Fall 2001 Genomics Exam #2
Genomic Variations and Expressions

There is no time limit on this test, though I have tried to design one that you should be able to complete within 5 hours, except for typing. There are three pages for this test, including this cover sheet. You are not allowed discuss the test with anyone until all exams are turned in at 9:30 am on Friday October 26. **EXAMS ARE DUE AT CLASS TIME ON FRIDAY OCTOBER 26**. You may use a calculator, a ruler, your notes, the book and the internet. However, you are not allowed to obtain and read journal articles as a part of your investigations. These questions are taken from the research literature and I do not want you to simply find the papers and read the answers. This is the Honor Code at its finest.

The **answers to the questions must be typed on a separate sheet of paper** unless the question specifically says to write the answer in the space provided. If you do not write your answers in the appropriate location, I may not find them. You may want to capture screen images as a part of your answers which you may do without seeking permission since your test answers will not be in the public domain.

-3 pts if you do not follow this direction.
Please do not write or type your name on any page other than this cover page.
Staple all your pages (INCLUDING THE TEST PAGES) together when finished with the exam.

Name (please print):

Write out the full pledge and sign:

How long did this exam take you to complete (excluding typing)?

You must answer 3 of the questions for each paper. Every one must answer the last question. Every question is worth 10 points.

Jaccoud et al.

1) Summarize figure 2. Print a copy (color or B&W) and point to specific spots that illustrate your interpretations.

2) Explain the significance of figure 3. Don't simply say that it validates the method. Explain why and support your explanation by citing specifics from the figure.'

3) Summarize figure 5 Explain how the data in panel A were derived and used to produce the dendrogram.

4) Using figure 6 as a starting place, design a way to use this approach to detect and identify biological weapons.

Daly et al.

1) Summarize figure 2. In your summary, just give me the main points, don't walk through every aspect of this large figure.

2) What significance does this paper have for linkage disequilibrium mapping of polygenic traits? Use the genes from figure 2 as examples in your answer, but you do not need to know the function of these genes. Just consider them generic genes that could contribute to a generic disease.

3) Which block is the least conserved of those shown in figure 2. Given the data shown, speculate why this is the case.

4) What is the next step after this paper? Summarize what you would do if you had the computer capacity to analyze all the data in TSC database.

Iyer et al.

1) Cite the data in figure 3 that support the claims that SBF and MBF can
a) activate different genes.
b) activate the same genes.

2) What is the significance of the genes marked by two dots in figure 3? How do these genes affect your interpretation of the figure as a whole.

3) Print figure 4 (color or B&W is fine) and then draw very clear arrows that are labeled clearly that point to only one gene:
a) that was induced during G1 and could have bound both transcription factors (based on sequence) but only bound SBF
b) that was induced in G1 that should not bind SBF but did and was classified as a gene activated by both transcription factors.
c) that was activated in G1 that should not have bound SBF (by sequence analysis) but did bind SBF. This gene must come from the group of genes characterized as an MBF-only binding target.

4) Draw a graph (similar to the other graphs in figure 4b) of what you would predict to see during meiosis for targets of these two transcription factors. You can use two colors of ink if this helps with clarity. It does not have to be done on a computer, you can draw it by hand.

Answer this one.
10)
a) Use expression data online and determine which of these transcription factors/factor are/is more likely to be induced when the cells are experiencing mutagenic alterations of their genome. Support your answer with images from the database (static images are fine, no hyperlinks necessary).
b)What gene or genes are coexpressed with your answer to part "a"?
c) Is this an example of aneuploidy? Support your answer with data.