Homework part 1

You have:

1. sample A = cDNA made on a blood sample from a patient infected with Ebola virus
2. sample B = 200 ng of viral genomic cDNA (it is an RNA virus)
3. the length of the viral genomic cDNA is 19 kb.

You made:

1. four 10-fold dilutions of the sample B
2. ran qPCR with sample A and dilutions of the sample b

Your data are:

dilution 1 C_t= 20
dilution 2 C_t= 23
dilution 3 C_t= 26.8
dilution 4 C_t= 30.4
sample A C_t= 32.7

Please find out:

1. Is it possible to estimate the efficiency of primers from these data?
2. If yes, what is it in %? (If not, assume it is 100%)
3. Amount of viral cDNA in the patients blood
4. Is it possible to estimate the amount of viruses in the patient's blood?

Homework part 2

Experiment

You have:
1. sample A = cDNA isolated from 100 mg of Arabidopsis roots (grown under normal conditions)
2. sample B = cDNA isolated from 100 mg of Arabidopsis roots (grown under stress conditions)
3. primers to ABA-receptor gene (E=98%), primers to reference gene E2F (E=93%)

You made:
1. ran qPCR with sample A and sample B using both primer sets

Your data are:
sample A ABA-receptor gene C_t= 29.4
sample A E2F gene C_t= 27.3
sample B ABA-receptor gene C_t= 25.1
sample B E2F gene C_t= 29.6

Please find out how much more/less of the ABA-receptor mRNA there is in the sample A by using:
1. delta Ct
2. Livak method
3. Pfaffl method

Homework part 3

Group 1:
Reza
Konstantia
Enid
Martin
Mohammed

Group 2:
Jun
Zaenab
Jule
Kiran

Group 3:
Anna
Maite
Enrique
Shirin
Anders

your topic is

RT with oligodT

your topic is

RT with random hexamers

your topic is

RT with gene-specific primers

Please answer the questions:
1. what is it?
2. is it applicable for qPCR (if not, what is it for)
3. what are advantages/disadvantages of it