Analytical and Bioanalytical Chemistry

Electronic Supplementary Material

Normalization in MALDI-TOF Imaging Datasets of Proteins: Practical Considerations

Sören-Oliver Deininger, Dale S. Cornett, Rainer Paape, Michael Becker, Charles Pineau, Sandra Rauser, Axel Walch, Eryk Wolski

Fig S1 Regions selected on the kindey and m/z 13780 signals with different normalization algorithms

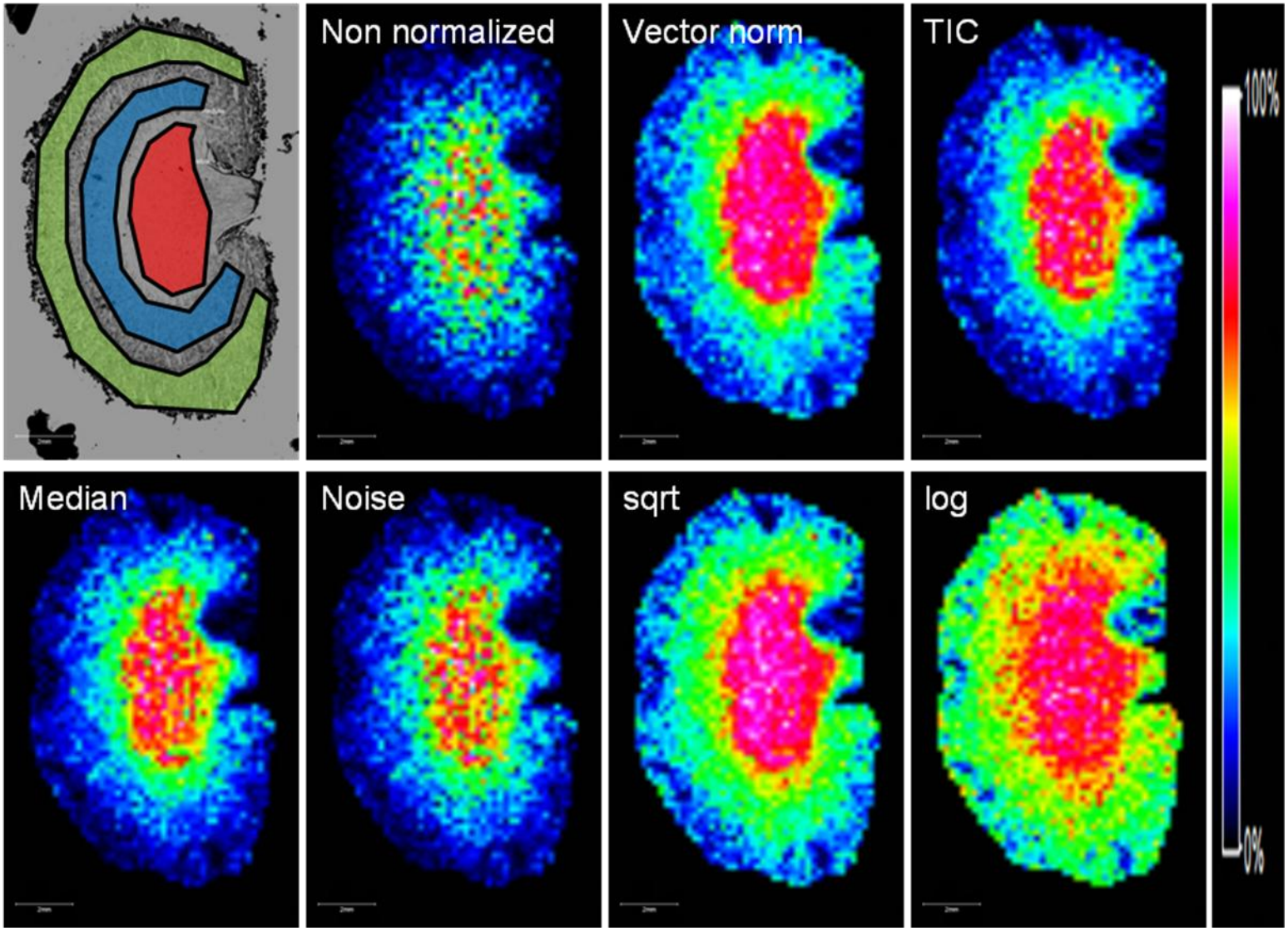

Fig S2 Comparison of averages spectra from 16 individual spectra from the testis dataset: Blue: Spectrum from the tubuli showing the strong signal at m/z 6263; Red: Spectrum from interstital area.

A) Spectra displayed on the same absolute scale. B) Zoomed view, the spectra are scaled to similar relative intensity in the displayed area. Red arrow: m/z 6177 signal used for recosntruction of figure 8 , Blue arrow: m/z 6263 signal

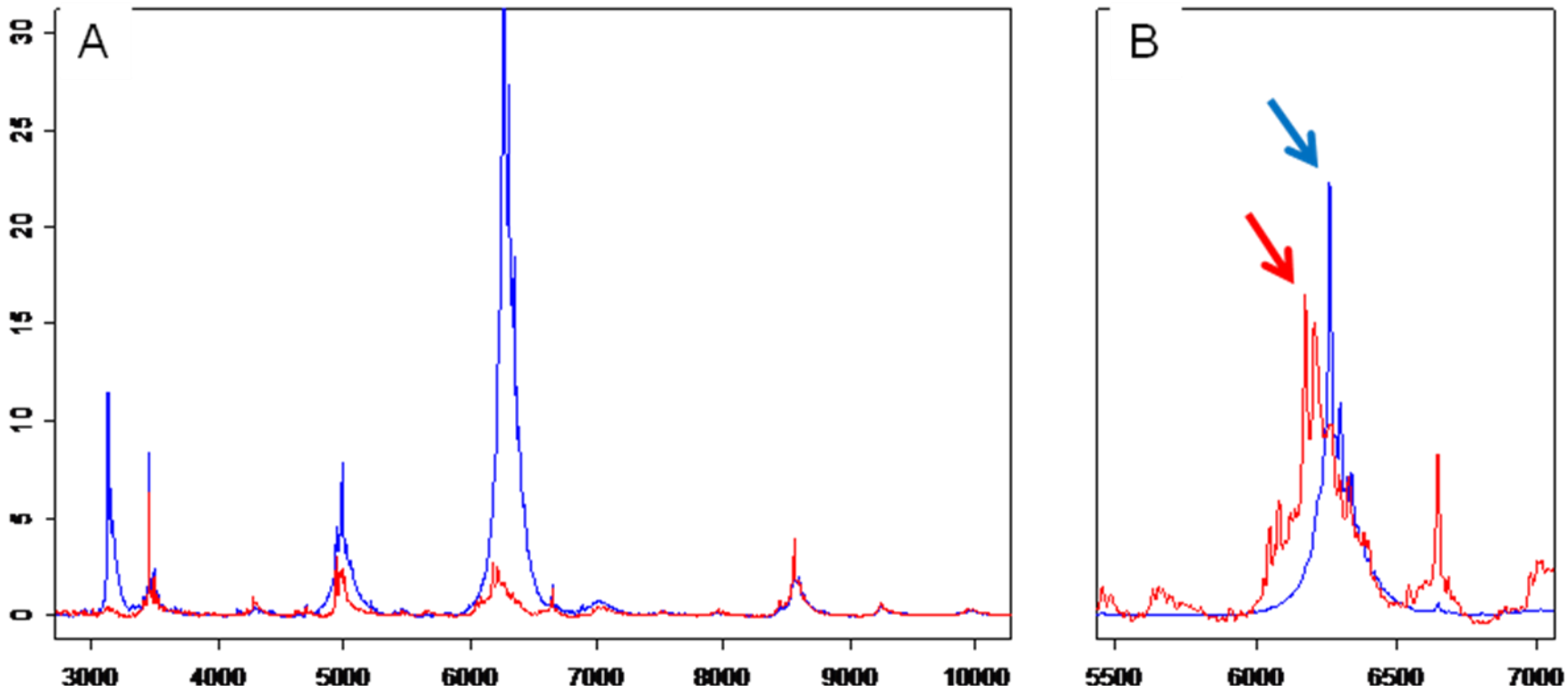

Fig S3 Rat testis, signal m/z 2397, with different normalization, scalebar 500 µm

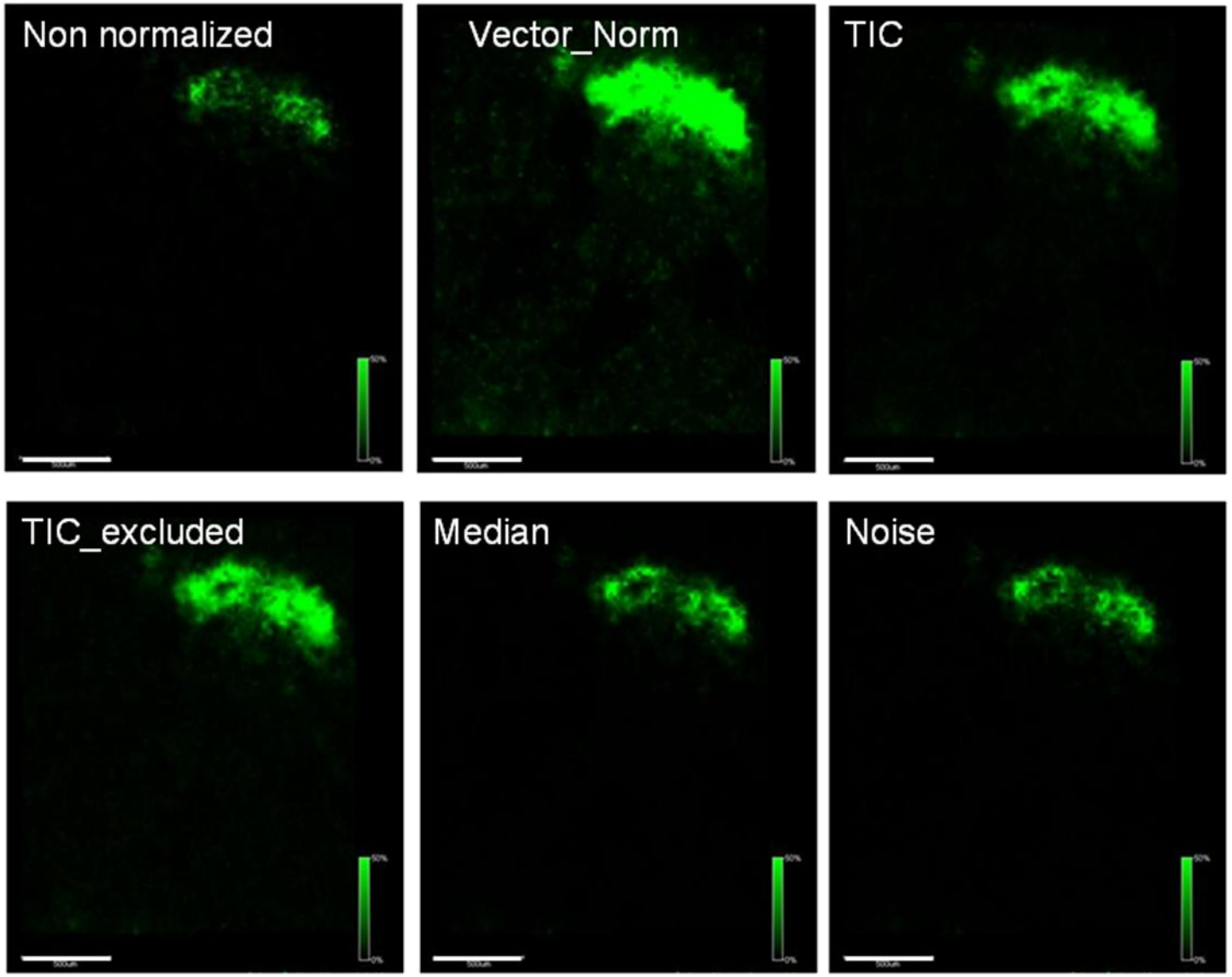

Fig S4 Rat testis, signal m/z 3457, with different normalization, scalebar 500 µm

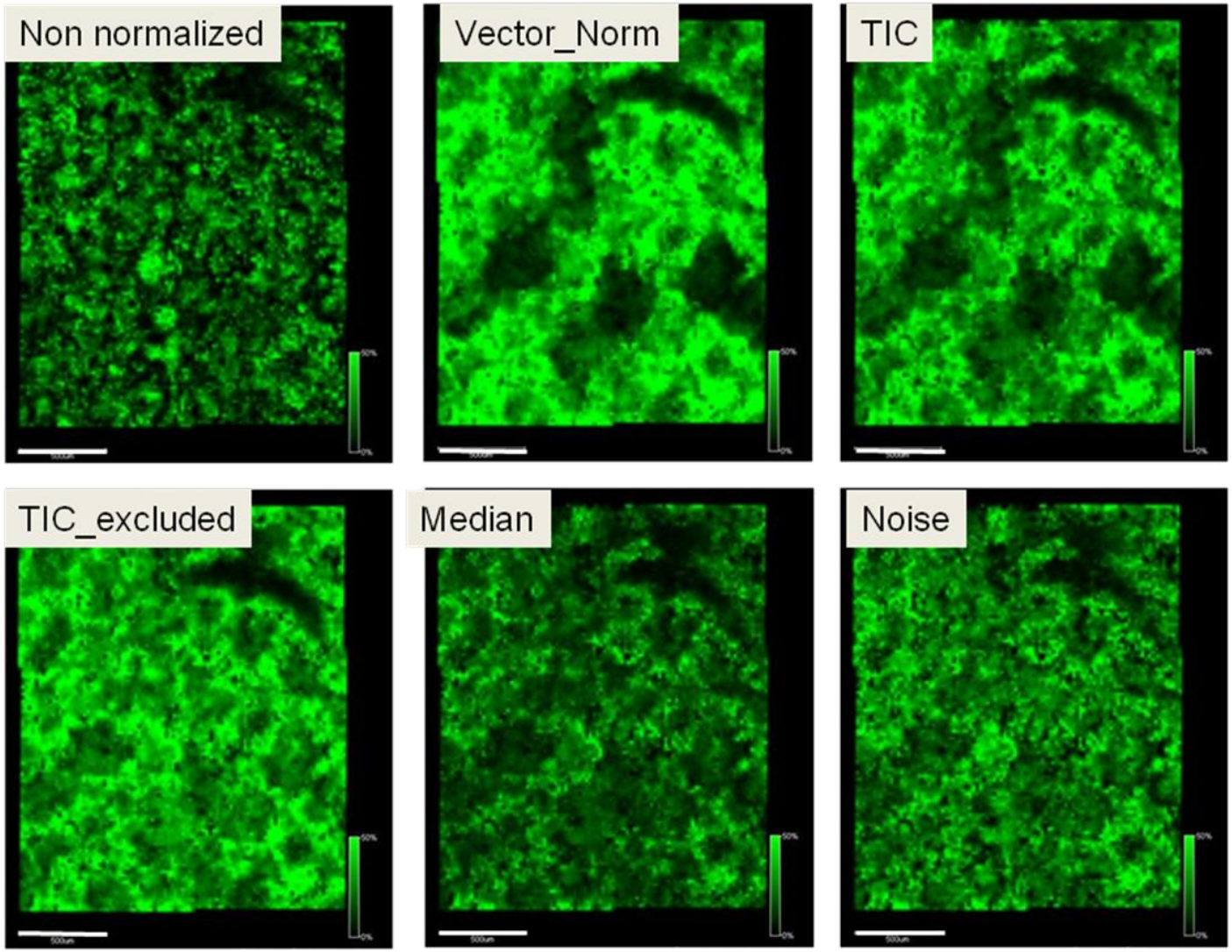

Fig S5 Rat testis, signal m/z 4984, with different normalization, scalebar 500 µm

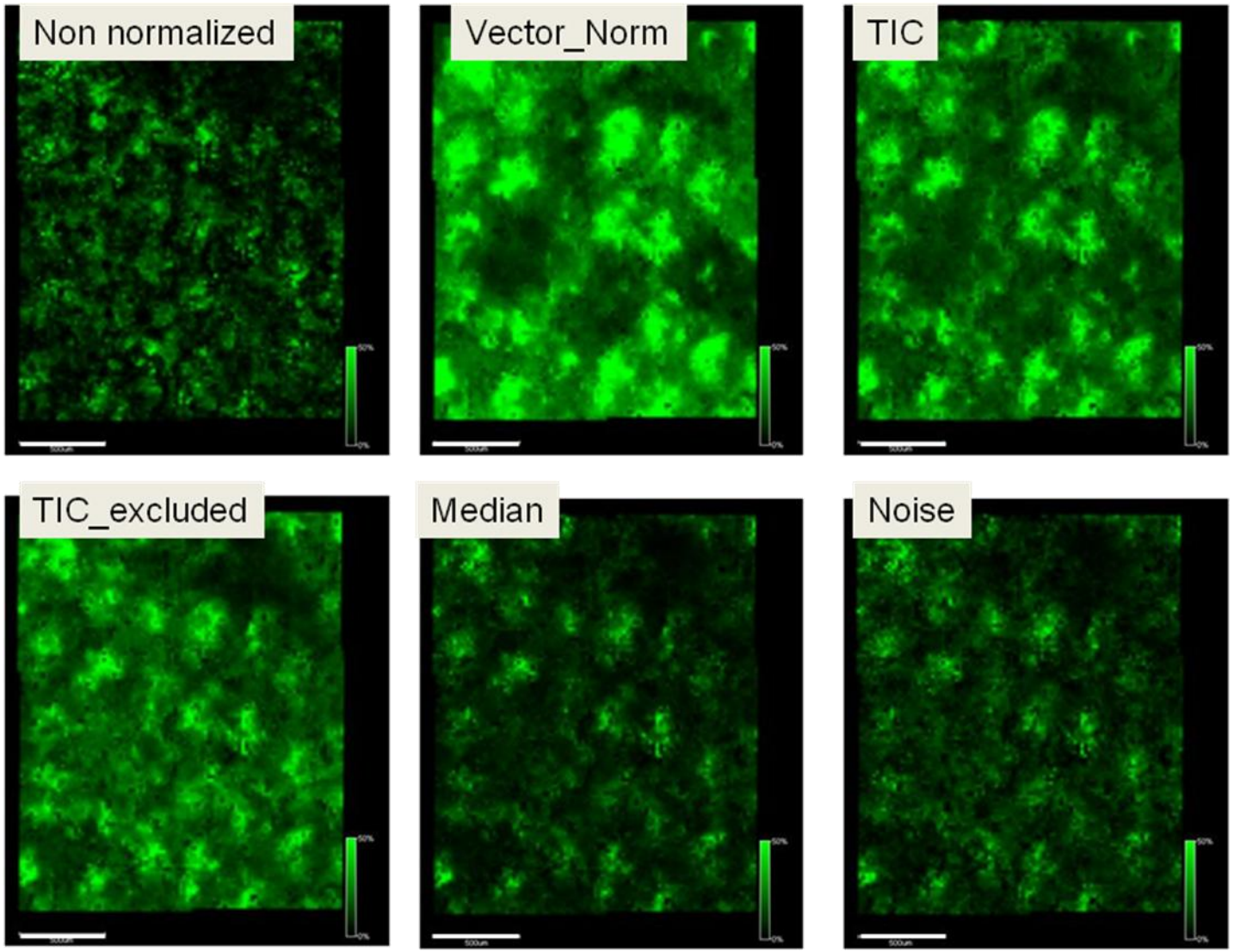

Fig S6 Rat testis, signal m/z 5456, with different normalization, scalebar 500 µm

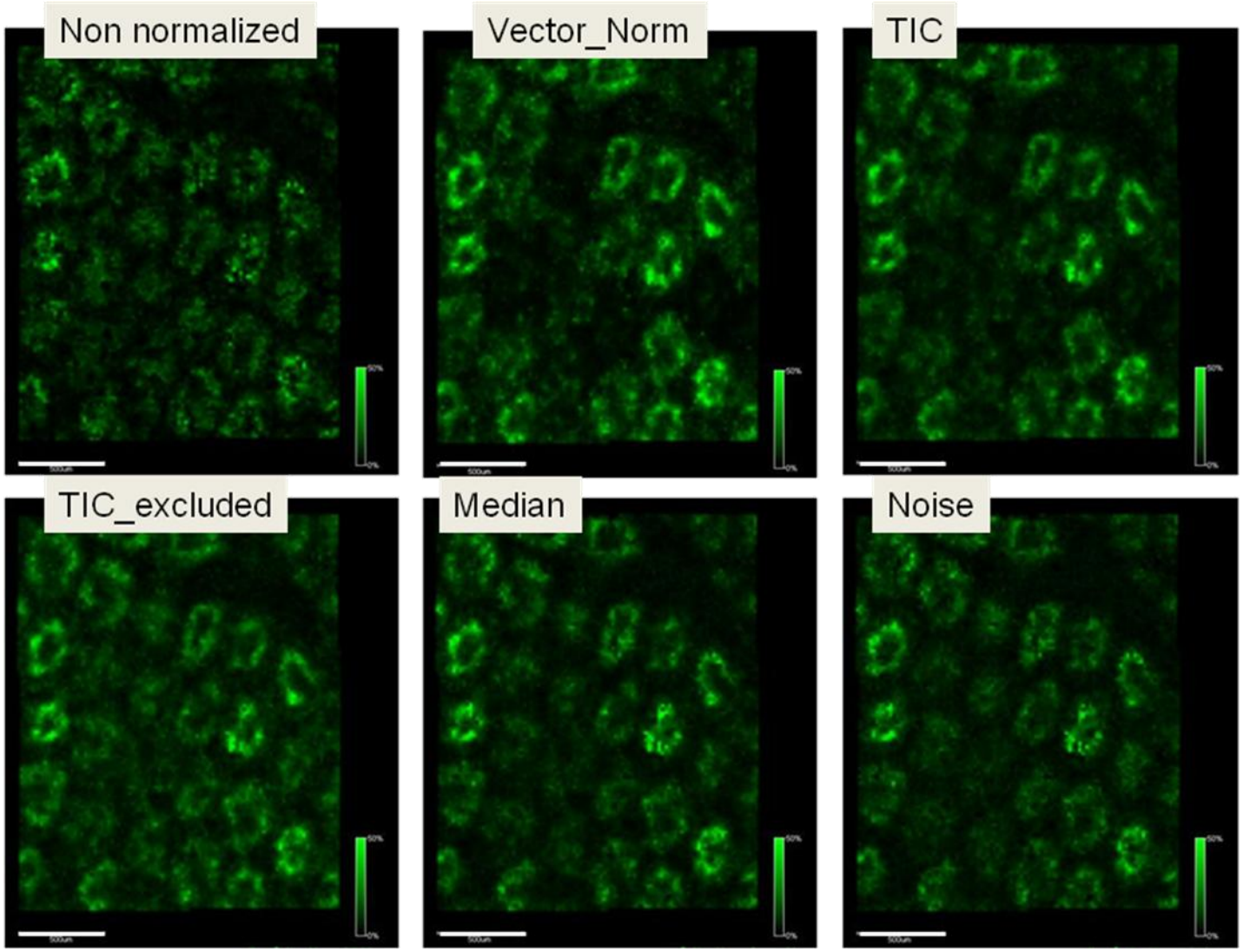

Fig S7 Rat testis, signal m/z 6264, with different normalization, scalebar 500 µm

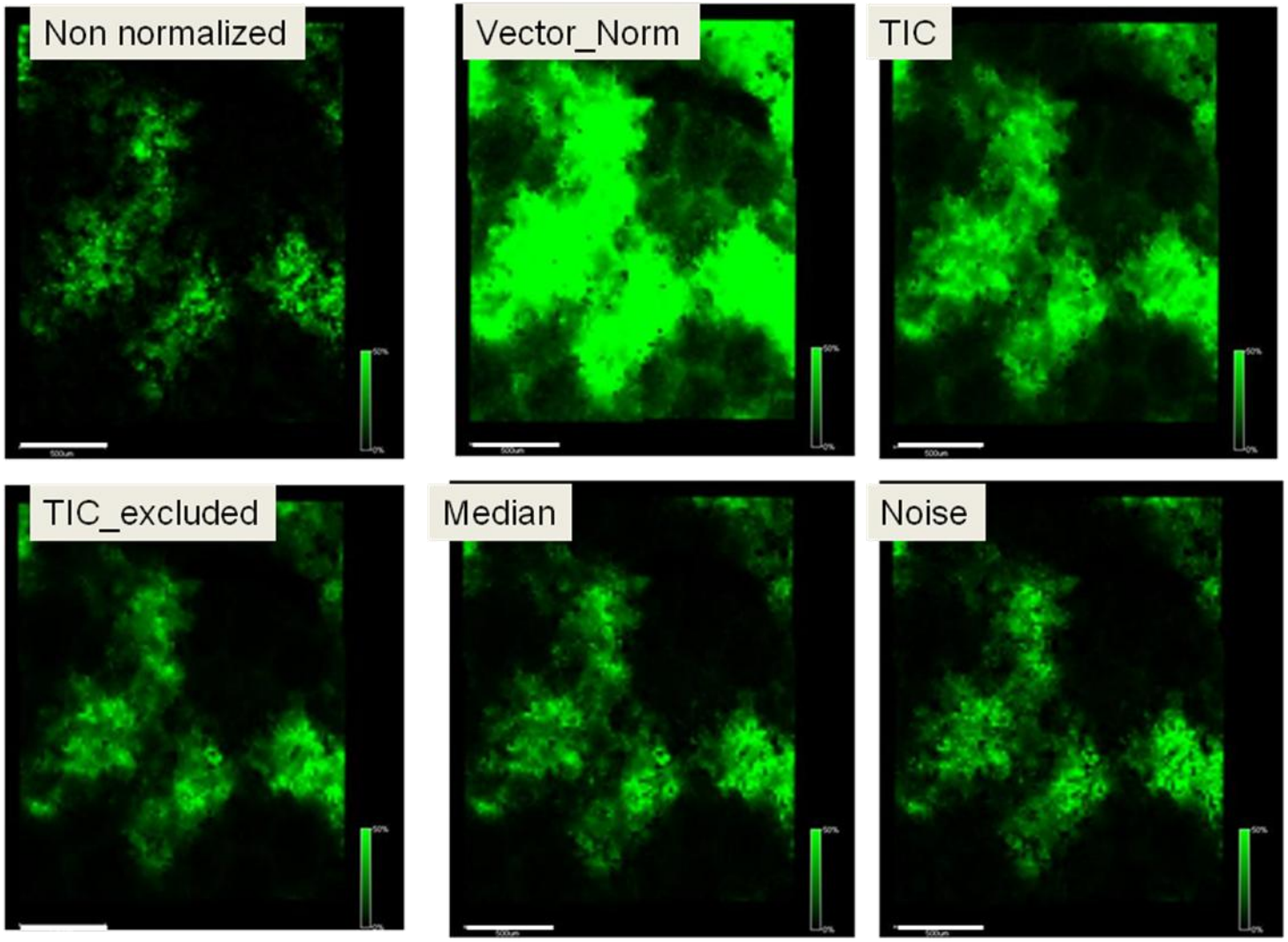

Fig S8 Rat testis, signal m/z 8563, with different normalization, scalebar 500 µm

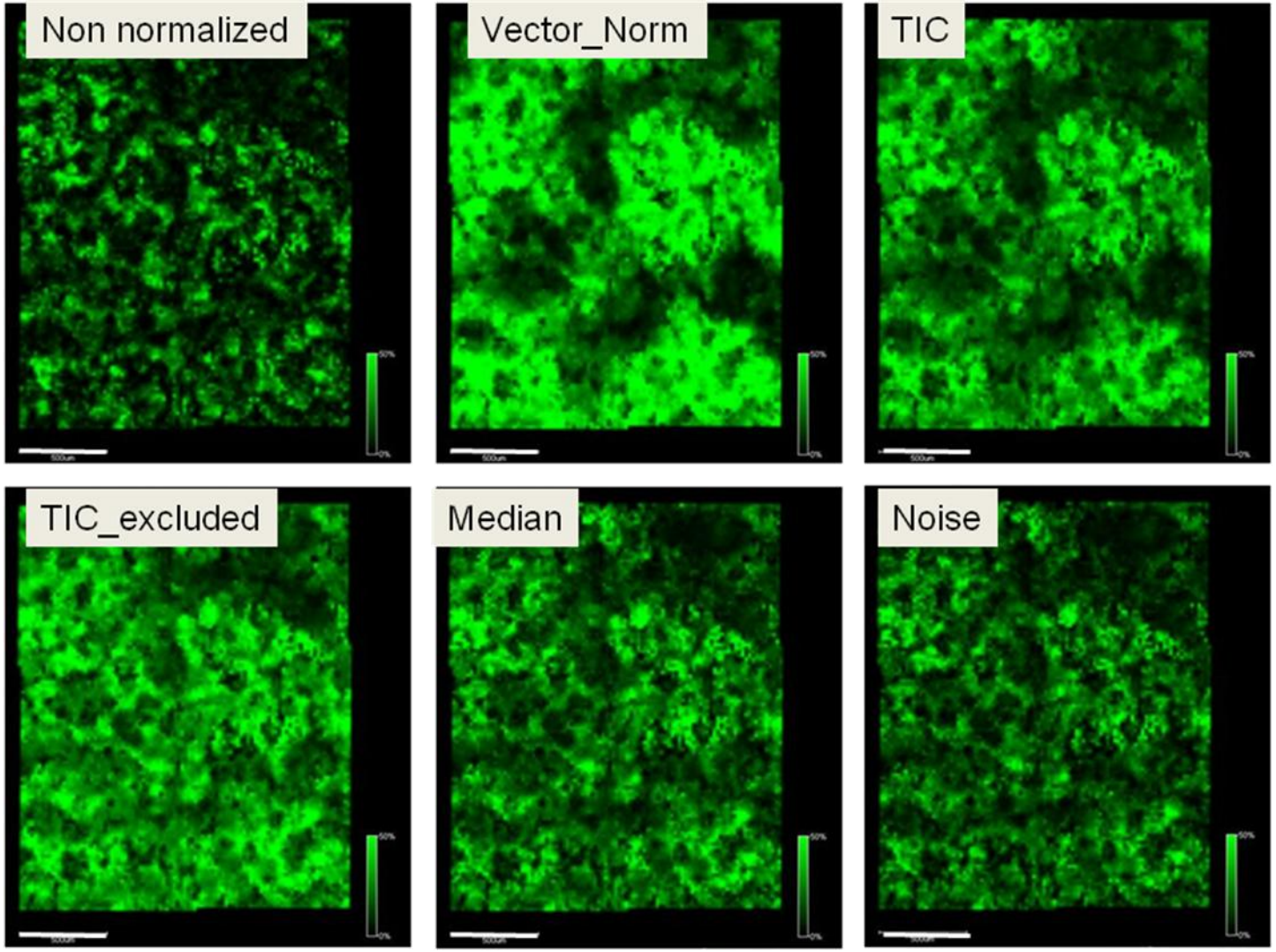

Fig S9 Rat testis, signal m/z 10260, with different normalization, scalebar 500 µm