Functional phenotypic screening of patient iPSC-derived motor neurons – in vitro HTS disease modeling with micro electrode arrays coupled with multi-variate analysis methods.





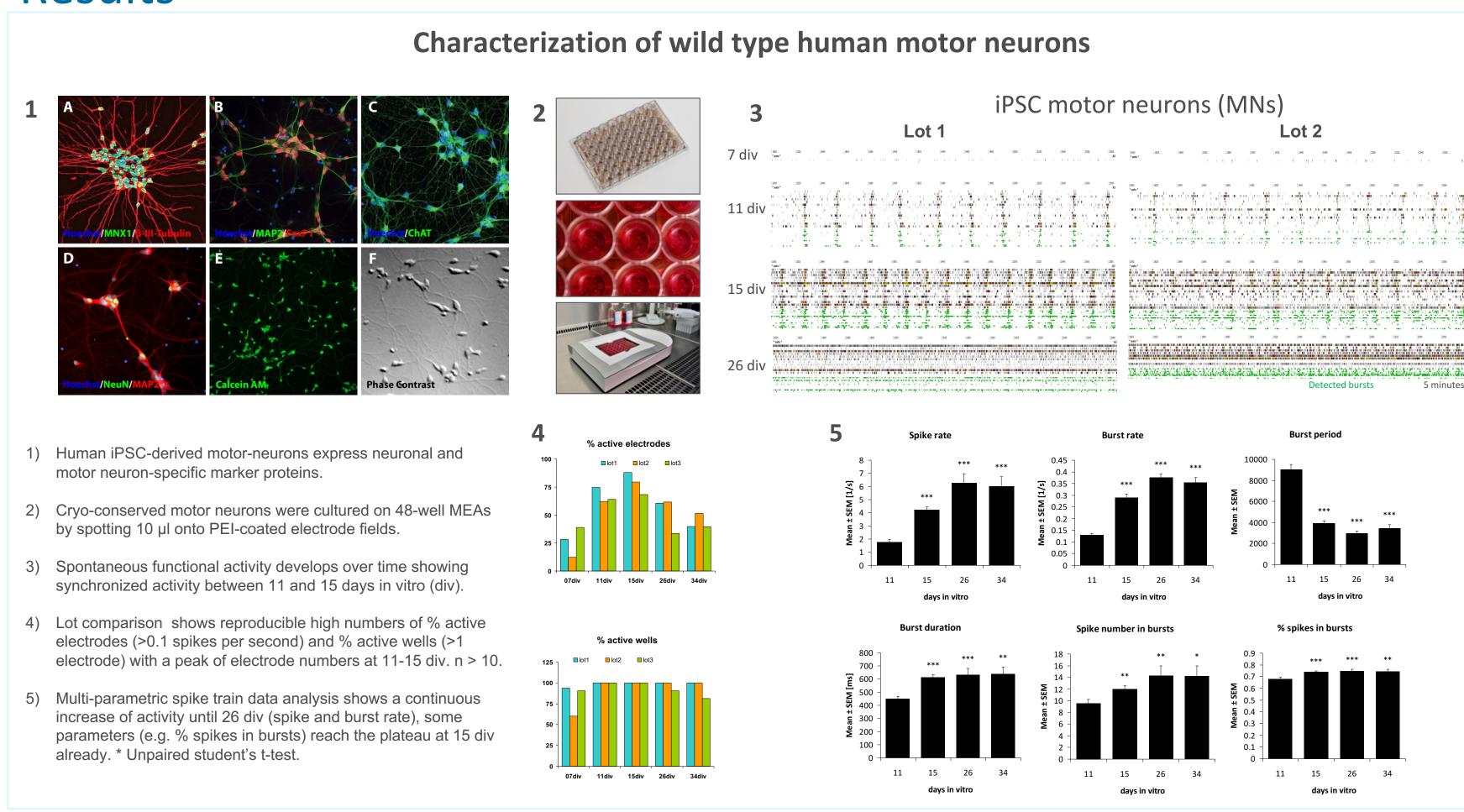
Monica Segura Castell¹, Luise Schultz¹, Konstantin Jügelt¹, Michael Hendrickson², Olaf H.-U. Schröder¹, Benjamin M. Bader¹

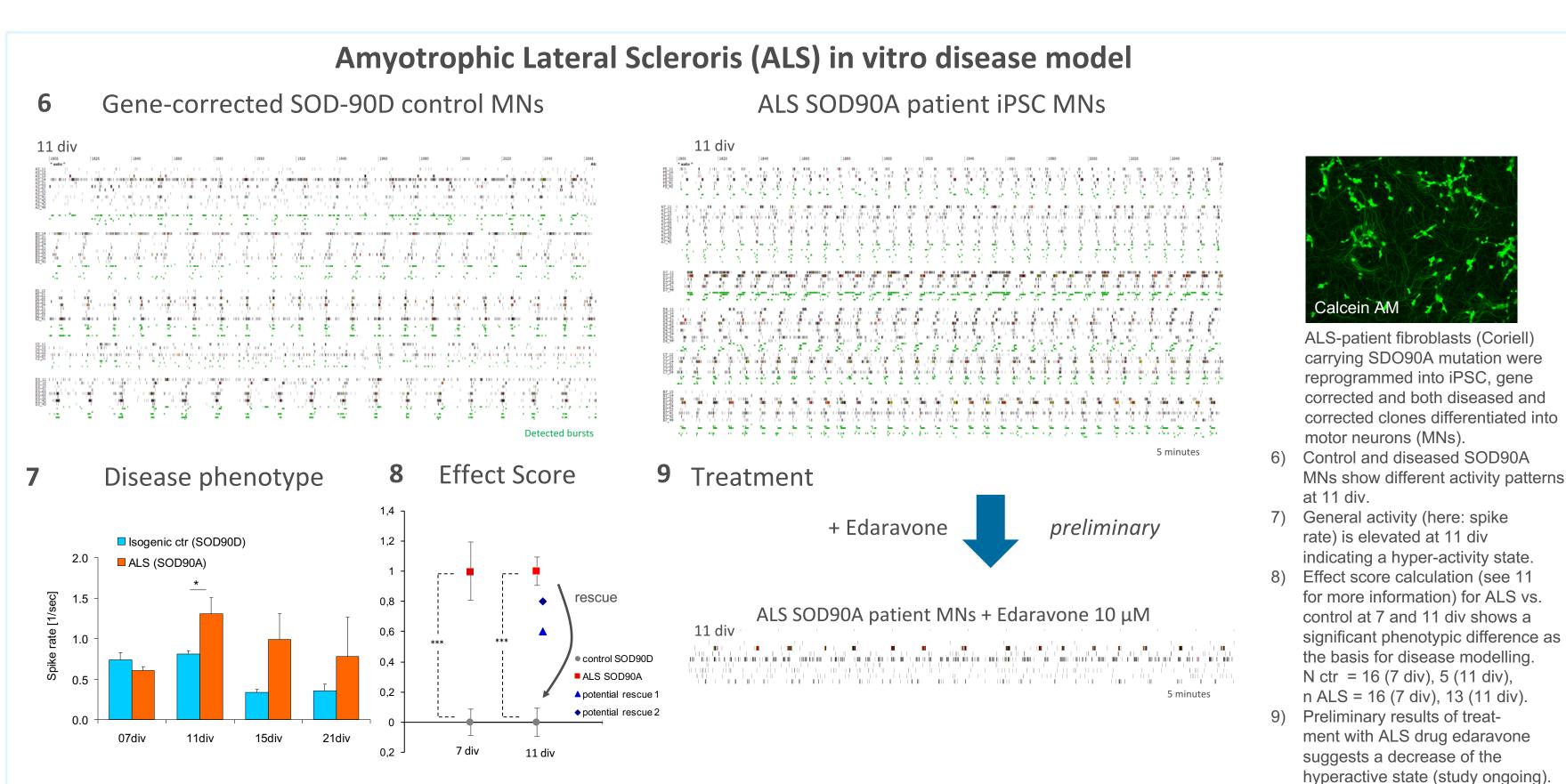
¹NeuroProof GmbH, Rostock, Germany, ²BrainXell Inc. Madison, Wi, USA. Contact and poster PDF: benjamin.bader@neuroproof.com

Objectives

One of the major challenges of drug discovery is decreasing attrition rates which requires developing more predictive pre-clinical in vitro models. Human induced pluripotent stem cell-derived (hiPSC) neuronal cultures promise higher physiological relevance and thus, better translation to the in vivo situation. Patient-derived iPSC models have been designed for various indications. We focused on investigating motor neuron diseases (MND) such as amyotrophic lateral sclerosis (ALS) and spinal muscular atrophy (SMA), which cause the loss of motor neurons. Our aims were to phenotypically describe the consequence of the genetic variation present in ALS and SMA patient iPSC-derived motor neurons on the functional activity and network connectivity. We further elucidated how functional ALS and SMA phenotypes separated from controls during network establishment to enabled compound testing to rescue the disease phenotypes.

Results



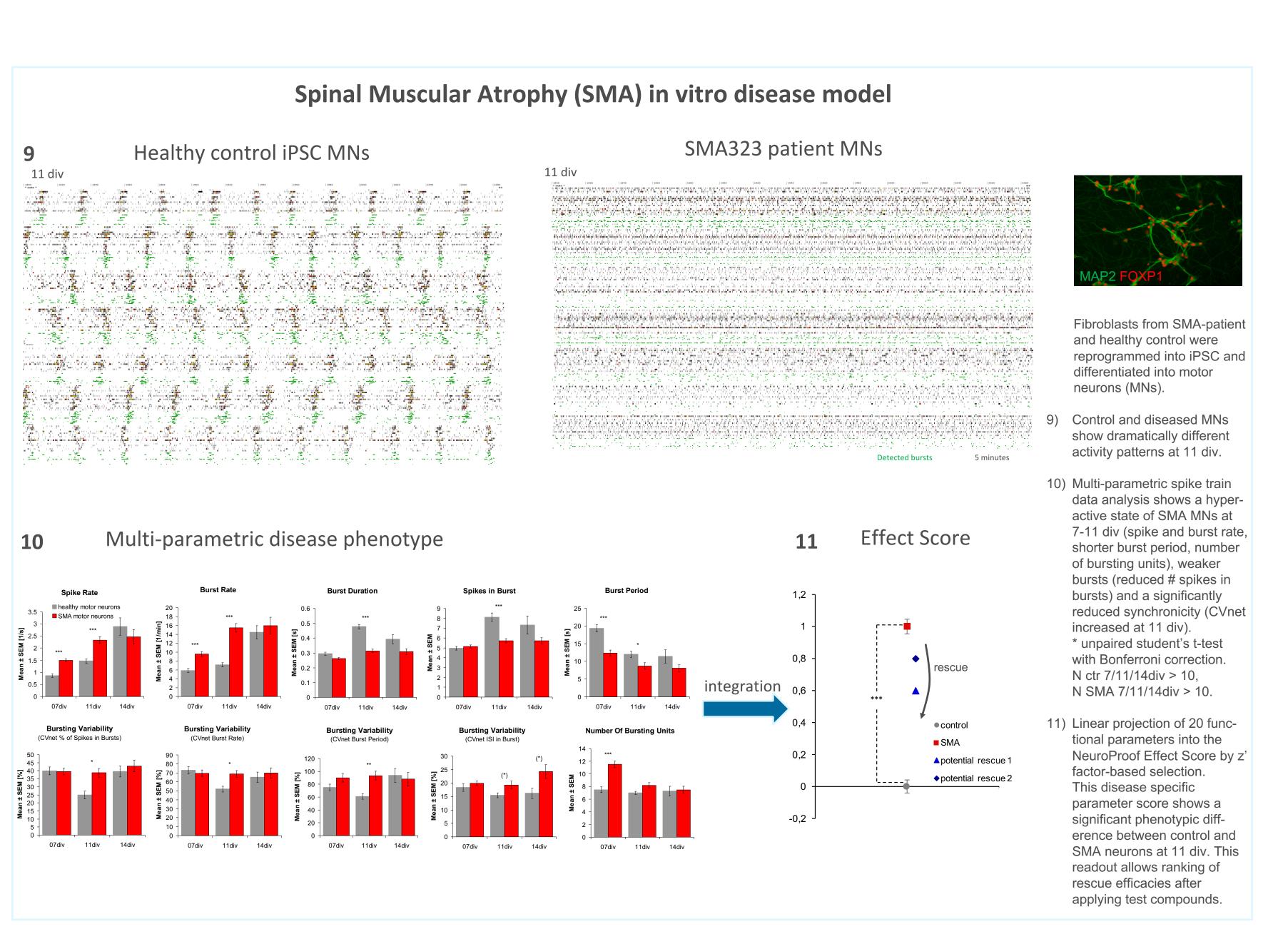


Methods

hiPSC culture: human iPSC-derived motor neurons from healthy control (lot 1-3), ALS patient and gene-corrected isogenic control and spinal muscular atrophy patient (SMA) (BrainXell) were cultured on 48 well MEAs (Axion Biosystems, USA).

MEA recording: MEAs were recorded on the MAESTRO recording station (Axion) at different days in vitro (div) during functional development. Per data point 60 minutes were recorded at 37°C und stable pH condition.

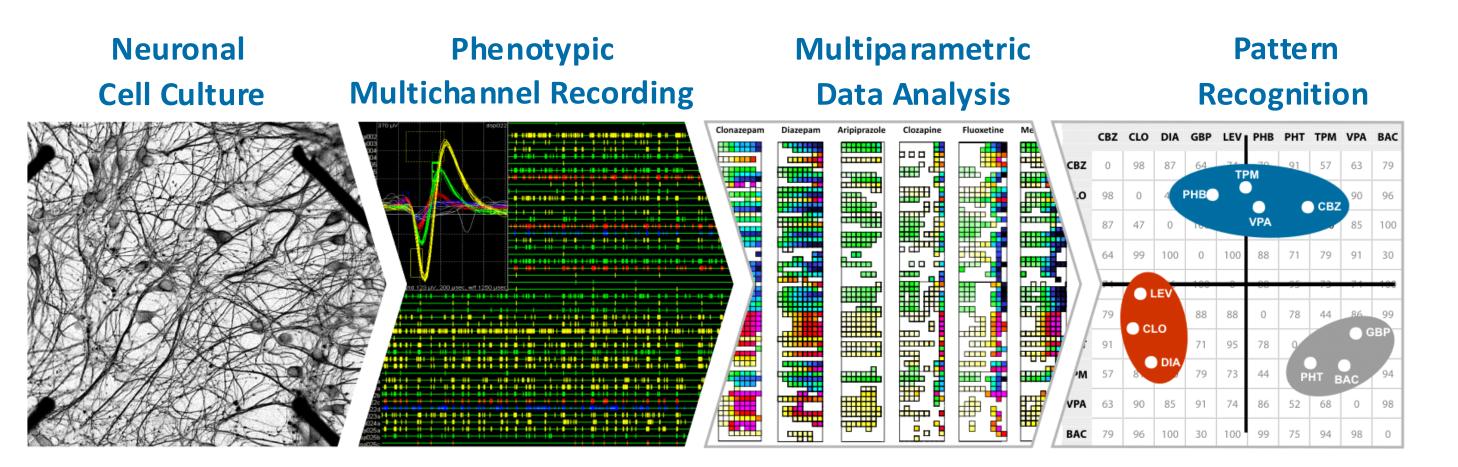
MEA Data analysis: Acquired spike train data was analysed multi-parametrically (NPWaveX software, NeuroProof). "Effect Score" calculation: Projection of multiple parameters into a single parameter based on Z' factor. For more information on Z'-factor, see Kuemmel et al. 2010. Biomol Screen 15(1):95-101 and Kozak et al. 2010.

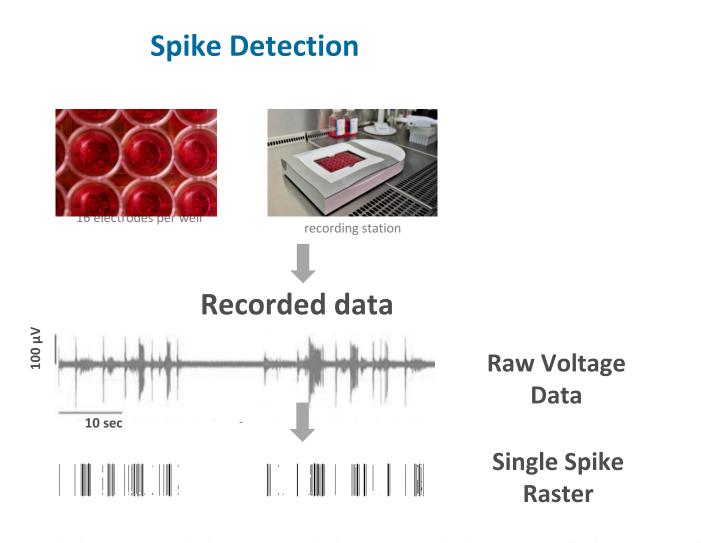


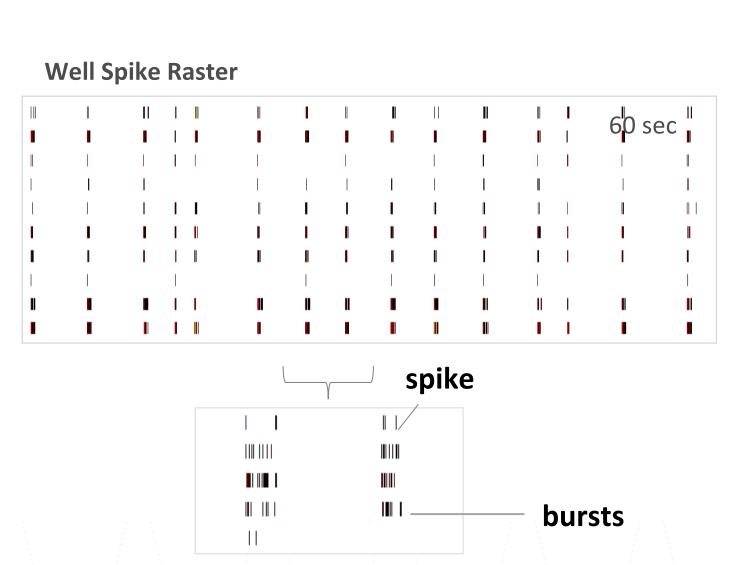
Summary and Conclusions

Our results show reproducible spontaneously active motor neuron networks with synchronized activity on the majority of the electrodes. We identified disease-specific functional phenotypes and show how reference compounds can affect them. In conclusion, we show that hiPSCderived motor neurons are able to produce meaningful functional in vitro phenotypes and that these phenotypes can be associated with known motor neuron diseases. By using artificial intelligence-based multivariate MEA data analyses combined with reproducible physiologically relevant iPSC neuron models we provide a functional phenotypic assay platform for high throughput compound screening.

NeuroProof Technology







Multi-parametric analysis Burst **Burst Area Burst Duration** Burst IBI **Burst Duration Burst Period Burst ISI**

Parameter sorted in 4 categories:

- General activity
- Burst structure
- Regularity/oscillation
- Synchronicity/connectivity