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First Last

LS3.1, MIDTERM EXAM II

5pm-6: 50pm, Thursday, Nov. 7, 2013

Dr. Chentao Lin

Version A

1. Write your name and student ID on the **Scantron**.

2. Check the exam to make sure you have every page before start. Read carefully the question, the multiple choices, and any figure included. You should select the **BEST** answer, and register your answer on both the Scantron and exam pages.

3. Hand in only the Scantron to TAs after you complete the exam. You can keep the question sheets and compare your answers with the key that will be posted online shortly after the exam.

4. Midterm II has 40 multiple-choice questions, 2.5 points each, 100 points total.

5. Use your common sense. Do not spend too much time on any single question. Good luck!

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1. Which of the following descriptions about transcription is correct?
A). Transcription is a DNA-dependent RNA polymerization process
B). Transcription is a DNA-dependent polypeptide polymerization process
C). Transcription is a DNA-dependent DNA polymerization process
D). Transcription is a RNA-dependent DNA polymerization process
E). Transcription produces RNA from the 3' end to the 5' end.

2. Which of the following descriptions about TFIID is incorrect?
A). TFIID is a multiple-subunit complex, including a DNA-binding subunit.
B). TFIID must bind to the TATA box, because TBP can only recognize TATA-containing promoter
C). TFIID must bind to not only DNA but also proteins.
D). TFIID is required for transcription of almost all eukaryotic genes.
E.) TFIID is not considered part of the RNA polymerase II holoenzyme by many researchers

3. Which of the following is not true about transcription initiation?
A). Transcription initiation requires sigma factor or TFIID. X
B). RNA polymerase II initiates transcription of most eukaryotic genes. X
C). Transcription initiation does not always rely on DNA sequence of the promoter. —
D). Transcription initiation only occurs in one direction of a chromosome. —
E). Formation of the closed/pre-initiation complex is essential for transcriptional initiation X

4. Which of the following is incorrect about transcription elongation?
A). Transcription elongation does not require promoter clearance. X
B). Transcription elongation requires the kinase activity of TFIIH. X
C). Transcription elongation does not require an E3 ubiquitin ligase activity of RNA polymerase.
D). Transcription elongation does not require a DNA topoisomerase.
E). Transcription elongation requires TFIIS.

5. Which of the following about sigma factor is incorrect?
A). The sigma factor cannot recruit histone acetyltransferase to activate transcription.
B). The sigma factor can bind to the TATA box and a subunit of the RNA polymerase
C). One cell may have more than one type of sigma factor.
D). Sigma factor is equivalent to the largest subunit of RNA polymerase II RPB1 = B'
E). One type of sigma factor may bind to more than one promoter.

6. Which of the following is not true about transcription regulation?
A). Transcription regulation only occurs before transcription initiation. attenuation
B). Transcription regulation is fundamentally similar in prokaryotes and eukaryotes —
C). Transcription regulation requires changes of DNA-protein interactions X
D). Transcription regulation may involve changes of both covalent bonds and non-covalent bonds of the DNA-protein complex. X
E). Transcription regulation requires transcription factors that are different from those required for transcription initiation. X

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7. Which of the following is correct about a bacterial operon?
A). A bacterial operon is a combination of bacterial genes encoding different mRNAs that are coordinately regulated by repressors
B). A bacterial operon is the collection of bacterial mRNAs encoding different proteins
C). A bacterial operon transcribes a single RNA regardless the number of proteins it may encode
D). A well-studied example of a bacterial operon is the lacZ gene
E). A bacterial operon transcribes multiple RNAs that encode multiple proteins.

8. Which of the following is most likely to occur in *E. coli* cells?
A). *E. coli* cells do not transcribe the lac operon in the presence of high lactose and low glucose.
B). *E. coli* cells actively transcribe the lac operon in the presence of low lactose and low glucose
C). *E. coli* cells do not transcribe the lac operon in the presence of high lactose and high glucose.
D). E. coli cells actively transcribe the lac operon in the presence of high lactose and low glucose.
E). None of above.

9. Which of the following best explains the selection you made in question #8?
A). Lactose binds to the lacI repressor, freeing the lac operator from lacI occupation to maximize transcription in the absence of cAMP.
B). cAMP binds to the lacI repressor, freeing the lac operator from lacI occupation to maximize transcription in the absence of lactose.
C) Lactose binds to the lacI repressor, freeing the lac operator from lacI occupation, cAMP binds to CAP to stabilize the DNA-RNA polymerase interaction.
D). Lactose binds to CAP repressor, freeing the lac operator from CAP occupation to stabilize the DNA-RNA polymerase interaction
E). Lactose binds to the lacI repressor to promote cAMP interaction with RNA polymerase, maximizing transcription in the absence of CAP.

10. Which of the following is incorrect?
A). Sigma factor is equivalent to TBP (TATA-binding protein)
B). TFIIH is required for the formation of the ssDNA bubble in the open complex
C). TFIID is required for the formation of pre-initiation complex
D) CTD is a required for the formation of pre-initiation complex but not the open complex
E). TFIIS is required for transcription elongation.

11. Which of the following is true?
A). The phage T7 RNA polymerase inactivates bacterial RNA polymerase to transcribe the T7 genes.
B). The phage T7 RNA polymerase activates bacterial RNA polymerase to transcribe the T7 genes.
C). The phage T7 RNA polymerase is active without the core enzyme of bacterial RNA polymerase.
D). The phage T7 RNA polymerase needs T7 sigma factor to transcribe the T7 genes
E). The phage T7 RNA polymerase encodes a novel β subunit of the bacterial RNA polymerase.

12. Which of the following best explains the function of histone modification?

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A). Histone acetylation increases positive charges of the core histones, resulting in increased density of nucleosomes and decreased transcription
B). Histone acetylation reduces positive charges of the core histones, resulting in decreased density of nucleosomes and increased transcription.
C). Histone methylation increases hydrophobicity of the core histones, resulting in increased condensation of nucleosomes and increased transcription.
D). Histone phosphorylation increases negative charges of DNA, resulting in increased density of nucleosomes and decreased transcription.
E). Histone acetylation and methylation both reduce positive charges of the core histones, resulting in increased density of nucleosomes and increased transcription.

13. Patients suffering from the genetic disease of Human Synpolydactyly (SPD) have abnormal number of fingers or toes. SPD is caused by mutations in the *HOX13* gene that encodes a transcription factor. Which of the following best describes the gene product of the *HOX13* gene?
A). A basic helix-loop-helix protein
B). A homeodomain protein
C). A zinc-finger protein
D). A basic leucine zip protein
E). A basic helix-turn-helix protein

14. Why is eukaryotic transcriptional regulation generally more complex than that of a prokaryote?
A). Eukaryotes are often multicellular organisms that need to coordinate between different cells.
B). Eukaryotes usually have larger genomes.
C). Eukaryotes have more complex protein-protein interactions.
D). Eukaryotes need to respond to more signals.
E). All of above.

15. Which of the following about eukaryotic promoter is incorrect?
A). Some eukaryotic promoters have GC-rich sequence.
B). Different eukaryotic promoters may have different transcription initiation site
C). Most eukaryotic promoters have a TATA box at the -25 position.
D). An actively transcribed eukaryotic promoter is usually free of nucleosomes
E). Some eukaryotic promoters cannot be transcribed by RNA polymerase II

16. Which of the following is the most abundant component of human chromosomes?
A). HAT (histone acetyltransferases)
B). RNA polymerase
C). Histones
D). HDAC (histone deacetylase)
E). Transcription repressors

17. Which is incorrect about the proto-oncogene and tumor suppressor genes?

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A). Proto-oncogenes usually encode proteins that promote cell proliferation
B). Tumor suppressor genes usually encode proteins that suppress cell proliferation
C). Gain-of-function mutations of oncogenes and loss-of-function mutations of tumor suppressor genes are closely associated with cancer development
D). Proto-oncogenes always encode transcription factors.
E). None of above

18. Which of the following about bacterial transcription termination is correct?
A). TFIIS is required for transcription termination in prokaryotes
B). Rho is required for Rho-independent transcription termination
C). A hairpin followed by AU-rich sequence constitutes the Rho-dependent transcription terminator
D). Rho may have an enzymatic activity similar to that of a helicase
E). Transcription termination is found for some gene but not other genes.

19. Which of the following best describes the combinatorial regulation of transcription?
A). One gene may have many enhancers, interacting with different transcription activators.
B). One gene may have many silencers, interacting with different transcription repressors.
C). Many transcription factors may be involved in the regulation of transcription in response to various internal or environmental factors.
D). RNA polymerase is regulated in many different ways.
E). All of above.

20. Which of the following is incorrect about the general transcription factors?
A). General transcription factors are required for transcription of all eukaryotic genes.
B). TFIIB can interact with both RNA polymerase II with TBP.
C). CTD is the core component of TFIID that binds to TATA box
D). TFIIH consumes ATP to break H bonds of a double-stranded DNA
E). TFIIS stimulates RNase activity of RNA polymerase II to cut RNA.

21. Which of the following about a nuclear receptor called glucocorticoid receptor is correct?
A). Glucocorticoid receptor is a general transcription factor.
B). Glucocorticoid receptor binds to its hormone ligand in the nucleus and moves to the cytosol.
C). Interaction with its hormone ligand inactivates glucocorticoid receptor, because it recruits a histone methyltransferase to suppress transcription.
D). Glucocorticoid receptor is a cytoplasmic/nuclear transcription regulator.
E). Glucocorticoid receptor binds to hsp90 and translocates together with hsp90 to the nucleus.

move heterochromatins to the promoter region.
D). An insulator usually de-phosphorylates transcription factors to activate transcription.
E). Insulators do not usually bind to DNA, but they often bind to histones.

24. Which of the following about chromosome, chromatid, and chromatin is correct?
A). Heterochromatin is heterozygous chromosomes, euchromatin is eukaryotic chromatin
B). Genes in heterochromatin are more actively transcribed than genes in euchromatin
C). Chromosomes are highly expressed regions of the genome
D). Euchromatin usually has a lower density of nucleosomes
E). Chromatids are transcription activator-binding regions of chromosomes

25. Which of the following best describes the histone code?
A). Histone code is the primary sequence of the histone proteins.
B). Histone code is the combination of chemical modifications of individual core histones.
C). Histone code is the combination of histone acetylation and deacetylation.
D). Histone code is the combination of chemical modifications of linker histones
E). Histone code defines the genetic code transmitted into the amino acid sequence of a protein.

26. Which of the following is incorrect about a riboswitch?
A). A riboswitch is a catalytic RNA that changes conformation upon binding to another molecule
B). An initial transcription product of the Trp operon may function as a riboswitch, although it may not necessarily be defined as a riboswitch.
C). The 3' UTR (un-translated region) of the RNA product of Trp operon is a riboswitch.
D). A small molecule may bind to a RNA to affect transcription of the gene encoding this RNA.
E). Aptamer is a co-factor of a riboswitch to exert an allosteric effect on the riboswitch.

27. Which of the following is true about chromatin remodeling?

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A). Chromatin remodeling involves chromosome segregation
B). Chromatin remodeling does not need ATP
C). Chromatin remodeling involves degradation of RNA polymerase
D). Chromatin remodeling usually does not change transcription activity
E). Chromatin remodeling usually involves nucleosome relocation.

28. Which of the following is false about nucleosomes?
A). Nucleosomes contain histones H2A, H2B, H3, and H4.
B). Nulceosomes usually locate in the nuclear pores.
C). Nucleosomes may migrate to allow active transcription.
D). Nucleosomes are basic units of chromatins.
E). A nucleosome contains 147bp of DNA.

29. Which of the following mechanisms is not found in chromatin remodeling?
A). Histone eviction
B). Histone transcription
C). Nucleosome unwrapping
D). Histone replacement
E). Nucleosome migration

30. Which of the following is not part of UPS (ubiquitin 26S proteasome system)?
A). E4 ubiquitin polymerase
B). E3 ubiquitin ligase
C). E1 ubiquitin activation enzyme
D). E2 ubiquitin conjugating enzyme
E). None of above

31. Brian Jonathan did an experiment to study how RNA polymerase acts. He mixed RNA polymerase with ^{32}P-labeled DNA and let them bind to each other at three different temperatures as indicated in Fig. 1. He then add unlabeled DNA to compete with ^{32}P-labeled DNA for RNA polymerase. He analyzed samples at different time (see "Time" in Fig. 1) from samples at different temperature, using a nitrocellulose filter assay. Brian measured the radioactivity left in the nitrocellulose filter (see "Labeled DNA bound" in Fig. 1).
Which of the following best explains Brian's result?
A). RNA polymerase has highest catalytic activity at 37°C
B). RNA polymerase has highest catalytic activity at 15°C
C). RNA polymerase has higher affinity to melted DNA
D). RNA polymerase has higher affinity to dsDNA
E). None of above

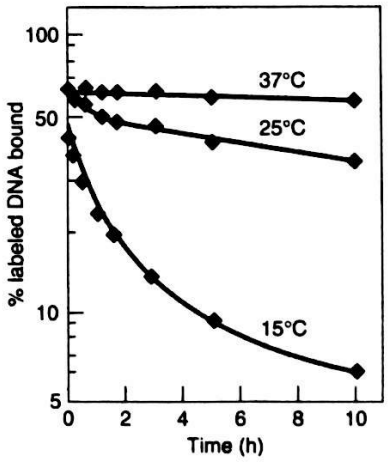

Fig. 1

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32. Tim Kim tries to figure out the mechanism of the *E. coli Trp* operon, which responds to the changing level of tryptophan in the cell. Kim isolated a *trp* mutant that contains the normal *Trp* promoter and *Trp* operator but a deletion of the *Trp* attenuator. Tim calls this mutant *trp-1*. Which of the following may not be observed by Tim in his study of the *trp-1* mutant?

A). The mutant *trp* operon will be transcribed under some conditions.
B). No tryptophan will be synthesized in the *trp-1* mutant cell.
C). The mutant *trp* operon is still negatively regulated by the cellular level of tryptophan.
D). The *mutant trp* mRNA will be transcribed at a level higher than that of the wild type *E. coli* in response to a high level of tryptophan.
E). None of above.

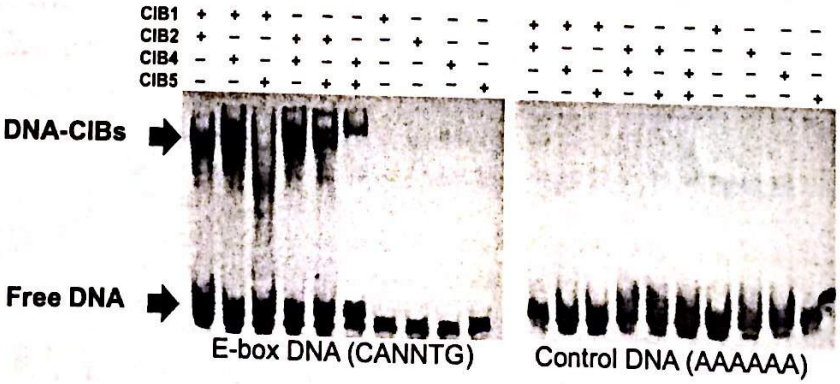
33. Tim identified two more *trp* mutants: the *trp-2* mutant that lacks the *Trp* operator (but normal for all other parts of the *Trp* operon), and the *trp-3* mutant that contains the normal sequence of the *Trp* operon but fails to express the Trp repressor protein. Which of the following is most likely to be observed by Tim in the study of these two new mutants?

A). The *trp-2* mutant should have the same phenotype as the *trp-3* mutant.
B). The *Trp-2* mutant should have the same phenotype as the *trp-1* mutant described in the question 32.
C). The *Trp-2* mutant should have the same phenotype as the *trp-3* mutant.
D). The *Trp-2* mutant completely loses its response to the changing level of tryptophan.
E). The *Trp-3* mutant cannot be transcribed under any condition.

34. In a recently published paper, an UCLA postdoc researcher Hongtao Liu reported a study of plant bHLH transcription factors CIB1, CIB2, CIB4, and CIB5. In this experiment, she mixed different CIB proteins with either the labeled E-box DNA or the labeled control DNA as indicated in Fig. 2, in which "+" means that the proteins listed on the left were included in the reaction and applied to the respective lane of the native gel, "-" means the respective protein listed on the left was not included in the reaction. Which of the following may be the best conclusion derived from Hongtao's results shown in Fig. 2?

A). bHLH transcription factors usually bind DNA indiscriminately.
B). CIB transcription factors bind DNA as homodimers
C). 4 transcription factors may together recognize more than 4 different DNA sequences.
D). bHLH transcription factors usually bind DNA as monomers
E). Different CIB proteins bind DNA with the identical affinity

Fig. 2



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35. Jane Rodriguez used the ChIP (chromatin immunoprecipitation) assay to study the Arabidopsis LS32 protein, which was thought to activate transcription in response to blue light (also called blue light induction). LS32 protein was hypothesized to be a DNA-binding protein that activates transcription of the gene X. Jane first exposed dark-grown Arabidopsis seedlings to blue light, harvested samples at different times at 1 to 12 hours after blue light treatment, and performed ChIP experiments of the all 12 samples, using different antibodies and the primer-pair encompassing the DNA sequence of the enhancer Y located in the first intron of gene X. Jane obtained the results shown in Fig. 3. Which of the following best explains Jane's discovery?

A). Acetylation of at least 3 different histones is required for the blue light suppression of gene X transcription

B). Acetylation of at least 2 different histones is required for blue light induction of gene X transcription

C). Histone H4 acetylation but not histone H3 acetylation is required for the blue light induction of gene X transcription

D). Histone H2B acetylation but not histone H3 acetylation is required for transcription elongation of the gene X in response to blue light

E). Histone H3K9 methylation but not histone H3K9 acetylation is required for the blue light induction of gene X transcription.

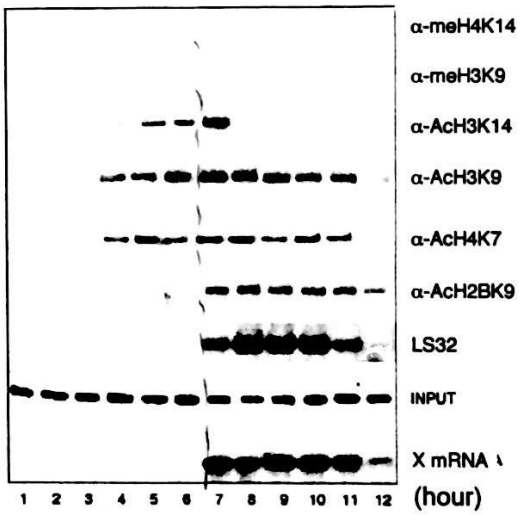
Fig. 3 (for questions 35-37)

The figure shows results of the ChIP reactions using the antibodies indicated and PCR primers encompassing the enhancer Y sequence of gene X (rows "α-meH4K14" to "LS32"). The genomic PCR ("Input") and the RT-PCR ("X mRNA") results are also shown.

Samples were taken 1-12hr after blue light treatment.

Antibodies used in the ChIP reaction and indicated on the right are:

α-meH4K14: anti-histone H4 methylated at K14;
α-meH3K9: anti-histone H3 methylated at K9;
α-AcH3K14: anti-histone H3 acetylated at K14;
α-AcH3K9: anti-histone H3 acetylated at K9;
α-AcH4K7: anti-histone H4 acetylated at K9;
α-AcH2BK9: anti-histone H2B acetylated at K9;
LS32: anti-LS32 antibody
Input: genomic PCR result using total genomic DNA of the samples used in ChIP (without immunoprecipitation).
X mRNA: RT-PCR result using a primer-pair encompassing the third exon of the gene X.



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36. Jane tried to further study how the LS32 protein may regulate transcription of gene X, she formulated a hypothesis based on the results shown in Fig. 3. Which of Jane's hypothesis makes the most sense?

A). LS32 recruits RNA polymerase II to the promoter in response to blue light.
B). LS32 binds DNA before most histone modification occurred after blue light treatment.
C). LS32 is most likely phosphorylated before it interacts with DNA
D). Acetylation of histones H3 and H4 facilitates association of LS32 to the enhancer Y.
E). LS32 recruits methylated histones in response to blue light

37. Based on the information provided in Questions 35 and 36, and assume all the experimental materials are readily available, how should Jane test the hypothesis you selected in Question 36?

A). Use the promoter deletion method to test exactly where the enhancer is in the gene X
B). Use the linker-scan method to test whether a histone methyltransferase interacts with LS32 in Arabidopsis plants overexpressing an epitope-tagged histone methyltransferase.
C). Use the NC filter assay to test whether LS32 binds to DNA better in response to blue light in transgenic Arabidopsis overexpressing (expressing more) histone acetyltransferase
D). Use the ChIP method to test whether LS32 has a higher affinity to chromatin in transgenic Arabidopsis overexpressing an appropriate histone acetyltransferase.
E). Using DNA foot-printing assay to test whether LS32 has a higher affinity to chromatin in transgenic Arabidopsis overexpressing an appropriate histone acetyltransferase

38. Mike Gomez tried to find a chemical reagent that can reduce the rate of transcription of the β-globin gene without reducing the rate of transcription of rRNA genes needed to synthesize the β-globin protein. Please help him select the most appropriate reagent with the respective reason provided in the following.

A). cAMP, because it affects only RNA polymerase I but not RNA polymerase II
B). α-amanitin, because it inhibits only RNA polymerase II but not RNA polymerase III
C). IPTG, because it effectively induces transcription of the lac operon
D). α-amanitin, because it has different inhibitory effects on different RNA polymerases that transcribe different genes
E). DTT, because it has different effects on different RNA polymerases that transcribe different genes.

39. Promoter deletion (promoter bashing) assay is commonly used to analyze DNA sequences important for transcription. Fig. 4 illustrates such an experiment that was used to analyze the promoter DNA of the human *TTR* gene, which encodes the thyroxine (a thyroid hormone) transport protein transthyretin. Which of the following is the best conclusion one may draw from the results shown in Fig. 4 (see the next page)?

A). The TRR transcription was regulated by three DNA elements.
B). There is a putative enhancer within the sequence between the 5' ends of deletion 1 and 2.
C). There is a putative enhancer within the sequence between the 5' ends of deletion 3 and 5.
D). There is a putative enhancer within the sequence between the 5' ends of deletion 2 and 3.
E). There is a putative enhancer within the sequence between the 5' ends of deletion 3 and 4.

40. Promoter bashing is a good method to identify the DNA regions important for transcription regulation, but this method requires that the complete sequence of the DNA under studied is

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known, and it does not tell us one important piece of information about the identified DNA element. Which of the following best explains the defect of this method?

A). This method cannot distinguish whether the identified DNA region contains an enhancer or a repressor.

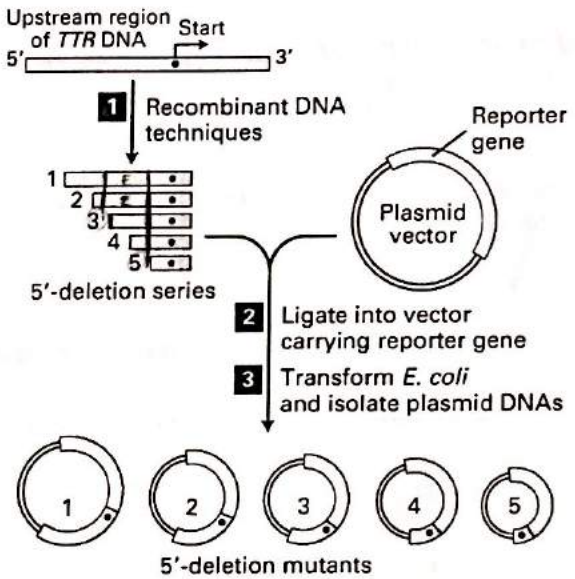
B). This method cannot distinguish whether the position or the DNA sequence of the identified DNA region is important for its function.

C). This method cannot distinguish whether the identified DNA region contains a TATA promoter or a TATA-less promoter

D). This method cannot distinguish whether the identified DNA region may interact with a transcription activator or with a transcription repressor

E). This method cannot distinguish whether the identified DNA region may interact with a histone acetyltransferase or with a histone deacetylase.

Fig. 4 (for question 39) A diagram depicting the experiment used to analyze the promoter DNA of the human *TTR* gene. The level of the reporter gene expression is analyzed by qPCR, and the results indicated by "+++" for high level of reporter expression, "+" for basal level of reporter expression, and "-" for no reporter expression.



Plasmid no.	Reporter-gene expression
1	+++
2	+++
3	+
4	+
5	-