

Progenesis SameSpots v4.1 – new features in the latest release

The latest version of Progenesis SameSpots is available now and comes with a brand new QC workflow which we've called SpotCheck. In addition to this, the tags feature, for the labelling of groups of spots, has also had some significant developments providing improved usability and greater flexibility.

Progenesis SpotCheck

SpotCheck is a separate QC workflow which allows you to quickly and objectively measure whether a 2D gel meets your lab's quality requirements.

There are 3 short steps in this process:

Analyse gel images that represent the gold standard

To get started with SpotCheck, you need a gold standard. This is used as a baseline to objectively measure the quality of your gels.

The gold standard is generated by doing a SameSpots analysis up to the point where you have aligned all of the gel images and detected spots – it is a very fast process. You are then ready to convert your experiment to a SpotCheck gold standard.

Convert analysis into SpotCheck gold standard

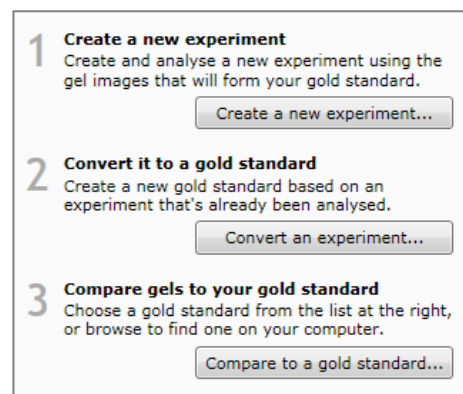
This is a simple process where you define the pass criteria that subsequent test images need to meet.

The default in the software is set to 80% of spots falling within 3 standard deviations of the gold standard – but you are able to adjust these numbers depending on the stringency of the quality control check you want to perform.

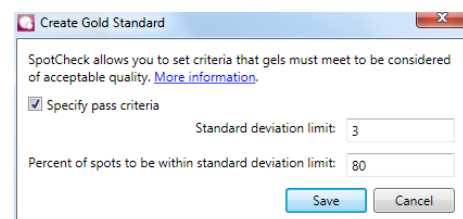
Monitor subsequent gel running

You can set up gold standards for each sample that you use, and then compare subsequent test images to make sure the gel running is maintained at an acceptable quality.

Gold standards can be shared between users and different labs, so you can manage the quality of gels that are analysed as part of the same project. This can help QC within a lab where different people and equipment may be involved in the gel running process and also collaboration across labs.



- 1 Create a new experiment**
Create and analyse a new experiment using the gel images that will form your gold standard.
[Create a new experiment...](#)
- 2 Convert it to a gold standard**
Create a new gold standard based on an experiment that's already been analysed.
[Convert an experiment...](#)
- 3 Compare gels to your gold standard**
Choose a gold standard from the list at the right, or browse to find one on your computer.
[Compare to a gold standard...](#)



Create Gold Standard

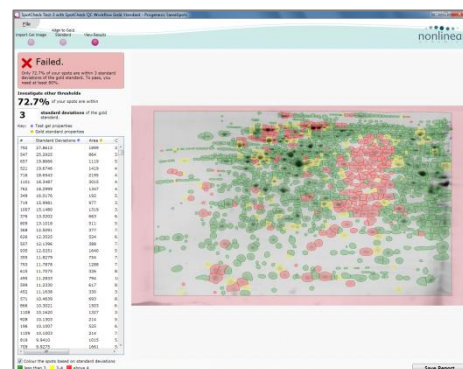
SpotCheck allows you to set criteria that gels must meet to be considered of acceptable quality. [More information.](#)

Specify pass criteria

Standard deviation limit:

Percent of spots to be within standard deviation limit:

[Save](#) [Cancel](#)



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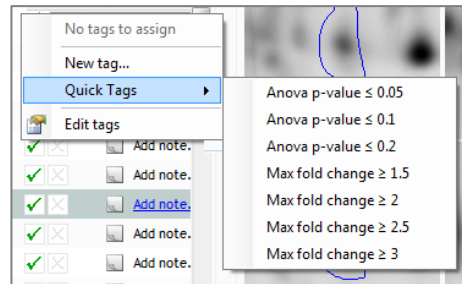
Improvements to Tags

Tags allow you to label a selection of spots according to the data associated with them (e.g. p-value, q-value, power, fold change etc), or their expression profile (e.g. up regulated in treatment 1). The existing tags feature has been updated to improve usability and provide more flexibility in the way tagged data can be displayed. There is also a new filter dialog that allows you to display spots based on a selection of their tags.

QuickTags

Using the new QuickTags feature, certain types of tag can be created without first having to select spots. For example, you can quickly tag all spots with a p-value of less than 0.05 and there is also the option to QuickTag spots by a range of fold changes.

You are still free to tag spots manually by selecting your group of spots and right-clicking to assign the tag.



Filtering your spots

While labelling your spots with tags is a helpful way to organize your data, filtering based on those tags is the more powerful analysis tool. By creating a filter, you can quickly reduce the amount of data you are viewing, enabling you to concentrate on the spots of real interest.

