

BIOL3104 **Midterm 2**, 2015, 6 pages, Total marks possible = 48

1) Define each of the following (/1 each)

/5 a) pseudogene

b) isoschizomer

c) paralog

d) proteome

e) selective sweep

2) A cross is performed between two true breeding strains of a diploid organism resulting in the phenotypic ratios at right. Draw the genetic map and include map distances based on this data.

	<u>Phenotype</u>	<u># progeny</u>
/2	+ + +	98
	g c r	86
	+ + r	406
	g c +	391
	g + r	12
	+ c +	7
		1000

/5

3) The following oligonucleotide sequence is called a palindrome in molecular genetics:
CCGCGATGCATCGCGG-3'

a) Briefly explain why this oligonucleotide would not be a good PCR primer? (/1)

b) In the space below, draw the melt curve graph that you would see for the primer dimer formed by this oligonucleotide if you were to increase the temperature slowly from 40 °C to 70 °C (/2). Label all axes (/1) and indicate the T_m point on your graph (/1).

/6

4) The terms a – f (below) are ways that Green et al. tried to ensure that sequences analyzed were from Neandertal. Briefly provide a reason why each was used. (/1 each)

a) clean room

b) “tagged” DNA fragments

c) restriction enzyme digests

d) comparisons of sequences obtained to genome sequences and GenBank entries.

e) mtDNA analysis

f) Y chromosome analysis

5) Shotgun sequencing was used to obtain the 4 sequences shown below.

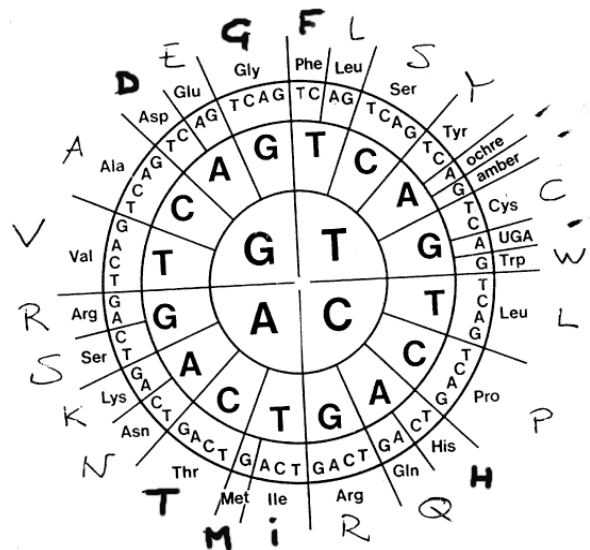
/6

- i) GCTAACTCTCTCCTCTTAGATGGCCGTCAGGAGCGCG
- ii) TGTCTAGAAGCGCGGTAAGTTCACGACTCTCCCTTCC
- iii) TACTAATACCATCATCACGCCACCAATGCTAACTCT
- iv) TTAGTAGGAAGGGAGAGTCGTGAACTTACCGCGCTTC

a) Briefly define and contrast shotgun sequencing and ordered clone sequencing. (/2)

b) In the space below, arrange the sequences into a single contig (/2). The fragments overlap by at least 6 nucleotides.

c) Give the amino acid sequence of the longest predicted ORF. (/2)



6) Write a unique characteristic of the sequencing strategy used with each of the following platforms.

a) Automated Sanger sequencing

/4

b) Illumina

c) Torrent

d) SMRT

7) An enzyme found in association with retroviral activity and involved in the synthesis of DNA from

/1

an RNA template is _____ (fill in blank, /1)

8) Introns are

/1

A. noncoding regions spliced out of primary transcripts.

B. the 5' and 3' untranslated regions of a gene.

C. coding regions joined together during RNA splicing.

D. multiple genes transcribed together.

E. none of the above.

9) What are three ways to identify/recognize coding regions (genes) in a DNA sequence?

/3

10) Look over the statements a – h, below. After each statement write which of the following four sequencing platforms is associated with the statement.

/6 Automated Sanger (AS) Illumina (IL)
 Torrent (TO) Single molecule real time (SM)

- a) based on DNA polymerization
- b) requires a PCR step
- c) sequence reads of > 2 kbp
- d) problems with mononucleotide repeats
- e) used to sequence Neandertal genome
- f) involves reversible terminators

11) Draw the key stages of “bridge amplification” as used in the Illumina sequencing platform.

/4

12) Three YAC clones of human DNA (YACs A - C) were tested for the presence of SNPs 1 - 5. The results are shown in the following table, in which a plus sign shows that the YAC contains that SNP:

/3

YAC	SNP				
	1	2	3	4	5
A	-	+	-	+	+
B	+	-	+	-	+
C	+	+	-	-	+

a. Briefly explain the meaning of 'SNP' (/1).

b. Draw a physical map showing the SNP order and align the YACs into a contig (/2)

13) You use PCR to amplify gene X and then ligate the amplicon into an expression vector. You wish to find a clone that has the insert in the correct orientation, i.e. downstream from a promoter that is located in the plasmid. You know the DNA sequence of the vector (and thus locations of S, E, A and N restriction sites) and of the target insert (below). *What restriction digest(s) would you do and what fragment pattern(s) are you looking for to identify the correct construct?*

/2

