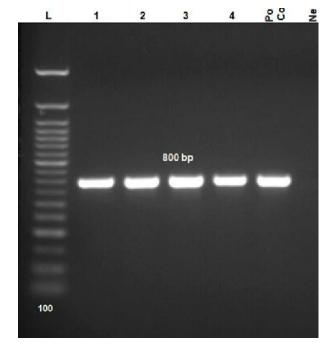
BCH 462- Biotechnology & Genetic Engineering [Practical]

Lab (8) Quantitative Reverse Transcription PCR (RT-qPCR) "Real-time PCR"

Polymerase chain reaction (PCR)

- One of the most powerful technologies in molecular biology.
- PCR is used in molecular biology to make many copies of (amplify) small sections of DNA or a gene
- In such traditional PCR (endpoint), detection of the amplicon is performed at the end of the reaction after the last PCR cycle, using gel electrophoresis. Why RT-PCR?



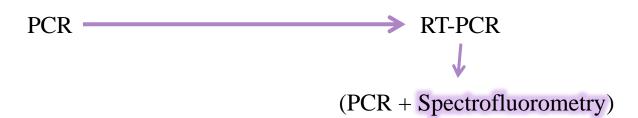
RT-PCR is <u>identical</u> to standard PCR <u>except</u> that the progress of the reaction is monitored <u>during each PCR cycle.</u>

Real-time quantitative (RT-qPCR)

- In real-time quantitative PCR fluorescent reporter dyes allow a PCR reaction to be visualized "in real time" as the reaction progresses by combine the amplification and detection steps in the PCR reaction.
- The assay relies on <u>measuring the increase in fluorescent signal.</u>
 - ➤ Is **proportional** to the amount of DNA produced during each PCR cycle.
 - Gives a quantitative information on the starting quantity of the amplified target.

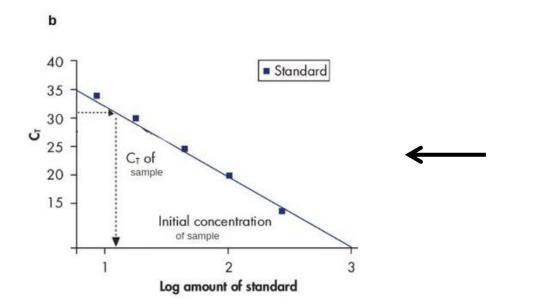
Applications:

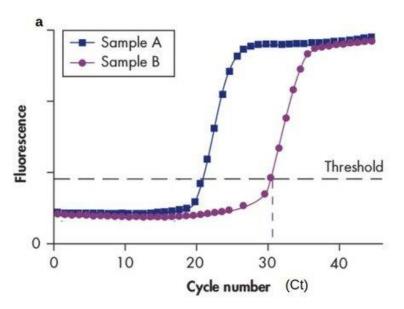
- 1. Gene expression (most common application).
- 2. Microbial load testing (type and # of microorganism)



RT-qPCR quantification methods

- 1. Absolute quantification: the exact concentration of sample can be determined, in which samples (typically a plasmid, oligonucleotide, or purified PCR product) of known quantity are serially diluted and then amplified to generate a standard curve.
 - Unknown samples are then quantified by <u>comparison with this curve</u>.
- 2. Relative quantification (Comparative): analyze changes in gene expression in a given sample relative to the same gene in another reference sample (disease vs normal control sample). The results are expressed as fold change (increase or decrease).
 - A normalizer gene (such as β -actin) is used as a control for experimental variability in this type of quantification.





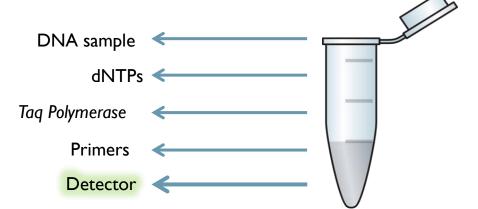
RT-qPCR chemistries (detection systems)

I. SYBR-green based assay:

Principle:

- The double-strands **DNA-intercalation** agent (DNA-binding dyes) such as **SYBR** Green.
- The SYBR Green 1 is **only** fluorescing <u>when intercalated into dsDNA</u>.
 - The <u>intensity of the fluorescence signal</u> is therefore **dependent** on the <u>quantity of dsDNA present in the reaction</u>.
- The main disadvantage of this method is that it is not specific since the dye <u>binds to all dsDNAs</u> formed during the PCR

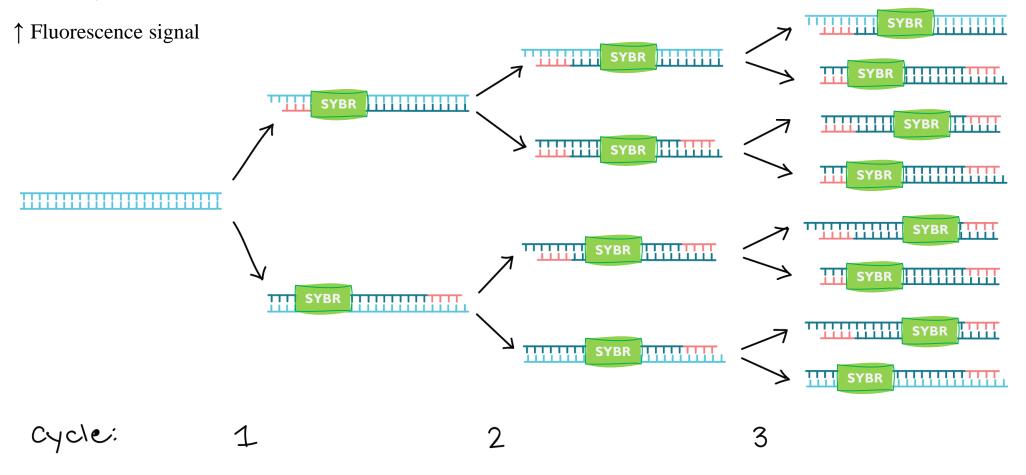
reaction (i.e., nonspecific PCR products and primer-dimers).





More dsDNA → More binding → More fluorescence

↑ Quantity of dsDNA



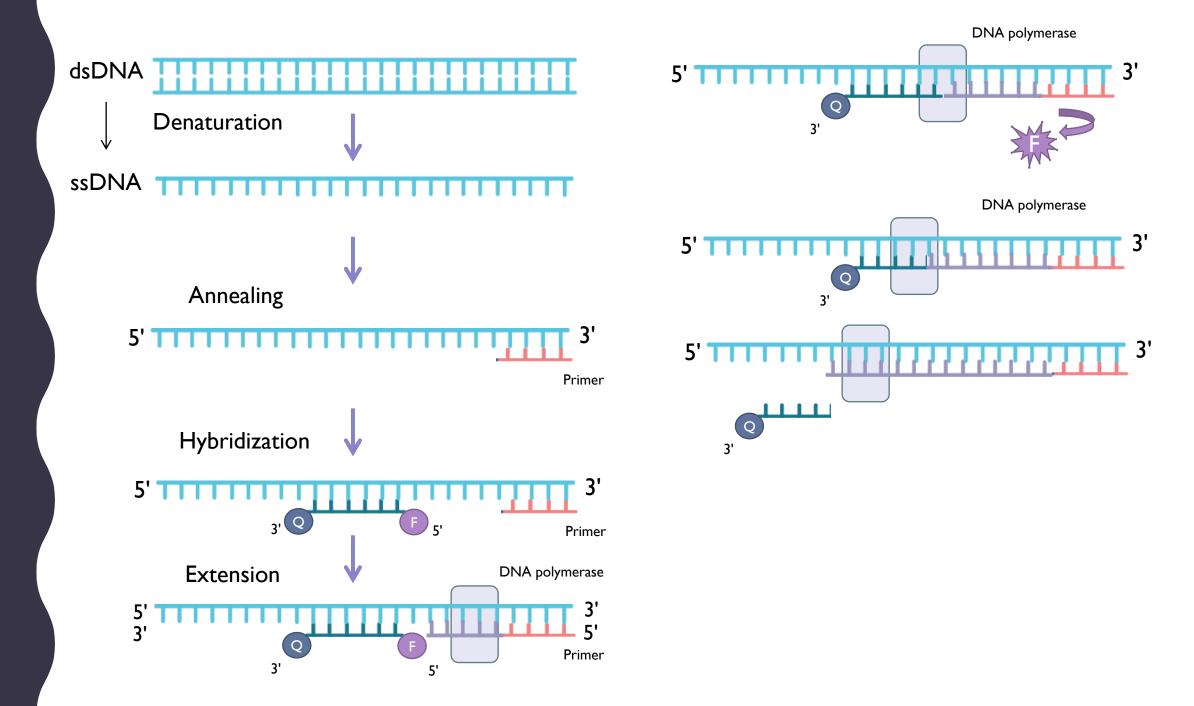
RT-qPCR chemistries (detection systems)

Fluorophore Quencher

II. Fluorogenic 5' nuclease assay (TaqMan® probe assay):

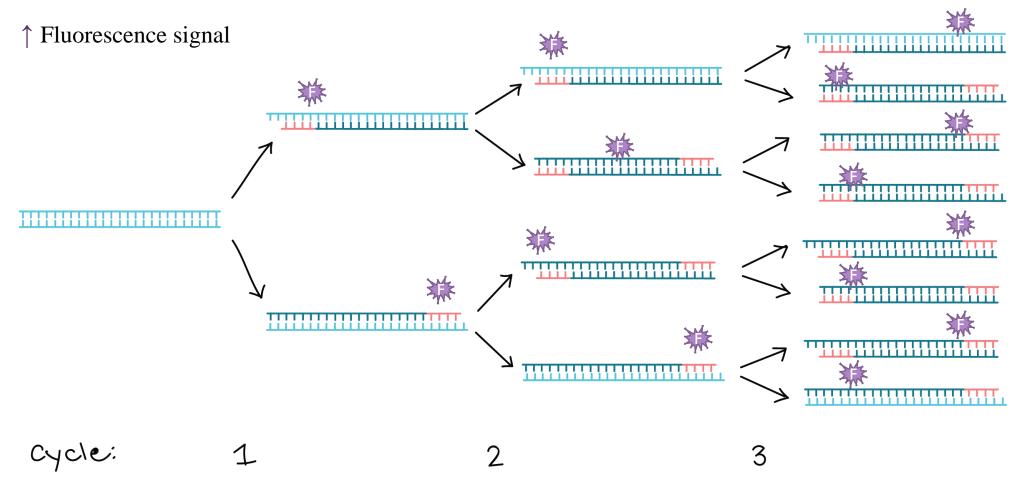
Principle:

- A probe is used in the real-time quantitative TaqMan assay.
- The **probe** is a specific sequence which has a fluorescent reporter dye linked to its 5 end and a non-fluorescent quencher at its 3 end.
- Whilst the probe is intact, the quencher absorbs the fluorescence emitted by the reporter dye.
- The TaqMan probe anneals downstream the target sequence from one of the primer sites and is cleaved by the 5['] nuclease activity of the *Taq polymerase* during the PCR extension phase.
- Cleavage of the probe by *Taq polymerase* during PCR will cause the separation of the reporter and quencher dyes, thereby allowing the reporter's fluorescent signal to be liberated.
- With each cycle additional reporter dye molecules are cleaved from their respective probes, leading to an increase in fluorescence intensity proportional to the amount of amplicon produced.



More dsDNA → More probe **displacement** and **cleavage**→ More fluorescence

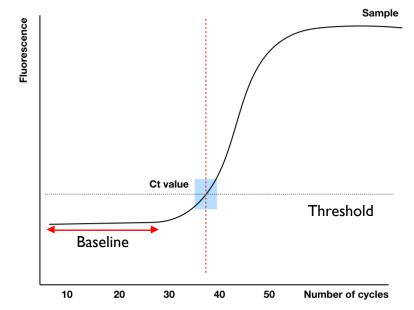
↑ Quantity of dsDNA



RT-qPCR amplification curve

Amplification plot is the plot of fluorescence signal versus cycle number.

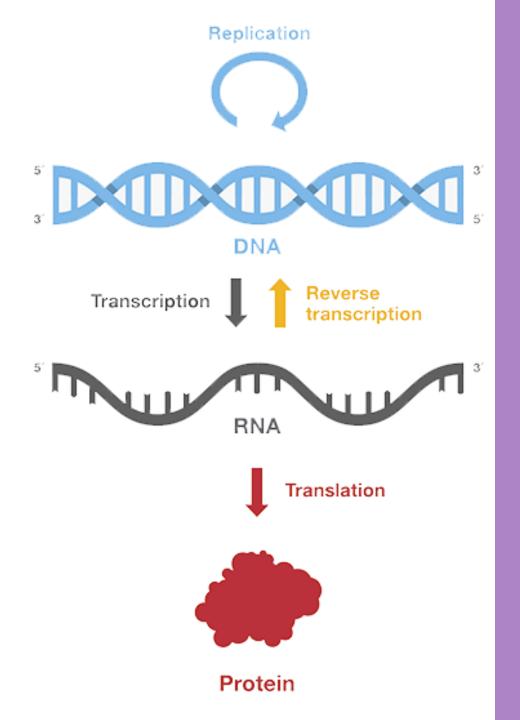
- 1. Baseline: The baseline of the real-time PCR reaction refers to the little change in fluorescent signal during the initial cycles of PCR (background or the "noise" of the reaction).
- 2. Threshold: is the level of detection or the point at which a reaction reaches a fluorescent intensity above background (baseline) levels.
- 3. C_t (threshold cycle): The threshold cycle (Ct) is the PCR cycle number at which your sample's reaction curve intersects the threshold line.



Practical Part 🧳

RT-qPCR for gene expression analysis

Gene expression is the process by which the heritable information in a **gene** is made into a functional **gene product**, such as **protein** or **RNA**.





Steps of evaluation gene expression by RT-qPCR

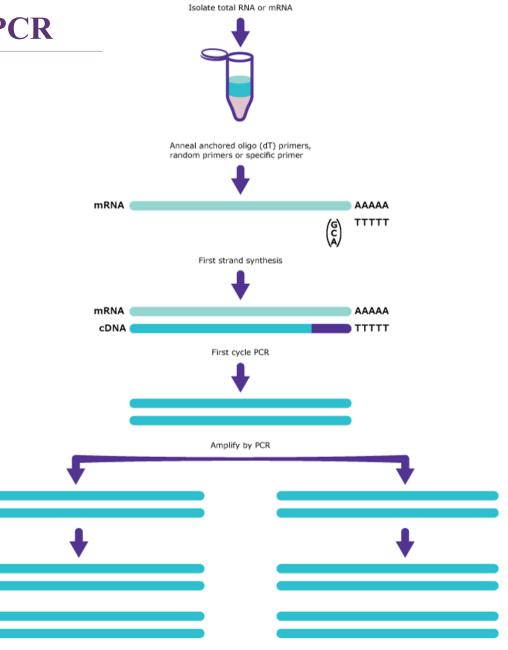
Step 1: RNA Extraction from Tissue/ Cell line or blood

Step 2: Reverse transcription to convert RNA to cDNA

Step 3: Determination of cDNA using real time PCR

Step 4: Data analysis

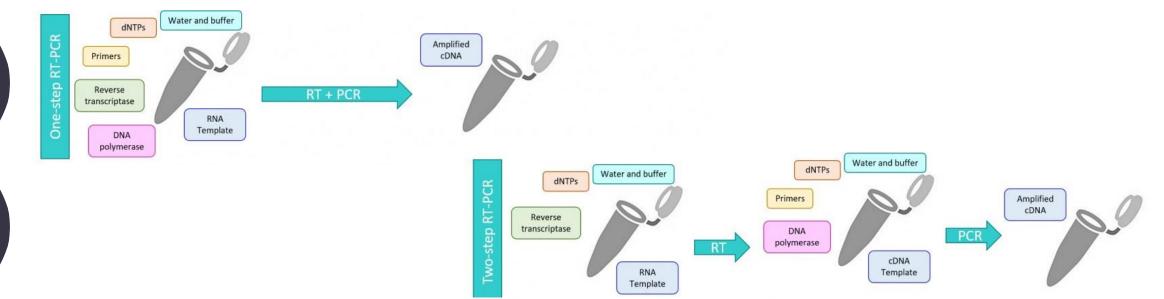
Pause and Think why do we use cDNA instead of gDNA or RNA?



RT-qPCR types

The RT-qPCR assay can be performed either as a <u>one-tube single RT and PCR enzyme method</u> or a <u>separate RT</u> and <u>PCR enzyme technique</u> using one or a two tubes.

- 1. One-step RT-qPCR, combines reverse transcription and PCR in a single tube and buffer, using a reverse transcriptase along with a DNA polymerase, simplifying reaction setup and reducing the possibility of contamination.
- 1. Two-step RT-qPCR, the <u>reverse transcription and PCR</u> steps are performed in separate tubes, with different optimized buffers, reaction conditions, and priming strategies.

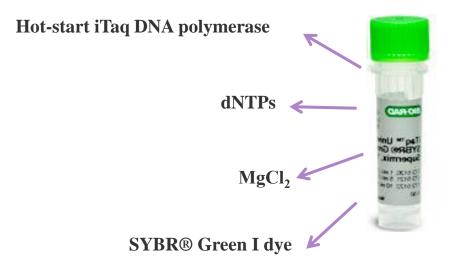


RT-qPCR for gene expression analysis

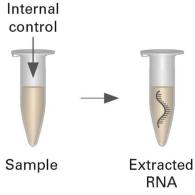
Reaction Components

Component	Volume per 12.5µl reaction
2X Green Master mix	6.25
Forward primer	0.25
Reverse primer	0.25
Nuclease free water	3.75
cDNA Template	2
Total:	Ι2.5 μΙ

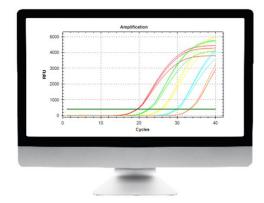
SYBR® Green PCR Master Mix



1. RNA isolation

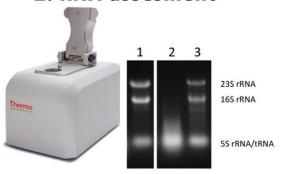


Sample: tissue, Cell-line



6. Data analysis

2. RNA assesment



To ensure RNA integrity and purity/concentration

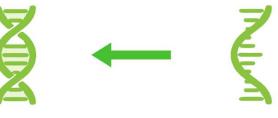


5. Real-Time PCR Thermal Cyclers

(Thermocycler + Spectrofluorometry)

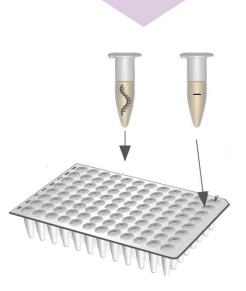
Quantitative real-time PCR workflow

3. Reverse transcription



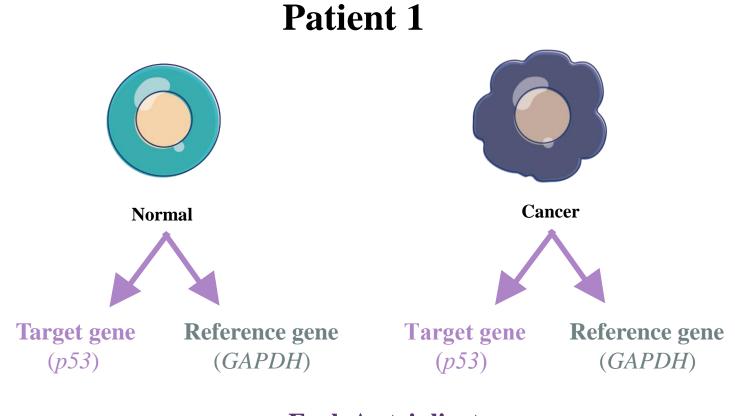
cDNA

RNA as the starting material



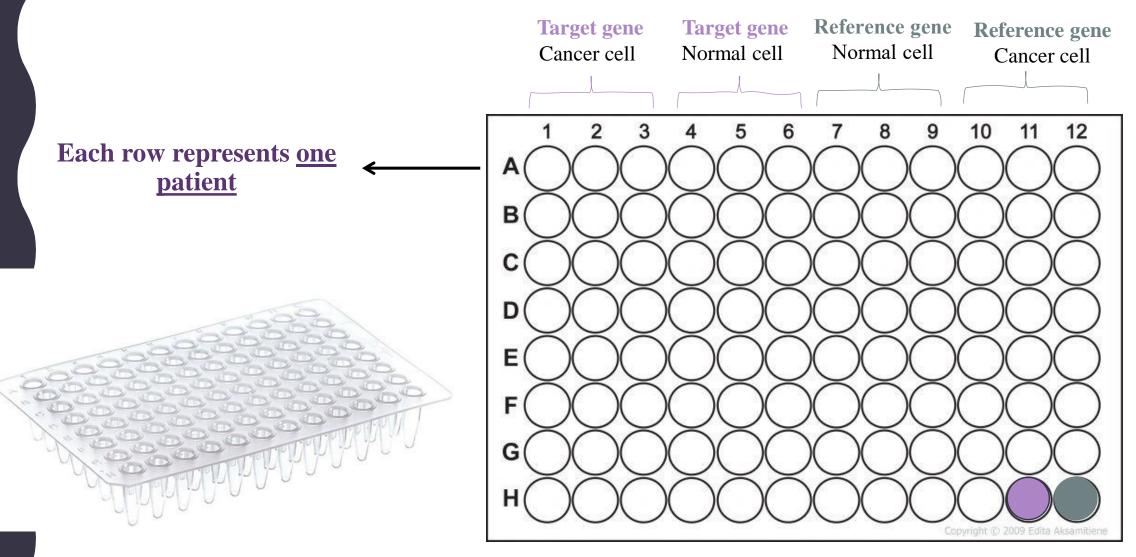
4. Plate load

■ Let's assume we want to study p53 expression in colorectal cancer patient using Relative RT-PCR.



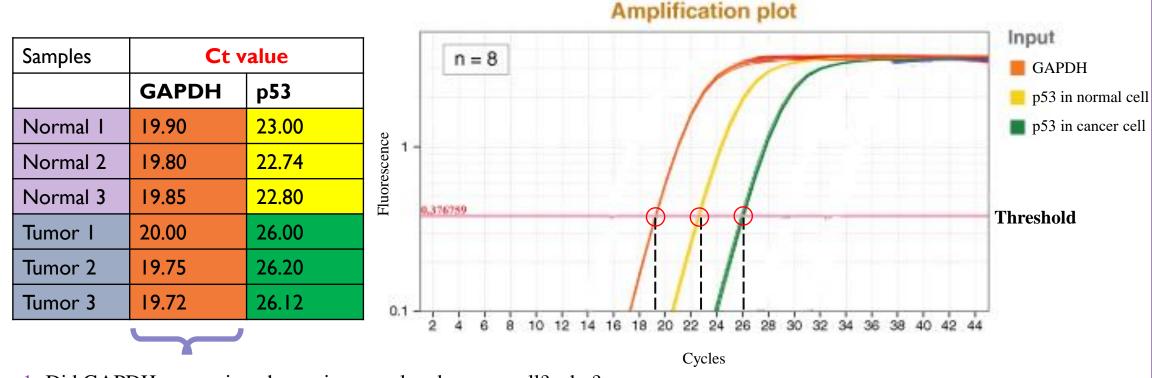
Each As triplicate

Each As triplicate

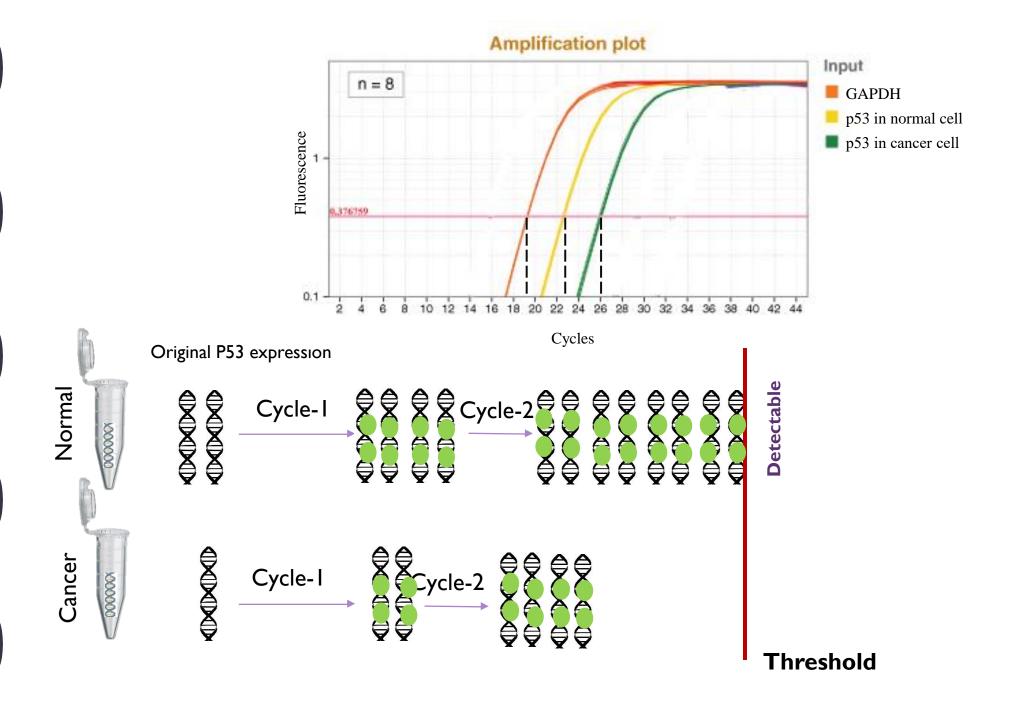


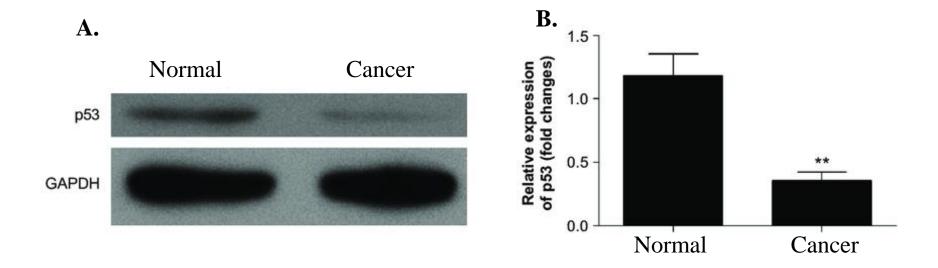
-ve control for each master mix (no template control)

Ct levels are inversely proportional to the amount of target nucleic acid expression in the sample (i.e.
the lower the Ct level the greater the amount of target nucleic acid in the sample).

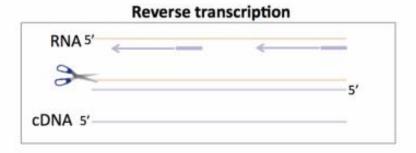


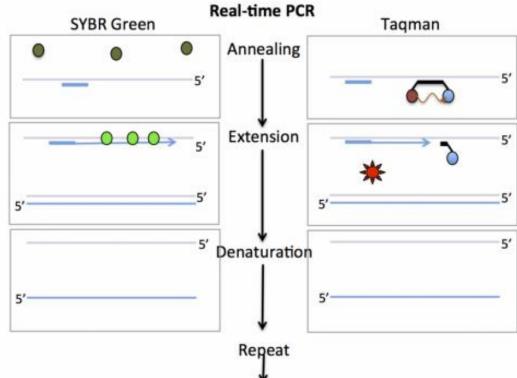
- 1- Did GAPDH expression change in normal and cancer cell? why?
- 2- What happened to p53 expression in cancer? Up/down?

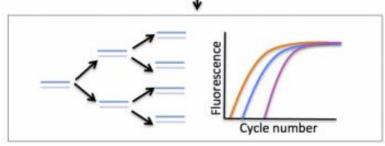




- Based on western blot and RT-PCR results we can conclude that **p53** is in CRC.
- And that could be explained through its function asgene.







Overview of RT-PCR technique

Comparison between Conventional PCR and RT-PCR

Conventional PCR	Real-time PCR
Qualitative / semi-quantitative	Quantitative
Endpoint	Real time
Gel-based PCR	Fluorescence-based PCR

Resources:

■ Gene Regulation Virtual Lab (both RT-PCR and Western blot are included)

https://www.labster.com/simulations/gene-regulation/

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