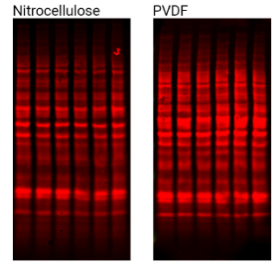


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REVERT™ Total Protein Stain Normalization Protocol V.2

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We use this protocol and it's working

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Abstract

REVERT™ Total Protein Stain is a near-infrared fluorescent membrane stain used for total protein detection and normalization. REVERT staining is imaged at 700 nm, and fluorescent signals are proportional to sample loading.

This protocol describes how to use REVERT™ Total Protein Stain for Western blot normalization and quantitative analysis.

Note: This protocol is intended for use with near-infrared fluorescent Western blots.

Guidelines

I. Introduction

In quantitative Western blotting (QWB), normalization mathematically corrects for unavoidable sample-to-sample and lane-to-lane variation by comparing the target protein to an internal loading control. The internal loading control is used as an indicator of sample protein loading, to correct for loading variation and confirm that observed changes represent actual differences between samples.

More Info: For more normalization related resources, see 'Further Reading' in section VIII.

Total Protein Staining as an Internal Loading Control

Total protein detection is becoming the “gold standard” for normalization of protein loading. After transfer, but prior to immunodetection, the membrane is treated with a total protein stain to assess actual sample loading across the blot. Because this internal loading control uses the combined signal from many different sample proteins in each lane, error and variability are minimized. This antibody-independent method corrects for variation in both sample protein loading and transfer efficiency, and monitors protein transfer across the blot at all molecular weights.

REVERT™ Total Protein Stain is a near-infrared fluorescent membrane stain used for total protein detection and normalization. REVERT staining is imaged at 700 nm, and fluorescent signals are proportional to sample loading.

This protocol describes how to use REVERT™ Total Protein Stain for Western blot normalization and quantitative analysis.

Note: This protocol is intended for use with near-infrared fluorescent Western blots.

II. Keys for Success

Saturation and linear range. Saturated bands and sample overloading frequently compromise the accuracy of QWB. Use a dilution series to verify that you are working within the linear range of detection, and signal intensity is proportional to sample loading. See the protocol: [Determining the Linear Range for Quantitative Western Blot Detection](#) for more information.

Replication. Replicate samples provide information about the inherent variability of your methods, to determine if the changes you see are meaningful and significant. A minimum of three technical replicates is recommended for each sample. Replicates are discussed further in section VI.

Uniform sample loading. Uniform loading of total sample protein across the gel is critical for accurate QWB analysis. A protein concentration assay (BCA, Bradford, or similar assay) must be used to adjust sample concentration and load all samples as consistently as possible.

III. Required Reagents

1. Treated and untreated samples

Protein concentration must be determined for all samples.

2. REVERT™ Total Protein Stain Kit (LI-COR, P/N 926-11010)

3. Electrophoresis reagents

4. Transfer Reagents

5. Western blot detection reagents (near-infrared fluorescence)

Perform near-infrared Western blot detection according to the Near-Infrared Western Blot Detection Protocol

[LI-COR NIRWesternProtocol with PVDF Membrane](#)

[LI-COR NIRWestern Protocol with Nitrocellulose Membrane](#)

IV. Protocol

See 'STEPS'

V. Total Protein and Target Quantification

Use Image Studio™ Software (for a free version, [download Image Studio Lite](#)) to quantify the fluorescent signals from REVERT staining (700 nm) and your target protein (800 nm).

See 'STEPS'

VI. Normalization Calculations and Analysis of Replicates

Replication is an important part of QWB analysis, and is used to confirm the validity of observed changes in protein levels. Biological and technical replicates are both important, but meet different needs (1, 2).

Biological replicates: Parallel measurements of biologically distinct samples, used to control for biological variation and examine the generalizability of an experimental observation.

Technical replicates: Repeated measurements used to establish the variability of a protocol or assay, and determine if an experimental effect is large enough to be reliably distinguished from the assay noise.

Technical replication can be performed by testing the sample multiple times on the same gel or membrane (intra-assay variation) or by testing the sample multiple times in several Western blot experiments. This procedure describes the normalization and analysis of technical replicates that were tested multiple times on the same membrane.

Calculate the Lane Normalization Factor for Each Lane (Total Protein Stain, 700 nm)

1. Prepare a spreadsheet that contains the total protein staining and target protein quantification data.
2. Using the Total Protein Stain data from the normalization channel, calculate the Average (arithmetic mean), Standard Deviation, and % Coefficient of Variation (% CV) of the replicate samples.

“Average” formula in Excel = AVERAGE(rep 1, rep 2,)

Standard Deviation formula in Excel = STDEV(rep 1 value, rep 2 value,)

% Coefficient of Variation =

$$\frac{\text{Standard Deviation of replicates}}{\text{Average Signal of replicates}} \times 100$$

REVERT Staining (700 nm)

Lane	Sample treatment	Replicate	700 nm signal	Average Signal	St Dev	% CV
1	none	1	10,000	9,000	1000	11%
2		2	8,000			
3		3	9,000			
4	UV	1	8,000	8,333	577	7%
5		2	9,000			
6		3	8,000			

Example values shown for illustration only.

3. Calculate the Lane Normalization Factor (LNF) for each lane.
 - a. Identify the lane with the highest signal for total protein staining.

b. Use this value to calculate the Lane Normalization Factor for each lane.

$$\text{Lane Normalization Factor} = \frac{\text{TPS for Each Lane}}{\text{TPS Signal from the Lane with the Highest TPS Signal}}$$

REVERT Staining (700 nm)

Lane	Sample treatment	Replicate	700 nm signal	Highest Signal	Lane Normalization factor
1	none	1	10,000	10,000	1
2		2	8,000	10,000	0.8
3		3	9,000	10,000	0.9
4	UV	1	8,000	10,000	0.8
5		2	9,000	10,000	0.9
6		3	8,000	10,000	0.8

Important: Normalization factors must be calculated for each blot. Normalization factors and standard curves cannot be reused between blots.

Calculate the Normalized Target Protein Signals (800 nm)

1. Using the Target Protein data from the 800 nm channel, calculate the Average, Standard Deviation, and % Coefficient of Variation of the replicate samples.

Target protein (800 nm), not normalized

Lane	Sample treatment	Replicate	Target (800 nm)	Average Signal	St Dev	% CV
1	none	1	650	600	50	8%
2		2	550			
3		3	600			
4	UV	1	450	477	25	5%
5		2	500			
6		3	480			

Example values shown for illustration only.

2. Calculate the Normalized Target Signal for each target band by applying the Lane Normalization Factor for that lane.

a. Divide the Target Signal for each lane by the corresponding LNF.

$$\text{Normalized Signal} = \frac{\text{Target Band Signal}}{\text{Lane Normalization Factor}}$$

Target protein (not normalized)	Normalization	Normalized to total protein				
Lane	Sample treatment	Replicate	Target (800 nm)	LNF (REVERT)	Norm. of Target	Norm. Target
1	none	1	650	1	650/1	650
2		2	550	0.8	550/0.8	688
3		3	600	0.9	600/0.9	667
4	UV	1	450	0.8	450/0.8	563
5		2	500	0.9	500/0.9	556
6		3	480	0.8	480/0.8	600

b. Calculate the Average, Standard Deviation, and % Coefficient of Variation of the replicates

Target protein (not normalized)	Target protein (normalized to total protein)							
Lane	Sample treatment	Replica te	Target (800 nm)	Normaliz ed Target	Avera ge signal	St Dev	% CV	
1	none	1	650	650	668	19	3%	
2		2	550	688				
3		3	600	667				
4	UV	1	450	563	573	44	4%	
5		2	500	556				
6		3	480	600				

VII. Data Interpretation

1. Use the normalized Target Protein values for relative comparison of samples.

In the example above, Target Protein level is 14% lower in UV-treated samples than in untreated samples.

2. % CV can be used to evaluate the robustness of QWB results, and determine if the magnitude of observed changes in Target Protein levels is large enough to be reliably distinguished from assay variability.

a. The percent coefficient of variation (% CV) describes the spread or variability of measured signals by expressing the standard deviation (SD) as a percent of the average value (arithmetic mean). Because % CV is independent of the mean and has no unit of measure, it can be used to compare the variability of data sets and indicate the precision and repeatability of an assay.

A low % CV value indicates low signal variability and high measurement precision.

A larger % CV indicates greater variation in signal and reduced precision

b. On a Western blot, a change in band intensity is meaningful only if its magnitude substantially exceeds the % CV.

Generally speaking, the magnitude of the reported change should be at least 2X greater than the % CV.

Example: To report a 20% difference between samples (0.8-fold or 1.2-fold change in band intensity), a CV of 10% or less would be recommended for replicate samples.

For a specific measurement, this threshold for the magnitude of change would correspond to the mean + 2 SD.

Faint bands or subtle changes in band intensity are more difficult to detect reliably. In these situations, QWB analysis requires more extensive replication and low % CV.

This is a general guideline only. Replication needs and data interpretation are specific to your experiment, and you may wish to consult a statistician.

3. Compare the % CV of Target Protein replicates before and after normalization.

a. Normalization should not greatly increase the % CV of replicate samples.

b. The purpose of normalization is to reduce the variability between replicate samples by correcting for lane-to-lane variation. A large increase in % CV after normalization of replicates is a warning sign that the normalization method is not sufficiently robust, and may be a source of experimental error.

VIII. Further Reading

Please see the following for more information about normalization.

Western Blot Normalization Handbook

[licor.com/handbook](https://www.licor.com/handbook)

The Normalization Handbook describes how to choose and validate an appropriate internal loading control for normalization.

Good Normalization Gone Bad

[licor.com/GNGB](https://www.licor.com/GNGB)

Good Normalization Gone Bad presents examples of normalization that have been adversely affected by common pitfalls and offers potential solutions.

Western Blot Normalization White Paper

[licor.com/normalizationreview](https://www.licor.com/normalizationreview)

This white paper comprehensively reviews the literature of Western blot normalization.

Determining the Linear Range for Quantitative Western Blot Detection

[licor.com/LinearRange](https://www.licor.com/LinearRange)

This protocol explains how to choose an appropriate amount of sample to load for QWB analysis.

Pan/Phospho Analysis For Western Blot Normalization

[licor.com/PanProteinNormalization](https://www.licor.com/PanProteinNormalization)

This protocol describes how to use pan-specific antibodies as an internal loading control for normalization.

Housekeeping Protein Validation Protocol

[licor.com/HKP-Validation](https://www.licor.com/HKP-Validation)

This protocol explains how to validate an HKP for use as an internal loading control, by demonstrating that HKP expression is stable in the relevant experimental samples.

Housekeeping Protein Normalization Protocol

[licor.com/HKP-Normalization](https://www.licor.com/HKP-Normalization)


This protocol describes how to use a housekeeping protein for Western blot normalization and quantitative analysis.

References


1. Robasky, K, Lewis NE, and Church GM. Nat. Rev. Genet. 15: 56–62 (2014).
<http://www.nature.com/nmeth/journal/v11/n9/pdf/nmeth.3091.pdf>
2. Naegle K, Gough NR, and Yaffe MB. Sci Signal. 8:fs7 (2015).
<https://www.ncbi.nlm.nih.gov/pubmed/25852186>

Materials

MATERIALS

 REVERT™ Total Protein Stain Kit **Licor Catalog #926-11010**

 Odyssey 28 KD Loading Indicator – 800 nm, 2 x 1 mL **Licor Catalog #926-20002**


 Odyssey 28 KD Loading Indicator – 700 nm, 2 x 1 mL **AppliChem Catalog #926-20004**



- 1 Generate a set of experimental samples (drug treatment, time course, dose-response, etc).

Note


Note: A minimum of three replicates should be performed for each sample.

- 2 Determine the protein concentration of each sample using a BCA, Bradford, or similar protein assay.
- 3 Dilute the samples to equal concentrations to enable consistent, uniform loading of total sample protein across the gel.
- 4 Prepare samples to be loaded on the gel with sample loading buffer.
- 5 Denature sample by heating at 95 °C for 3 min (or 70 °C for 10 min).
 00:03:00
- 6 Load a uniform amount of sample protein in each lane.
- 7 Separate sample proteins by SDS-PAGE.
- 8 Transfer proteins to blotting membrane.

Stain membrane with REVERT™ Total Protein Stain using the Single-Color Western Blot protocol

- 9 After transfer is complete, stain membrane with REVERT™ Total Protein Stain using the Single-Color Western Blot protocol:
- 10 Add methanol to the stain reagents as indicated on each bottle.

- 11 Rinse membrane in water, and incubate in 5 mL of REVERT Total Protein Stain solution for 5 minutes, with gentle shaking.

 00:05:00

- 12 Decant Total Protein Stain solution thoroughly.

- 13 Rinse membrane with Wash solution.

Note

REVERT Wash solution (P/N 926-11012): 6.7% (v/v) Glacial Acetic Acid, 30% (v/v) Methanol, in water.

- 14 Rinse membrane with Wash solution again.

Image total protein stain in 700nm chan

- 15 Image the membrane in the 700 nm channel with an Odyssey® imaging system (Classic, CLx, or Fc).

Adjust settings so that no saturation appears in the bands to be quantified.

Blocking and immunodetection

- 16 Rinse membrane briefly with water, and proceed immediately to blocking and immunodetection steps.

- 17 Perform immunoblotting using IRDye® 800CW conjugated secondary antibody to detect the HKP. Blocking and immunodetection

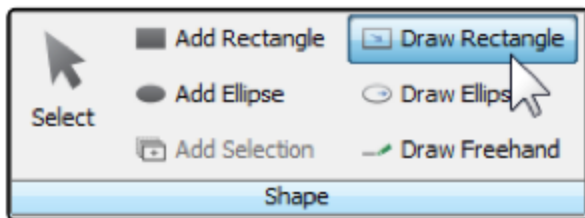
Image membrane in 800nm chan

- 18 Image the membrane in the 800 nm channel with an Odyssey imaging system. Adjust settings so that no saturation appears in the bands to be quantified.

Total Protein Quantification (700 nm image)

19 Use the Draw Rectangle in Image Studio™ Software to quantify the Total Protein signal in each lane. Draw a shape around the first lane on the Total Protein Stain image (700 nm channel).

20 In the Shape group on the Analysis tab, click Draw Rectangle.



21 Draw a rectangle around the first lane. If lanes are skewed, rotate the shape by clicking Rotate in the Edit group.

Note

More Info: For help choosing the right background subtraction method, see [licor.com/BgSubtractHelp](https://www.licor.com/BgSubtractHelp).

22 Copy the shape from the first lane to each remaining lane. With the first shape selected, click Add Selection.

23 Click the next lane to copy the shape. If necessary, adjust the shape borders to ensure that each shape encloses the signal from one and only one lane.

24 Export total protein quantification data. Click Shapes to open the Shapes data table.



- 25 Select shape data, then copy and paste data into a spreadsheet.

For information on how to perform the normalization calculations and data interpretation, go to **Sections VI - VII in the Guidelines.**

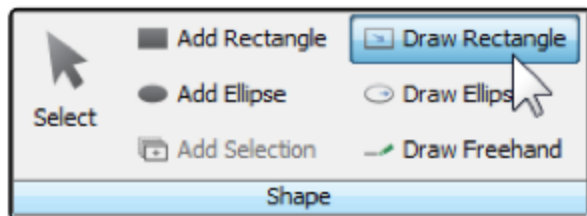
Note

Note: All data fields will be exported, but “Signal” is the field of interest for analysis.

Total Protein Quantification (800 nm image)

- 26 Use the Add Rectangle tool in Image Studio Software to quantify the target protein band in each lane (800 nm channel).

Add shapes to bands. In the Shape group on the Analysis tab, click Add Rectangle.

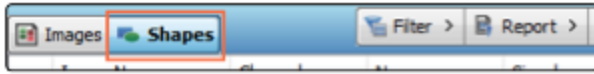


- 27 Click each band to be analyzed, and an appropriately sized shape will be added around the band.

Note

More Info: For help choosing the right background subtraction method, see [licor.com/BgSubtractHelp](https://www.licor.com/BgSubtractHelp).

- 28 Export total protein quantification data. Click Shapes to open the Shapes data table.



29 Select shape data, then copy and paste data into a spreadsheet.

For information on how to perform the normalization calculations and data interpretation, go to **Sections VI - VII in the Guidelines.**

Note

Note: All data fields will be exported, but “Signal” is the field of interest for analysis.