

Genomic DNA QC Using Standard Gel Electrophoresis (For Collaborators)

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Summary

Before shipping your DNA sample(s), please be sure to follow the JGI sample preparation and sample submission guidelines located at <u>http://my.jgi.doe.gov/general/gettingstarted.html</u>.

This protocol describes how to run a standard agarose gel utilizing concentration and size standards as well as Qubit[™] fluorometer to evaluate the quality, quantity, and molecular weight of your DNA sample(s). We recommend all DNA samples to be evaluated with this protocol before they are shipped to JGI.

Materials & Reagents

Materials/Reagents/Equipment	Vendor	Stock Number
Disposables		
Microcentrifuge Tubes	VWR	
Pipette Tips		
Qubit™ Assay Tubes	Invitrogen	Q32856
<u>Reagents</u>		
GenePure LE Agarose (Generates)	ISC BioExpress	E-3120-500
50X TAE Buffer	Invitrogen	24710-030
SYBR® Safe DNA gel stain (10,000X concentrate in DMSO)	Invitrogen	S33102
Or Ultra Pure Ethidium Bromide (10mg/ml)	Invitrogen	15585011
5X Loading Dye		
TE Buffer, pH 8.0 500ml	Ambion	9849
DNA Molecular Weight Marker II (0.12–23.1 kbp) (~25ng/ul)	Roche	10 236 250 001
DNA Mass Standards (Lambda DNA) 15, 31, 63, 125, 250, 500ng / 6ul	Life Technologies	14420-012
Quant-iT [™] dsDNA BR Assay Kit, 500 assays (2-1000 ng)	Invitrogen	Q32853
Quant-iT [™] dsDNA HS Assay Kit, 500 assays (0.2-100 ng)	Invitrogen	Q32854
Equipment		



Pipettes		
12X14 Horizontal Device Comb (25 well 1.5mm)	CLP	75.1214-MT-25D
12X14cm Horizontal Gel Electrophoresis Device	CLP	75.1214
Gel Doc Imager	Bio-Rad	
Qubit [™] fluorometer 1.0 or 2.0	Invitrogen	Q32857 or Q32866

EH&S

PPE Requirements:

Safety glasses, lab coat, and nitrile gloves should be worn at all times while performing this protocol. Additional safety equipment is required at designated steps.

Procedure

NOTE: All reagents/stock solutions should be prepared prior to the start of the procedure.

1. Gel & Sample Preparation

- 1.1 Cast a ~100ml 1% agarose gel with 1X TAE and ethidium bromide (.15ug/ml) or SYBR® Safe DNA gel stain (10,000X concentrate in DMSO). Use a narrow well comb.
- 1.2 Transfer 1µl of your genomic DNA sample(s) (concentration between 50ng to 500ng) into clean labeled tube(s) and bring the total volume up to 4µl with 1X TE Buffer, pH 8.0.
 - a. If the genomic DNA concentration is thought to be lower than $50ng/\mu l$, then transfer 2-4 μl of the sample(s). For example, if the DNA concentration is around $25ng/\mu l$, then transfer 2 μl of the DNA sample and add 2 μl of TE Buffer to a final volume of 4 μl to be loaded on the gel.
 - b. If the genomic DNA concentration is thought to be higher than $500ng/\mu l$, then create a dilution of the sample(s) in TE Buffer to reduce the concentration between $50ng/\mu l$ and $500ng/\mu l$. For example, if the DNA concentration of the sample is around $1000ng/\mu l$, then create a 1:10 dilution of the sample in TE buffer by adding $1\mu l$ of the original sample to $9\mu l$ of TE buffer. Then transfer $1\mu l$ of 1:10 diluted sample and add $3\mu l$ of TE Buffer to a final volume of $4\mu l$ to be loaded on the gel.
- 1.3 Add 1µl of 5X loading dye. The amount of loading dye should remain consistent among all samples to maintain even DNA migration on the gel. Vortex and spin down sample tube(s).

2. Gel Electrophoresis

Note: Refer to Appendix 1 for the gel loading guide.



- 2.1 Load the gel according to the format listed below:
 - a. Well $1 6\mu l$ of 2.50 ng/ μl standard (total mass = 15 ng)
 - b. Well $2 6\mu l$ of 5.17 ng/ μl standard (total mass = 31 ng)
 - c. Well $3 6\mu l$ of 10.50 ng/ μl standard (total mass = 63 ng)
 - d. Well $4 5\mu l$ of Marker 2 (~25ng/ μl)
 - e. Well $5 5\mu l$ of DNA sample (from above sample preparation)

Note: If multiple samples are being run, load all samples and complete loading f-i after the last sample.

- f. Well $6 5\mu l$ of Marker 2 (~25ng/ μl)
- g. Well 7 6 μ l of 20.83 ng/ μ l standard (total mass = 125ng)
- h. Well $8 6\mu l$ of $41.67 \text{ ng/}\mu l$ standard (total mass = 250ng)
- i. Well $9 6\mu l$ of 83.33 ng/ μl standard (total mass = 500ng)
- 2.2 Run gel for 90 min at ~120V in 1X TAE buffer. If a different electrophoresis set-up is being used, ensure the genomic DNA bands have ran ≥ 2 cm down from well and separation of marker is apparent.
- 2.3 Remove gel from gel box and image.

3. DNA QC Gel Analysis

- 3.1 Analyze genomic DNA for molecular weight, quantity, and quality. Refer to the JGI Guidelines document to see the specific guidelines in the following areas for your genome type.
 - a. **MOLECULAR WEIGHT** (If large long mate-pair analysis is needed, the size of DNA needs to be in the high molecular weight. In this case, DNA band should be above the 23kb band. If possible, pulse field gel should be performed to properly determine the molecular weight)

b. QUANTITY

- i. Compare genomic DNA band with mass standard bands (15, 31, 63, 125, 250, 500ng) to obtain a concentration estimate. Then use the concentration estimate to calculate the total DNA available for this sample.
- ii. If Quantity One Software (Bio-Rad) is available, please refer to Appendix 2 for instructions.

c. QUALITY

i. How does the DNA look? Is the DNA a tight band or does it appears to be streaky, displaying signs of degrading and/or shearing? Is RNA present in your sample? A protocol to remove RNA from the sample can be located at http://my.jgi.doe.gov/general/index.html.



Note: Refer to Appendix 3 and 4 for examples of QC gels that have passed and failed JGI DNA QC requirements.

4. <u>Sample Quantitation with the QubitTM fluorometer</u>

- 4.1 Set up the number of 0.5ml Qubit[™] assay tubes that will be needed for the samples and one standard.
- 4.2 Label the tube lids; these tubes are temperature sensitive so do not hold these too long in your hand as you label them.
- 4.3 Add 1 μ l of Quant-iTTM standard (100ng/ μ l) and exactly 1 μ l of each of the samples to the appropriate tubes (Careful pipetting is critical to ensure that exactly 1 μ l was added to each tube to accurately determine the sample concentration).
- 4.4 Make the Quant-iT[™] working solution by diluting the Quant-iT[™] dsDNA BR reagent 1:200 in Quant-iT[™] dsDNA BR buffer. Use a clean plastic tube each time you make Quant-iT[™] working solution. Do not mix the working solution in a glass container.
 - a. The final volume in each assay tube must be 200µl and each tube will require 199µl. Prepare sufficient Quant-iT[™] working solution to accommodate all samples and standard. For example, for 8 samples, prepare enough working solution for the samples and 1 standard: prepare a total volume of 2ml of working solution (10µl of Quant-iT[™] reagent plus 1,990µl of Quant-iT[™] buffer).
- 4.5 Load 199µl of Quant-iT[™] working solution into each of the tubes used for samples and the standard.
- 4.6 Mix by vortexing for 2–3 seconds, being careful not to create bubbles. The final volume in each tube should be 200µl.
- 4.7 Allow all tubes to incubate at room temperature for 2 minutes in dark since the reagent is light sensitive.
- 4.8 Plug in and press any key to turn on the Qubit[™] fluorometer.
- 4.9 Press HOME, use the arrow \downarrow and \uparrow keys to highlight Quant-iTTM DNA, BR, and press GO to initiate the assay.
- 4.10 On the calibration screen, highlight Use last calibration and press GO.
 - a. For each assay, there will be an option to run a new calibration or to use the values from the previous calibration. If the values seem off then use the *Calibrating the Qubit*TM *Fluorometer* from the manufacturer's protocol for calibration guidelines.
- 4.11 Insert a sample tube into the Qubit[™] fluorometer, close the lid and press **GO**.



- 4.12 When the QubitTM fluorometer displays the QF value, choose **Calculate sample** concentration and select the volume of sample added to each of the assay tube (which should be 1 μ L).
- 4.13 When the QubitTM fluorometer displays the concentration of dsDNA in your original sample, record that number $(1\mu g/ml = 1ng/\mu l)$.
- 4.14 Continue reading samples and recording values until all samples are read.
 - a. If you did not choose **Calculate sample concentration** then you must calculate the concentration of your original sample by using the equation supplied below.

Calculating the Concentration of Your Sample:

The QubitTM fluorometer gives values for the Quant-iTTM dsDNA BR assay in μ g/mL. This value corresponds to the concentration after your sample was diluted into the assay tube. To calculate the concentration of your sample, use the following equation:

Concentration of your sample = QF value \times (200/x)

where:

QF value = the value given by the QubitTM fluorometer x = the number of microliters of sample you added to the assay tube This equation generates a result with the same units as the value given by the QubitTM fluorometer (i.e., if the QubitTM fluorometer gave a concentration in µg/mL, the result of the equation will be in µg/mL).

- 4.15 The following should be done if the concentration reading is out of range:
 - a. If the concentration reads too low, then use the Quant-iT[™] dsDNA HS kit and repeat section 2 and use the ↓ and ↑ keys to highlight **Quant-iT[™] DNA**, **HS** assay.
 - b. If the concentration reads too high, then dilute the sample to 200-500ng/µl with TE buffer, pH 8.0 and repeat section 2 with **Quant-iT[™] DNA**, **BR** assay.

Reagent/Stock Preparation

<u>1X TAE Buffer</u> 40ml 50X TAE Buffer 1960ml Milli-Q ddH₂O 5X Loading Dye 125ml Nuclease free H₂O 75ml 100% glycerol 0.01g Bromophenol Blue 0.01g Xylene Cyanole FF



APPENDIX 1: GENOMIC DNA QC GEL LOADING GUIDE

Lane 1	Lane 2	Lane 3	Lane 4	Lane 5	Lane 6	Lane 7	Lane 8	Lane 9
5µl of 3.125ng/µl	5μl of 6.25ng/μl	5μl of 12.5ng/μl	5µl of Marker II	5µl of sample	5µl of Marker II	5μl of 25ng/μl	5µl of 50ng/µl	5µl of 100ng/µl
Total mass = 15.625ng	Total mass = 31.25ng	Total mass = 62.5ng				Total mass = 125ng	Total mass = 250ng	Total mass = 500ng
				-	Longer a		-	

Figure 1: Gel loading Guide.





APPENDIX 2: USING QUANTITY ONE SOFTWARE TO ANALYZE DNA QC GELS



1) Click on Quantity One Program Icon 🚺

2) Open gel file image to be analyzed.



3) Click on the "Draw a box and expand the image inside" Icon Draw a box around first set of concentration standards to expand.



4) Click the "Contour" Icon 👼. The following sub-Icon box appears. Volume Tools × ▶ ♥ ♥ ♥ ♥ ♥ ♥ ■ **95 1** 2 ۶Ū

5) Click on the "Volume Contour Tool" Icon 😰. Place cursor arrow on outer edge of concentration standard, left click & HOLD. Slightly move cursor outward until the contour's bounding outline completely encompasses the desired band.





For older versions of the software the contour tool is not available. Use the "Volume Rectangle Tool" Icon 🔳 instead.



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Edit User Label	
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6) Place cursor in center of the bounding area and double click. The "Volume Properties" box will appear.

Make sure "Standard" is selected and input only the numerical value for that particular concentration standard.

Click on the OK button. Repeat for the remaining concentration standards.



7) After all of the concentration standards have been assigned, repeat Steps #5 & #6 for the unknown samples. Make sure "Unknown" is selected. Remember when outlining the "Unknown samples" ONLY select the high molecular weight section for analysis.



SII.

- 8) Click on the "Display Volume Report" Icon in the sub-Icon toolbar 🗐. Volume Tools × k 😨 J 🗮 🔍 🏭 👘 % 🔞 2
- 9) The following window will appear, make sure all of the appropriate boxes are selected.

volume Report Op	tions
Volume Objects To Report All objects Selected objects Data To Display Name Min. Value Type Max. Value Volume Density Adj. Vol. Mean Backgd. % Volume Num. Pixels X Concentration X Location Area V Location	Image Display Options IDisplay image in report Print image on report IShow overlays in image Image on 1st page only Background Subtraction Method Global CLocal Regression Method Point To Point CLinear
Mean Value Width	Cubic Quadratic Cogistic Opline Display R-Squared Value Display Method Equation Show curve
Font size: Small Line Spacing: Very Small	▼ ▼



10) Click on the "Show Curve" button to display graphic plot of the standards & samples. Standards are red plus symbols (+) and unknown samples are blue triangles (Δ). All value points should be in close proximity to linear curve plot. The closer the "R-Squared" value (*at the bottom of the page*) is to 1.0 the greater the accuracy. *For this example the R-Squared* = 0.983483



11) Click on the "OK" button. Page returns to "Volume Report Options" displayed in Step #9. Click the "Done" button on that page to see the final report.
Volume Report



12) Determine the "Concentration" of each sample in "ng/ul".

Sample #1 = **188ng/ul**

Sample #2 = **246ng/ul.**

Note: If the sample volume loaded is greater than 1ul, divide the concentration estimate by the sample volume loaded.

13) Determine the total "Quantity" for each sample in "ug".

Sample #1) 188ng/ul * 500ul (total volume of sample) = **94,000ng Total (94ug)** Sample #2) 246ug/ul * 250ul (total volume of sample) = **61,500ng Total (61.5ug)**



APPENDIX 3: EXAMPLE OF QC GELS THAT PASSED JGI DNA QC REQUIREMENTS



Figure 1: Example of DNA samples that have a tight band with minimal smearing and have molecular weight greater than 23kb.



Figure 2: Example of MDA DNA product which has some smearing present but most of the DNA has a molecular weight at 23kb.



RNA Contamination DNA degradation

APPENDIX 4: EXAMPLE OF QC GELS THAT FAILED JGI DNA QC REQUIREMENTS

Figure 1: Example of DNA samples with RNA contamination and signs of DNA degradation.



Figure 2: Example of DNA samples with impurities (proteins and polysaccharides that can inhibit chemical reactions during library construction).