

Video Article

Erratum: In vivo Clonal Tracking of Hematopoietic Stem and Progenitor Cells Marked by Five Fluorescent Proteins using Confocal and Multiphoton Microscopy

URL: http://www.jove.com/video/5515

DOI: doi:10.3791/5515

Keywords:

Date Published: 9/24/2014

Citation: Erratum: In vivo Clonal Tracking of Hematopoietic Stem and Progenitor Cells Marked by Five Fluorescent Proteins using Confocal and Multiphoton Microscopy. J. Vis. Exp. (), e5515, doi:10.3791/5515 (2014).

Abstract

A correction was made to In vivo Clonal Tracking of Hematopoietic Stem and Progenitor Cells Marked by Five Fluorescent Proteins using Confocal and Multiphoton Microscopy. At the time of publication, there was a typo in the discussion, which displayed an incorrect depth.

This was corrected in the discussion from:

This approach combines the benefits of single-cell resolved high resolution imaging together with optical sectioning via confocal microscopy. Very large x - y (mm²) regions of the intact dense tissue volume can be examined by generating tiled-images. These high resolution images from optical sections can be used to computationally reconstruct (automatically and "on-the-fly") complete 3D volumes of great complexity to depths of ~ 30 μ m, comprising ~ 20 -30 layers of cells, vascular, bone and collagen structures. 3D reconstructions can be used for morphometric non-invasive quantitative analyses of biologic interest. One important caveat to point out is that large volume/high resolution imaging is time-consuming, for instance 1 hr per ~ 1 mm³ of tissue (one fossae of the sternum), therefore we recommend imaging no more than 1 mouse per experiment per day when bone marrow as well as different tissues need to be examined in detail.

to:

This approach combines the benefits of single-cell resolved high resolution imaging together with optical sectioning via confocal microscopy. Very large x - y (mm²) regions of the intact dense tissue volume can be examined by generating tiled-images. These high resolution images from optical sections can be used to computationally reconstruct (automatically and "on-the-fly") complete 3D volumes of great complexity to depths of ~ 300 μ m, comprising ~ 20 -30 layers of cells, vascular, bone and collagen structures. 3D reconstructions can be used for morphometric non-invasive quantitative analyses of biologic interest. One important caveat to point out is that large volume/high resolution imaging is time-consuming, for instance 1 hr per ~ 1 mm³ of tissue (one fossae of the sternum), therefore we recommend imaging no more than 1 mouse per experiment per day when bone marrow as well as different tissues need to be examined in detail.

Protocol

A correction was made to In vivo Clonal Tracking of Hematopoietic Stem and Progenitor Cells Marked by Five Fluorescent Proteins using Confocal and Multiphoton Microscopy. At the time of publication, there was a typo in the discussion, which displayed an incorrect depth.

This was corrected in the discussion from:

This approach combines the benefits of single-cell resolved high resolution imaging together with optical sectioning via confocal microscopy. Very large x - y (mm²) regions of the intact dense tissue volume can be examined by generating tiled-images. These high resolution images from optical sections can be used to computationally reconstruct (automatically and "on-the-fly") complete 3D volumes of great complexity to depths of ~ 30 µm, comprising ~ 20 -30 layers of cells, vascular, bone and collagen structures. 3D reconstructions can be used for morphometric non-invasive quantitative analyses of biologic interest. One important caveat to point out is that large volume/high resolution imaging is time-consuming, for instance 1 hr per ~ 1 mm³ of tissue (one fossae of the sternum), therefore we recommend imaging no more than 1 mouse per experiment per day when bone marrow as well as different tissues need to be examined in detail.

to:

This approach combines the benefits of single-cell resolved high resolution imaging together with optical sectioning via confocal microscopy. Very large x - y (mm²) regions of the intact dense tissue volume can be examined by generating tiled-images. These high resolution images from optical sections can be used to computationally reconstruct (automatically and "on-the-fly") complete 3D volumes of great complexity to depths of ~ 300 μ m, comprising ~ 20-30 layers of cells, vascular, bone and collagen structures. 3D reconstructions can be used for morphometric non-invasive quantitative analyses of biologic interest. One important caveat to point out is that large volume/high resolution imaging is time-consuming, for instance 1 hr per ~1 mm³ of tissue (one fossae of the sternum), therefore we recommend imaging no more than 1 mouse per experiment per day when bone marrow as well as different tissues need to be examined in detail.



Disclosures

No conflicts of interest declared.