Bio067: SARS in San Francisco? A PCR-based case study

You are a medical professional working in San Francisco in March 2004. On Monday, you see a patient who has a dry cough, headache, a fever of 101°F and body aches. After examining the patient, you decide that the infection is likely to be viral. So after you take throat swabs for potential testing, you tell the patient to rest, to drink plenty of liquids, to avoid using alcohol and tobacco and to take aspirin or Tylenol to help reduce the fever (and not to go to work, to avoid spreading the virus to others).

In talking with your colleagues over lunch, it becomes clear that many of them have also seen patients with similar symptoms. Since the SARS epidemic is still fresh in your collective memory, you all decide to test the samples you have taken for the presence of viruses that are known to cause similar symptoms.

Laboratory technicians purify RNA from each sample and use reverse transcriptase to make a double-stranded DNA copy of any viral RNA in the sample. They then divide this DNA into four tubes that contain different pairs of DNA primers to detect genes from the following viruses using the polymerase chain reaction (PCR):

SARS coronavirus (SARS CoV)
Avian Influenza A (H5N1)
Influenza B
Human metapneumovirus (a virus in the same family as influenza)

The PCR includes 40 rounds of denaturing the DNA (pulling apart the two strands), binding the primers to the DNA and adding nucleotides to the primers. After PCR, the amount of DNA has significantly increased in only one of the four tubes, suggesting that you may have identified the virus causing the patient's symptoms.

Using the sequence of this piece of DNA and the sequence of the primers for each virus, determine which virus is likely to be infecting your patient. The arrows indicate the end of the primer to which nucleotides are added during each round of PCR. **Fill in your diagnosis on the overhead at the front of the room.**

If you finish your diagnosis before other groups, discuss what steps you will take next (consider both your patients as individuals and the broader population).