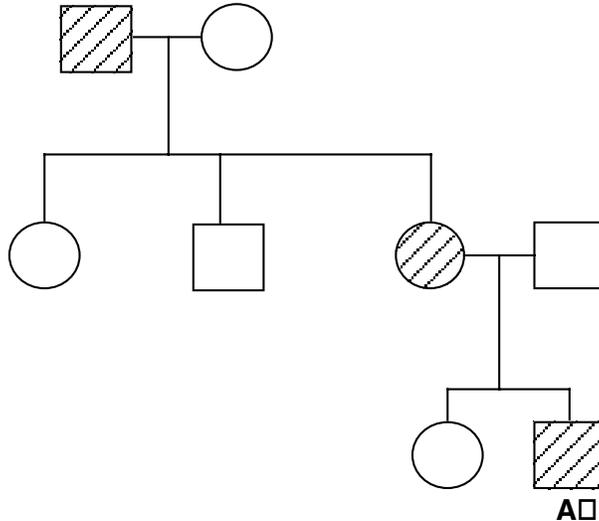## 7.013 Cancer Pedigree Section

Individual A has been diagnosed with familial adenomatous polyposis - a type of colon cancer. Investigation of the individual's family history yields the following pedigree for colon cancer (where the shaded individuals have colon cancer). Assume people marrying into this family carry 2 wildtype alleles.

a) Based on the pedigree, what is the mode of inheritance? (X-linked recessive, X-linked dominant, autosomal dominant, autosomal recessive)? How do you know?

In order to isolate the disease gene responsible for this type of colon cancer, you look for markers linked to the disease phenotype. You score each family member for the presence of a marker with 4 alleles: 1, 2, 3, and 4. The results are listed below.
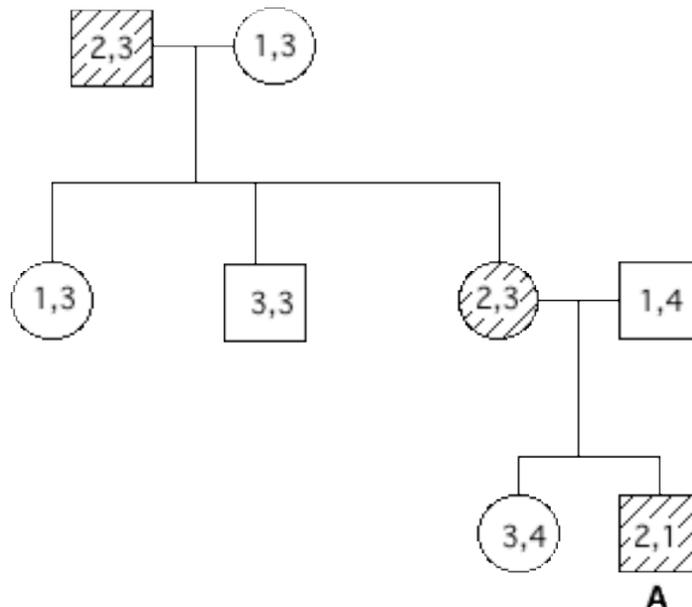
b) Which marker(s), if any, are linked to the colon cancer phenotype? Briefly explain.

One year later you identify the disease gene – "adneomatous polyposis coli" or *APC* - and you perform an analysis to find the mutations causing colon cancer in this affected family.

Using PCR followed by sequencing techniques, a nonsense mutation in the *APC* gene of Individual A is found. This mutation creates an *HpaI* restriction site in the gene. Using PCR, you amplify the *APC* DNA fragment from various tissue samples and perform RFLP analysis with the restriction enzyme *HpaI*. These digests are run out on an agarose gel shown below.

(Use A to define the wild-type allele.)
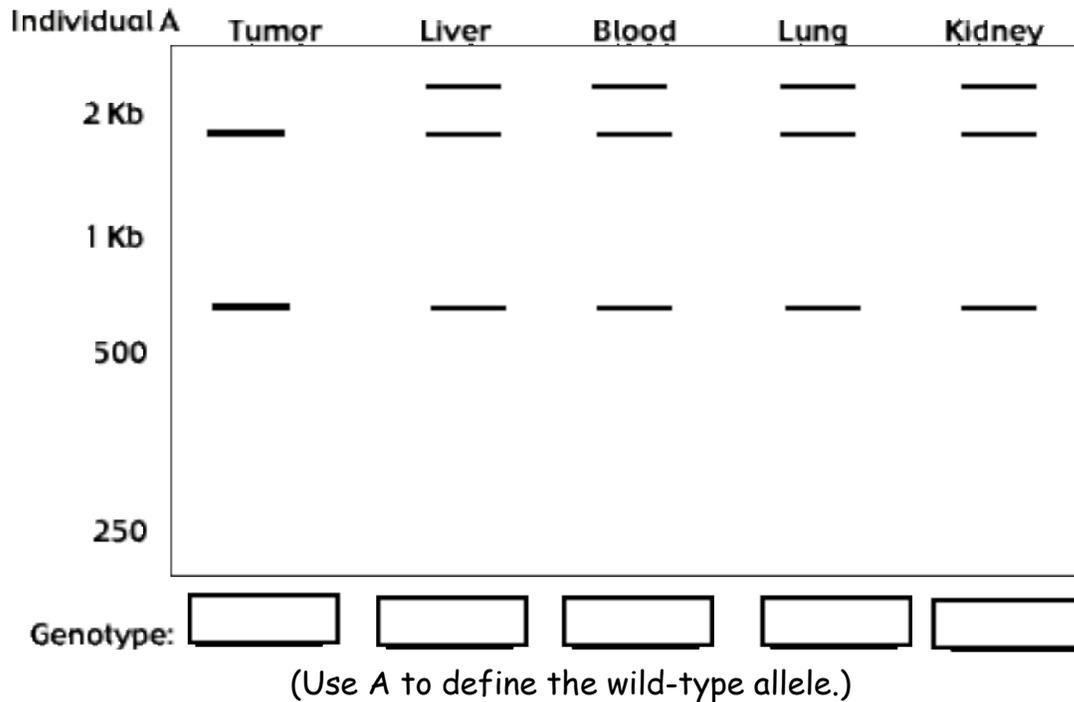
c) In the spaces provided above, fill in the *APC* genotype for each tissue.

d) How do you account for the results in part c?

e) At the **cellular** level, is the cancer phenotype of the mutant *APC* gene...

dominant   or   recessive? Circle one.

In order to study the colon cancer further, you propose making a mouse model for the human disease. The first step is to identify the mouse gene.

f) Given the human *APC* gene and an agarose gel of sized cut mouse genomic DNA, name the technique or process that would allow you to determine if there's a mouse gene similar to the human *APC* gene.

_____

g) Given you find the mouse gene and are able to create a deletion within it, how could you create a transgenic mouse where some of its cells will have this deletion?