

# Integrated Separation and Readout – Towards Field-diagnosis of Trypanosomiasis

Carlos Honrado<sup>1</sup>, Stefan H. Holm<sup>2</sup>, Jason P. Beech<sup>2</sup>, Bao D. Ho<sup>2</sup>, Daniel Spencer<sup>1</sup>, Michael P. Barrett<sup>3</sup>, Jonas O. Tegenfeldt<sup>2</sup> and Hywel Morgan<sup>1\*</sup>

<sup>1</sup>*Faculty of Physical Sciences and Engineering and Institute for Life Sciences, University of Southampton, Southampton, UK, SO17 1BJ*

<sup>2</sup>*Division of Solid State Physics, NanoLund, Lund University, Lund, Sweden, PO Box 118, S-221 00*

<sup>3</sup>*Wellcome Centre for Molecular Parasitology, Institute of Infection, Immunity and Inflammation, College of Medical, Veterinary and Life Sciences & Glasgow Polyomics, University of Glasgow, Glasgow, UK, G12 8TA*

The dataset contains the experimental data and Matlab codes needed to generate the figures of the article. In particular:

- “Figure5\_S2.mat” and “Figure5\_S2.m”, corresponding to the experimental data and code, respectively, to plot Figures 5 and S2;
- “Figure6.m”, containing the experimental data and code, to plot Figure 6;
- “Figure7.mat” and “Figure7.m”, corresponding to the experimental data and code, respectively, to plot Figure 7;
- “Figure8.m”, containing the experimental data and code, to plot Figure 8;
- “FigureS3\_S5.mat” and “FigureS3\_S5.m”, corresponding to the experimental data and code, respectively, to plot Figures S3 and S5;
- “FigureS4.mat” and “FigureS4.m”, corresponding to the experimental data and code, respectively, to plot Figure S4;

Extract the “.mat” (data) and “.m” (code) to the same directory. Run the script files in Matlab 2016 (or later) to generate the plots corresponding to each figure.