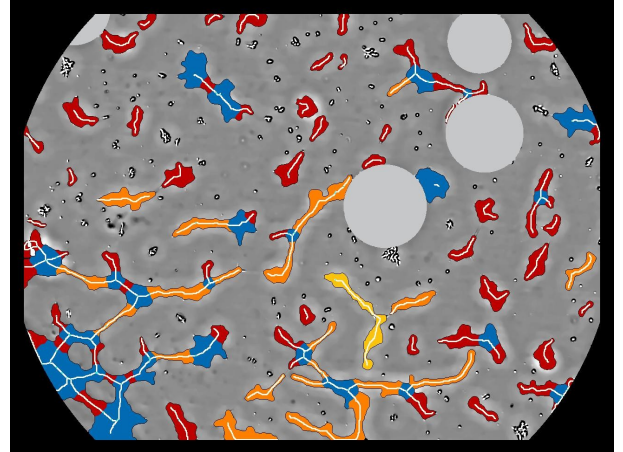
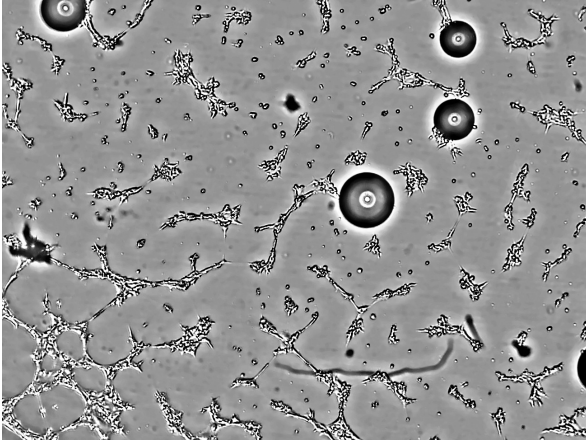


Specification Sheet

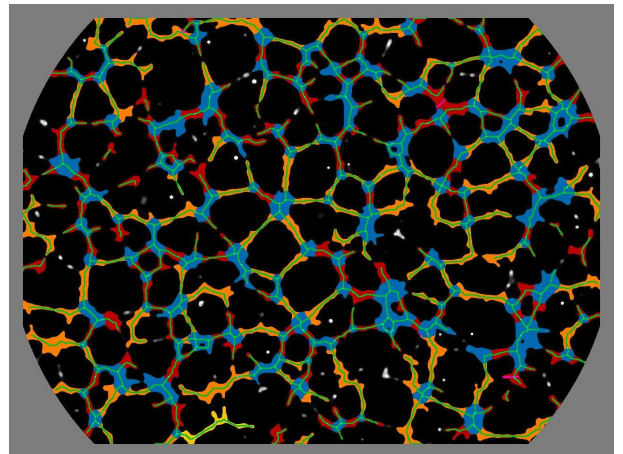
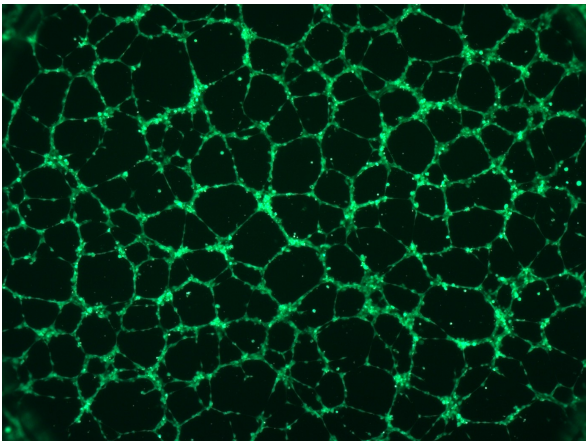
Module

Tube Formation Assay

Tube Formation, native



Tube Formation, fluorescent



Method

To avoid miss analysis due to artificial optical edge effects a mask projected on the image which defines the region of analysis.

By using the object oriented image analysis approach based on the first-class Cognition Network Technology of our partner Definiens AG, we divide the cellular parts into 3 categories:

- Confluent Areas (white)
- Nodal structures (blue)
- Tubes (yellow, orange, red)

Air bubbles are automatically excluded (grey).

The S.CORE tube formation quantification includes the analysis of three aspects:

1. **Single tube quality:** tubes are thin, long and linear
2. **Confluent areas:** the more confluent areas the less tube formation potential
3. **Tube network:** the more complex the tube network the more tube formation potential

Specification Sheet

Evaluation of single tube quality

S.CORE calculates a 'Single Tube Index' for each tube segment which considers the length-width-ratio and the linearity of the tubes. On the basis of the tube index the developmental stage of the tubes is classified in well-developed (yellow), satisfactory (orange), or poorly developed (red).

Quantification of confluent areas

Cellular areas in which a circle of a distinct diameter (multiple of maximal cell size) can be totally projected are classified as confluent areas.

Evaluation of tube network

For all elements - except confluent areas - the formation of the cellular parts is described by the projection of a skeleton (*white*). The complexity of the tube network is described by the ratio of 'Number of branching points' and 'Total length skeleton'.

All three aspects are integrated in the definition of the S.CORE Tube Formation Index.

List of output values:

Output value	Description
1. S.CORE Tube Formation Index	$(\text{Mean single tube index})^2 \times (1 - \text{Confluent area}^*) \times (\text{No. branching points} / \text{Total length skeleton})$
2. Mean single tube index	Sum of all single tube indexes** / No. tubes
3. Total length skeleton (green) [px]	Total length of the skeleton structure (green)
4. No. branching points (green)	No. of branching points within the skeleton (green)
5. No. tubes (yellow, orange, red)	No. of all tubes (yellow+orange+red) in the particular image
6. No. nodal structures (blue)	No. of all nodal structures (blue) in the particular image
7. Mean tube length [px]	Mean length of all tubes
8. Confluent area (white) [%]	Area of confluent areas (white) [px] / total image size [px]

* for definition of 'Confluent area' see 'Output value 8.' (referred to 1)

** Single tube index = linearity factor x tube length-width ratio

For more information on S.CORE and this module please do not hesitate to contact us.

Your S.CORE Team

Reference:

Senft C, Priester M, Polacin M, Schröder K, Seifert V, Kögel D, Weissenberger J
Inhibition of the JAK-2/STAT3 signaling pathway impedes the migratory and invasive potential of human glioblastoma cells.
J Neurooncol 2010 Jun 30.