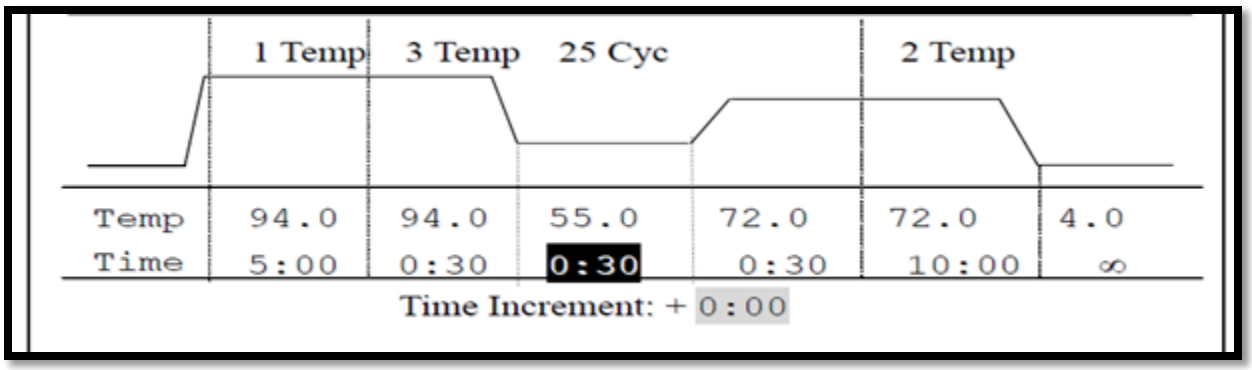
Q1 A- MultiGene OptiMax/ Thermo-cyclers / Conventional polymerase chain reaction (PCR)

B-



Q2- Sample 1=192.5 , Sample 2=188.3, Sample 3=223.77, Sample 4=133.6 (two only)

C1V1=C2V2

C1V1=100 * 50

V 1 =25.97--------add DEBIC =24.02

V 2=26.55-------add DEBIC= 23.44

V3 = 22.34------add DEBIC =27.65

V4= 37.42--------add DEBIC= 12.57

Q3-

$2^{-\Delta\Delta CT}$ = Normalized expression ratio

ΔCT(calibrator) = CT(target, calibrator) – CT(ref, calibrator)= -2

ΔCT(test) = CT(target, test) – CT(ref, test) = -4

$\Delta\Delta$CT = ΔCT(test) – ΔCT(calibrator) = -4-(-2) = -2

$2^{-\Delta\Delta CT} = 2^{-(-2)}$

Normalized expression ratio= 4

Q4-

PCR----------RT-PCR

Buffer 10 X	Buffer 10 X
Deoxynucleotide Triphosphates(dNTPs)	Deoxynucleotide Triphosphates(dNTPs)
oligonucleotides,20 nucleotides 2 primers	random primes
ThermostablePolymerase (TaqDNApolymerase)	reverse transcriptase
nuclease-free water	nuclease-free water

DNA Template RNA template

Q5-

M-------DNA marker

1-2 ----- RNA

3-5-----cDNA

Q6-

1-4-------RNA

M--------DNA marker

5-8------genomic DNA

Q7- 2 or 5

Q8-A

1.primers should be 17-28 bases in length;
2. base composition should be 50-60% (G+C);
3. primers should end (3') in a G or C, or CG or GC: this prevents dimer formation and increases efficiency of priming;
4. Tms between 55-80^{o}C are preferred.
5. 3'-ends of primers should not be complementary (ie. base pair), as otherwise primer dimers will be synthesised preferentially to any other product.
6. presence of three or more Cs or Gs at the 3'-ends of primers may promote mispriming at G or C-rich sequences (because of stability of annealing), and should be avoided.

B- Self Dimer

Q9-
sample 1= 2 pure
sample 2= 1.6 contaminated with phenol
sample 3= 4 contaminated with protean

Q10-
1- plateau phase
2- exponential phase
3- amplification production
4- threshold cycle (ct)