

2027-05-07 · 80 minutes

pGLO plate observations and gel analysis

Your goal: Record observations from the approved pGLO plates after overnight incubation, then analyze the supplied gel evidence. Use clearly labeled invented practice if plates or authentic images are unavailable.

One product: One plate-observation and gel-analysis record: actual pGLO condition labels, count or uncountable-growth description, fluorescence and status; then ladder distances, a standard curve, sample-size estimates and a conclusion about pattern consistency with an identity limit. Keep any invented fallback separately labeled within that same record.

Question: When do estimated band sizes fit a supplied pattern, and why does that not confirm DNA identity?

Start the work

Prior Thursday May 6 teaching inputs are supplied in full. Student completion, actual photograph, measured distances and laboratory approval remain unverified.

1. Friday May 7 pGLO read: the teacher provides the closed plates prepared Thursday May 6 and incubated overnight at 37°C under the approved Bio-Rad kit SOP. Record each actual plate label, count or uncountable-growth description and fluorescence observation under the teacher's approved viewing setup. Wear UV-protective eyewear or view through a UV-blocking shield, and never look directly at the UV lamp. Never reopen plates. Keep growth and fluorescence as different observations; arabinose-induced GFP expression is not the antibiotic selection step. If plates are absent or failed, record that status and use C1 from May 6 as explicitly invented practice, not replacement observations. Then analyze the assigned authentic gel image or the D1 nominal fallback. A band pattern does not prove plasmid identity. A self-contained count fallback is C1: positive comparison $P=12$, negative comparison $N=0$, sample $S=8$. These invented role labels are not pGLO plate identities or evidence that any kit worked.
2. Paper analysis only. Use supplied nominal records, not actual measurements. Do not perform or design a biological experiment. A matching band-size pattern cannot confirm plasmid or sequence identity. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending. Step: Build a standard curve relating distance to fragment size.

3. Paper analysis only. Use supplied nominal records, not actual measurements. Do not perform or design a biological experiment. A matching band-size pattern cannot confirm plasmid or sequence identity. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending. Step: Estimate the size of each sample band from the curve.
4. Paper analysis only. Use supplied nominal records, not actual measurements. Do not perform or design a biological experiment. A matching band-size pattern cannot confirm plasmid or sequence identity. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending. Step: Compare estimated sizes to the expected restriction map.
5. Paper analysis only. Use supplied nominal records, not actual measurements. Do not perform or design a biological experiment. A matching band-size pattern cannot confirm plasmid or sequence identity. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending. Step: Conclude whether the plasmid matches the predicted construct.

Paper analysis only. Use supplied nominal records, not actual measurements. Do not perform or design a biological experiment. A matching band-size pattern cannot confirm plasmid or sequence identity. Save the same analysis record with missing input, next action and receipt pending.

Words you will use

nominal

Assigned teaching value, not a new measurement.

lane

Labeled column of the supplied band diagram.

band

Drawn mark at a stated nominal position.

ladder

Reference set of known DNA fragment lengths.

migration distance

Distance from the declared origin to band center, nominal here.

origin

Common reference line labeled 0 mm.

millimeter

Length unit abbreviated mm, used here for migration distance.

base pair

Pair of complementary DNA bases; bp also counts fragment length.

bp

Abbreviation for base pair.

fragment size

DNA length in bp, different from distance in mm.

linear DNA

DNA with two ends rather than a circular form.

double-stranded DNA

DNA containing two paired strands.

topology

Molecular form, such as linear or circular.

standard curve

Reference relation used to estimate an unknown value within its stated domain.

base-10 logarithm

Exponent to which 10 is raised to obtain a positive number.

exponent

Number indicating a power, as 3 in 10 cubed.

inverse

Operation that reverses another; 10 to a power reverses log10.

log space

Scale on which values are logarithms instead of original sizes.

interpolation

Estimate between reference points within their domain.

extrapolation

Estimate beyond the reference range; not allowed here.

domain

Input range where the stated model applies.

midpoint

Position halfway between two reference positions.

rounding

Reporting a value at a stated precision.

nearest 10

Closest multiple of ten, using the stated halfway rule.

estimate

Value inferred through a declared model, not a direct identity measurement.

expected pattern

Supplied comparison lengths and band count, not proof of a construct.

tolerance

Declared allowed difference for comparison; not measured uncertainty here.

inclusive

Including the stated endpoints.

pattern consistency

Agreement with all stated pattern rules; not confirmation of identity.

sequence identity

Exact order of DNA bases; not established by size alone.

construct

An engineered DNA arrangement; none is designed or identified here.

restriction map

Description of positions where specified enzymes cut DNA; no real map is supplied here.

gene orientation

Direction of a gene within DNA, not determined by these sizes.

limitation

Evidence boundary restricting a conclusion.

uncertainty

What the supplied information cannot settle.

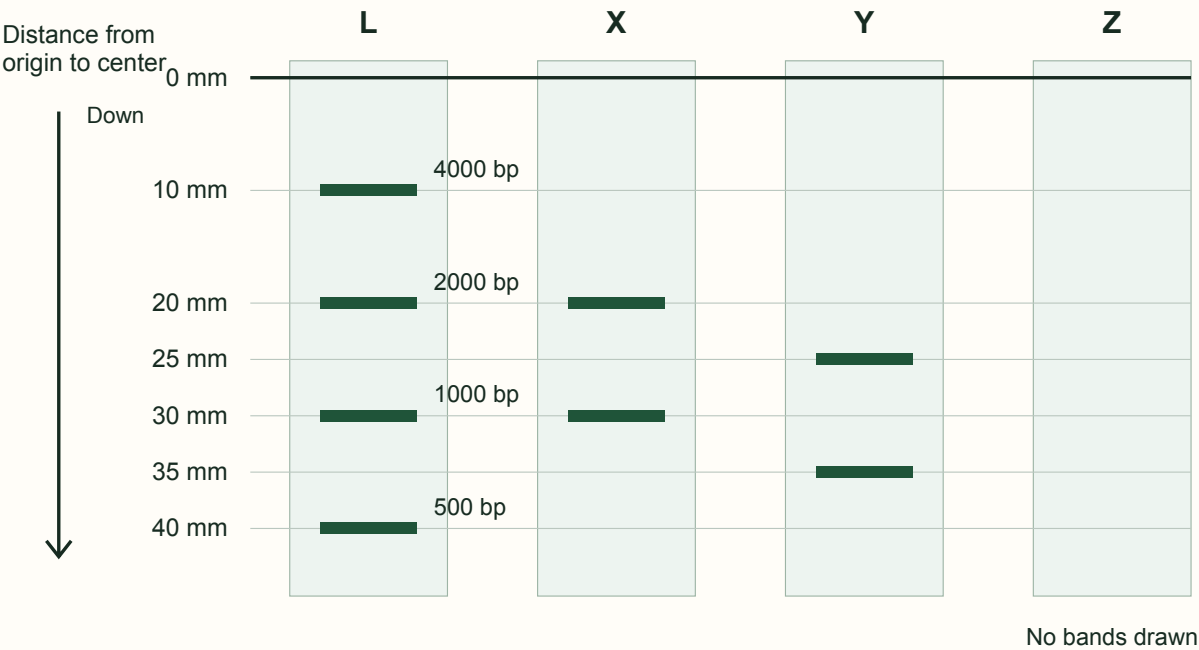
receipt

Evidence that work reached its confirmed destination.

Approved nominal band reference

Supplied band record: BI-GEL-PAPER-01

Original idealized linear-DNA schematic. Not a photograph or actual measurement.
Distances are nominal labels. Do not measure the printed page with a ruler.



L = known-size ladder; X and Y = abstract sample labels; Z = blank comparison lane.
D1 gives every value in text. Actual records replace practice; authentic photograph remains pending.

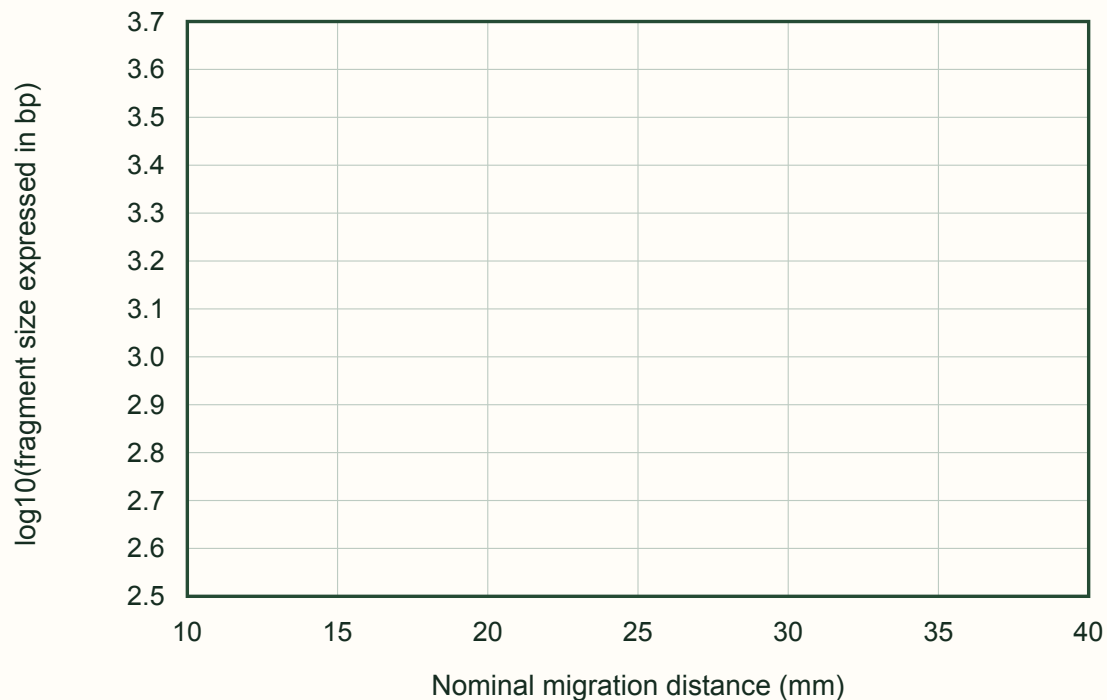
Original idealized teaching figure, not actual data. Full text values and rule are supplied. Actual approved inputs replace practice; complete one assigned graph.

Text description: D1 gives L at 10/20/30/40 mm with 4000/2000/1000/500 bp, X 20/30, Y 25/35 and Z no bands; common origin 0.

Blank standard-curve response

One standard curve: original paper response

Original idealized linear-DNA teaching record. No actual measured calibration.



Plot four ladder points from G1. Domain 10–40 mm; do not extend the line beyond it.

Actual approved inputs replace practice. Text tables and rules supply a full equivalent.

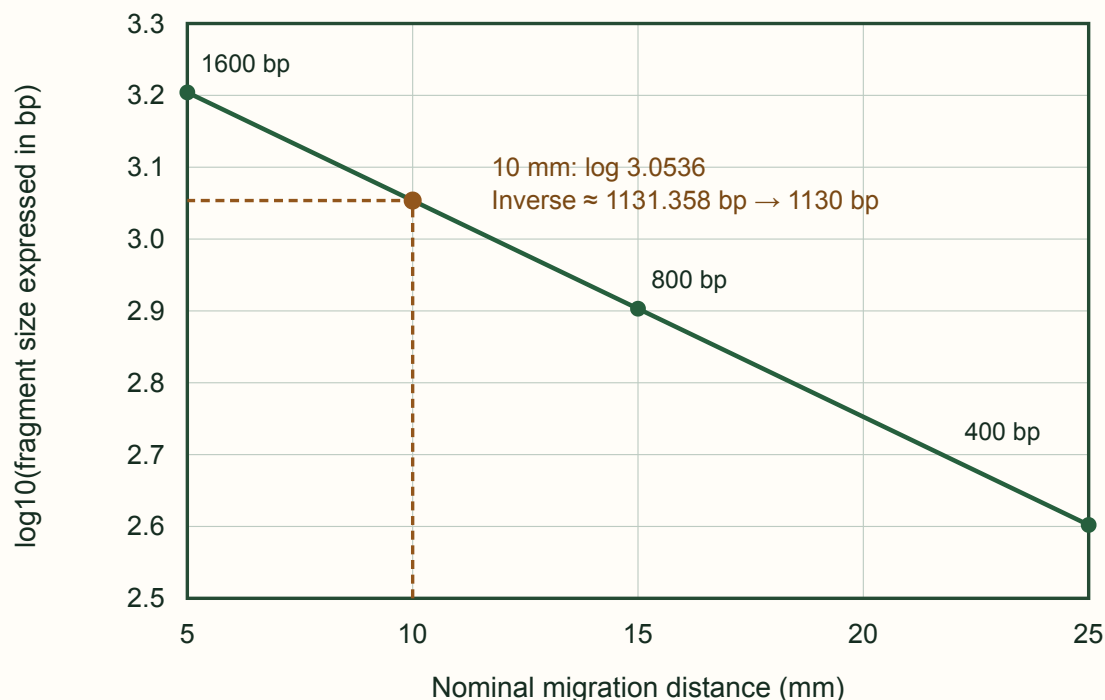
Original idealized teaching figure, not actual data. Full text values and rule are supplied. Actual approved inputs replace practice; complete one assigned graph.

Text description: G1 gives x range 10–40 mm and y range 2.5–3.7 $\log_{10}$ size, four reference points and full plotting rules.

Distinct worked model graph

M1: distinct worked mathematical model

Original idealized linear-DNA teaching record. No actual measured calibration.



Model domain 5–25 mm. Do not submit this model as the assigned graph.

Actual approved inputs replace practice. Text tables and rules supply a full equivalent.

Original idealized teaching figure, not actual data. Full text values and rule are supplied. Actual approved inputs replace practice; complete one assigned graph.

Text description: M1 supplies three reference points at 5/15/25 mm and the 10-mm midpoint calculation, inverse 1131.358 bp and rounded 1130 bp.

H1: Distance is not identity

Friday May 7 pGLO read: the teacher provides the closed plates prepared Thursday May 6 and incubated overnight at 37°C under the approved Bio-Rad kit SOP. Record each actual plate label, count or uncountable-growth description and fluorescence observation under the teacher's approved viewing setup. Wear UV-protective eyewear or view through a UV-blocking shield, and never look directly at the UV lamp. Never reopen plates. Keep growth and fluorescence as different observations; arabinose-induced GFP expression is not the antibiotic selection step. If plates are absent or failed, record that status and use C1 from May 6 as explicitly invented practice, not replacement observations. Then analyze the assigned authentic gel image or the D1 nominal fallback. A band pattern does not prove

plasmid identity. A self-contained count fallback is C1: positive comparison P=12, negative comparison N=0, sample S=8. These invented role labels are not pGLO plate identities or evidence that any kit worked.

Opening input: in this idealized linear-DNA comparison, shorter fragments travel farther through the same gel than longer ones. NHGRI explains this size-separation principle. At 8–10, after the plate-record stage, state why a farther band would suggest a smaller fragment in this model, not a known sequence. One short answer is enough. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Today is Friday May 7. The May 6 source record is supplied again in full; no prior student completion, actual gel photograph or experiment is assumed. The next listed class is Monday May 10. Start S1 status marks during work and update changes only.

D1: The complete May 6 teaching record

BI-GEL-PAPER-01 is the same original fictional record supplied for May 6. It represents idealized linear double-stranded DNA, not an actual gel photograph, restriction map or construct. Lane order from left to right is L, X, Y, Z. L is the known-size ladder; X and Y are abstract sample labels; Z is a blank comparison lane.

The top reference line is the common origin, 0 mm. Nominal distance increases downward to each drawn band's center. Values are whole millimeters supplied by the author, not measurements students made. Do not measure the printed page. No actual measurement uncertainty is supplied.

Complete ladder: L1 at 10 mm is 4000 bp; L2 at 20 mm is 2000 bp; L3 at 30 mm is 1000 bp; L4 at 40 mm is 500 bp. Base pairs, abbreviated bp, count DNA length. Millimeters, abbreviated mm, give migration distance. They are different quantities.

Complete samples: X1 at 20 mm; X2 at 30 mm; Y1 at 25 mm; Y2 at 35 mm. Z has no bands drawn. Keep that statement; do not create a zero-mm band or take a logarithm of zero. No band drawn is not proof that DNA or contamination is absent.

Full text alternative to the reference image: L has four centers at 10/20/30/40 mm; X has two at 20/30 mm; Y has two at 25/35 mm; Z has none. Each lane begins at the same top 0-mm line. At 5–20 record the four ladder rows with distance, known size and supplied log value from G1. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

G1: One standard curve with a complete log lookup

At 20–40 make one standard curve in the same analysis record. A base-10 logarithm is the exponent that produces a number when 10 is raised to that power. For example, $\log_{10}(1000)=3$ because 10 cubed is 1000. Logs require positive input; Z is not a zero-sized fragment.

Use these supplied numerical values, to four decimal places: 4000 bp $\rightarrow$ 3.6021; 2000 bp $\rightarrow$ 3.3010; 1000 bp $\rightarrow$ 3.0000; 500 bp $\rightarrow$ 2.6990. No calculator or outside log table is required. Do not round these logs further before interpolation.

Horizontal axis: Nominal migration distance (mm), from 10 through 40 with ticks every 5. Vertical axis: $\log_{10}(\text{fragment size expressed in bp})$, from 2.5 through 3.7 with ticks every 0.1. The supplied blank grid includes those labels. This line graph covers a defined interval; neither axis must start at zero.

Plot the four ladder points (10,3.6021), (20,3.3010), (30,3.0000), (40,2.6990). Draw the idealized straight trend through the points; four-decimal lookup rounding may produce tiny differences. Caption: Original idealized linear-DNA teaching record, not measured calibration. Do not add error bars or invent repeats.

The model applies only from 10 to 40 mm, including both ends. Do not extend it beyond that range. A 45-mm band would be not estimable by this rule. The full-precision relation behind these supplied positions is $\text{size}(\text{bp})=4000 \times 2^{-(\text{distance_mm}-10)/10}$. This is an authored math rule, not a universal gel law. Use P1's supplied lookup route instead of calculating powers if preferred. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

P1: Interpolate in log space, then convert back

At 40–55 estimate all four X/Y bands. A sample at a listed ladder distance uses that point's log value. For a position halfway between adjacent ladder distances, average the two log values, not the two bp sizes. Both Y positions are midpoints. Record each selected or interpolated log before converting back.

The inverse of $\log_{10}$ is 10 raised to the log value. Complete lookup, log $\rightarrow$ approximate bp: 3.6021 $\rightarrow$ 4000.369; 3.4515 $\rightarrow$ 2828.134; 3.3515 $\rightarrow$ 2246.467; 3.3010 $\rightarrow$ 1999.862; 3.2505 $\rightarrow$ 1780.328; 3.1515 $\rightarrow$ 1417.425; 3.1505 $\rightarrow$ 1414.165; 3.1495 $\rightarrow$ 1410.912; 3.0505 $\rightarrow$ 1123.311; 3.0000 $\rightarrow$ 1000.000; 2.9495 $\rightarrow$ 890.225; 2.8505 $\rightarrow$ 708.761; 2.8495 $\rightarrow$ 707.131; 2.8485 $\rightarrow$ 705.505; 2.7495 $\rightarrow$ 561.694; 2.6990 $\rightarrow$ 500.035. These values cover every required sample and reference. No outside tool is needed.

Round only the final size to the nearest 10 bp. For this positive-number rule, a value below the halfway point rounds down; at or above it rounds up. Example unrelated to the record: 1234 rounds to 1230 and 1235 rounds to 1240. Keep the log and inverse value visible so the estimate is traceable.

Use columns lane/band, nominal mm, selected or interpolated log, inverse bp, and final rounded bp. Make four sample rows, X1/X2/Y1/Y2, plus Z saying no bands drawn and no size estimated. A hand-drawn line can be imprecise; use the supplied numerical midpoint rule for the final answer. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

T1: Complete fictional expected pattern and comparison rule

At 55–70 compare every sample lane with teaching pattern T. T has exactly two bands, expected sizes 2000 bp and 1000 bp, ordered from larger to smaller. No real restriction-map prediction is supplied, so this abstract length pattern stands in for one during practice. It is not a DNA sequence, real construct or designed restriction map.

Declared rule: the band count must match, and each final rounded estimate must be within 5% of its corresponding expected size. This is a classroom comparison convention, not measured error, a confidence interval or a validated identity test. The bounds are supplied: larger band 1900–2100 bp; smaller band 950–1050 bp, inclusive.

Sort each lane's estimated sizes from larger to smaller. Compare X and Y to both bounds and check their band counts. Compare Z's no-band state with T's two-band requirement. An extra or missing band fails the stated pattern rule; do not ignore one to make a match.

Write one short conclusion in the same record. State each lane's consistency or inconsistency with T under this rule. Cite its estimates or missing-band state, and give one evidence limit. Pattern consistency does not confirm plasmid identity, sequence or gene orientation. Do not describe an actual restriction digest or transformation as successful.

One useful limit is the idealized linear-DNA assumption. This supplied mapping is not validated for a real circular or other-shaped DNA molecule. Topology means molecular form, such as linear versus circular. Another limit is that different sequences can have the same length; a size pattern alone does not identify sequence. No new experiment is requested. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Q1: Check one analysis record

At 70–80 check the same ladder table, graph, four estimates, Z statement and conclusion. Verify axis labels and ranges, base 10, midpoint logs, inverse conversion and final nearest-10 rounding. Verify that all lanes were considered and the conclusion says pattern consistency rather than identity confirmation.

Correct a real discrepancy or note one verified match. If a peer truly comments, record that genuine deidentified comment; otherwise mark self review. Do not invent a mistake, actual gel observation or completed earlier lab. The final sentence restates the same conclusion, not a second report. Actual

route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

S1: Preserve genuine status

Track ten short statuses: 1 teacher acceptance and genuine data/reference; 2 real rubric and expected pattern; 3 actual photograph and measured distances; 4 genuine prior laboratory work and approval. Also track 5 real sequence/identity evidence; 6 actual peer participation; 7 enrolled task/access/completion; 8 confirmed destination/deadline; 9 saved analysis; 10 genuine receipt. Mark completed, pending or not checked with an evidence pointer or missing input.

The pGLO manufacturer SOP is linked for the approved plate route. No authentic gel, restriction map, sequence, gel SOP, photograph or measured band distances are supplied here; those remain separate teacher inputs. The nominal analysis does not complete those obligations. Ask your teacher whether myPLTW Project 6.1.2 applies today and where to stop; paper practice does not complete that portfolio milestone.

Open the linked BI assignment in Turn in your work. If blocked, save the same analysis with missing input, next action and receipt pending. Monday May 10 is the next date; no actual lab completion is carried forward. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

M1: Complete distinct log-space model

Optional distinct mathematical model, not a second task. Another invented linear-DNA ladder has 1600 bp at 5 mm, 800 bp at 15 mm and 400 bp at 25 mm. Its log₁₀ values are 3.2041, 2.9031 and 2.6021. One sample is at 10 mm. Nominal distance uses the same top origin, 0 mm; valid model range is 5–25 mm.

M1 graph is fully plotted. Horizontal axis is nominal distance, 5–25 mm, ticks every 5. Vertical axis is log₁₀(size expressed in bp), 2.5–3.3, ticks every 0.1. Points are (5,3.2041), (15,2.9031), (25,2.6021), joined by the idealized line. The marked 10-mm sample lies halfway between the first two references.

Worked calculation: $(3.2041 + 2.9031)/2 = 3.0536$. Supplied inverse: $10^{3.0536} \approx 1131.358$ bp. Round to the nearest 10 bp: 1130 bp. Averaging 1600 and 800 directly would give 1200 bp and is not this log-space rule.

Complete model expectation: one band of 1100 bp, with a declared 5% teaching interval of 1045–1155 bp. The one 1130-bp estimate lies inside that interval, so its pattern is consistent under that convention. Identity is not confirmed. No real DNA molecule or experiment was observed. Self-check: midpoint was taken in log space and inverse applied before rounding. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Try the decision

Original route: suppose a lane's estimated sizes fit T. What does that support? Actual route: use the genuine comparison and limits.

- The size pattern is consistent under this rule; identity remains unconfirmed.
- Matching the estimated sizes confirms the plasmid sequence, without further identity evidence.
- Prior transformation must have succeeded because the estimated sizes fit T.

Explain your choice using the reading. Discuss it or say it to yourself. This practice does not add another submission.

Your 80-minute flow

0–10 minutes	Friday May 7 pGLO read: the teacher provides the closed plates prepared Thursday May 6 and incubated overnight at 37°C under the approved Bio-Rad kit SOP. Record each actual plate label, count or uncountable-growth description and fluorescence observation under the teacher's approved viewing setup. Wear UV-protective eyewear or view through a UV-blocking shield, and never look directly at the UV lamp. Never reopen plates. Keep growth and fluorescence as different observations; arabinose-induced GFP expression is not the antibiotic selection step. If plates are absent or failed, record that status and use C1 from May 6 as explicitly invented practice, not replacement observations. Then analyze the assigned authentic gel image or the D1 nominal fallback. A band pattern does not prove plasmid identity. A self-contained count fallback is C1: positive comparison P=12, negative comparison N=0, sample S=8. These invented role labels are not pGLO plate identities or evidence that any kit worked.
10–20 minutes	Use D1/G1 to record nominal ladder inputs; no actual measurement. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.
20–40 minutes	Use G1 to plot one standard curve with the supplied logs. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.
40–55 minutes	Use P1 to estimate four bands and retain the Z no-band state. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.
55–70 minutes	Use T1 for all-lane pattern comparison and one bounded conclusion. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.
70–80 minutes	Use Q1/S1 to check, revise and save the same analysis. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Your response record

Use these labels on paper or in your document. The space below also works when this page is printed.

Plate observations and size-ordering answer

At 0–8, add four kit-condition rows to the same record: +pGLO LB/amp; +pGLO LB/amp/ara; -pGLO LB/amp; -pGLO LB. Columns: actual plate label/ID, preparation and read dates, colony count or uncountable-growth description, fluorescence observation, and status (observed, absent, failed or not assessed). Keep lids closed and use the approved viewing setup. Wear UV-protective eyewear or view through a UV-blocking shield, and never look directly at the UV lamp. Do not predict observations into empty cells. If plates are absent or failed, retain that status; use C1’s three invented P/N/S rows only as a separately labeled practice alternative, never as kit observations. At 8–10, answer H1’s size-ordering question before the gel analysis.

Use the manufacturer plate labels and actual observation record. The P/N/S count fallback has different roles and is not a four-condition pGLO dataset. Keep all work in one product.

Use this space or the same labeled section in your existing document. Add paper when your table, graph or drawing needs more room.

Condition	Actual plate ID	Prep date	Read date	Count or growth description	Fluorescence	Status
+pGLO LB/amp						
+pGLO LB/amp/ara						
-pGLO LB/amp						
-pGLO LB						

Size-ordering answer, using H1:

Four supplied ladder rows

Original route: Use D1/G1 for the four distances, sizes and supplied logs.

Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Use this space or the same labeled section in your existing document. Add paper when your table, graph or drawing needs more room.

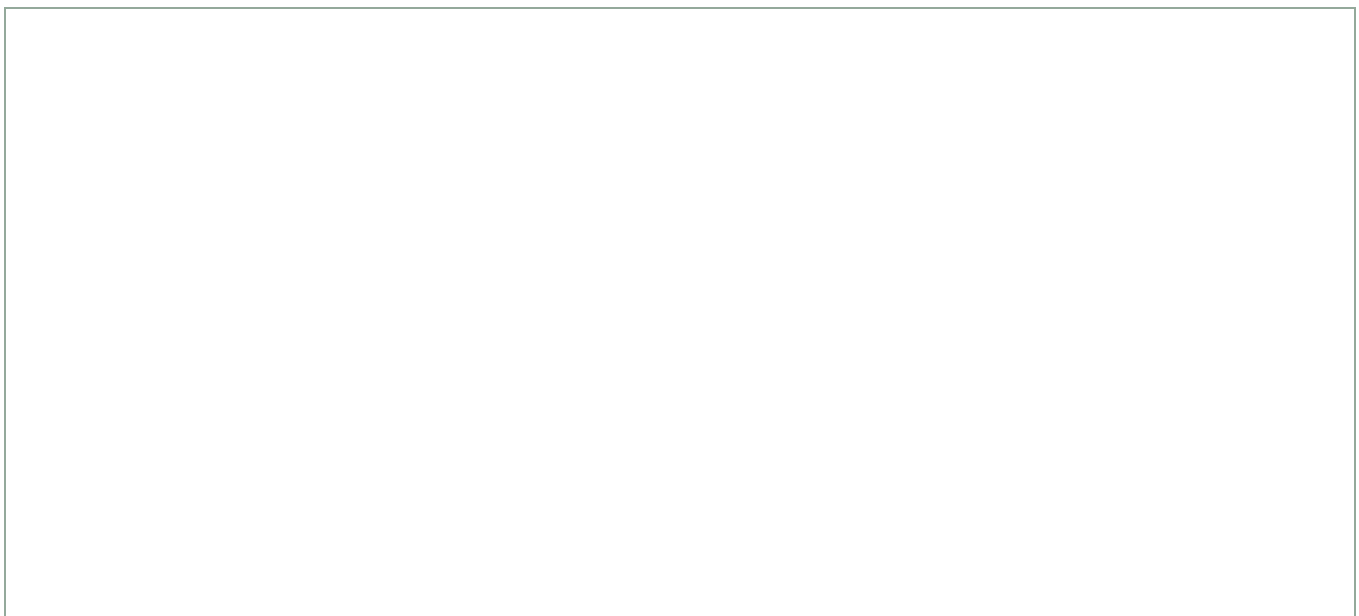


One standard curve

Original route: Use G1 to plot the four ladder points on the response grid.

Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Use this space or the same labeled section in your existing document. Add paper when your table, graph or drawing needs more room.



Four estimates and Z status

Original route: Use P1 for all X/Y estimates and explicit no-band Z row.

Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Use this space or the same labeled section in your existing document. Add paper when your table, graph or drawing needs more room.

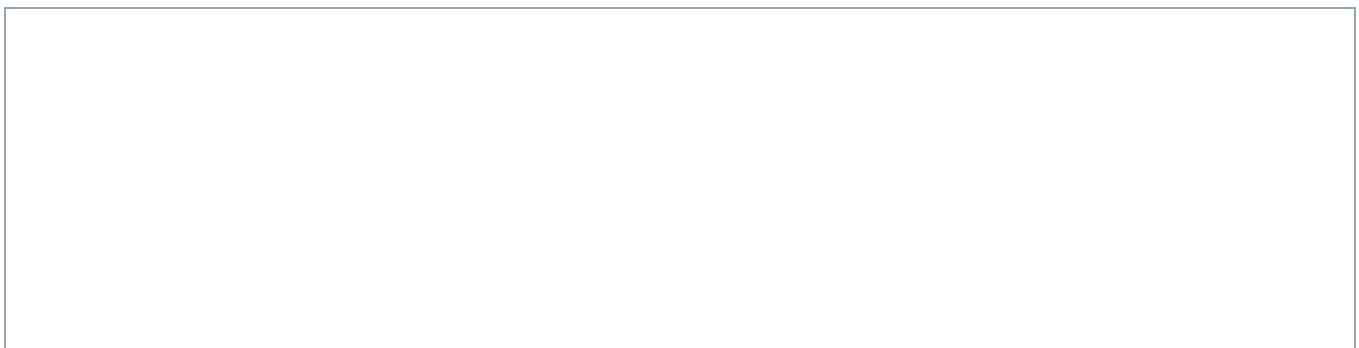


All-lane comparison and bounded conclusion

Original route: Use T1 to compare X/Y/Z with the complete pattern and declared bounds.

Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Use this space or the same labeled section in your existing document. Add paper when your table, graph or drawing needs more room.



Check and save the same analysis

Original route: Use Q1/S1 to verify and save the same product and genuine statuses.

Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Use this space or the same labeled section in your existing document. Add paper when your table, graph or drawing needs more room.

A large, empty rectangular box with a thin black border, intended for students to perform their analysis, create tables, graphs, or drawings.

Check your product

- Original route: all ladder and sample positions preserve approved BI-GEL-PAPER-01, with mm distinct from bp.
- Original route: one graph uses the four base-10 log values, exact axis ranges and the declared 10–40 mm domain.
- Original route: all four sample estimates show the selected/interpolated log, inverse and nearest-10-bp result; Z remains no bands drawn.
- Original route: every lane is compared with both band count and declared size bounds, with one bounded conclusion and limitation.
- Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.
- Both routes: a pattern match does not confirm identity, actual experiment, approval, official completion or receipt.

Keep the limit: This idealized linear-DNA model supports only a bounded size-pattern comparison. It cannot establish any real construct, sequence identity, gene orientation, transformation or completed experiment.

Turn in your work

Open the linked BI assignment in Turn in your work. Confirm real prompt, rubric and deadline. Actual route: use the teacher's genuine data, comparison rule and rubric in place of this practice. Complete one analysis record. Missing authentic inputs, approval and receipt remain pending.

Paper analysis only. Use supplied nominal records, not actual measurements. Do not perform or design a biological experiment. A matching band-size pattern cannot confirm plasmid or sequence identity. Save the same analysis record with missing input, next action and receipt pending.

[Open this assignment in Schoology.](#)

Carry forward

A matching size pattern can support consistency; it cannot identify a DNA sequence by itself.

Monday May 10 is the next lesson. Carry the labeled paper analysis, not an invented laboratory completion or identity confirmation. What can the band pattern support in your notebook conclusion?

Sources and resources

[Open today's page](#)

NHGRI-SEPARATION · Separating the Sequencing Products: Transcript

NHGRI; general size-ordering concept only

<https://www.genome.gov/25019982/online-education-kit-separating-the-sequencing-products-transcript>

NHGRI-BP · Base Pair

NHGRI; base-pair concept and DNA length

<https://www.genome.gov/genetics-glossary/Base-Pair>

NIST-LOG10 · LOG10 mathematical reference

NIST Dataplot; positive inputs and base-10 inverse relationship

<https://www.itl.nist.gov/div898/software/dataplot/refman2/ch6/log10.pdf>

BIO-RAD-PGLO · pGLO Transformation Kit Quick Guide

Bio-Rad, manufacturer SOP for approved educational kit

https://www.bio-rad.com/webroot/web/pdf/lse/literature/Bulletin_3052.pdf