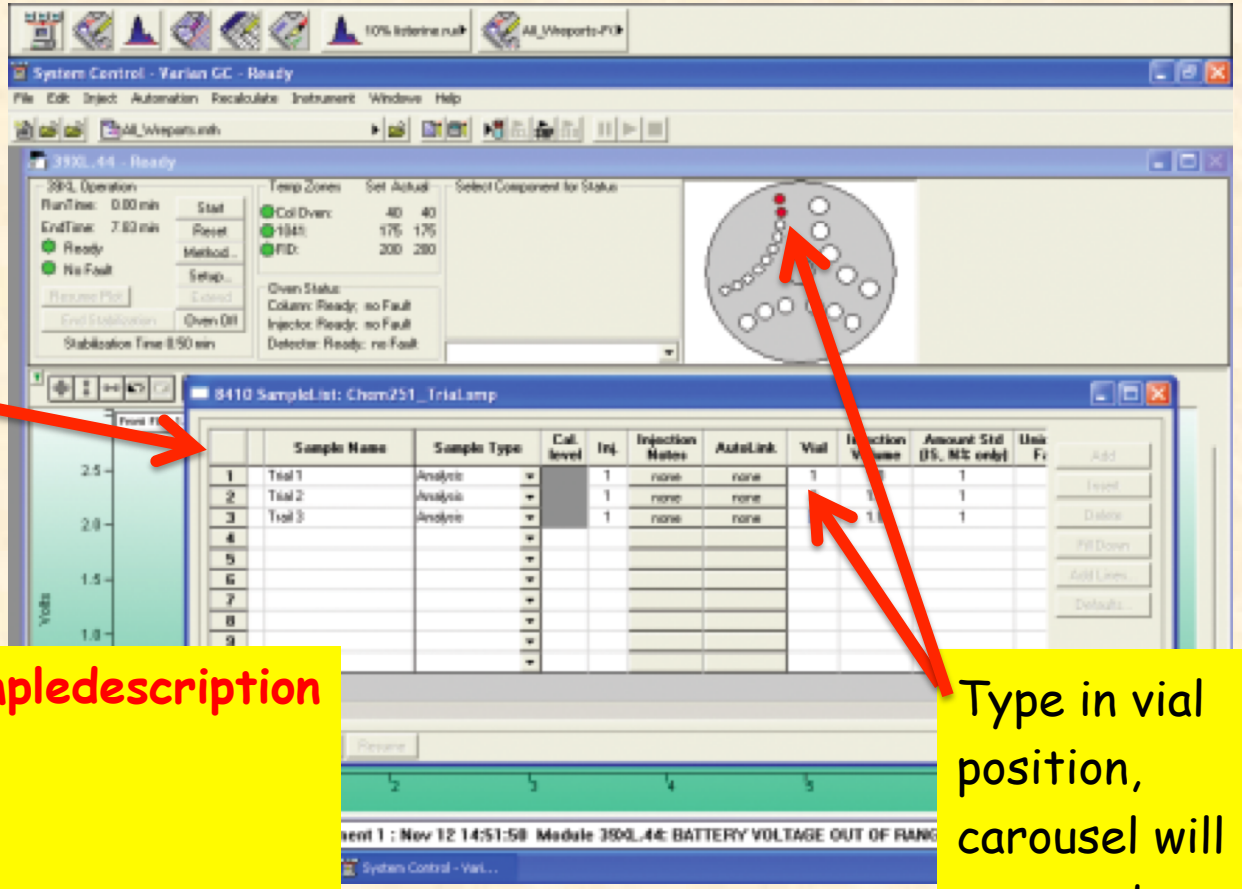
11. Navigate to folder where SampleList file is stored or where old Samplelist files have been stored.
12. Create a new sample list or open an old file.

Find folder where Samplelist parameter is to be stored.



III. Setup Experiment and Method

13. Fill in the SampleList .
14. Write description of Samplelist and fill in vial position.



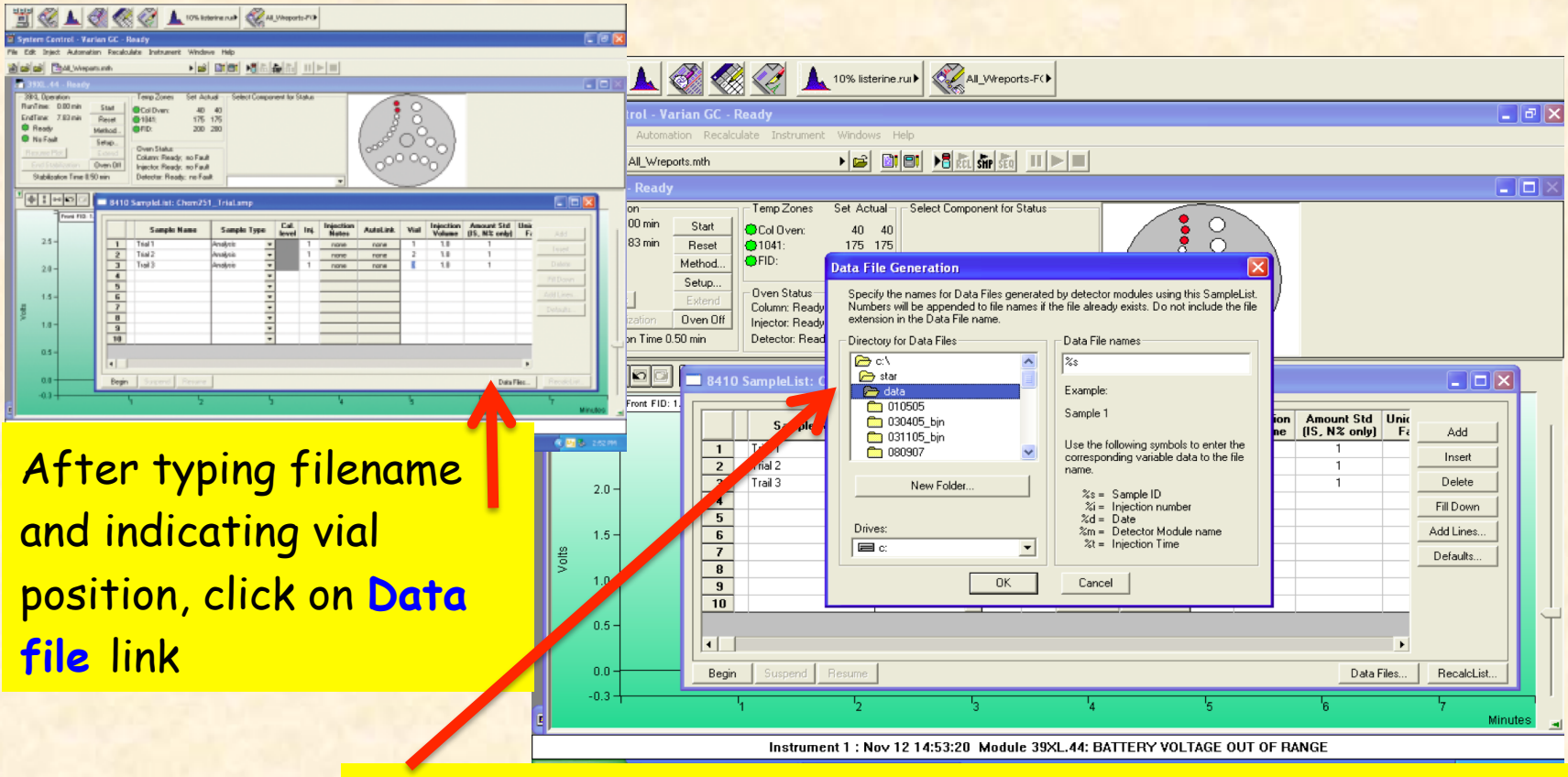
Write description of samples to be analyze. Use format of-

username_counter_sampledescription
ie.,
fg_a1_5%EtOH
fg_a2_10%EtOH

Type in vial position, carousel will turn red.

III. Setup Experiment and Method

15. Find folder to save chromatogram files in the Data File Generation menu

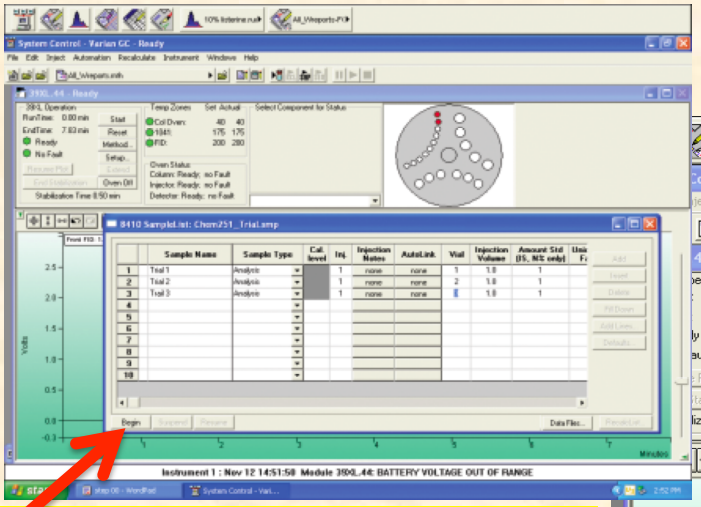


After typing filename and indicating vial position, click on **Data file** link

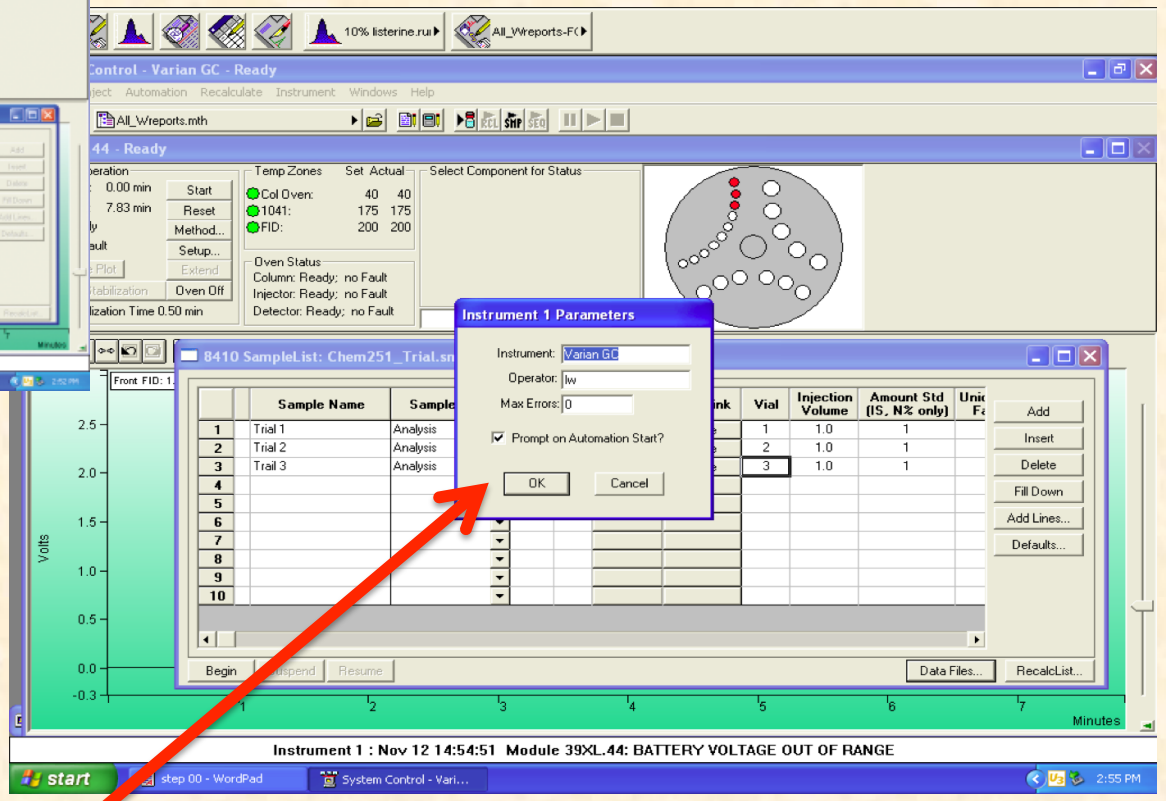
Navigate to folder where chromatograms are to be stored, Click **OK** when done.

III. Setup Experiment and Method

16. Click on **Begin** to activate Method.



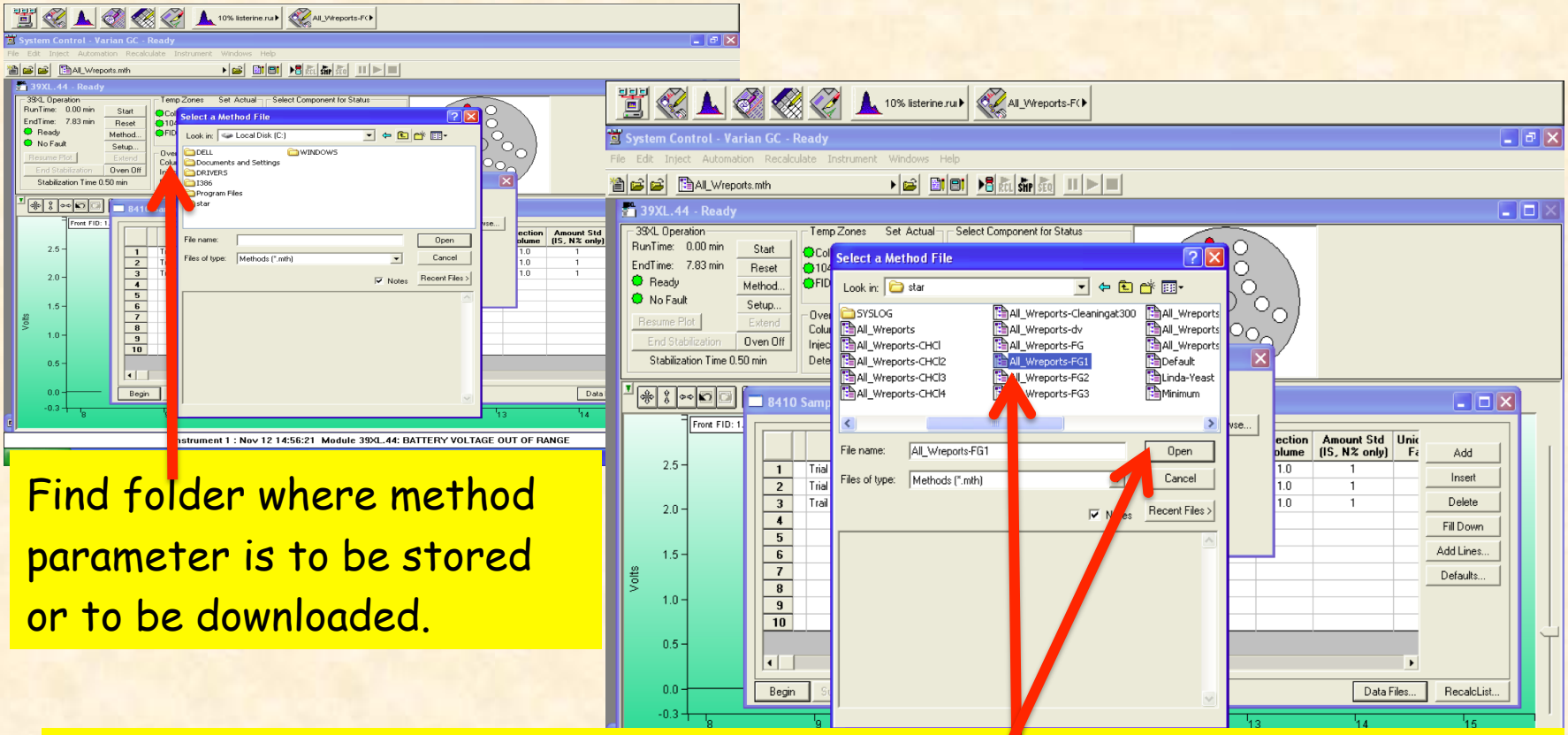
Click on **Begin** to upload method files and to activate data collection.



Instrument 1 Parameter menu display. Click on **OK**.

III. Setup Experiment and Method

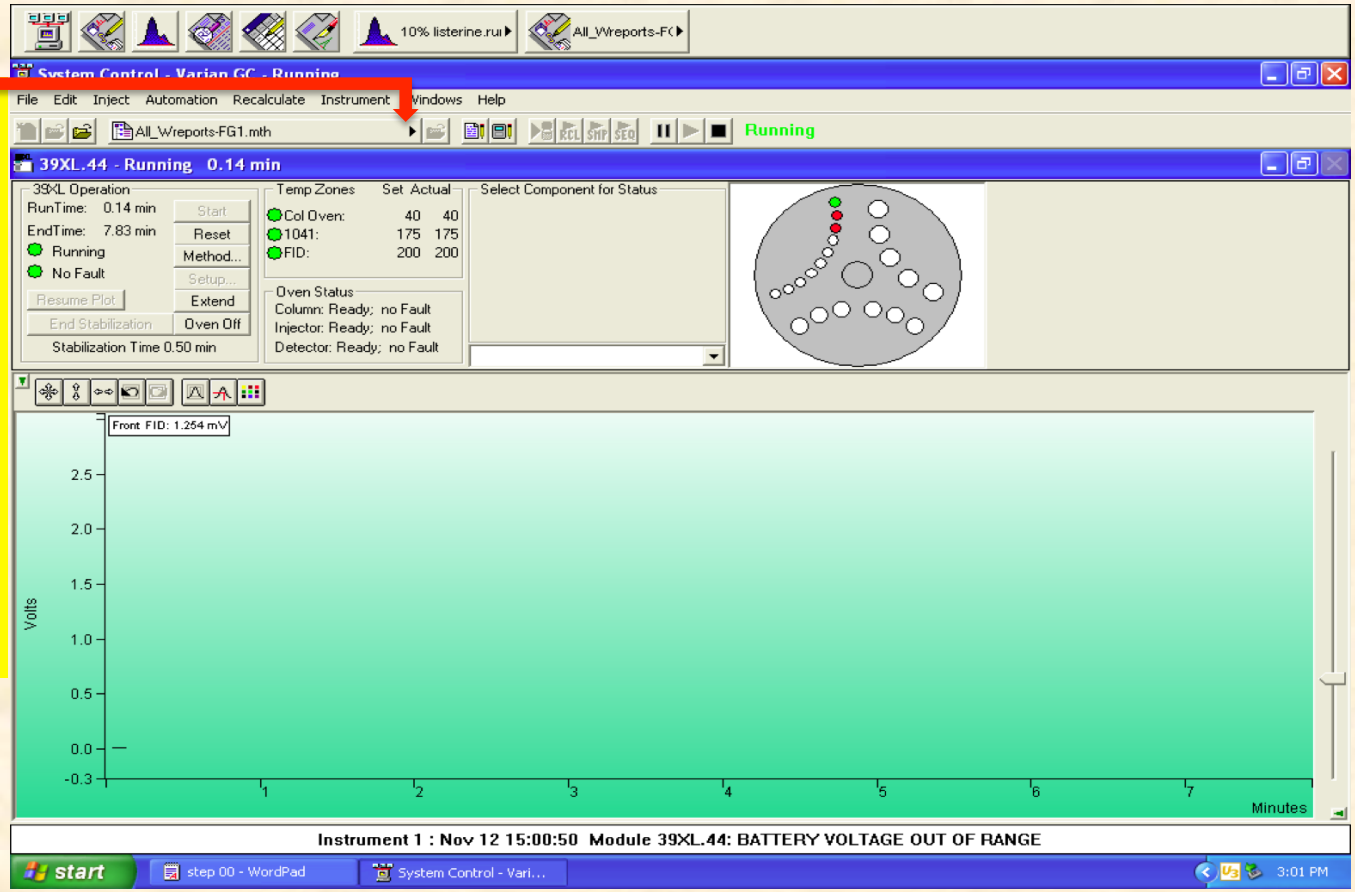
17. Navigate to folder where Methods[*.mth] file is stored. Select a method file with proper parameters for experiment.



IV. Activate the Method collection

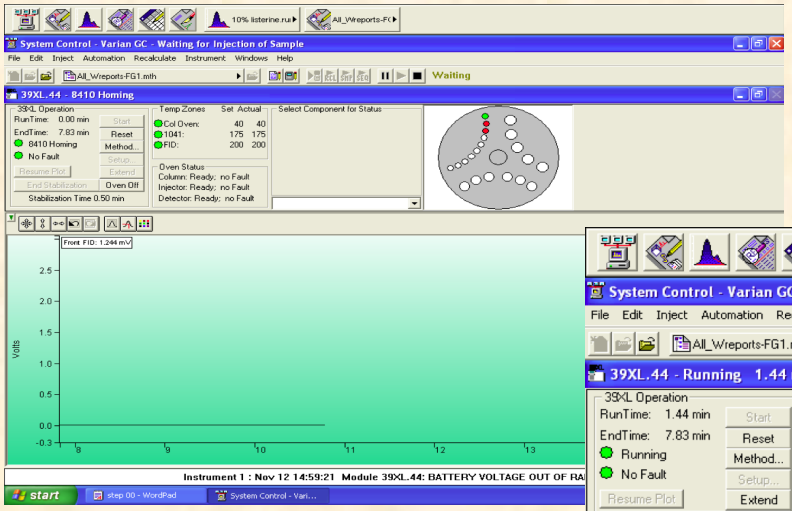
18. Instrument will begin equilibrating the temperature and initiate stabilization routine. If the instrument is not activate, click on method link were the All_Wreports.mth shows and reactivate the method.

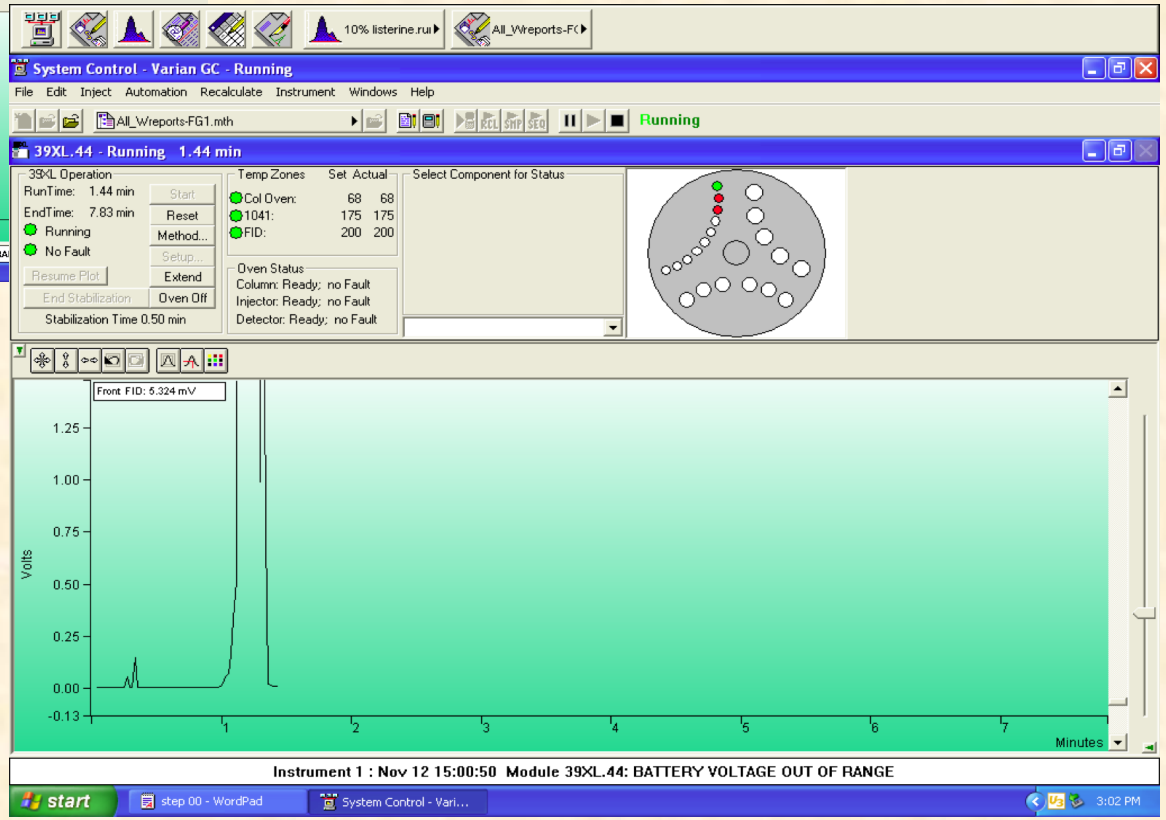
If the GC does not begin the initialization routine, then click on this menu to reactivate the methods



IV. Activate the Method collection

19. GC begins to collect chromatogram.



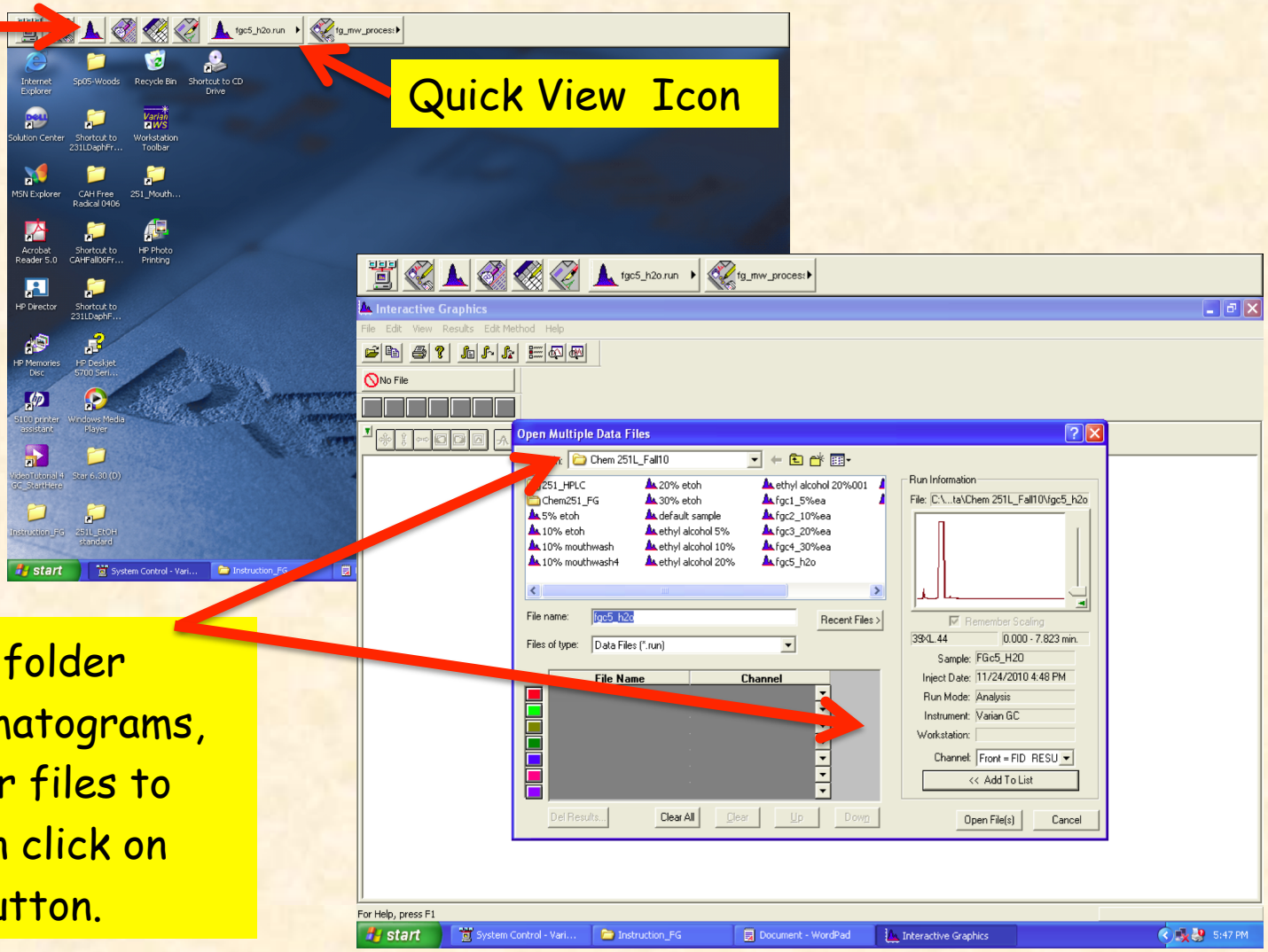


Chromatogram begins to collect.

V. Processing the Data

20. In the Interactive Graphic menu and select files to display.

Click on Interactive Graphic menu or the Quick View to access chromatogram.

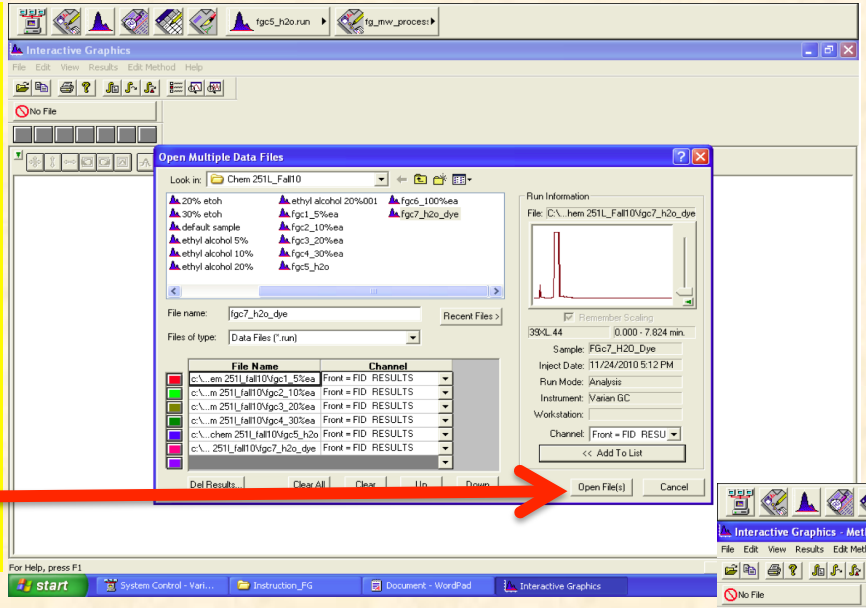


Navigate to the folder containing chromatograms, select the file or files to analyze and then click on "**Add to List**" button.

V. Processing the Data

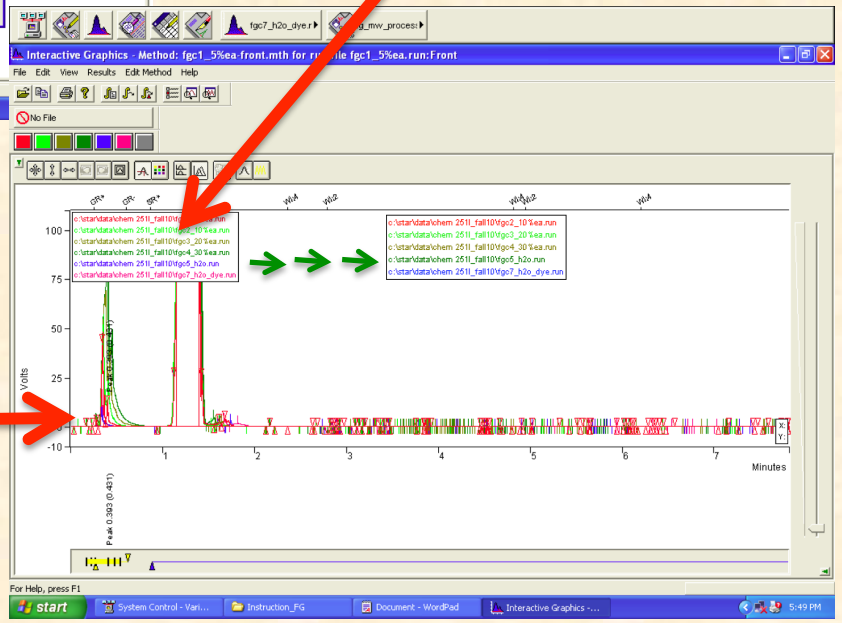
21. After selecting chromatogram, open the files.

After selecting files to be display, click on "**Open Files**".



Move Legend out of the way.

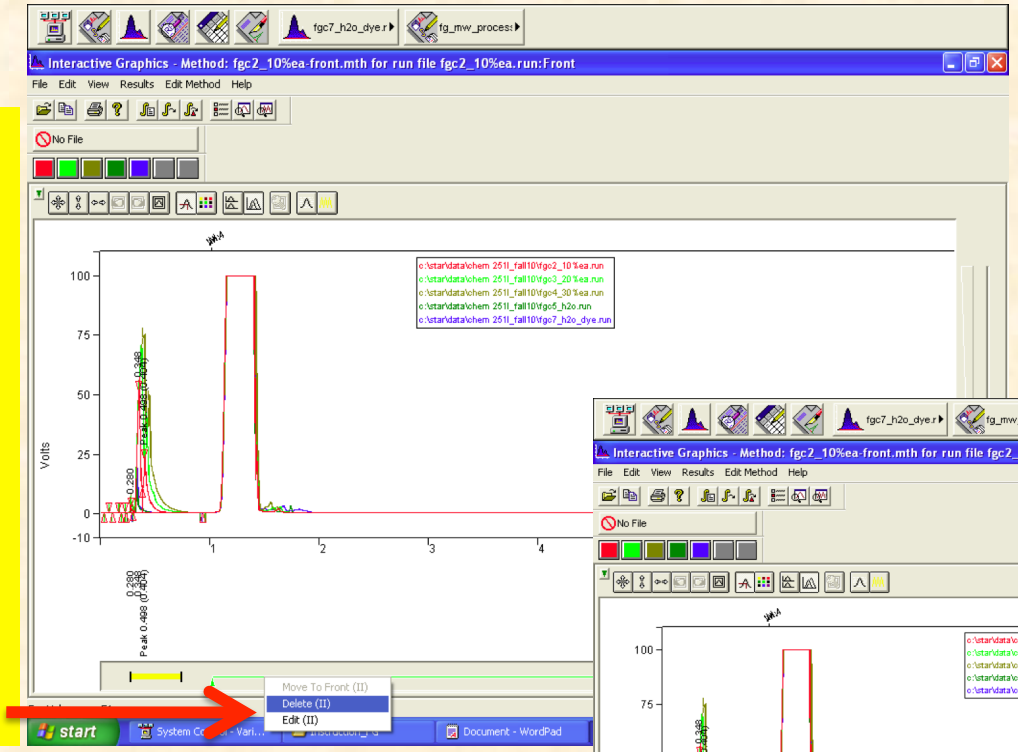
Peaks displays in the display screen.

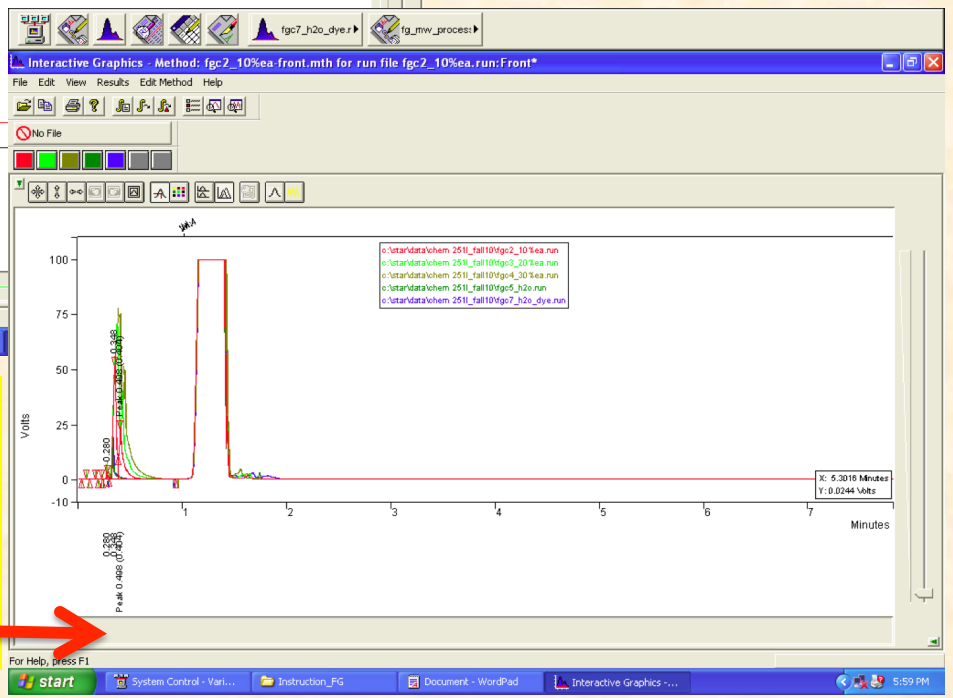


V. Processing the Data

22. Remove peak markers.

Hold left mouse button down on the peak label area and delete peak markers



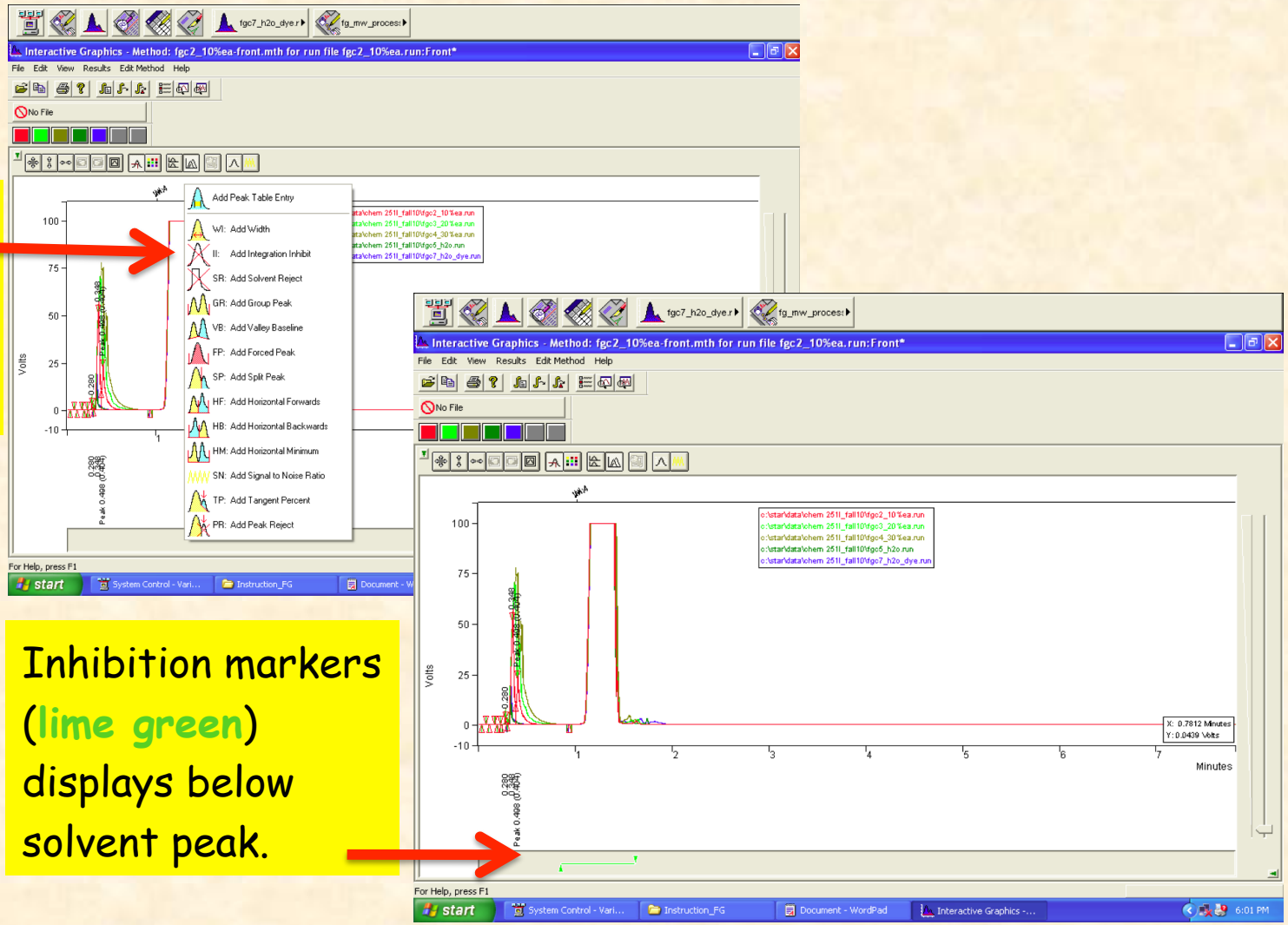


No markers left on the **peak label** area for any of the chromatogram peaks.

V. Processing the Data

23. Move cursor below solvent peak and hold right mouse button down.

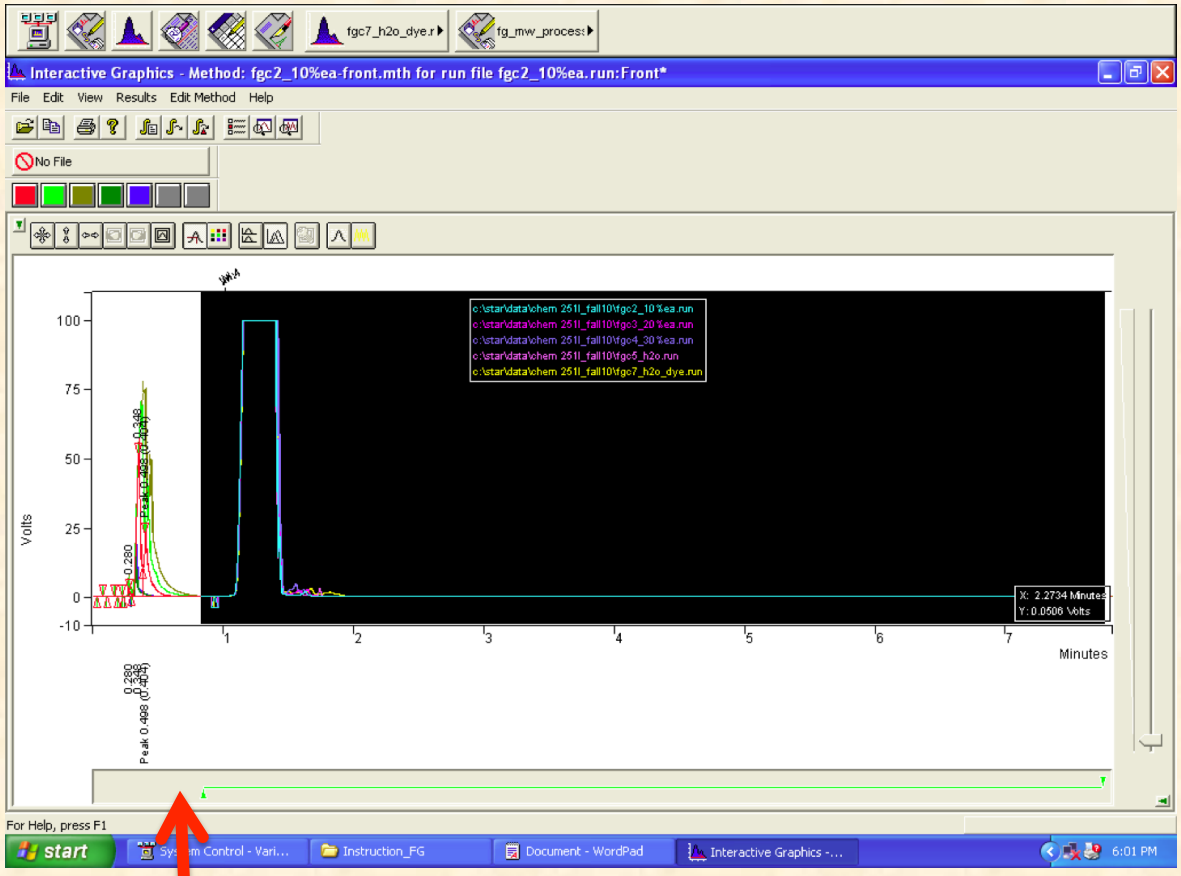
Add **Integration Inhibition** mark.



Inhibition markers (**lime green**) displays below solvent peak.

V. Processing the Data

24. Stretch inhibition markers so all peaks with retention times greater than the solvent is ignored in the analysis.

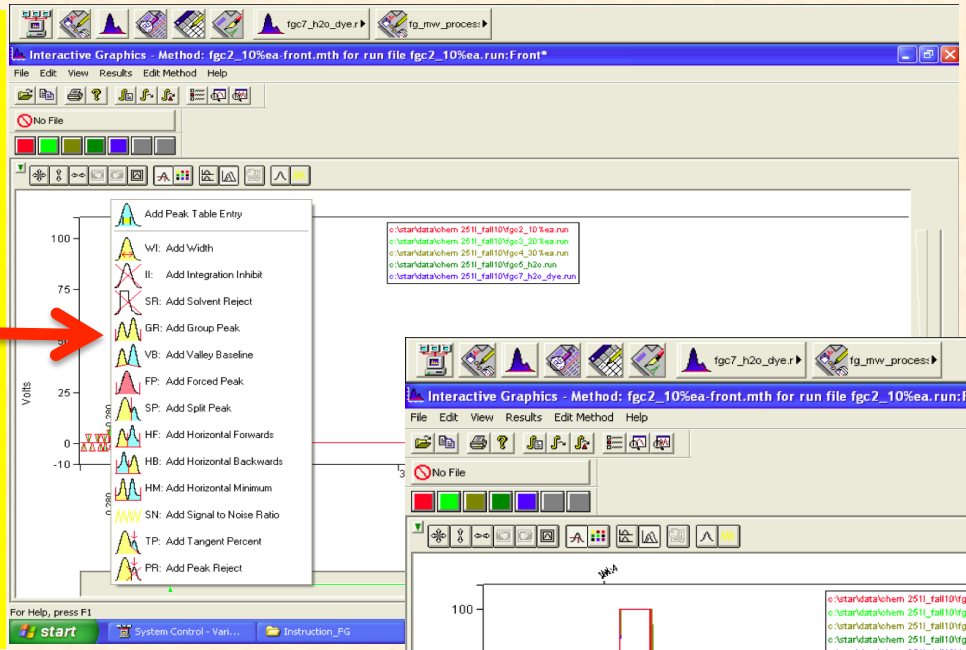


Click on right handle of inhibition marker and stretch to the end of time line so rest of signals are inhibited for integration in the analysis.

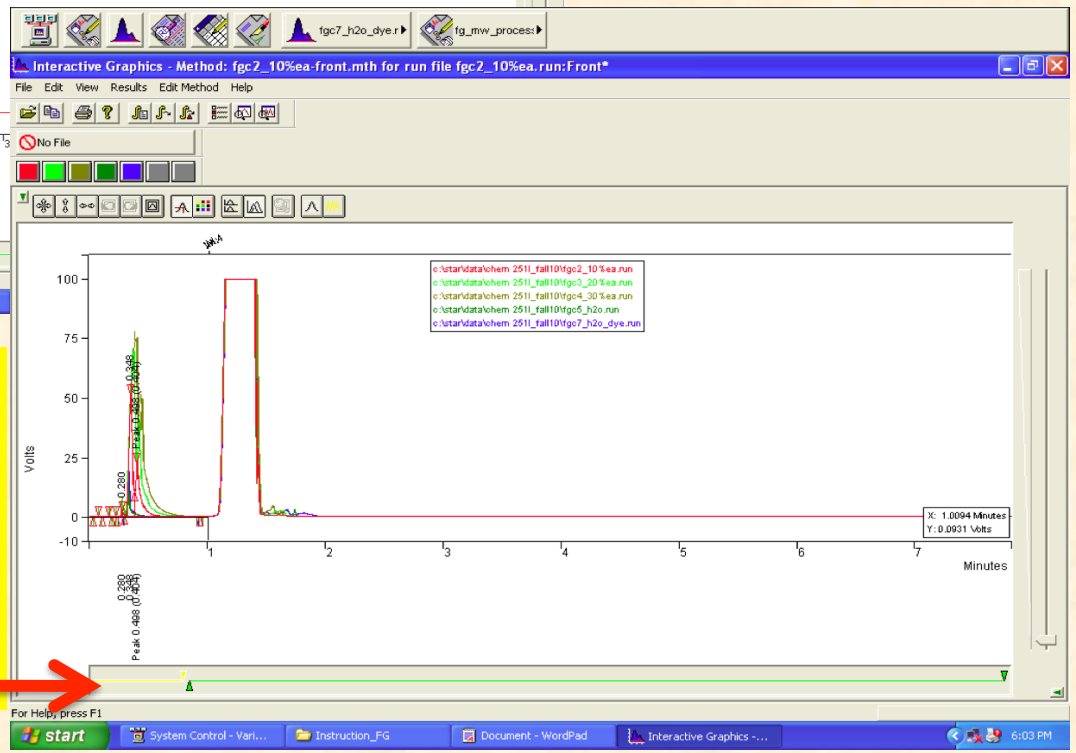
V. Processing the Data

25. Select peak or group of peaks to be analyze and mark the peak(s)

Select peaks to be analyze and right click on the peak label area then move cursor up to "Add Group Peaks".



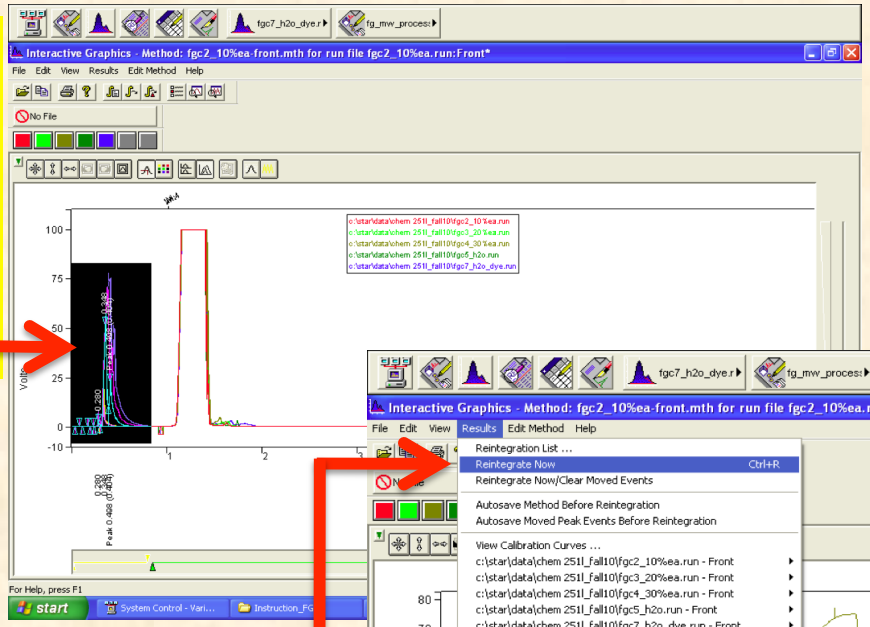
Add Group Peak marker (yellow).



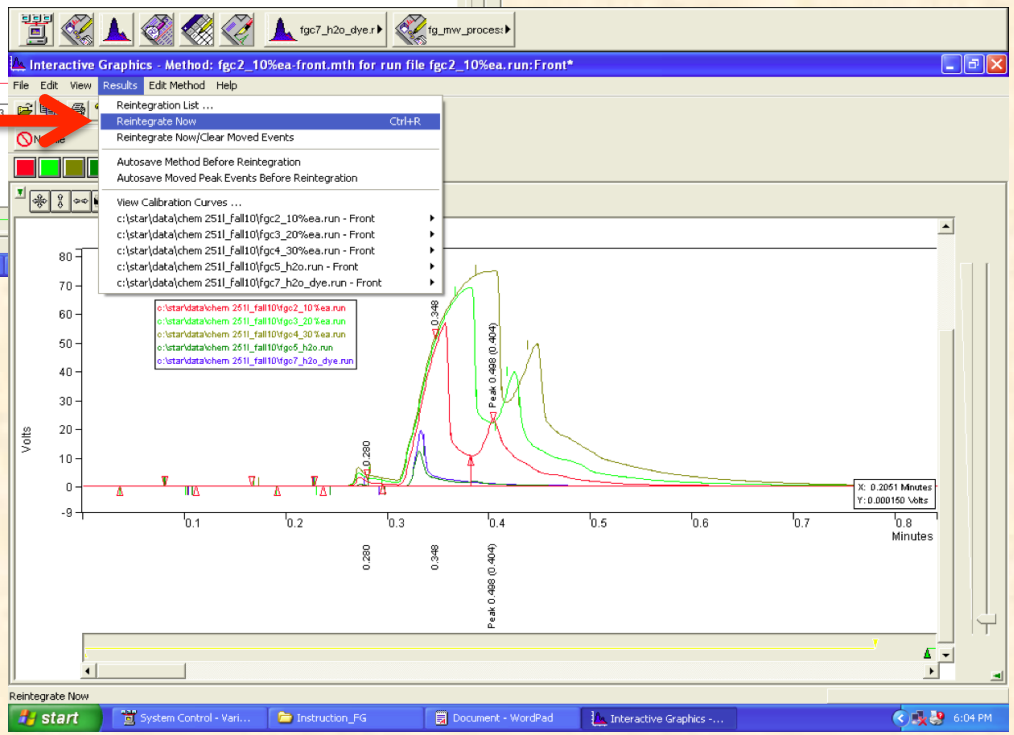
V. Processing the Data

26. Zoom in to peaks to be analyzed by boxing with cursor

Box region in the chromatogram to expand. Use mouse cursor to box the area.



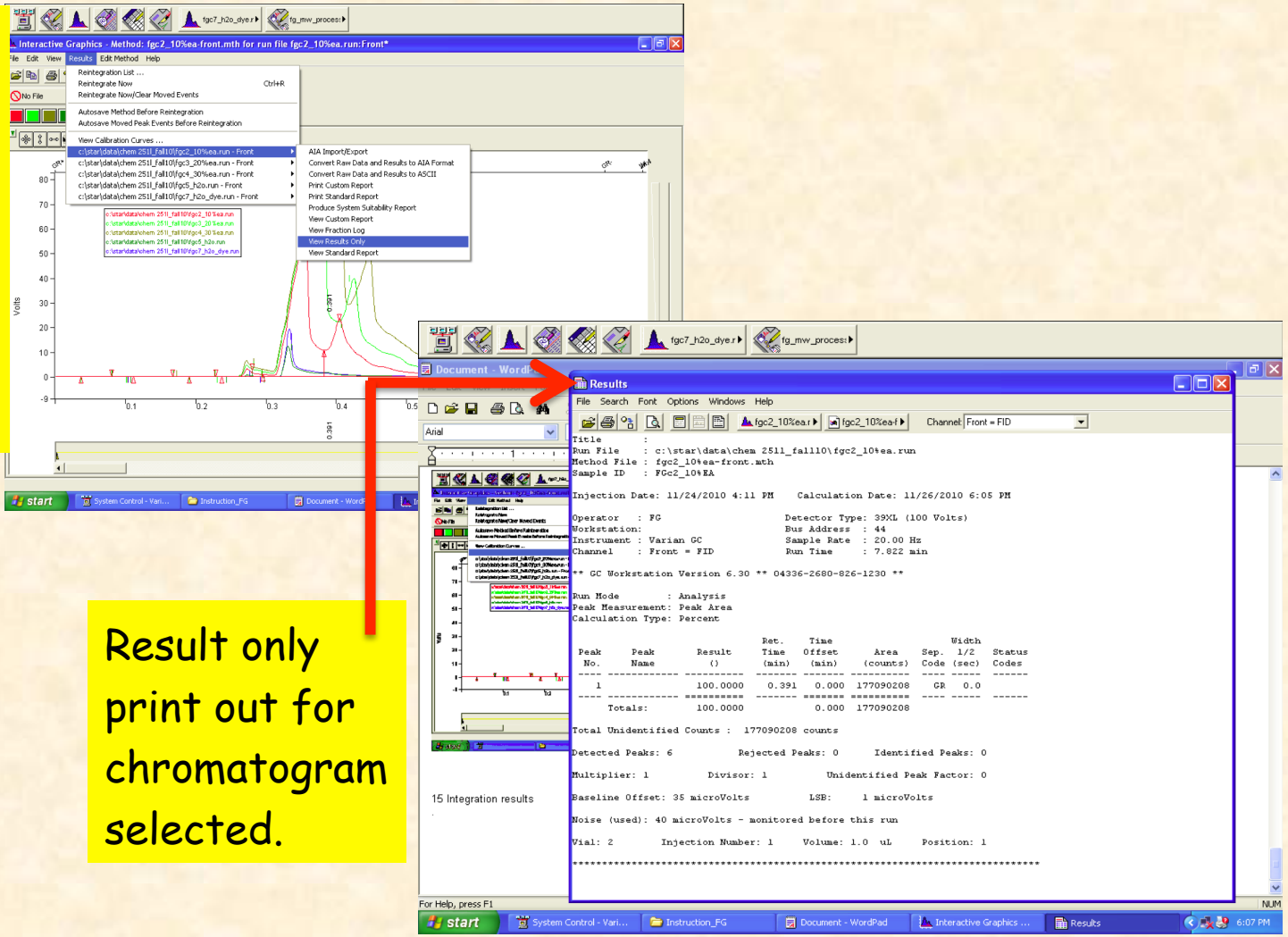
After zooming into to area of interest in the graphic interactive screen, click on **Result** heading to display result printout of the chromatogram that are displayed.



V. Processing the Data

27. Show "Results Only" for chromatogram selected. Result print out is displayed for specific chromatogram chosen.

Navigate in the Result menu to to the specific chromatogram in which detail results are to be displayed.

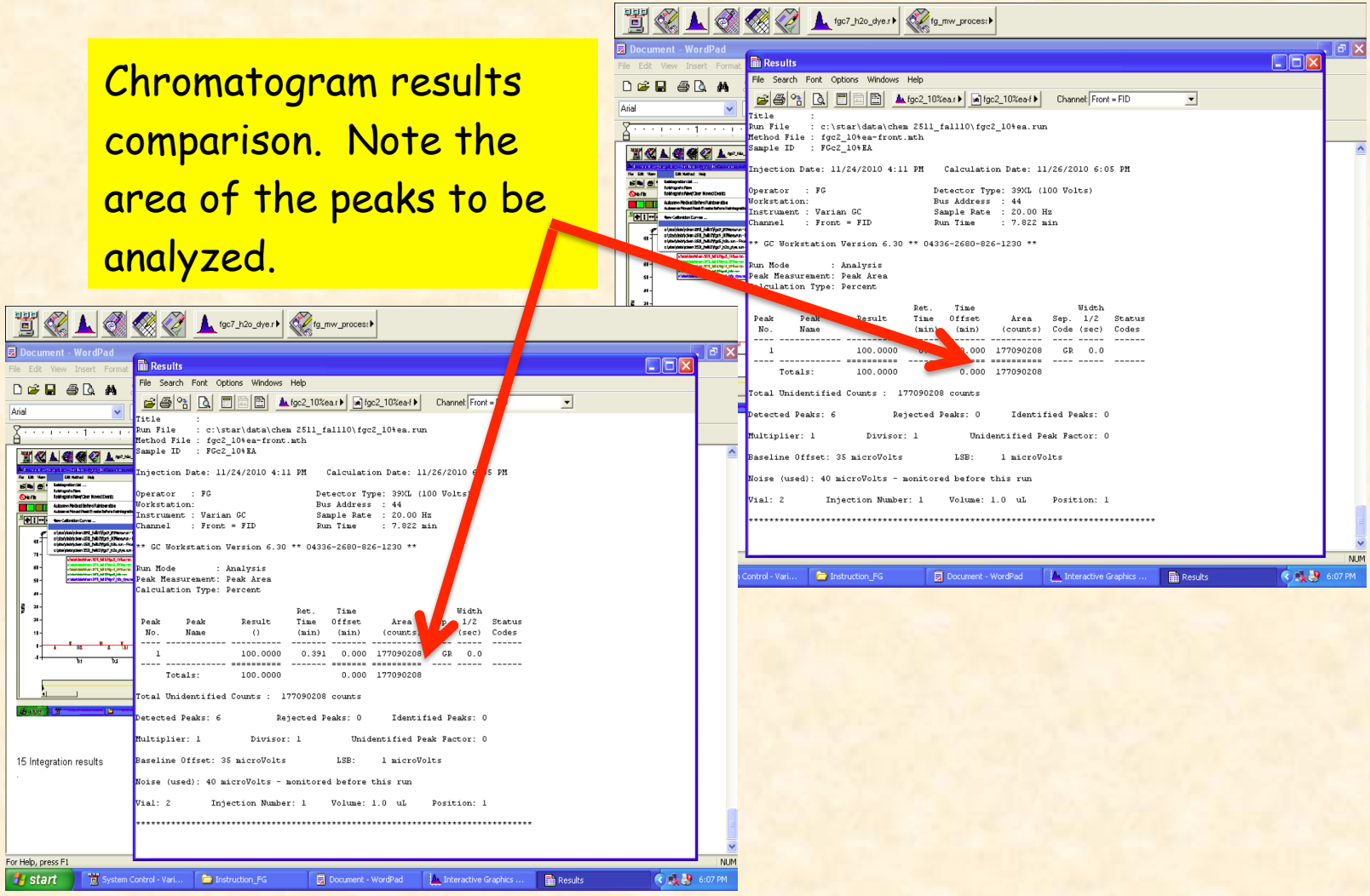


Result only print out for chromatogram selected.

V. Processing the Data

28. "Results Only" comparison of print out for a couple of chromatograms that were selected for closer investigation.

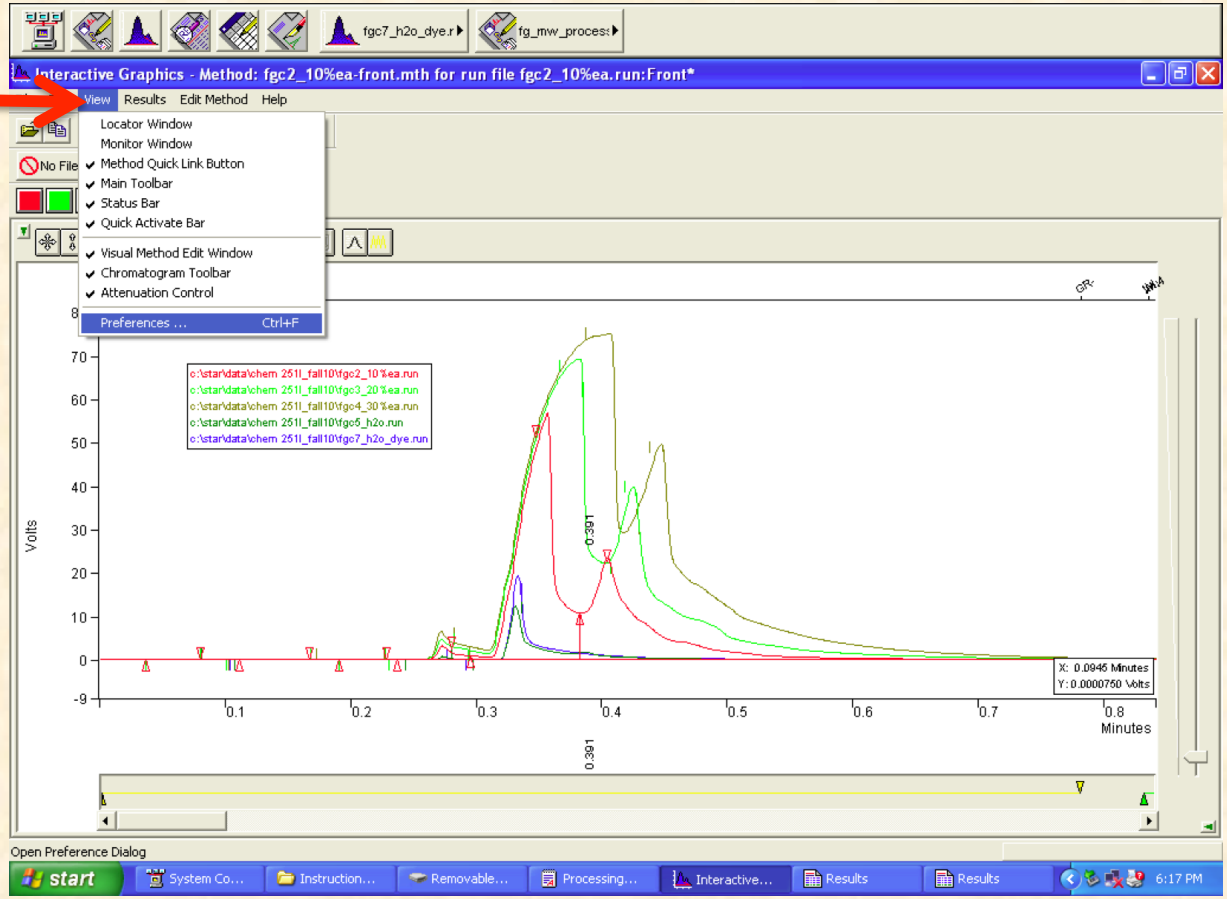
Chromatogram results comparison. Note the area of the peaks to be analyzed.



V. Processing the Data

29. Compare Chromatogram profile comparison by changing trace colors.

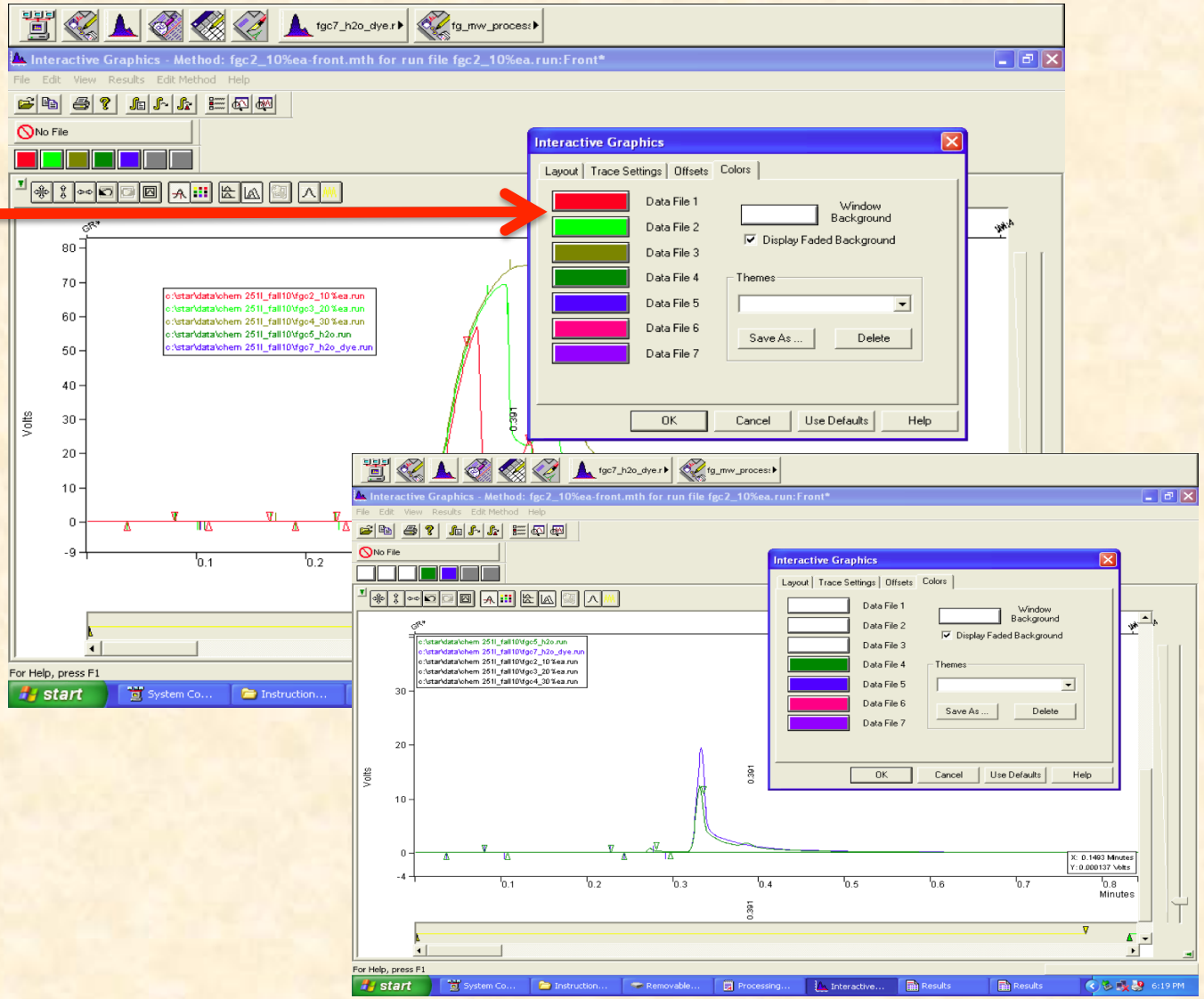
Chromatogram profile comparison. To further investigate detail profile of each chromatogram, navigate to "View then to Preference"



V. Processing the Data

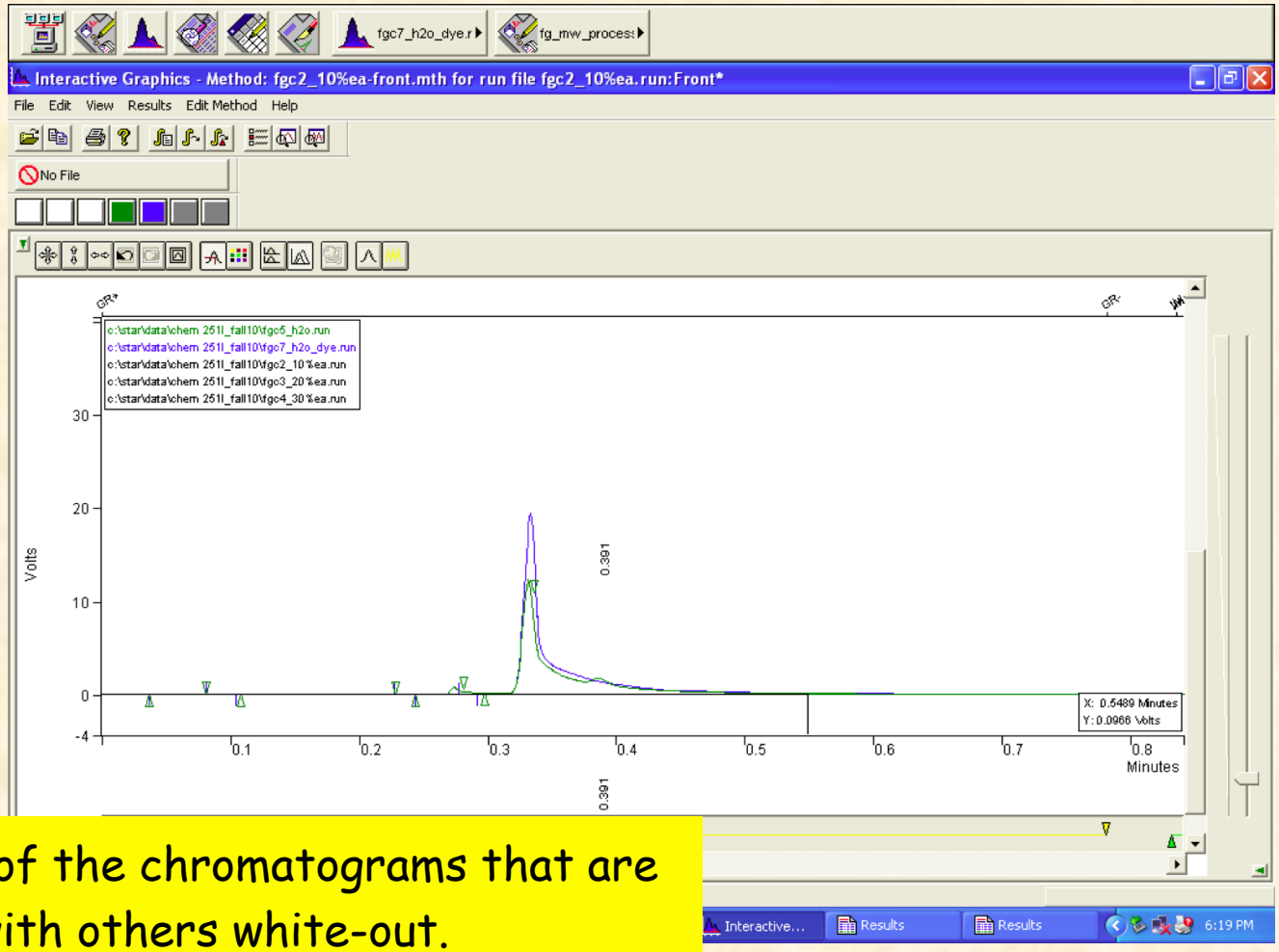
30. Under View → Preference, go to "**Trace Setting**" and adjust color.

For chromatograms that are to be ignored, change the color of the chromatogram traces to white so only chromatogram of interest are shown in the screen.



V. Processing the Data

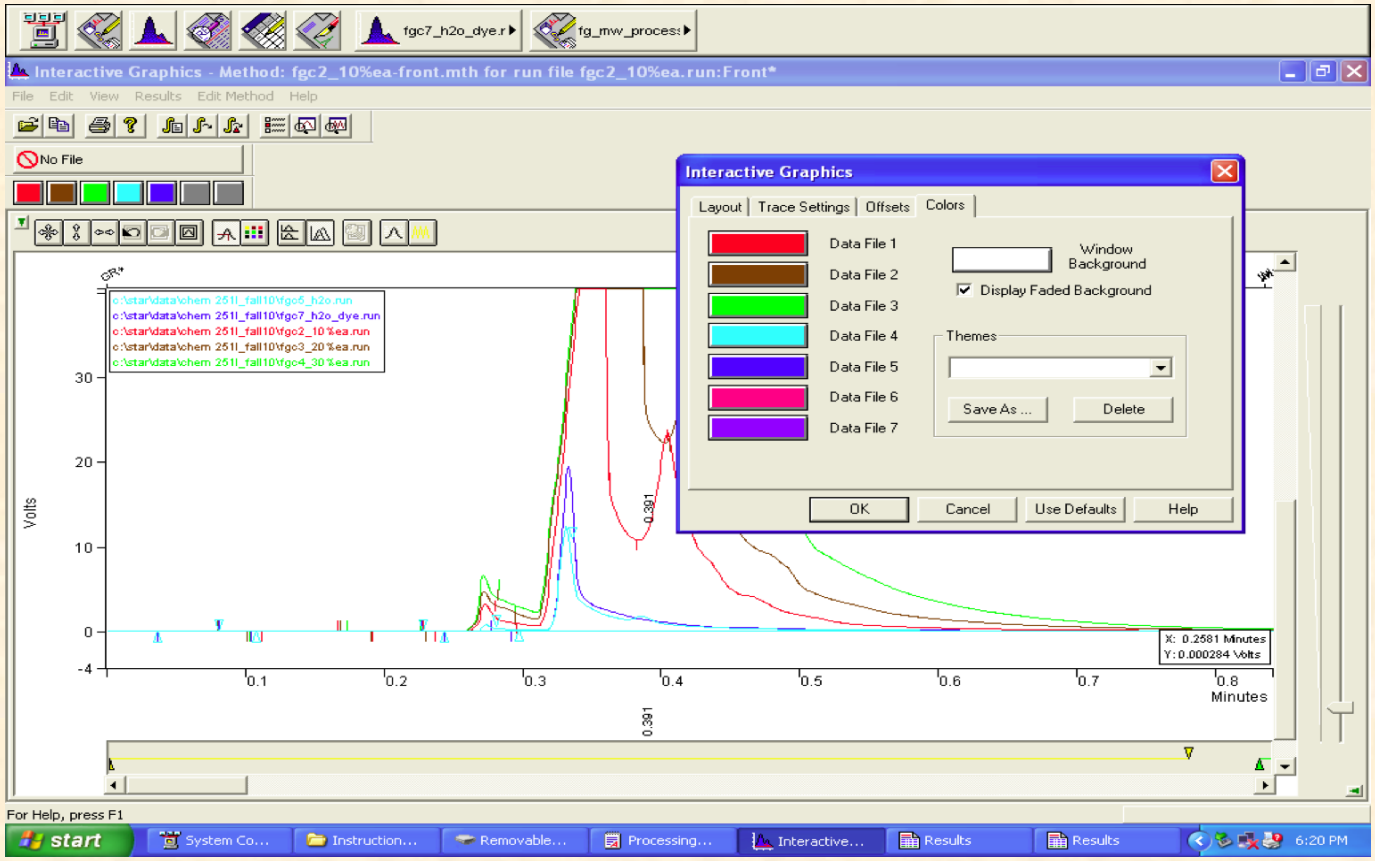
31. Chromatogram profile comparison.



Final comparison of the chromatograms that are to be compared with others white-out.

V. Processing the Data

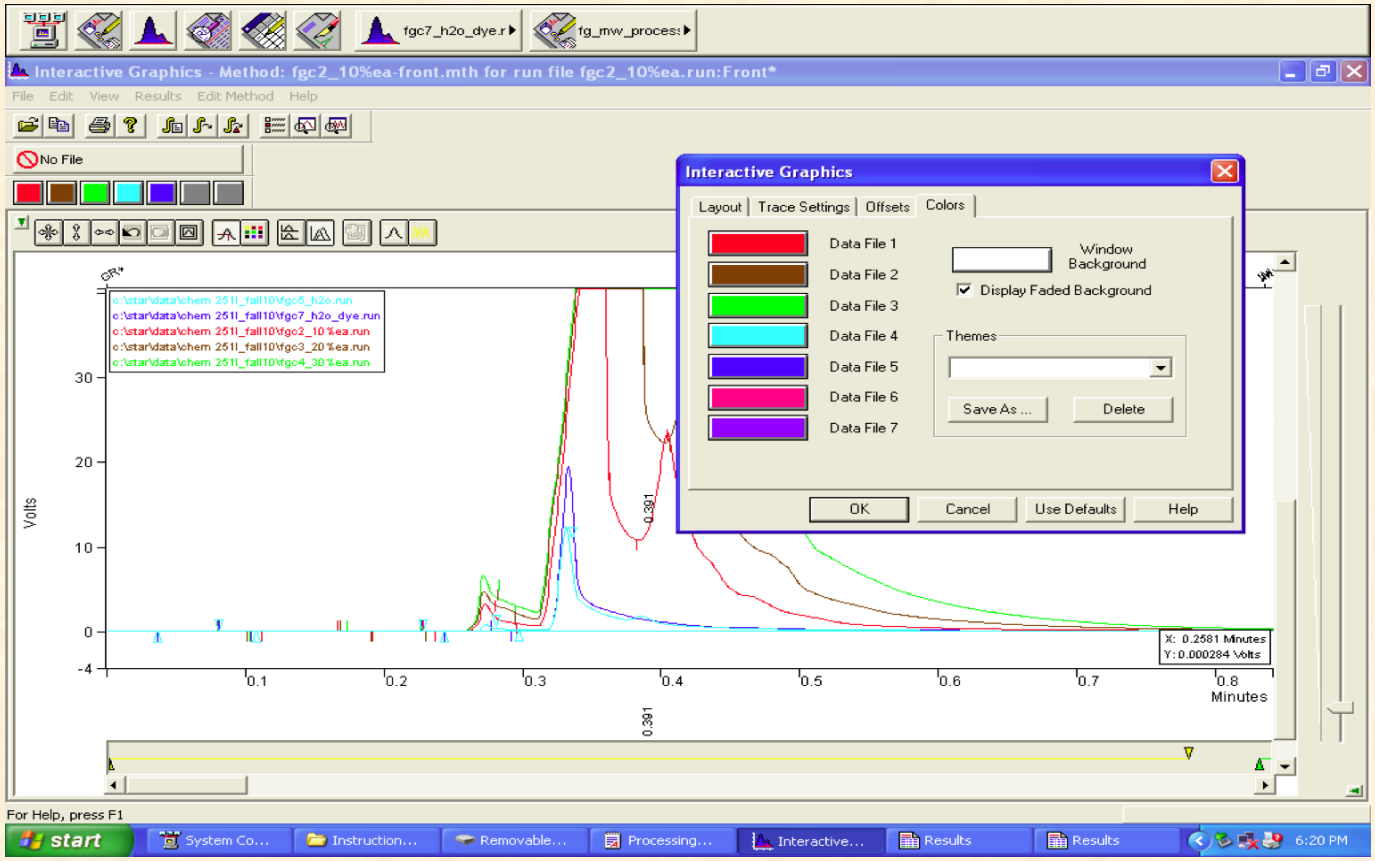
32. Revert trace colors back to original settings



Revert chromatogram colors back so that all can be displayed. Otherwise, the color will stay as white.

V. Processing the Data

33. Revert trace colors back to original settings



Revert chromatogram colors back so that all can be displayed. Otherwise, the color will stay as white.

VI. Clean up GC and Work Area

Remove your samples from the auto-sampler holder.

Close gas cylinder tank Do not adjust primary and secondary valve in regulator!

Clean the work area around the GC.

Shut down computer and turn off GC.