



Advanced Cell Biology & Biotechnology

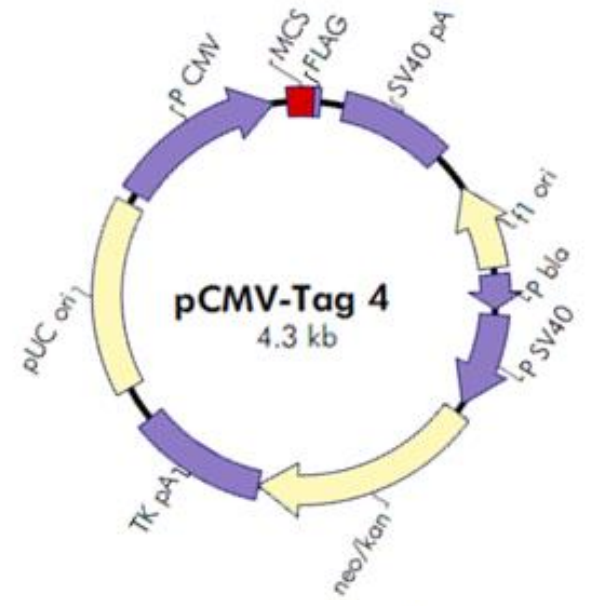
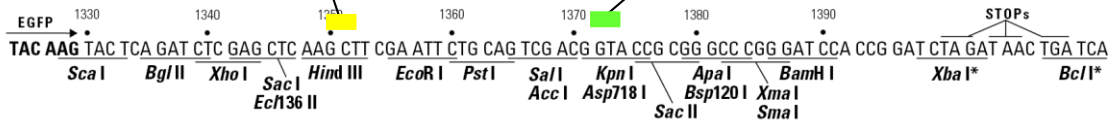
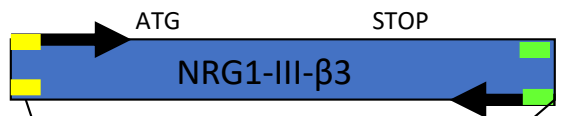
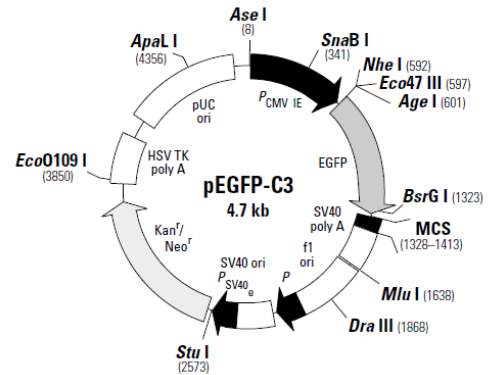
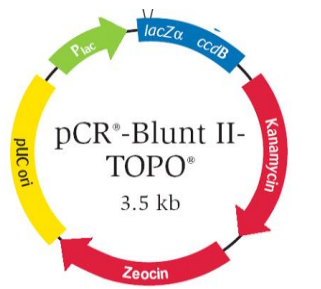
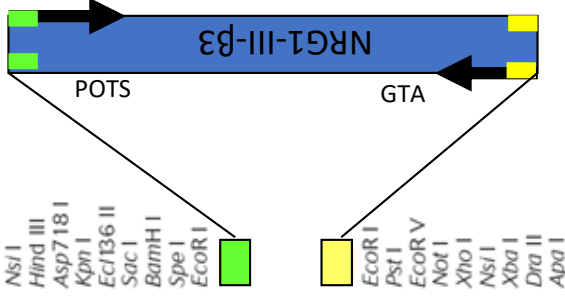
Biotechnology Project Lab

Giovanna Gambarotta
& Isabella Tarulli

The lecture of November 28th 2021 is about to begin....

- summary of the previous lesson
- quantitative real time PCR (qRT-PCR-26-11-2021)
- example of qRT-PCR data analysis
- exercise with qRT-PCR data (Excel files)

Subcloning NRG1IIIβ3 into the expression vector pCMV-Tag4 containing a FLAG



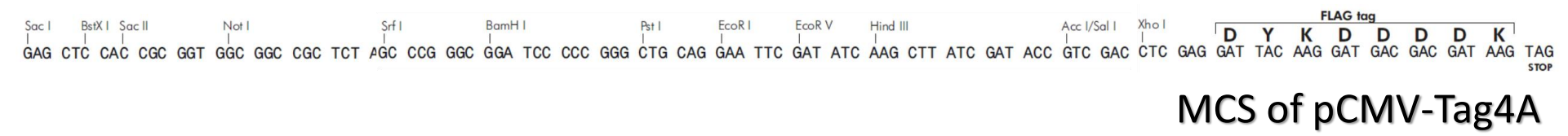
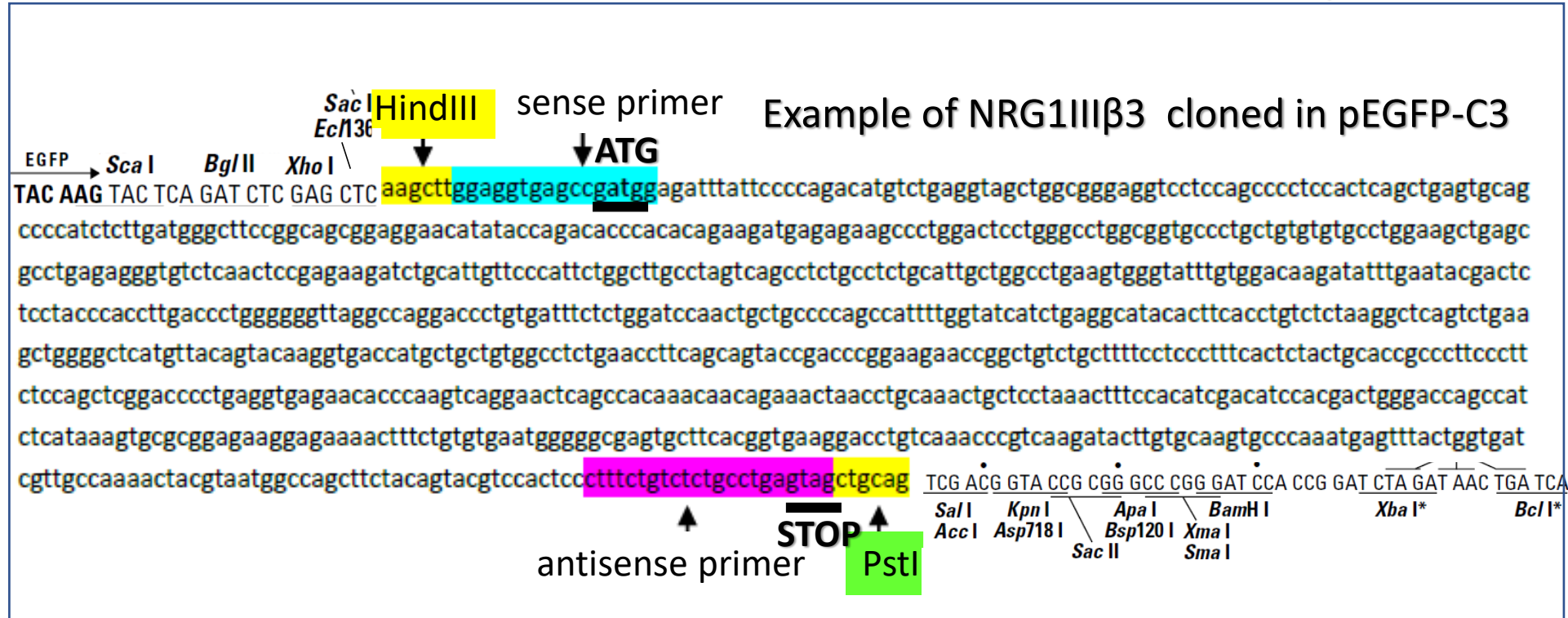
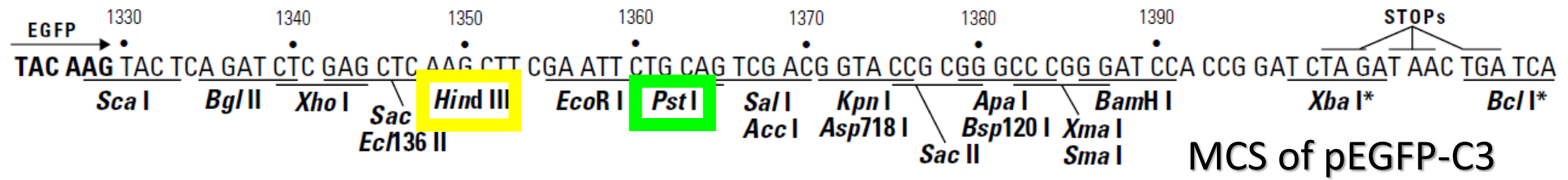
T3 promoter
 A ATT AAC CCT CAC TAA AGG GAA CAA AAG CTG GAG CTC CAC CGC GGT GGC GGC CGC TCT A...

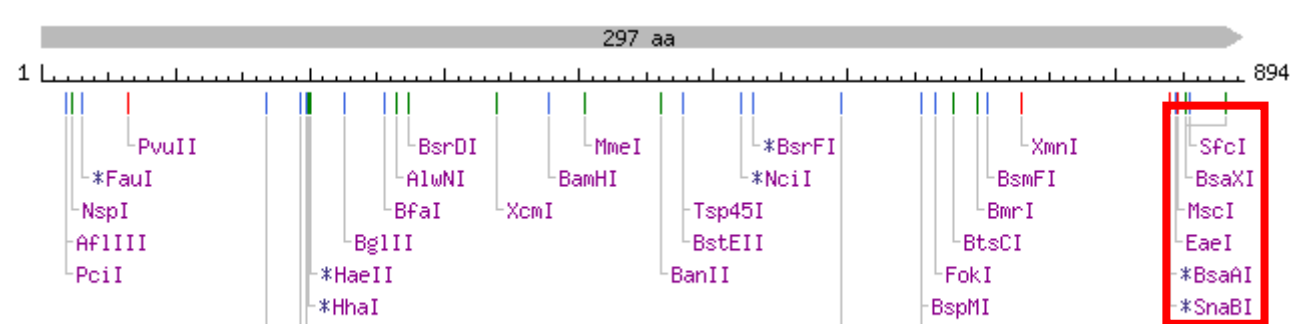
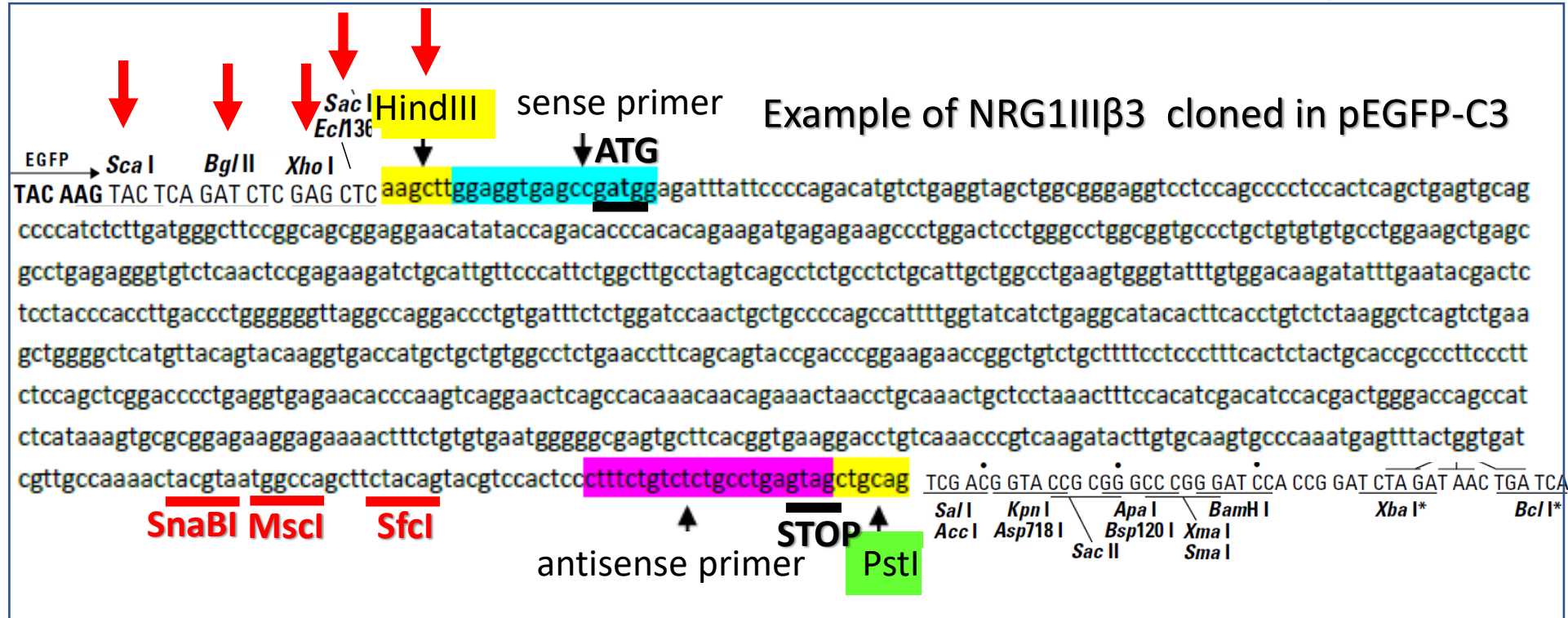
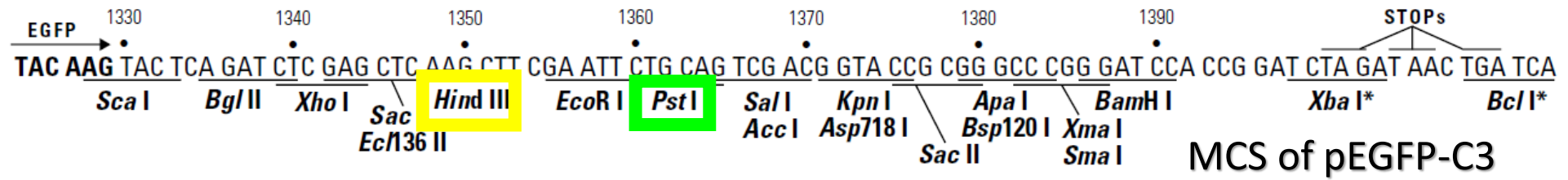
Srf I BamH I Pst I EcoR I EcoR V Hind III Acc I/Sal I
 ...GC CCG GGC GGA TCC CCC GGG CTG CAG GAA TTC GAT ATC AAG CTT ATC GAT ACC GTC GAC*

Xho I **FLAG tag**
 ...CTC GAG GAT TAC AAG GAT GAC GAC GAT AAG TAG GGCCCGGTACCT...
 STOP

T7 promoter
 ...TAATTAATTAAGGTACCAGGTAAGTGTACCAATTGCGCCTATAGTGAGTCGTATTA
 MULTIPLE STOP CODONS







Single cutters of NRG1IIIβ3

Enzymes you can use for subcloning in pCMV-Tag4

pCMV-Tag 4A Multiple Cloning Site Region

ATT AAC CCT CAC TAA AGG GAA CAA AAG CTG **GAG CTC** CAC **CGC GGT** GGC
GGC CGC TCT AGC CCG GGC **GGA TCC** CCC GGG **CTG CAG** **GAA TTC** **GAT ATC**
AAG CTT ATC GAT ACC GTC GAC*CTC GAG **GAT TAC AAG GAT GAC GAC GAT**
AAG TAG GGC CCG GTA CCT TAA TTA ATT AAG GTA CCA GGT AAG TGT ACC
CAA TTC GCC CTA TAG TGA GTC GTA TTA

pCMV-Tag 4B Multiple Cloning Site Region

TTA ACC CTC ACT AAA GGG AAC AAA AGC TGG **AGC TCC** ACC **GCG GTG** GCG
GCC GCT CTA GCC CGG GCG **GAT CCC** CCG GGC **TGC AGG** **AAT TCG** **ATA TCA**
AGC TTA TCG ATA CCG TCG ACA CTC GAG **GAT TAC AAG GAT GAC GAC GAT**
AAG TAG GGC CCG GTA CCT TAA TTA ATT AAG GTA CCA GGT AAG TGT ACC
CAA TTC GCC CTA TAG TGA GTC GTA TTA

pCMV-Tag 4C Multiple Cloning Site Region

TAA CCC TCA CTA AAG GGA ACA AAA GCT GGA **GCT CCA** **CCG CGG** TGG CGG
CCG CTC TAG CCC GGG **GG ATC CCC** CGG **GCT GCA GGA** **ATT CGA TAT CAA**
GCT TAT CGA TAC CGT CGA **CAA** CTC GAG **GAT TAC AAG GAT GAC GAC GAT**
AAG TAG GGC CCG GTA CCT TAA TTA ATT AAG GTA CCA GGT AAG TGT ACC
CAA TTC GCC CTA TAG TGA GTC GTA TTA

EcoRI	PstI	SacII
EcoRV	BamHI	
HindIII	SacI	FLAG

-> Translate the protein that you obtain after the subcloning:
if you have the correct frame you will obtain the NRG1
followed by the **FLAG: DYKDDDDK**



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quantitative real time PCR (qRT-PCR)

- ✿ PCR reaction
- ✿ conventional versus real time PCR
- ✿ real time PCR principles
- ✿ threshold cycle C_T
- ✿ efficiency
- ✿ relative quantification
- ✿ reference genes
- ✿ primers
- ✿ **detection chemistry**
- ✿ GLP in real time PCR

A microscopic image of biological tissue, possibly muscle or connective tissue, showing fibrous structures in shades of purple and blue. A white rectangular text box is overlaid in the center, containing the title.

Real-Time PCR Detection Chemistry

1. DNA-binding (intercalating) agents (SYBR Green I, Eva Green, LC Green)
2. Hydrolysis probes (TaqMan)
3. Hybridization (Beacons, Scorpions, Pleiades)
4. Hybridization with FRET probes (Light Cycler)

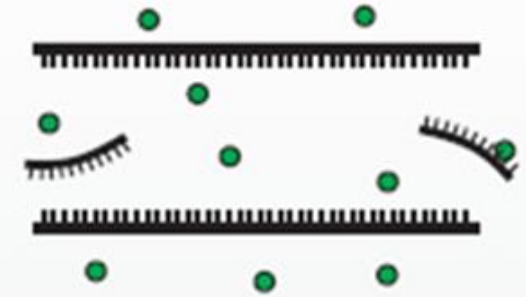
Principles of Real-Time Detection Chemistry

SYBR Green technique:

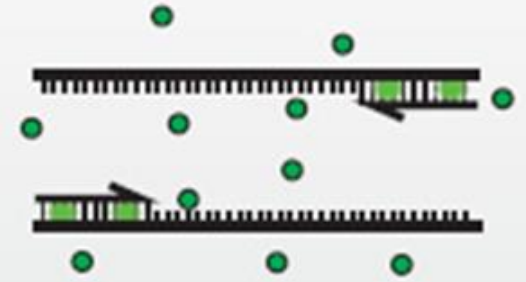
- **SYBR Green fluorescence** is enormously increased upon binding to double-stranded DNA.
- during the extension phase, more and more SYBR Green will bind to the PCR product, resulting in an increased fluorescence.
- consequently, during each subsequent PCR cycle, more fluorescence signal will be detected.

SYBR Green I fluoresces only when bound to dsDNA.

Denature



Anneal



Extend



* Pros: relatively cheap, doesn't require probe design

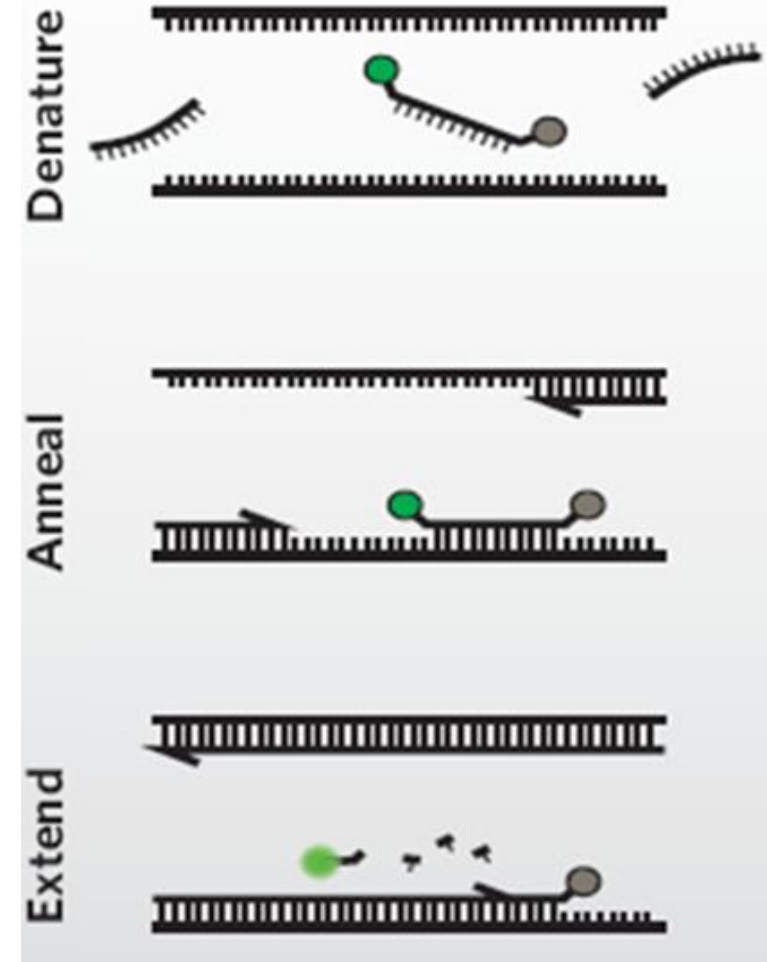
* Cons: nonspecificity can lead to false positives, not attuned for complex protocols

Principles of Real-Time Detection Chemistry

Hydrolysis probe technique:

- the hydrolysis probe is conjugated with a **quencher fluorochrome**, which absorbs the fluorescence of the **reporter fluorochrome** as long as the probe is intact.
- upon amplification of the target sequence, the hydrolysis probe is displaced and subsequently hydrolyzed by the Taq polymerase.
- this results in the separation of the reporter and quencher fluorochrome and consequently the fluorescence of the reporter fluorochrome becomes detectable.
- during each consecutive PCR cycle this fluorescence will further increase because of the progressive and exponential accumulation of free reporter fluorochromes.

TaqMan requires a sequence-specific probe that connects fluorophore and quencher.



* Pros: specificity, different colors can be used in multiplex assays

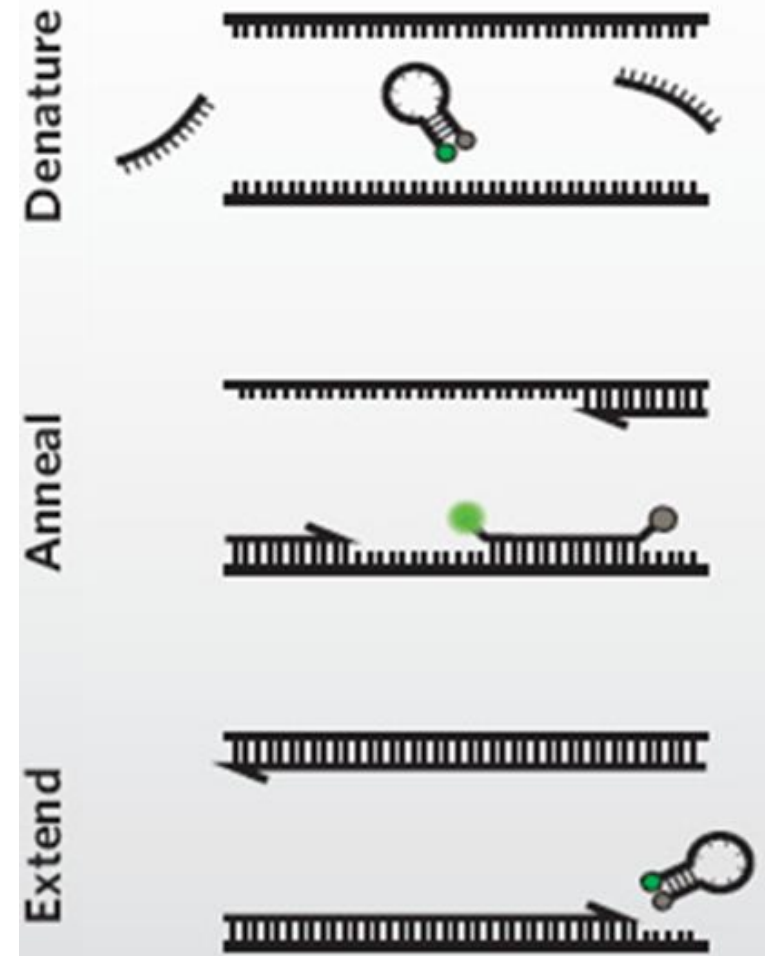
* Cons: some background noise due to irreversibility of the reaction

Principles of Real-Time Detection Chemistry

Hybridization probes technique:

- in this technique the probe is labelled with a **reporter fluorochrome** at the 3' end and a **quencher fluorochrome** at the 5' end.
- in the unbound conformation the quencher interacts with the reporter: the fluorescence is OFF
- when the probe anneals to the target sequence this results in the separation of the reporter and quencher fluorochrome and consequently the fluorescence of the reporter fluorochrome becomes ON
- upon amplification of the target sequence, the probe is displaced, and the fluorescence is OFF

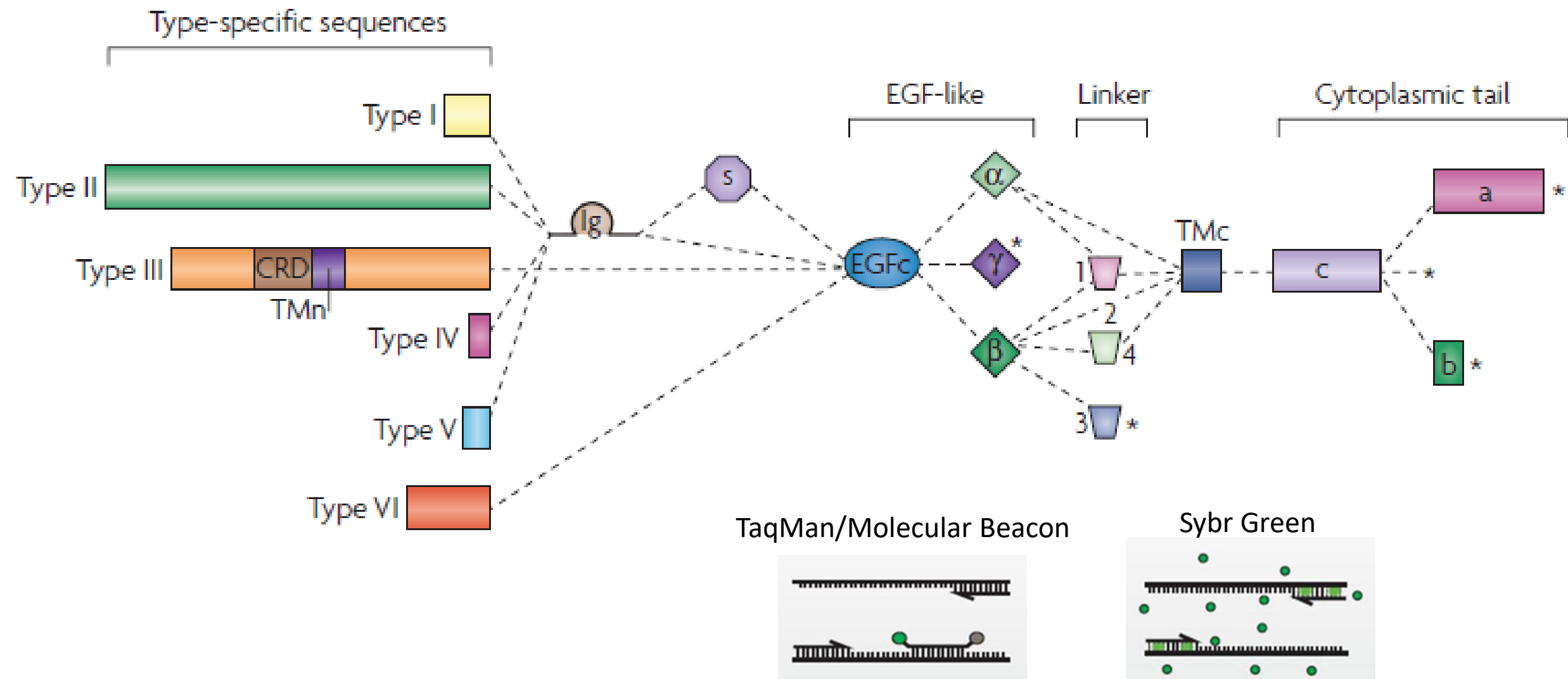
Molecular Beacons uses sequence specific probes that take on a hairpin structure.



* Pros: greater specificity, reversible fluorescence means lower background

* Cons: some non-specific interactions of the hairpins can lead to false positives

Real-Time PCR for NRG1 isoforms





SYBR Green (double-stranded DNA binding dye)

- ✿ emits a strong fluorescent signal upon binding to double-stranded DNA
- ✿ non-specific binding is a disadvantage
- ✿ requires extensive optimization
- ✿ requires melting curve analysis to ensure specificity
- ✿ longer amplicons create a stronger signal
- ✿ may be multiplexed when coupled with melting curve analysis

When to Choose SYBR Green

- ✿ detection of thousands of molecules
- ✿ general screening of transcripts prior to moving to probe based assays
- ✿ when the PCR system is fully optimized
- ✿ no primer dimers or non-specific amplicons

When Not to Choose SYBR Green

- ✿ allelic discrimination assays
- ✿ multiplex reactions
- ✿ amplification of rare transcripts



GLP in qRT-PCR

The highest risk in PCR is the contamination

- it is important to have two separate laboratory rooms for real time and DNA manipulation
- use pipettes and reagents dedicated only to PCR
- change gloves when you go to the PCR room
- check everytime for contamination by introducing negative controls in your reactions
- after the PCR reaction, discard the plate in a different room
- run the agarose gel in a different room (in the conventional PCR)
- never introduce plasmidic DNA in the PCR room!!!!



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RT (reverse transcriptase)

	stock	RT +	RT-	mix	final concentration
RNA		0,5-1 µg	0,5-1 µg		1 µg
Buffer	5x	5 µl	5 µl		1x
BSA	1 µg/µl	2,5 µl	2,5 µl		0.1 µg/µl
Triton	1%	1,25 µl	1,25 µl		0.05%
dNTPs	10mM	1,25 µl	1,25 µl		0,5mM
random primers	50 µM	3,75 µl	3,75 µl		7.5 µM
reverse transcriptase	200u/µl	1 µl	—		200u
RNAse inhibitor	33u/µl	1 µl			33u
water	 µl µl		
tot	25 µl	25 µl	25 µl		

- the cDNA can be diluted 10 folds or more for real time PCR analysis
- if you dilute 10 folds, you add 225 µl water to each sample
- for each gene, you will use 15 µl for the technical triplicate
- if you dilute 10 folds you can analyse 15 genes
- if you dilute 20 folds you can analyse 30 genes
- when you dilute 10 folds, the Ct shifts 3,3 cycles, when you dilute 2 folds Ct shifts 1 cycle

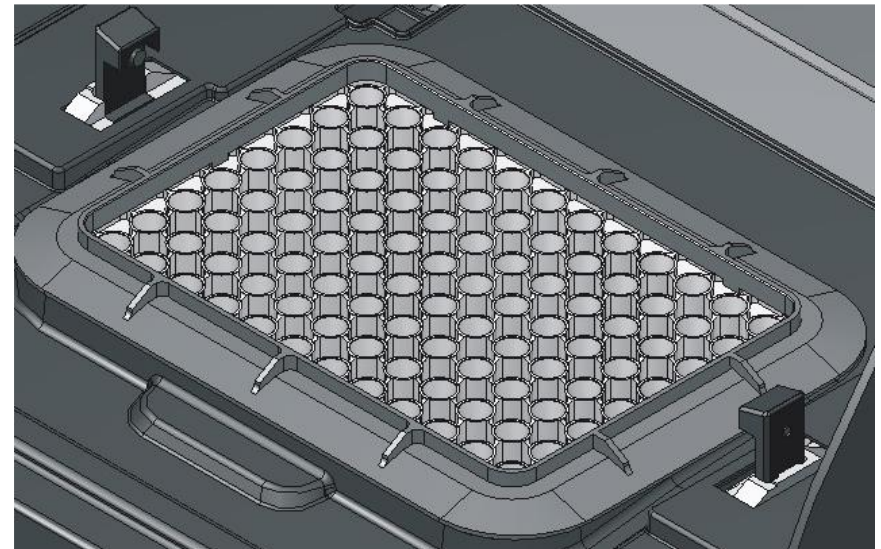
For each gene (target or reference) prepare a mix containing primers and syber mix:

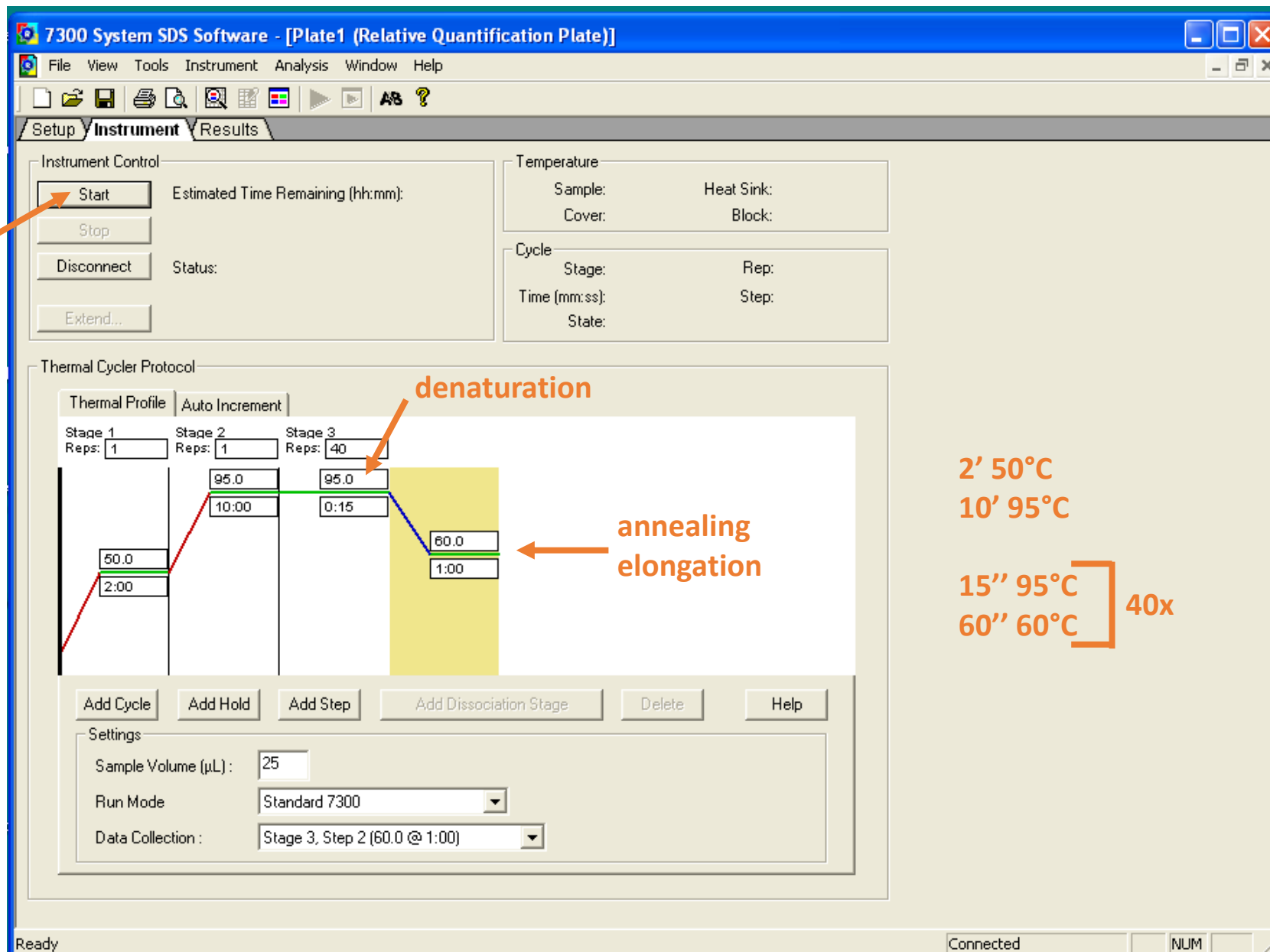
Mix for n samples x 3 (technical triplicate)

MIX/each gene		1 sample	MIX	final concentration
primer sense	7,5 μ M			300 nM
primer antisense	7,5 μ M			300 nM
SYBR green I	2 x			1x
water				
tot		20 μ l		

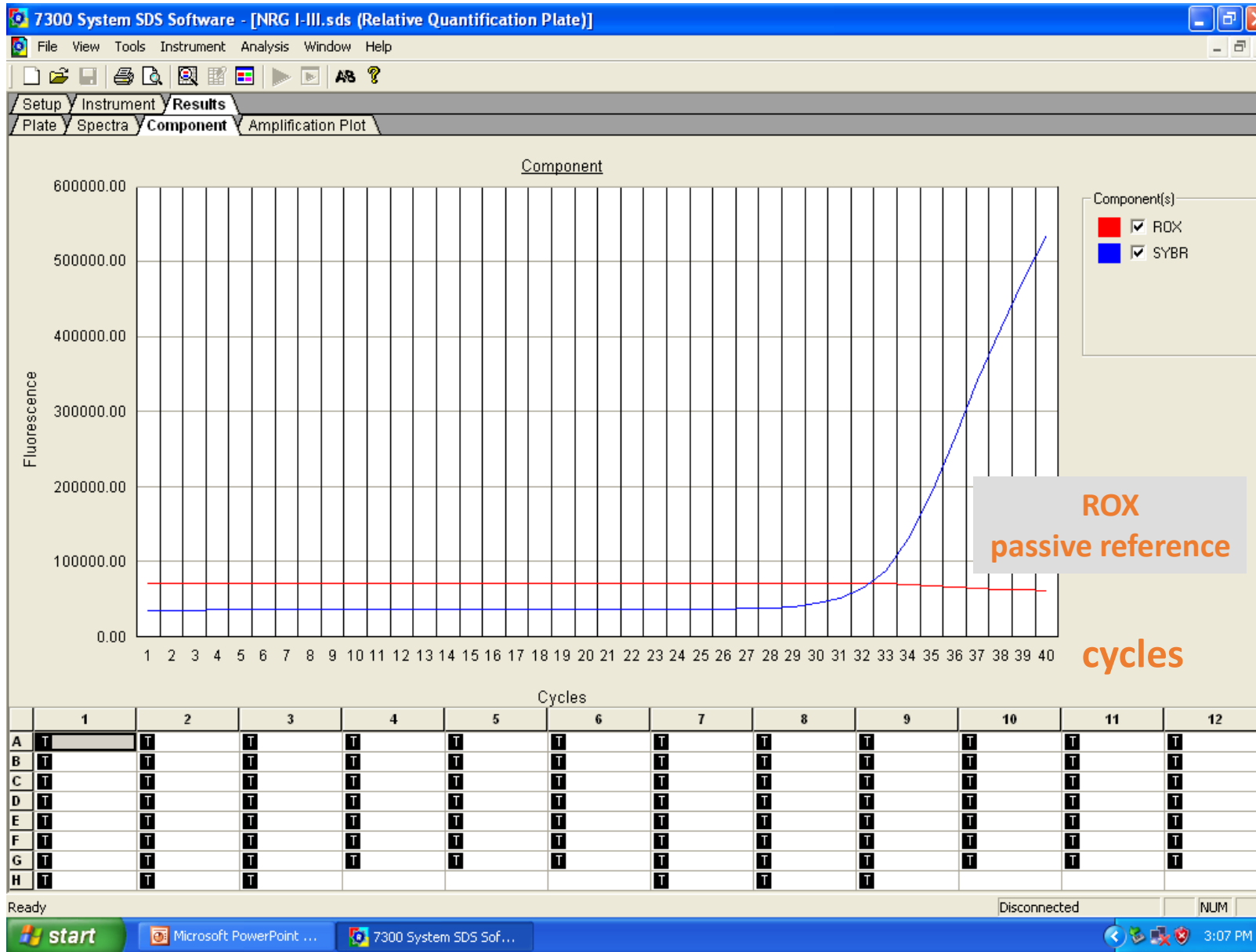
For each sample (to be done in technical triplicate)
mix 5 μ l diluted cDNA and 20 μ l mix

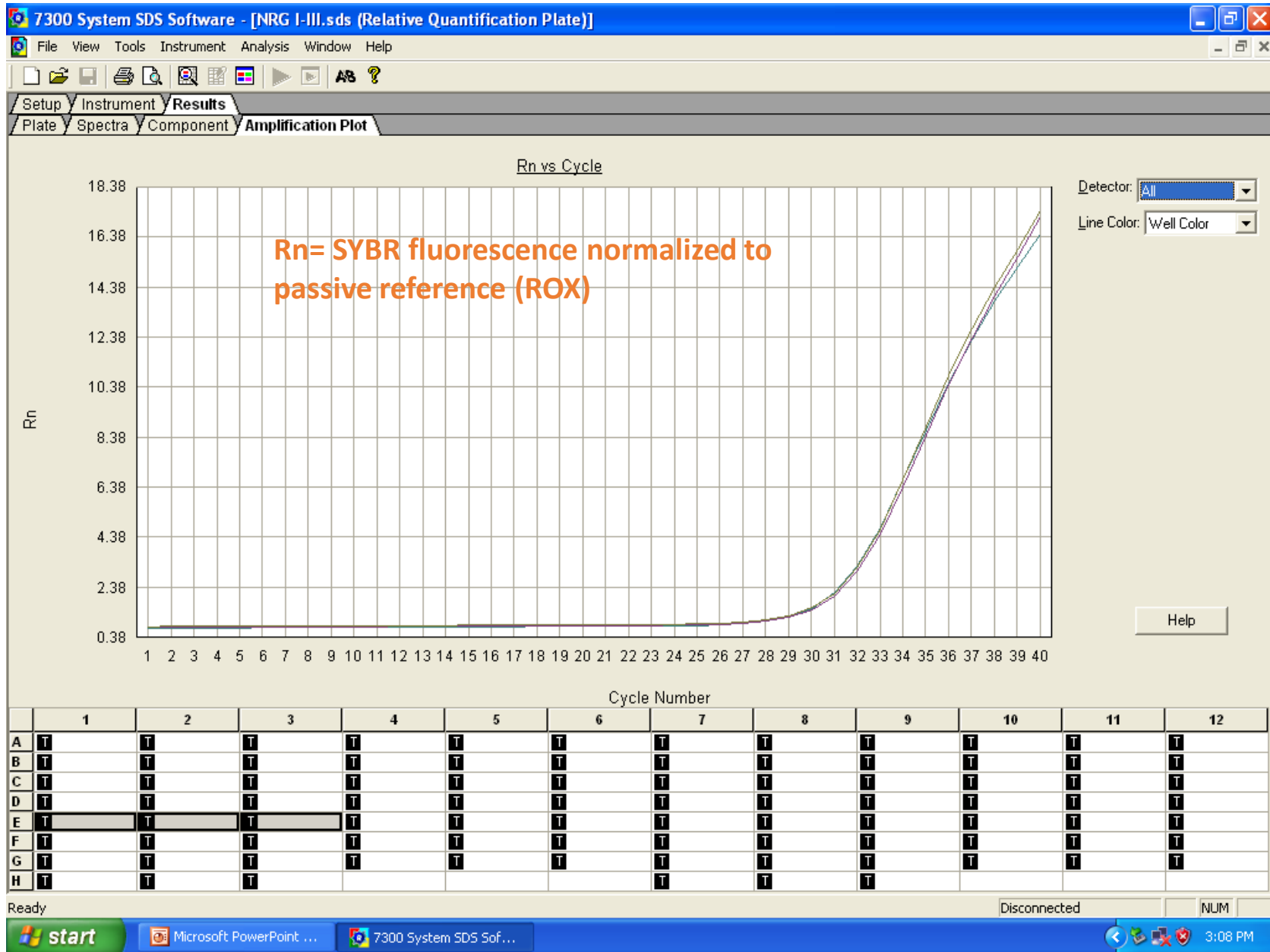


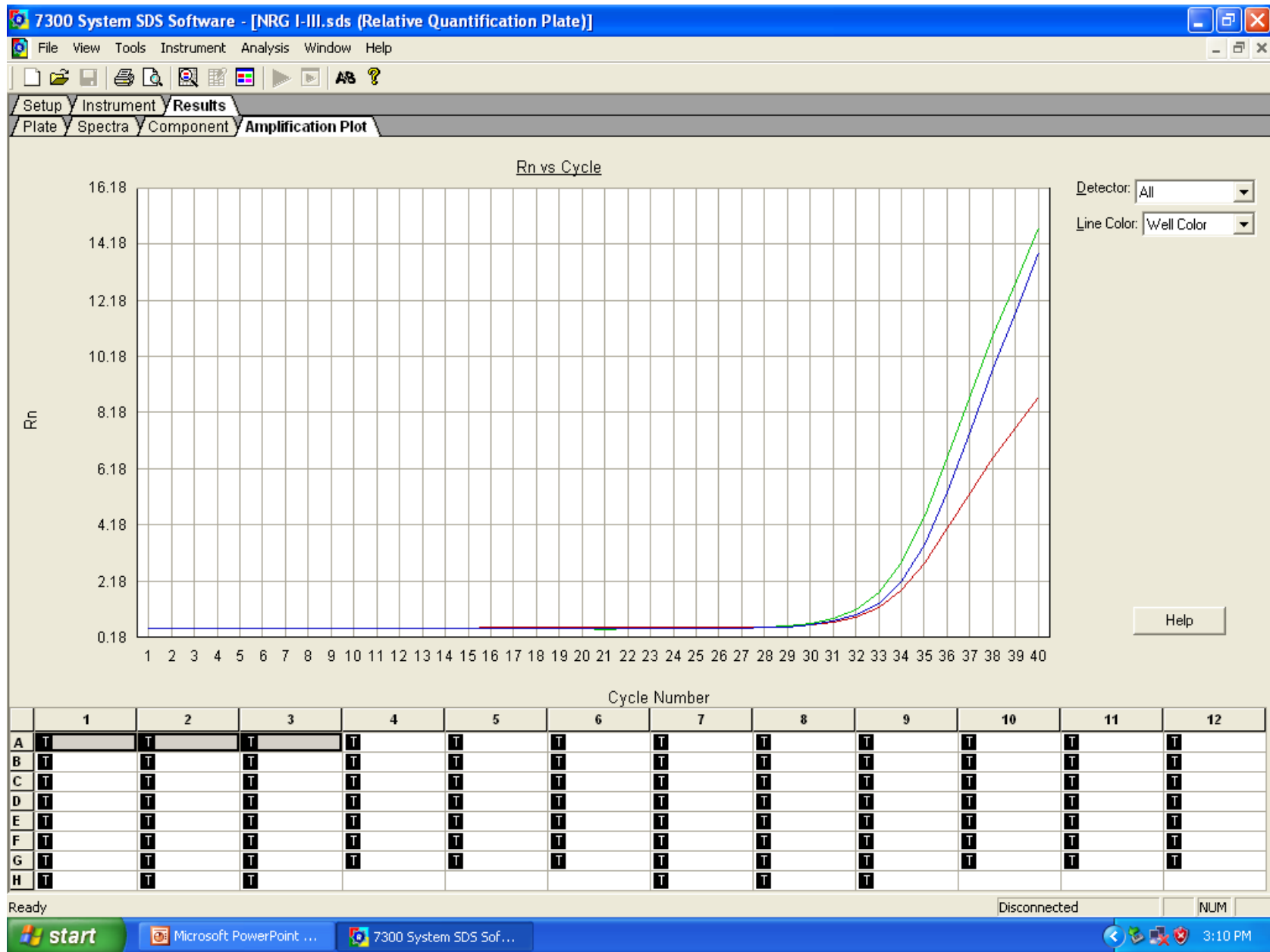


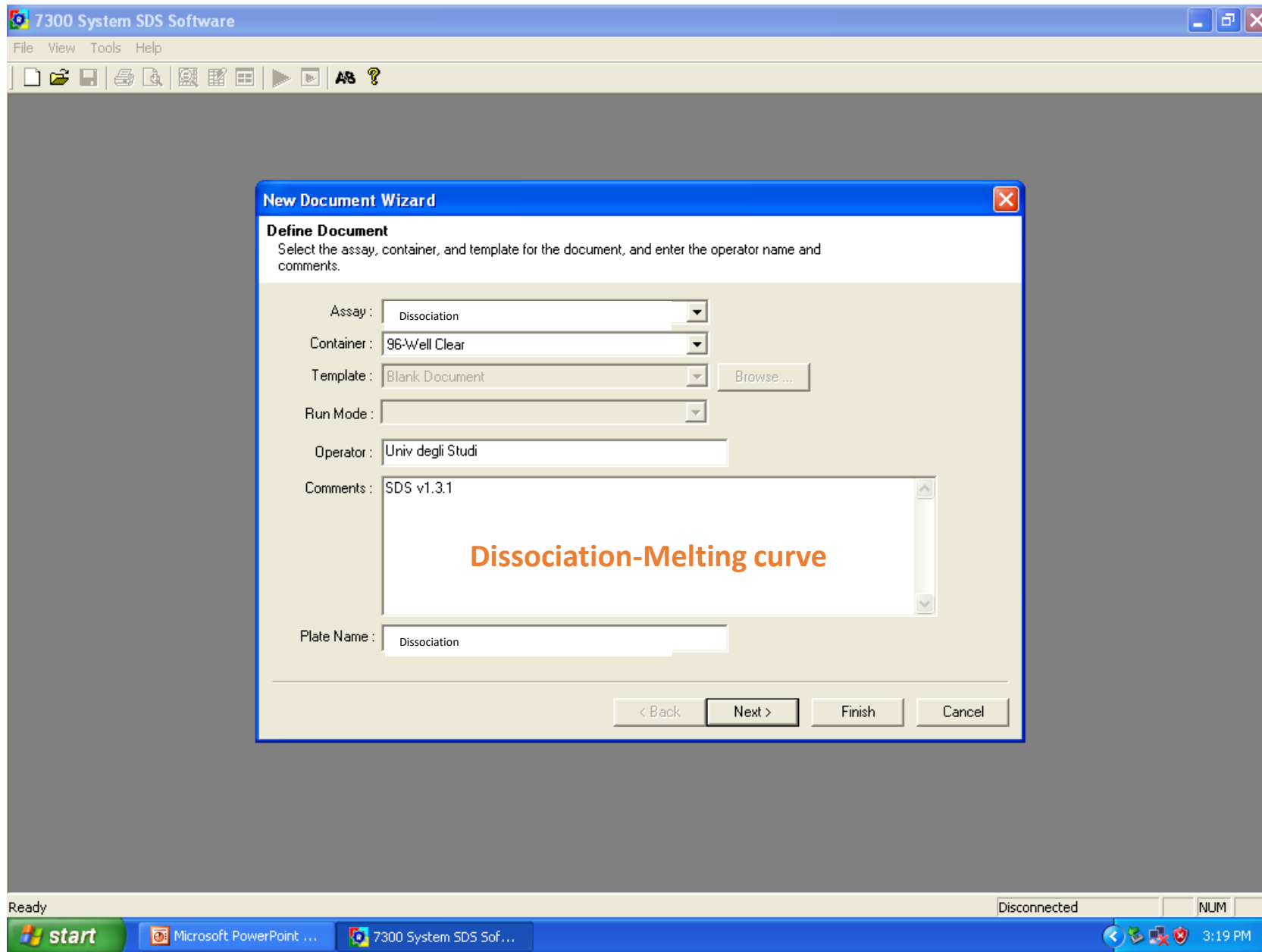


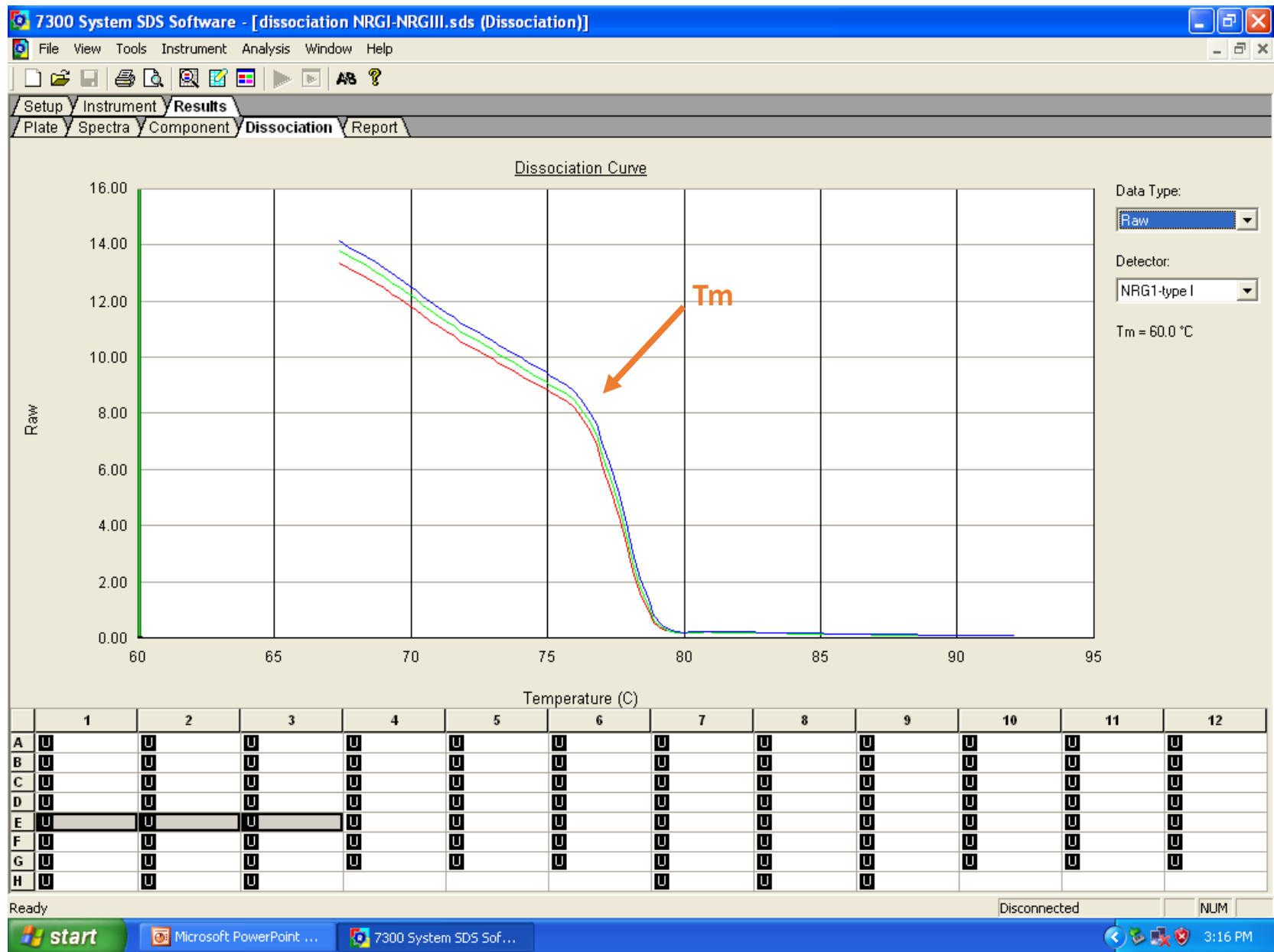
Fluorescence

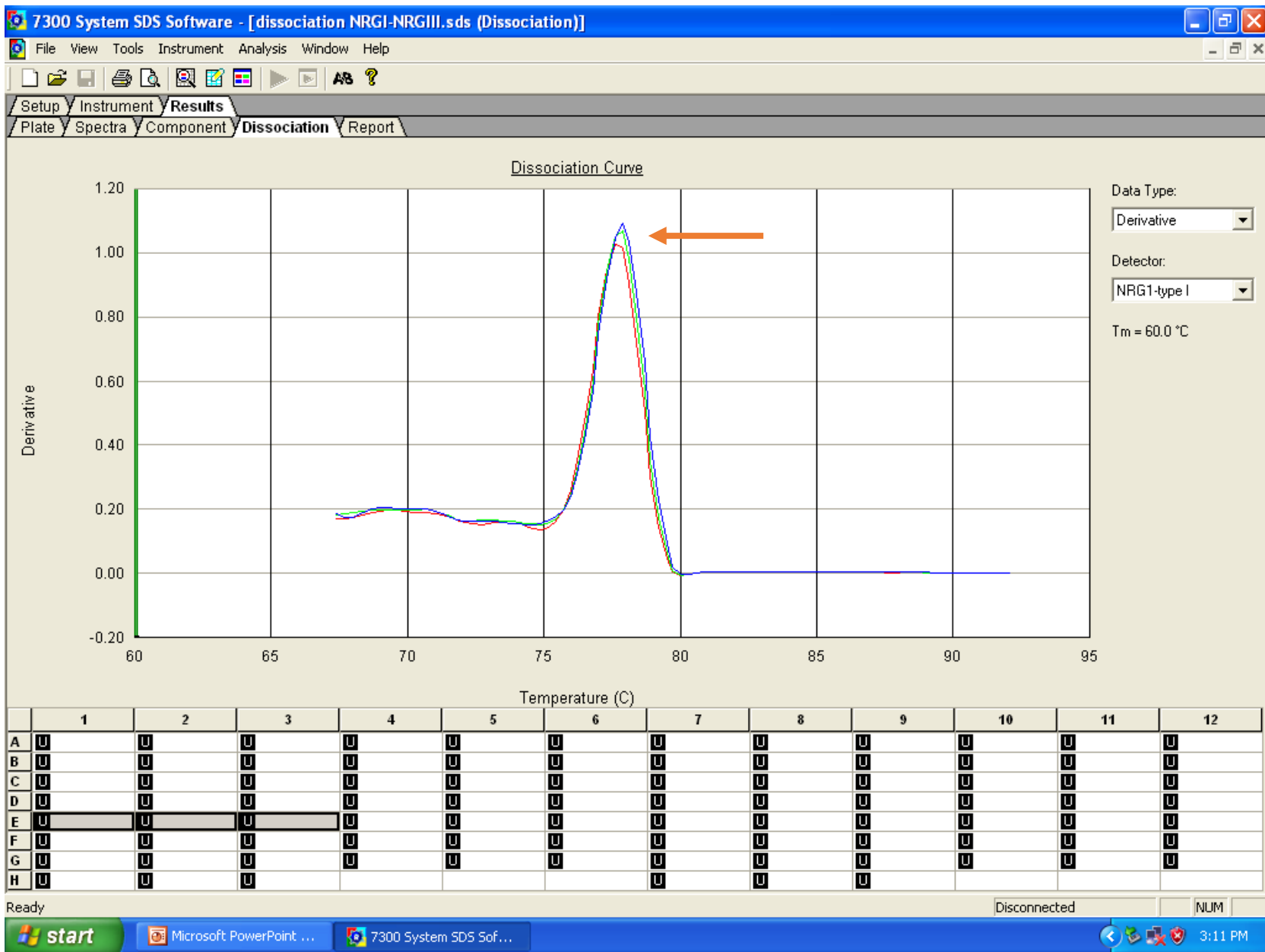


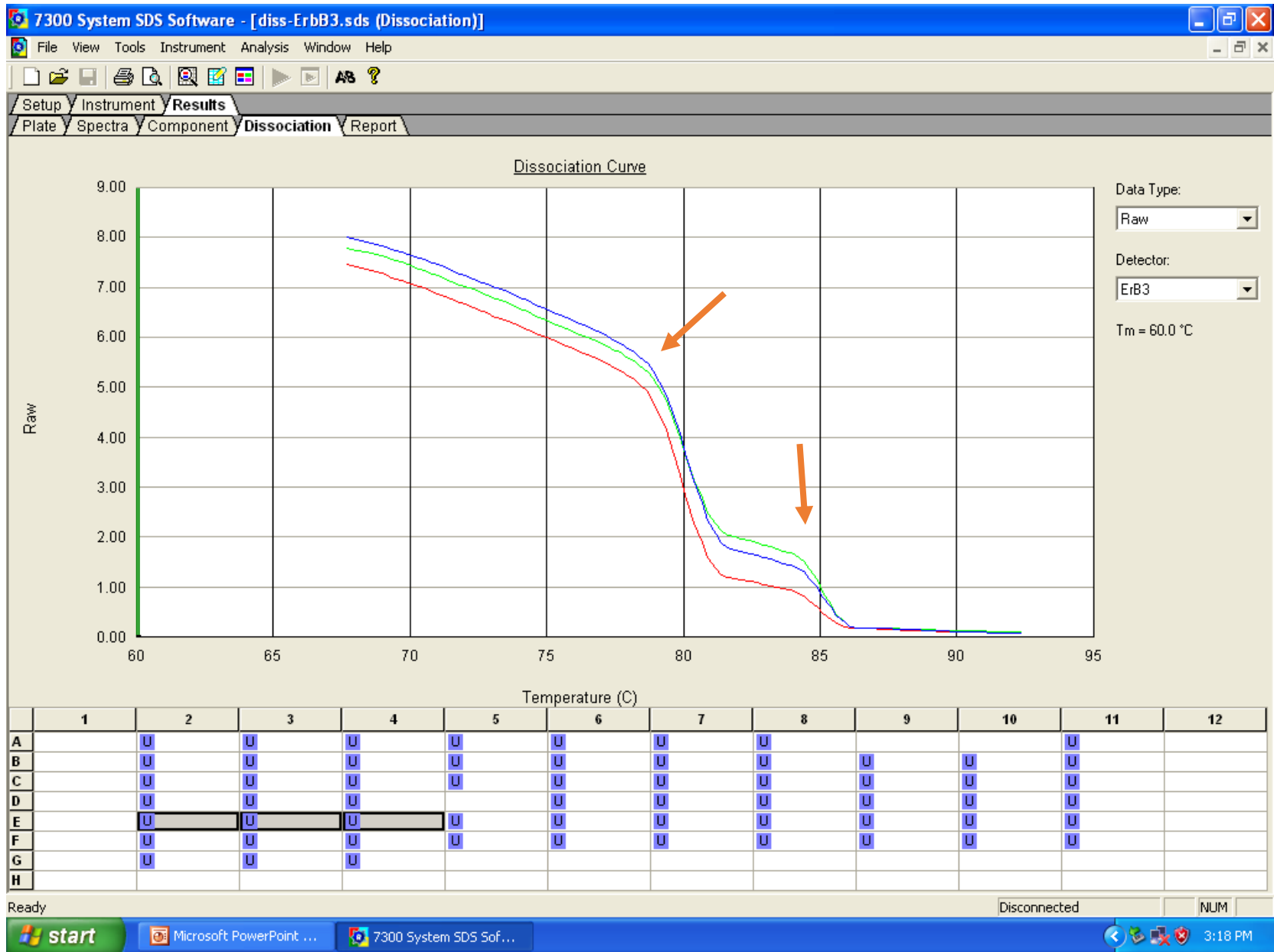


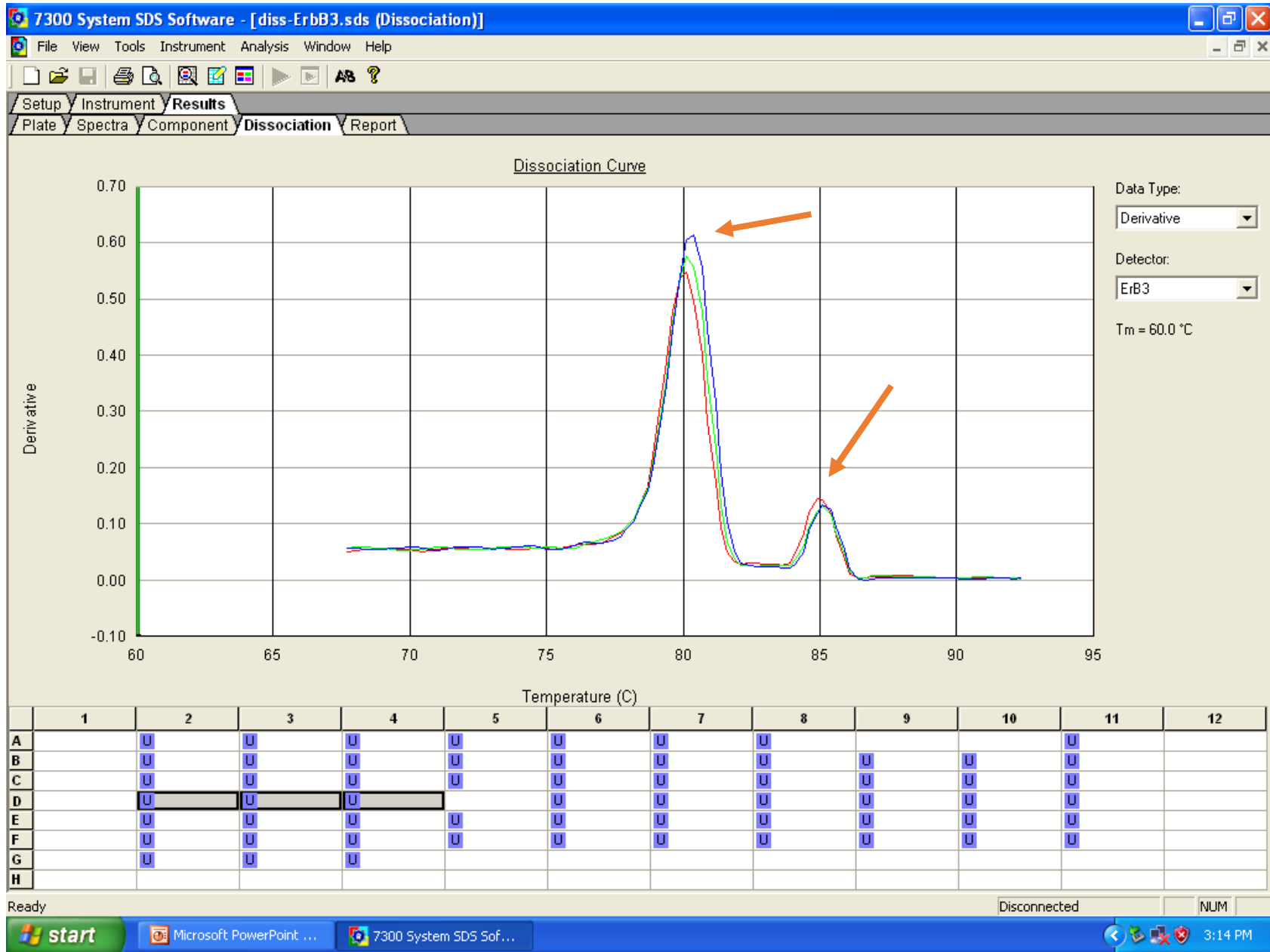


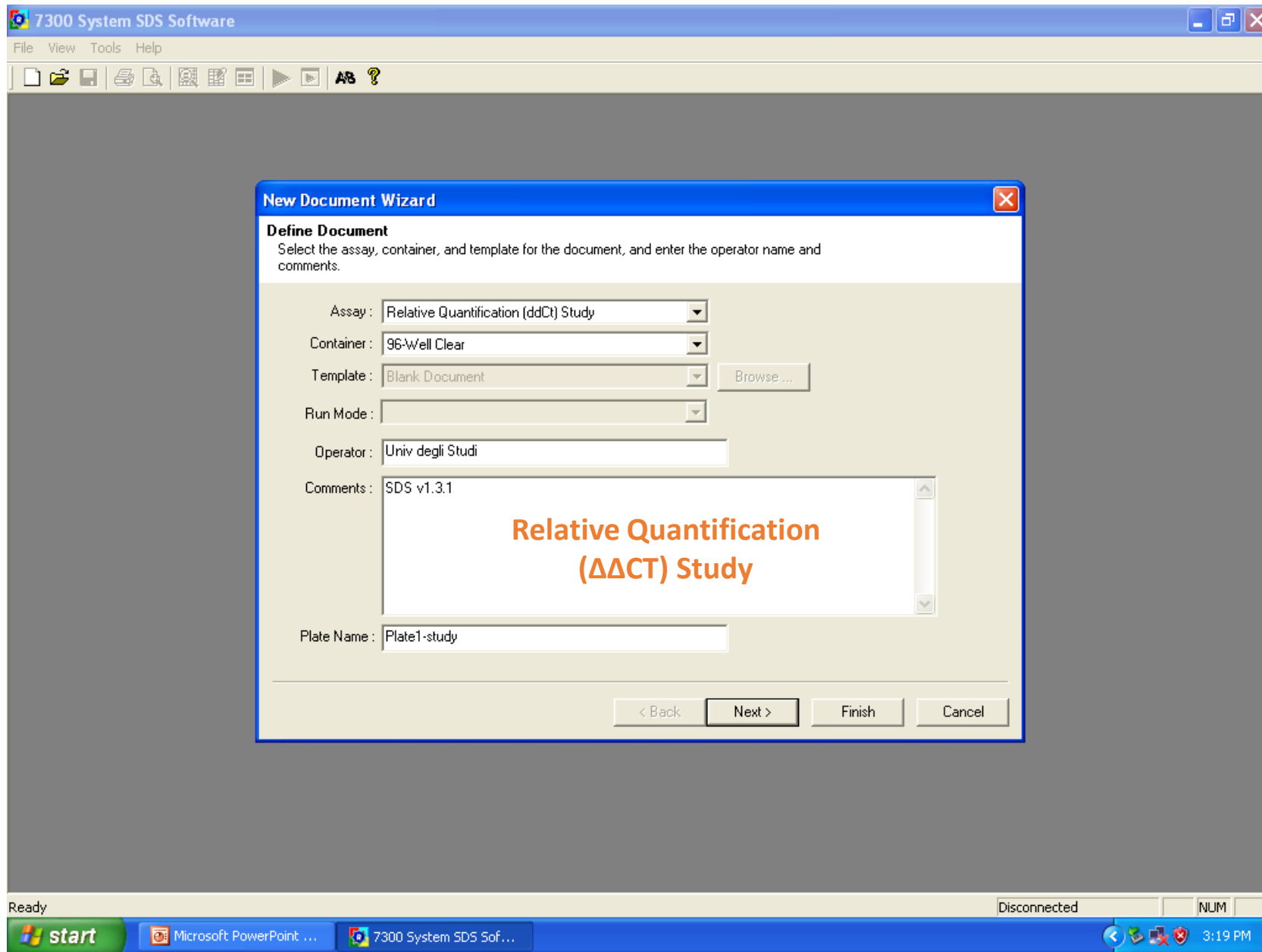


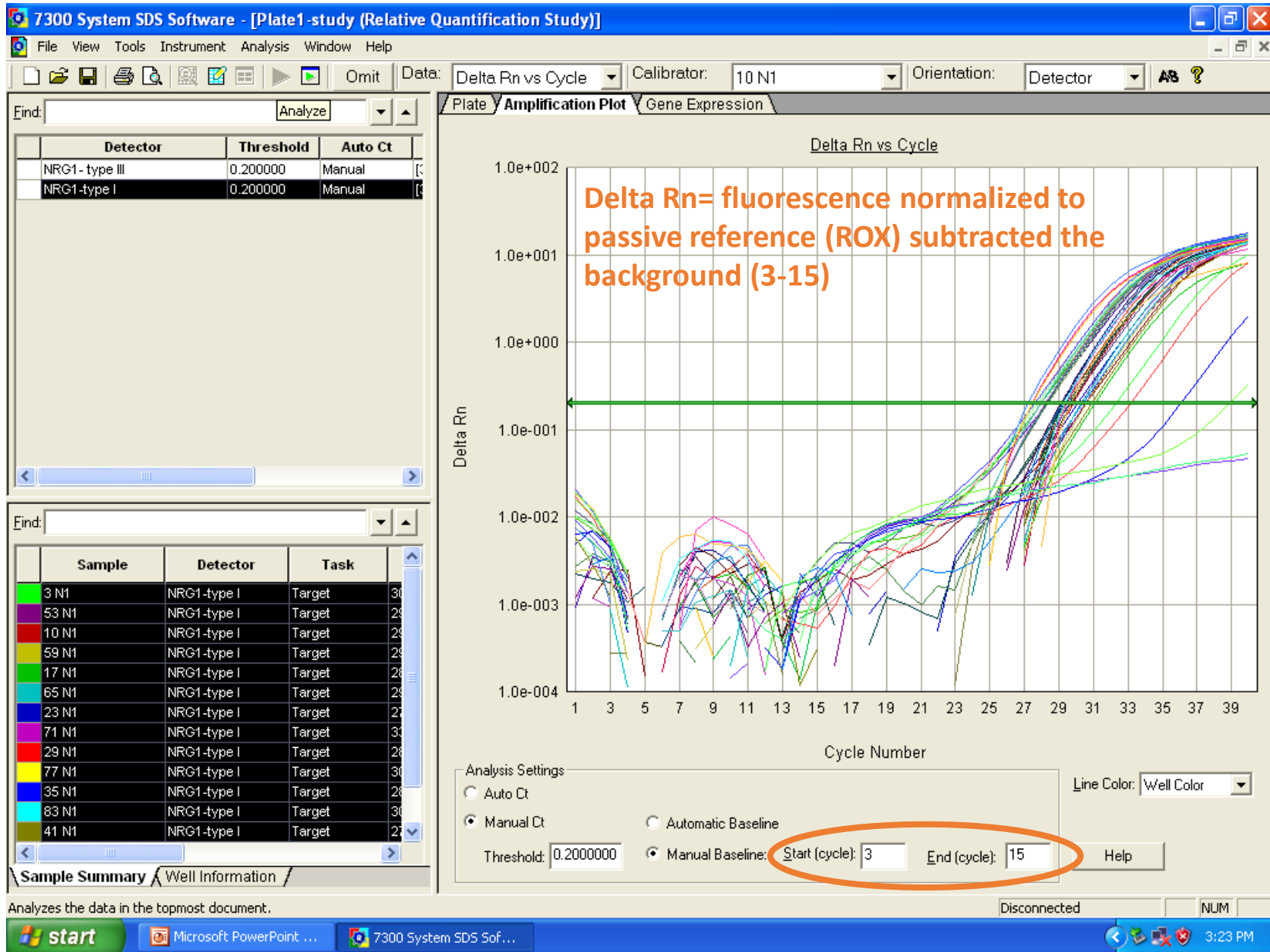












7300 System SDS Software - [Plate1-study (Relative Quantification Study)]

File View Tools Instrument Analysis Window Help

Omit Data: Delta Rn vs Cycle Calibrator: 10 N1 Orientation: Detector AS ?

Find: []

Detector	Threshold	Auto Ct	Baseline
NRG1-type III	0.200000	Manual	[6,14]
NRG1-type I	0.200000	Manual	[6,14]

CTR=water+mix= negative control

Undetectable or 39,045 Ok!!

Find: []

Plate	Well	Sample	Detector	Ct	Ct std err	Omit
NRG I-III	F3	35 N1	NRG1-type I	27.930	0.060	<input type="checkbox"/>
NRG I-III	F4	83 N1	NRG1-type I	30.235	0.103	<input type="checkbox"/>
NRG I-III	F5	83 N1	NRG1-type I	30.555	0.103	<input type="checkbox"/>
NRG I-III	F6	83 N1	NRG1-type I	30.258	0.103	<input type="checkbox"/>
NRG I-III	G1	41 N1	NRG1-type I	27.331	0.078	<input type="checkbox"/>
NRG I-III	G2	41 N1	NRG1-type I	27.428	0.078	<input type="checkbox"/>
NRG I-III	G3	41 N1	NRG1-type I	27.162	0.078	<input type="checkbox"/>
NRG I-III	G4	CTR N1	NRG1-type I	Undet.		<input type="checkbox"/>
NRG I-III	G5	CTR N1	NRG1-type I	39.045		<input type="checkbox"/>
NRG I-III	G6	CTR N1	NRG1-type I	Undet.		<input type="checkbox"/>
NRG I-III	H1	47 N1	NRG1-type I	29.320	0.080	<input type="checkbox"/>
NRG I-III	H2	47 N1	NRG1-type I	29.500	0.080	<input type="checkbox"/>
NRG I-III	H3	47 N1	NRG1-type I	29.227	0.080	<input type="checkbox"/>

Sample Summary Well Information

Ready Disconnected NUM

start Microsoft PowerPoint ... 7300 System SDS Sof... 3:30 PM

Plate Amplification Plot Gene Expression

Delta Rn vs Cycle

Delta Rn

Cycle Number

Analysis Settings

Auto Ct Manual Ct Automatic Baseline Manual Baseline

Threshold: 0.2000000 Start (cycle): 6 End (cycle): 14

Line Color: Well Color

Help

Microsoft Excel - NRG1-NRGIII.xls

File Modifica Visualizza Inserisci Formato Strumenti Dati Finestra ?

Digitare una domanda.

W30

	A	B	C	D	E	F	G	H	I	R	S	T	U	V	W	X
28	Endogeno															
29																
30	Plate	Well ID	Well	Sample	Detector	Task	Ct	Ct std err	Avg Ct	Threshold	Auto Ct	Baseline	Start	End		
31																
32	NRG I-III	7 A7	3 NIII	NRG1- typ	Target		33.119	0.293	32.588	0.2	Manual	Manual	7	15		
33	NRG I-III	8 A8	3 NIII	NRG1- typ	Target		32.539	0.293	32.588	0.2	Manual	Manual	7	15		
34	NRG I-III	9 A9	3 NIII	NRG1- typ	Target		32.107	0.293	32.588	0.2	Manual	Manual	7	15		
35	NRG I-III	10 A10	53 NIII	NRG1- typ	Target											
36	NRG I-III	11 A11	53 NIII	NRG1- typ	Target		32.749	0.225	32.975	0.2	Manual	Manual	7	15		
37	NRG I-III	12 A12	53 NIII	NRG1- typ	Target		33.2	0.225	32.975	0.2	Manual	Manual	7	15		
38	NRG I-III	19 B7	10 NIII	NRG1- typ	Target											
39	NRG I-III	20 B8	10 NIII	NRG1- typ	Target		31.587	0.118	31.705	0.2	Manual	Manual	7	15		
40	NRG I-III	21 B9	10 NIII	NRG1- typ	Target		31.824	0.118	31.705	0.2	Manual	Manual	7	15		
41	NRG I-III	22 B10	59 NIII	NRG1- typ	Target		32.801	0.127	32.937	0.2	Manual	Manual	7	15		
42	NRG I-III	23 B11	59 NIII	NRG1- typ	Target		33.19	0.127	32.937	0.2	Manual	Manual	7	15		
43	NRG I-III	24 B12	59 NIII	NRG1- typ	Target		32.82	0.127	32.937	0.2	Manual	Manual	7	15		
44	NRG I-III	31 C7	17 NIII	NRG1- typ	Target		32.753	0.022	32.732	0.2	Manual	Manual	7	15		
45	NRG I-III	32 C8	17 NIII	NRG1- typ	Target		32.71	0.022	32.732	0.2	Manual	Manual	7	15		
46	NRG I-III	33 C9	17 NIII	NRG1- typ	Target											
47	NRG I-III	34 C10	65 NIII	NRG1- typ	Target											
48	NRG I-III	35 C11	65 NIII	NRG1- typ	Target		33.647	0.151	33.798	0.2	Manual	Manual	7	15		
49	NRG I-III	36 C12	65 NIII	NRG1- typ	Target		33.949	0.151	33.798	0.2	Manual	Manual	7	15		
50	NRG I-III	43 D7	23 NIII	NRG1- typ	Target		33.543	0.083	33.586	0.2	Manual	Manual	7	15		
51	NRG I-III	44 D8	23 NIII	NRG1- typ	Target		33.468	0.083	33.586	0.2	Manual	Manual	7	15		
52	NRG I-III	45 D9	23 NIII	NRG1- typ	Target		33.747	0.083	33.586	0.2	Manual	Manual	7	15		
53	NRG I-III	46 D10	CTR NIII	NRG1- typ	Target	Undet.				0.2	Manual	Manual	7	15		
54	NRG I-III	47 D11	CTR NIII	NRG1- typ	Target	Undet.				0.2	Manual	Manual	7	15		
55	NRG I-III	48 D12	CTR NIII	NRG1- typ	Target	Undet.				0.2	Manual	Manual	7	15		
56	NRG I-III	55 E7	29 NIII	NRG1- typ	Target											
57	NRG I-III	56 E8	29 NIII	NRG1- typ	Target		34.482	0.314	34.796	0.2	Manual	Manual	7	15		
58	NRG I-III	57 E9	29 NIII	NRG1- typ	Target		35.109	0.314	34.796	0.2	Manual	Manual	7	15		
59	NRG I-III	58 E10	71 NIII	NRG1- typ	Target		34.093	0.32	34.413	0.2	Manual	Manual	7	15		
60	NRG I-III	59 E11	71 NIII	NRG1- typ	Target											
61	NRG I-III	60 E12	71 NIII	NRG1- typ	Target		34.733	0.32	34.413	0.2	Manual	Manual	7	15		
62	NRG I-III	67 F7	35 NIII	NRG1- typ	Target		34.249	0.296	33.786	0.2	Manual	Manual	7	15		

Pronto NUM

start Microsoft PowerPoin... 7300 System SDS So... NRG1-NRGIII.xls NRG1-NRGIII.csv D:\Applied Biosyste... 3:36 PM

1 - copy the Ct of the target gene and of the reference gene for calibrator and samples

	Ct-target gene	Ct-Reference gene
Calibrator	$Ct_{(target)C} = 25$	$Ct_{(reference)C} = 24$
Sample 1	$Ct_{(target)1} = 22$	$Ct_{(reference)1} = 23$
Sample 2	$Ct_{(target)2} = 23$	$Ct_{(reference)2} = 24$
Sample 3	$Ct_{(target)3} = 27$	$Ct_{(reference)3} = 23$

2 - normalize the Ct of the target gene to that of the reference gene for calibrator and samples, calculating the ΔCt

	Ct-target gene	Ct-Reference gene	ΔCt
Calibrator	$Ct_{(target)C} = 25$	$Ct_{(reference)C} = 24$	$\Delta Ct_C = Ct_{(target)C} - Ct_{(reference)C} = 1$
Sample 1	$Ct_{(target)1} = 22$	$Ct_{(reference)1} = 23$	$\Delta Ct_1 = Ct_{(target)1} - Ct_{(reference)1} = -1$
Sample 2	$Ct_{(target)2} = 23$	$Ct_{(reference)2} = 24$	$\Delta Ct_2 = Ct_{(target)2} - Ct_{(reference)2} = -1$
Sample 3	$Ct_{(target)3} = 27$	$Ct_{(reference)3} = 23$	$\Delta Ct_3 = Ct_{(target)3} - Ct_{(reference)3} = 4$

3 - normalize the ΔCt of the samples to the ΔCt of calibrator, calculating the $\Delta\Delta Ct$

	$\Delta\Delta Ct$	$-\Delta\Delta Ct$	$2^{-\Delta\Delta Ct}$
Calibrator	$\Delta\Delta Ct_C = \Delta Ct_C - \Delta Ct_C = 1 - 1 = 0$	0	$2^{-\Delta\Delta Ct_C} = 2^0 = 1$
Sample 1	$\Delta\Delta Ct_1 = \Delta Ct_1 - \Delta Ct_C = -1 - 1 = -2$	2	$2^{-\Delta\Delta Ct_1} = 2^2 = 4$
Sample 2	$\Delta\Delta Ct_2 = \Delta Ct_2 - \Delta Ct_C = -1 - 1 = -2$	2	$2^{-\Delta\Delta Ct_2} = 2^2 = 4$
Sample 3	$\Delta\Delta Ct_3 = \Delta Ct_3 - \Delta Ct_C = 4 - 1 = 3$	-3	$2^{-\Delta\Delta Ct_3} = 2^{-3} = 0,125$

4 - finally, calculate the normalized relative quantification = $2^{-\Delta\Delta Ct}$



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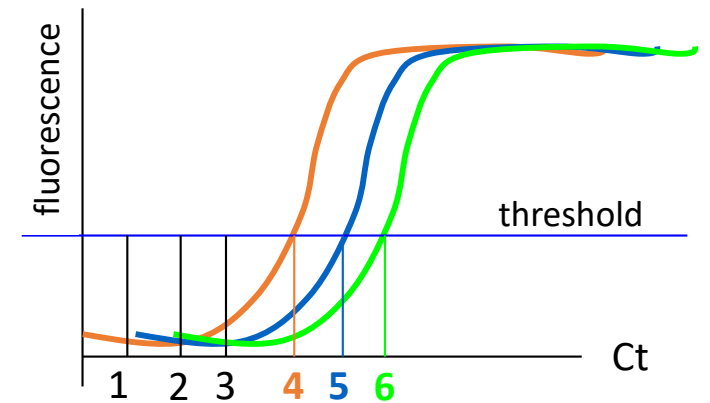
Biotechnology Project Lab

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& Isabella Tarulli

The lecture of November 28th 2021 is about to begin....

- summary of the previous lesson
- quantitative real time PCR (qRT-PCR-26-11-2021)
- example of qRT-PCR data analysis
- **exercize with qRT-PCR data (Excel files)**

cycle	Sample A (calibrator)	Sample B	Sample C
0	2	4	8
1	4	8	16
2	8	16	32
3	16	32	64
4	32	64	128
5	64	128	256
6	128	256	512



- If the detectable amount of DNA is **128**
- the Ct value for sample A will be 6,
- the Ct value for sample B will be 5,
- the Ct value for sample C will be 4

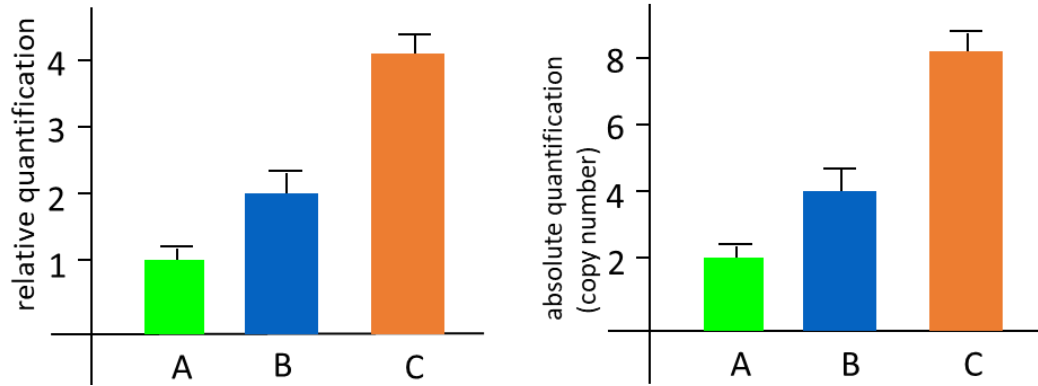
The logarithm of a number is the exponent to which another number, the base, must be raised to produce that number.

At each cycle, during the exponential phase, the DNA doubles

Ct is the number of amplification cycles necessary to obtain a detectable amount of DNA ->

Ct are base 2 logarithms.

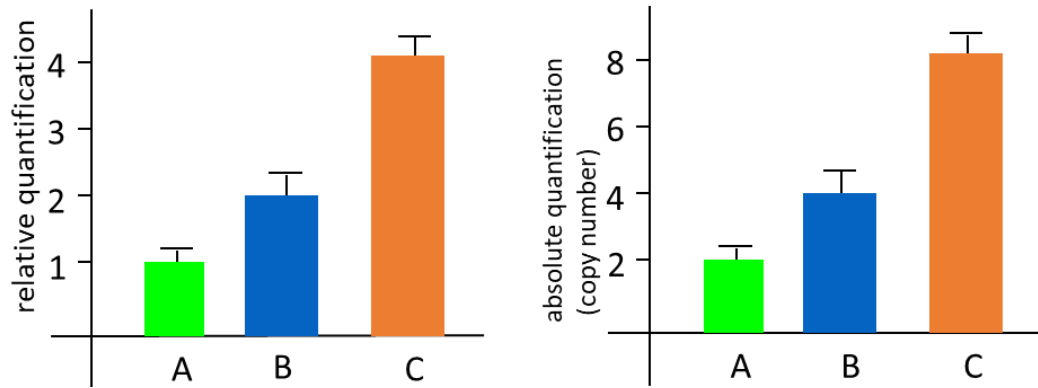
- if the starting material is low, you will need many amplification cycles (Ct high),
- if the starting material is high, you will need less amplification cycles (Ct low).



If calibrator is B, which will be relative expression of A and C?

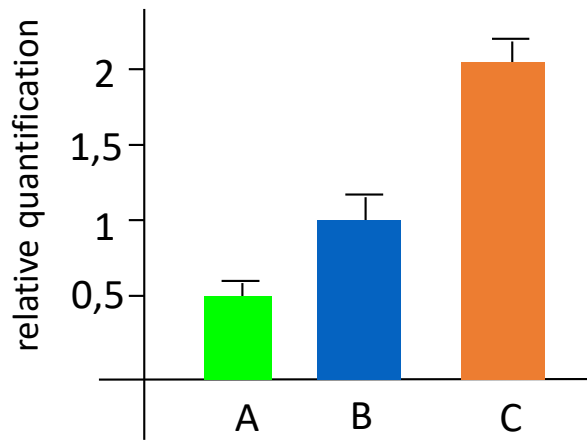
cycle	Sample A (calibrator)	Sample B	Sample C
0	2	4	8
1	4	8	16
2	8	16	32
3	16	32	64
4	32	64	128
5	64	128	256
6	128	256	512

If calibrator is C, which will be relative expression of A and B?

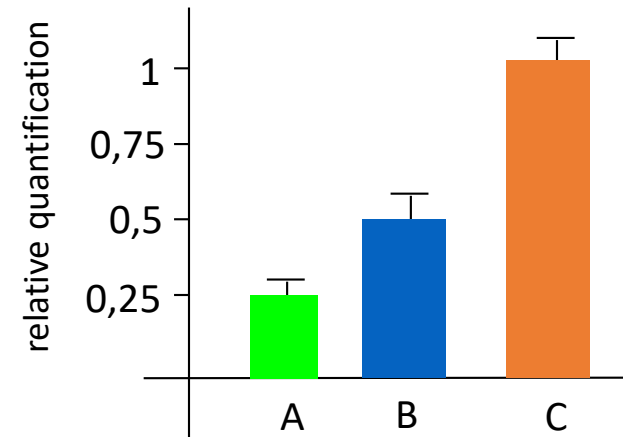


cycle	Sample A (calibrator)	Sample B	Sample C
0	2	4	8
1	4	8	16
2	8	16	32
3	16	32	64
4	32	64	128
5	64	128	256
6	128	256	512

If calibrator is B, which will be relative expression of A and C?



If calibrator is C, which will be relative expression of A and B?





Ct meaning

- how does Ct change when you dilute your sample?
- how does Ct change when you have different copy numbers?

If the CT of my calibrator is 18,

Which will be the CT if

- I dilute it 2 fold? 10 fold?
 - I dilute it 4 fold? 100 fold?
 - I dilute it 8 fold? 1000 fold?
 - I dilute it 16 fold? 10000 fold?
- ($\log_2 10 = 3.322$)

If the CT of my calibrator is 20

- Which will be the CT of a sample in which the gene expression is 2 fold?
- Which will be the CT of a sample in which the gene expression is 4 fold?
- Which will be the CT of a sample in which the gene expression is 8 fold?
- Which will be the CT of a sample in which the gene expression is 16 fold?

- Which will be the CT of a sample in which the gene expression is $1/2$? (=0,5)?
- Which will be the CT of a sample in which the gene expression is $1/4$ (=0,25)?
- Which will be the CT of a sample in which the gene expression is $1/8$ (=0,125)?
- Which will be the CT of a sample in which the gene expression is $1/16$ (=0,0625)?

If the CT of my calibrator is **18**,

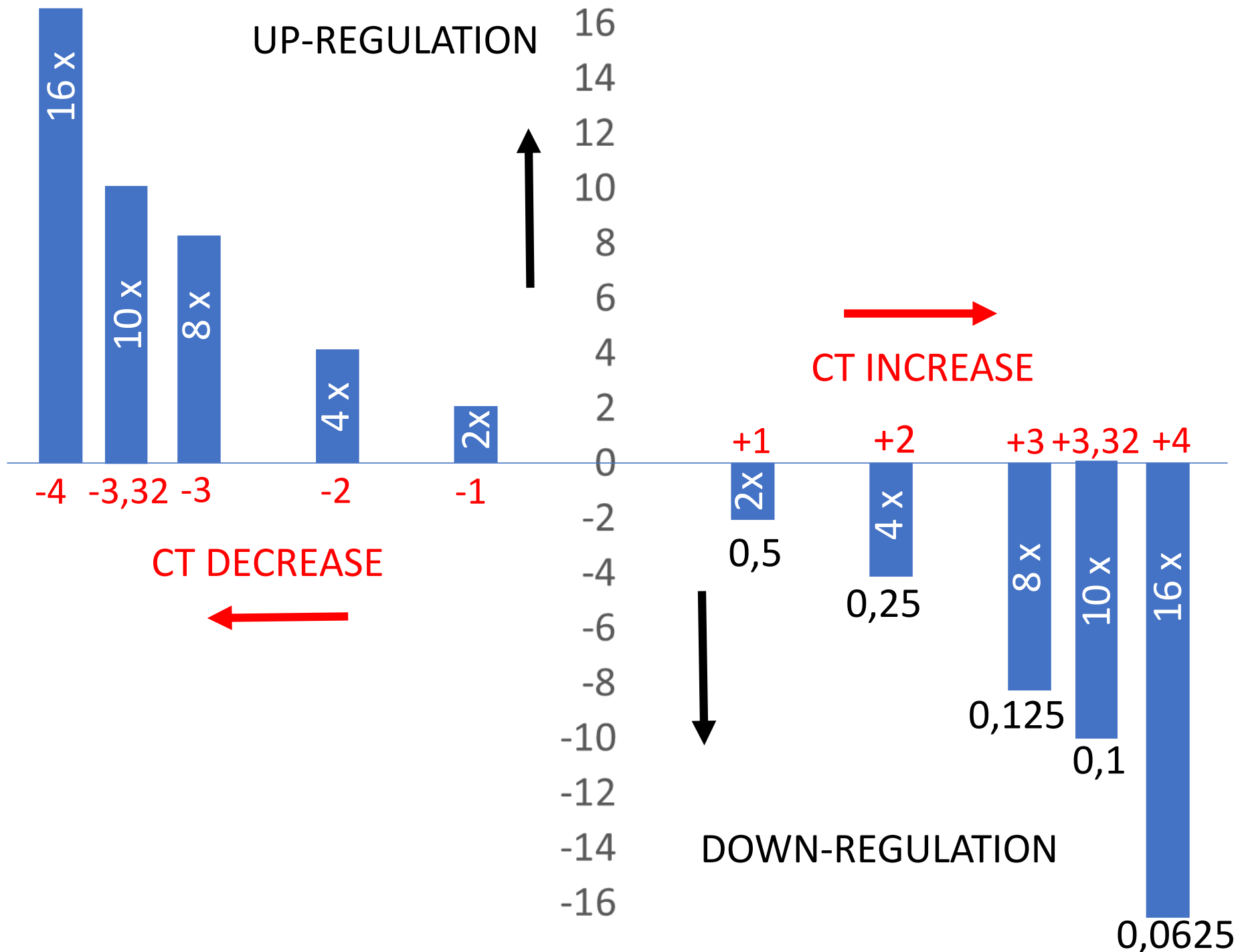
Which will be the CT if

- I dilute it 2 fold? **19**
 - I dilute it 4 fold? **20**
 - I dilute it 8 fold? **21**
 - I dilute it 16 fold? **22**
- 10 fold? **21,322**
 - 100 fold? **24,633**
 - 1000 fold? **27,966**
 - 10000 fold? **31,288**

($\log_2 10 = 3.322$)

If the CT of my calibrator is **20**

- Which will be the CT of a sample in which the gene expression is 2 fold? **19**
 - Which will be the CT of a sample in which the gene expression is 4 fold? **18**
 - Which will be the CT of a sample in which the gene expression is 8 fold? **17**
 - Which will be the CT of a sample in which the gene expression is 16 fold? **16**
-
- Which will be the CT of a sample in which the gene expression is 1/2 (=0,5)? **21**
 - Which will be the CT of a sample in which the gene expression is 1/4 (=0,25)? **22**
 - Which will be the CT of a sample in which the gene expression is 1/8 (=0,125)? **23**
 - Which will be the CT of a sample in which the gene expression is 1/16 (=0,0625)? **24**





Exercise with qRT-PCR data (Excel files)

- Please, prepare an expression graphic for soluble NRG1 & ErbB2 expression, like in the following examples focused on ErbB3
- If you need help, I will show you how to carry out CT analysis & graphic preparation

	strain	age	sample number	CT soluble NRG1	CT ErbB2	CT HKG	
4	WT	P3	59.55	31,393	22,62	24,33	
5			59.57	30,725	22,33	24,23	
6			59.59	30,416	22,33	24,09	
7		P16	59.67	29,293	23,83	24,68	
8			59.68	29,415	23,7	25,06	
9			59.69	28,97	23,51	24,63	
10		1 month	59.73	31,263	25,25	25,32	
11			59.74	30,977	25,96	25,74	
12			59.75	30,649	24,72	25,24	
13		2 months	59.79	32,22	27,13	27,12	
14			59.80	32,027	27,82	26,7	
15			59.81	33,01	28,12	27,41	
16		CMT1A +/-	P3	59.61	30,658	22,87	24,69
17	59.63			30,221	22,41	24,14	
18	59.65			29,808	22,3	23,99	
19	P16		59.70	25,753	22,6	24,65	
20			59.71	25,477	23,75	24,59	
21			59.72	25,852	23,02	24,79	
22	1 month		59.76	25,096	23,86	24,65	
23			59.77	25,851	24,08	24,74	
24			59.78	25,588	24,83	25,05	
25	2 months		59.82	26,295	25,57	26,2	
26		59.83	27,057	26,04	26,19		
27				soluble NRG1	ErbB2	ErbB3	HKG

	B	C	D	E	F	G	H	I	J	K	L
4	strain	age	sample number	CT ErbB3	CT HKG	Δ CT	$\Delta\Delta$ CT	$-\Delta\Delta$ CT	$2^{-\Delta\Delta$ Ct	average	standard deviation
5	WT	P3	59.55	20,115	24,33	-4,219	0,218	-0,218	0,85975649	1,07189	0,5081638
6			59.57	19,072	24,23	-5,161	-0,724	0,724	1,65175533		
7			59.59	20,155	24,09	-3,931	0,506	-0,506	0,70417211		
8		P16	59.67	20,933	24,68	-3,748	0,689	-0,689	0,62028365	0,70646	0,1885933
9			59.68	21,418	25,06	-3,642	0,795	-0,795	0,57634317		
10			59.69	20,309	24,63	-4,321	0,116	-0,116	0,92274249		
11		1 month	59.73	22,639	25,32	-2,678	1,759	-1,759	0,29545289	0,44461	0,2981065
12			59.74	23,296	25,74	-2,44	1,997	-1,997	0,2505204		
13			59.75	21,15	25,24	-4,093	0,344	-0,344	0,78785389		
14		2 months	59.79	24,729	27,12	-2,392	2,045	-2,045	0,24232245	0,23037	0,0399401
15			59.80	24,694	26,7	-2,009	2,428	-2,428	0,18582287		
16			59.81	24,899	27,41	-2,51	1,927	-1,927	0,26297544		
17	CMT1A	P3	59.61	20,242	24,69	-4,44567	-0,009	0,00867	1,00602768	0,97079	0,0756747
18			59.63	19,881	24,14	-4,259	0,178	-0,178	0,88392753		
19			59.65	19,524	23,99	-4,469	-0,032	0,032	1,02242853		
20		P16	59.70	20,628	24,65	-4,025	0,412	-0,412	0,75158074	0,68878	0,1222355
21			59.71	20,54	24,59	-4,054	0,383	-0,383	0,76684133		
22			59.72	21,218	24,79	-3,569	0,868	-0,868	0,54790588		
23		1 month	59.76	20,988	24,65	-3,664	0,773	-0,773	0,58519932	0,71455	0,2651889
24			59.77	20,279	24,74	-4,465	-0,028	0,028	1,01959768		
25			59.78	21,502	25,05	-3,545	0,892	-0,892	0,53886657		
26		2 months	59.82	22,956	26,2	-3,243	1,194	-1,194	0,43708931	0,46516	0,1945434
27			59.83	22,323	26,19	-3,864	0,573	-0,573	0,6722175		
28			59.84	23,591	26,22	-2,632	1,805	-1,805	0,28618104		

soluble NRG1

ErbB2

ErbB3

HKG



