Minilab report on RNA isolation due 10/11/07

One Figure – electrophoresis gel
One Table – Spectrophotometric analysis
A type-written analysis of the results

Figure

Figure must be in a professional format. You will need to crop the gel photo and then label it. See some of the figures in your textbook for how to do this (e.g. 10.27)

Figure must also include a figure legend. Don't use the textbook figure legends as a model as they contain a bit too much detail. See the following legends that come from the original papers. All figure legends should contain the following components.

1. Figure number
2. Figure title. A fragment or a sentence that summarizes what the figure demonstrates or test. Often the figure title is in bold.
3. Brief description of experiment
4. Description of all the components of the figure. For example on a gel, it should be clear what is in each lane. There should be no components of the figure that are not described on the gel.
5. Figures should be self-sufficient

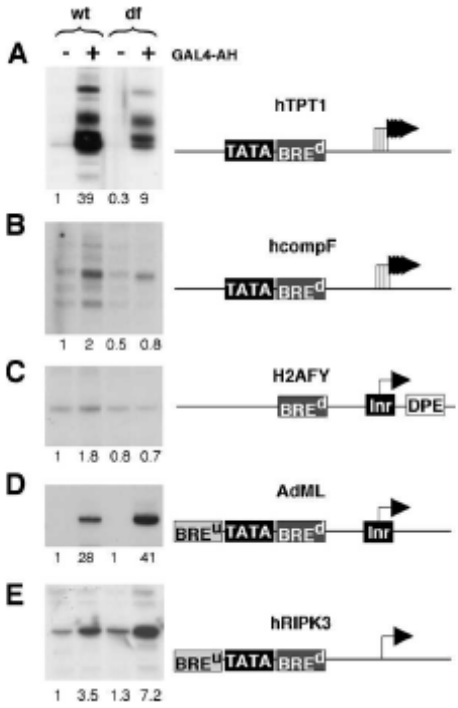

Figure 5. The function of the BREd is context-dependent. The core promoters indicated in A–E (wild type; wt) were tested in transcription assays alongside a derivative of each promoter that contained a mutated BREd sequence (df). The numbers below each panel are quantitation of the level of transcription relative to that observed at basal level for each wild-type promoter. Schematics of each promoter are shown at the right with the core promoter elements indicated; arrows depict the transcription start sites. The core promoters were compared in an in vitro transcription assay with HeLa nuclear extract in the absence or presence of the activator GAL4-AH(50 ng).

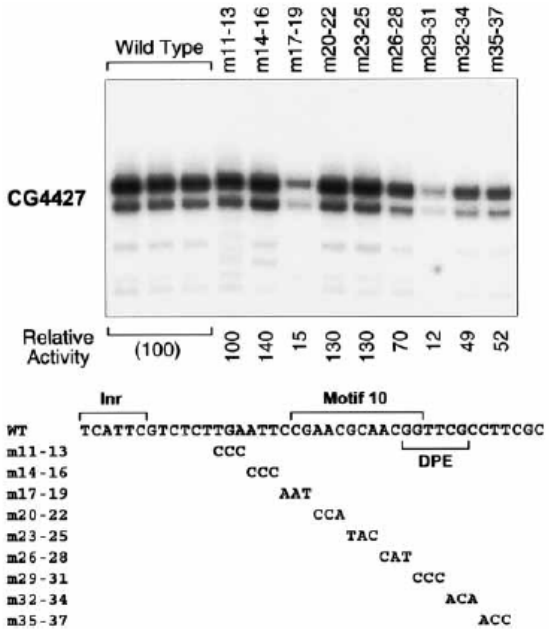

Figure 2. Scanning mutational analysis of the motif 10 sequence. A series of mutant CG4427 core promoters was constructed in which triple nucleotide substitutions were introduced in the downstream promoter region that encompasses the motif 10 sequence and the DPE. Outside the motif 10 sequence, A, T, and G nucleotides were mutated to C, and C nucleotides were mutated to A. Within the motif 10 sequence, the substitution mutations were designed to minimize the similarity of the sequence to the motif 10 consensus. The wild-type and mutant promoters were subjected to in vitro transcription analysis with a *Drosophila* nuclear extract. The transcriptional activity of each mutant promoter is reported relative to that of the wild-type promoter.

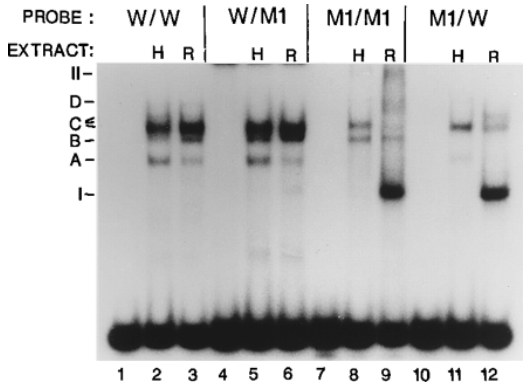

Figure 2. Gel shift assays show nuclear factor binding patterns of HT29 (H) and RINm5F (R) nuclear extracts to wild-type (W/W) and mutant (W/M1, M1/M1, M1/W) -131/-92 sequences. Each lane contains 10 000 cpm of probe with or without nuclear extracts, separated on a 3.5% polyacrylamide gel. Lanes 1 to 3, W/W probe: lane 1, no extract; lane 2, HT29 nuclear extract; and lane 3, RINm5F extract. Lanes 4 to 6, W/M1 probe: lane 4, no extract; lane 5, HT29 extract; and lane 6, RINm5F extract. Lanes 7 to 9, M1/M1 probe: lane 7, no extract; lane 8, HT29 extract; and lane 9, RINm5F extract. Lanes 10 to 12, M1/W probe: lane 10, no extract; lane 11, HT29 extract; and lane 12, RINm5F extract. Complexes A, B, C, and D were found with the W/W probe and to varying degrees with the mutant probes. Complex I was formed only with the RINm5F extracts and the M1/M1 or M1/W probe. Complex II was only formed with the RINm5F extract and the M1/M1 probe.

Tables

All figures must follow a professional format. See the following example tables derived from papers. The all demonstrate components of a proper table.

1. Tables are numbered on the top line followed by a table title that describes the whole table
2. Column headings are separated from title and contents by lines
3. Data related to a give characteristic should be organized vertically
4. Footnotes or legends should be separated from the data by a line.
5. Never grid information within the data. Use spacing instead
6. Tables should be self-sufficient

Table 1. General class II transcription initiation factors from human cells

Factor		Subunits, kDa	(no.)	Function
TFIID	⁄TBP	38	(1)	Binds to TATA, promotes TFIIB binding
	\TAFs*	15–250	(12)	Regulatory functions (+ and −)
TFIIB		35	(1)	Promotes TFIIF–pol II binding
TFIIF		30, 74	(2)	Targets pol II to promoter
RNA pol II		10–220	(12)	Catalytic function
TFIIE		34, 57	(2)	Stimulates TFIIH kinase and ATPase activities
TFIIH		35–89	(9)	Helicase, ATPase, CTD kinase activities
All class II GTFs		> 2 MDa	(>42)	

Function and subunit composition of the human class II general initiation factors. The factor denoted with an asterisk is not absolutely required for *in vitro* basal or core promoter-dependent pol II transcription initiation. TBP, TATA box-binding protein; TAF, TBP-associated factor; GTF, general transcription factor.

TABLE 2. Determination of a DPE functional range set[a]

Promoter	DPE sequence	Relative transcription[b]
	+28 +33	
Wild-type *G*	A G A C G T	100
Mutants		
G 11-1	G C A T G G	86 ± 20
G 11-2	T G A T C C	81 ± 20
G 6-1	T C A C A C	79 ± 7
G 6-2	G C A C C T	74 ± 27
G 6-3	A G T T G T	70 ± 11
G 6-4	T C A T G T	68 ± 7
G 6-5	A G A T C T	63 ± 10
G 6-6	A C G C A C	54 ± 7
G 6-7	A G A G A C	54 ± 9
G 6-8	A G T T G A	53 ± 4
G 6-9	A A C T G C	52 ± 2
G 6-10	G G A T G C	51 ± 6
G 6-11	C C A T G T	51 ± 12
DPE functional range set[c]	A/G/T C A C A/C/G C/T	

[a] The DPE functional range set represents sequences that contribute to or are compatible with DPE function.
[b] Mean ± standard deviation from four independent experiments.
[c] The T nucleotide at positions +30 is included on the basis of the presence of T at this position in the DPE-containing promoters tested in Fig. 1.

Analysis

Write a brief summary of your results analysis. One to two typed pages, 12pt font, double spaced. Refer to figures when appropriate. However, the summary should make sense even if the reader doesn't refer to the figure.

Organization

Goal of Experiment (Evaluate Trizol RNA isolation protocol for classroom use)

Experiment (Sample of students isolate RNA from worms using Trizol reagent, then evaluate the RNA by electrophoresis and Spectrometry.)

Results (Brief summary of the electrophoretic and spectrometry results and what they mean)

Conclusion: Address goal of experiment.