

BIOINFORMATICS ASSIGNMENT 1 (Day 1 - 5)

1. Gene Name : SRY

2. Function of the Gene : The SRY gene (Sex-determining Region Y) is a critical gene located on the Y chromosome in mammals, including humans. It plays a fundamental role in the development of male characteristics during embryogenesis. Here are the key functions of the SRY gene:

a. Initiation of Testis Development: The SRY gene is responsible for triggering the differentiation of the undifferentiated gonads into testes in male embryos. It acts as a transcription factor, activating other genes involved in male sexual development.

b. Formation of Sertoli Cells: Sertoli cells are essential supportive cells within the testes. The SRY gene is responsible for promoting the development and differentiation of these cells. Sertoli cells play a crucial role in the production of sperm and the regulation of spermatogenesis.

c. Suppression of Ovarian Development: In the absence of the SRY gene or its malfunction, the default development pathway in humans is toward female characteristics. The SRY gene suppresses the development of ovaries and inhibits the expression of genes associated with female sexual development.

d. Regulation of Anti-Müllerian Hormone (AMH): The SRY gene controls the production of Anti-Müllerian Hormone (AMH), also known as Müllerian inhibiting substance. AMH is responsible for causing the regression of the Müllerian ducts, which would otherwise develop into female reproductive structures (such as the uterus and fallopian tubes).

Overall, the SRY gene plays a pivotal role in initiating male sexual development, promoting testis formation, suppressing female sexual characteristics, and regulating key hormonal factors involved in sexual differentiation during embryogenesis.

3. NCBI accession number : NC_000024.10

4. Forward Primer : TCAACAGCGATGATTACAGTCCA

5. Reverse primer : GCTGATCTCTGAGTTTCGCATTC

6. Features of primers :

OLIGO	Start	Length	Temperature	GC%	Sequence
Forward Primer	114	23	60.06	43.48	TCAACAGCGATGATTACAGTCCA
Reverse primer	352	23	60.00	47.83	GCTGATCTCTGAGTTTCGCATTC

7. Amplicon length and sequence :

Amplicon length	239
Amplicon sequence	TCAACAGCGATGATTACAGTCCAGCTGTGC AAGAGAATATTCCCGCTCTCCGGAGAAGCT CTTCCTTCCTTTGCACTGAAAGCTGTAAC CTAAGTATCAGTGTGAAACGGGAGAAAACA GTAAAGGCAACGTCCAGGATAGAGTGAAGC GACCCATGAACGCATTATCGTGTGGTCTC GCGATCAGAGGCGCAAGATGGCTCTAGAG AATCCCAGAATGCGAAACTCAGAGATCAGC

qPCR Data analysis (DAY 5)

Housekeeping genes(GAPDH)	Ct values	
	Ct 1	Ct 2
Untreated (control)	18.5	18.5
Untreated (control)	17.8	17.8
Untreated (control)	17.5	17.5
Treated	18.3	18.3
Treated	18.5	18.5
Treated	18.2	18.2

Gene of interest (HER2)	Ct values	
	Ct 1	Ct 1
Untreated(control)	23.3	22.5
Untreated(control)	22.5	22.2
Untreated(control)	21.2	21.9
Treated	25.3	25.3
Treated	26.5	26.5
Treated	27.5	27.5

The following data are results of qPCR from cancer cell lines. HER2 stands for human epidermal growth factor. It's healthy in normal amounts, but too much may be a sign of a certain type of breast cancer. Calculate the 2 Delta Ct values for the following data and plot the values on a graph using graphpad prism.

Housekeeping genes(GAPDH)	Ct values		Gene of interest (HER2)	Ct values		Average Ct value for HG	Average Ct value for GOI	Δ Ct value	Δ Δ Ct value	Fold change
	Ct 1	Ct 2		Ct 1	Ct 2					
Untreted	18.5	18.5	Untreted	23.3	22.5	18.5	22.9	4.4	0	1
Untreted	17.8	17.8	Untreted	22.5	22.2	17.8	22.35	4.55	0.15	0.9012504626
Untreted	17.5	17.5	Untreted	21.2	21.9	17.5	21.55	4.05	-0.35	0.7845840979
treated	18.3	18.3	treated	25.3	25.3	18.3	25.3	7	2.6	0.1649384888
treated	18.5	18.5	treated	26.5	26.5	18.5	26.5	8	3.6	0.08246924442
treated	18.2	18.2	treated	27.5	27.5	18.2	27.5	9.3	4.9	0.0334929207