

# Extracellular vesicles isolated from human induced pluripotent stem cell-derived neurons contain a transcriptional network

David A. Hicks<sup>1\*</sup>, Alys C. Jones<sup>1#</sup>, Nicola J. Corbett<sup>1†</sup>, Kate Fisher<sup>1</sup>, Stuart M. Pickering-Brown<sup>1</sup>, Mark P. Ashe<sup>2</sup> and Nigel M. Hooper<sup>1\*</sup>

<sup>1</sup>Division of Neuroscience and Experimental Psychology and <sup>2</sup>Division of Molecular & Cellular Function

School of Biological Sciences, Faculty of Biology, Medicine and Health, University of Manchester, Manchester Academic Health Science Centre, Manchester, M13 9PT, United Kingdom

Current address: <sup>#</sup>Manchester University NHS Foundation Trust, Manchester, United Kingdom; <sup>†</sup>Discovery Research UK, MSD, London, United Kingdom

\* Correspondence:

David A. Hicks

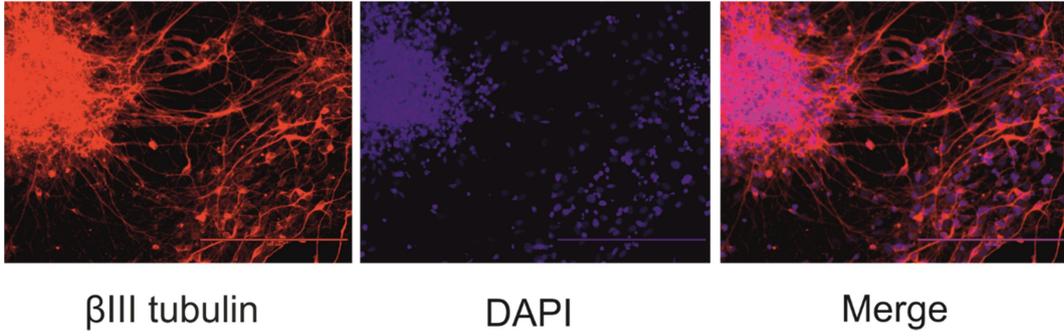
[david.hicks-2@manchester.ac.uk](mailto:david.hicks-2@manchester.ac.uk) (ORCID: [0000-0001-6045-1063](https://orcid.org/0000-0001-6045-1063))

Nigel M. Hooper

[nigel.hooper@manchester.ac.uk](mailto:nigel.hooper@manchester.ac.uk)

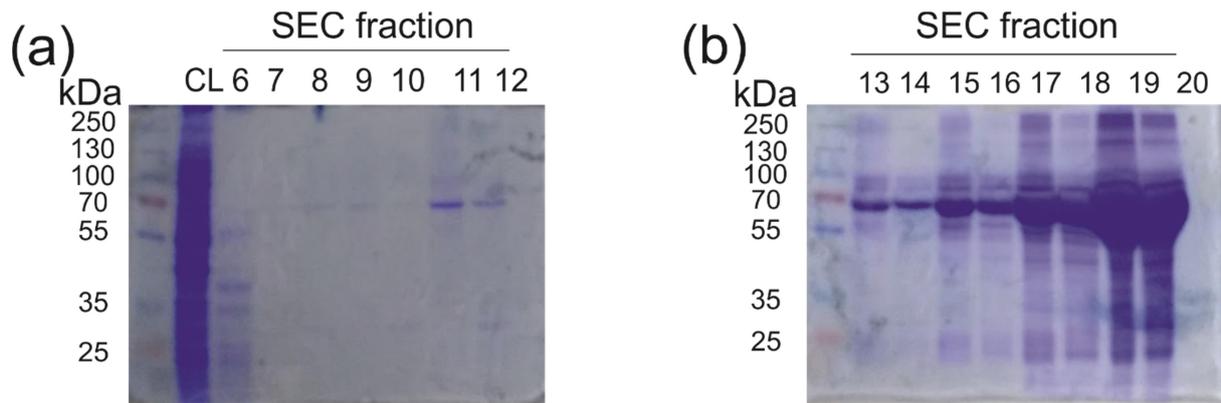
**Keywords:** Extracellular vesicles, neurons, RNA seq, proteomics, cell signalling

Running title: *Extracellular vesicle subtypes and transcriptional networks*



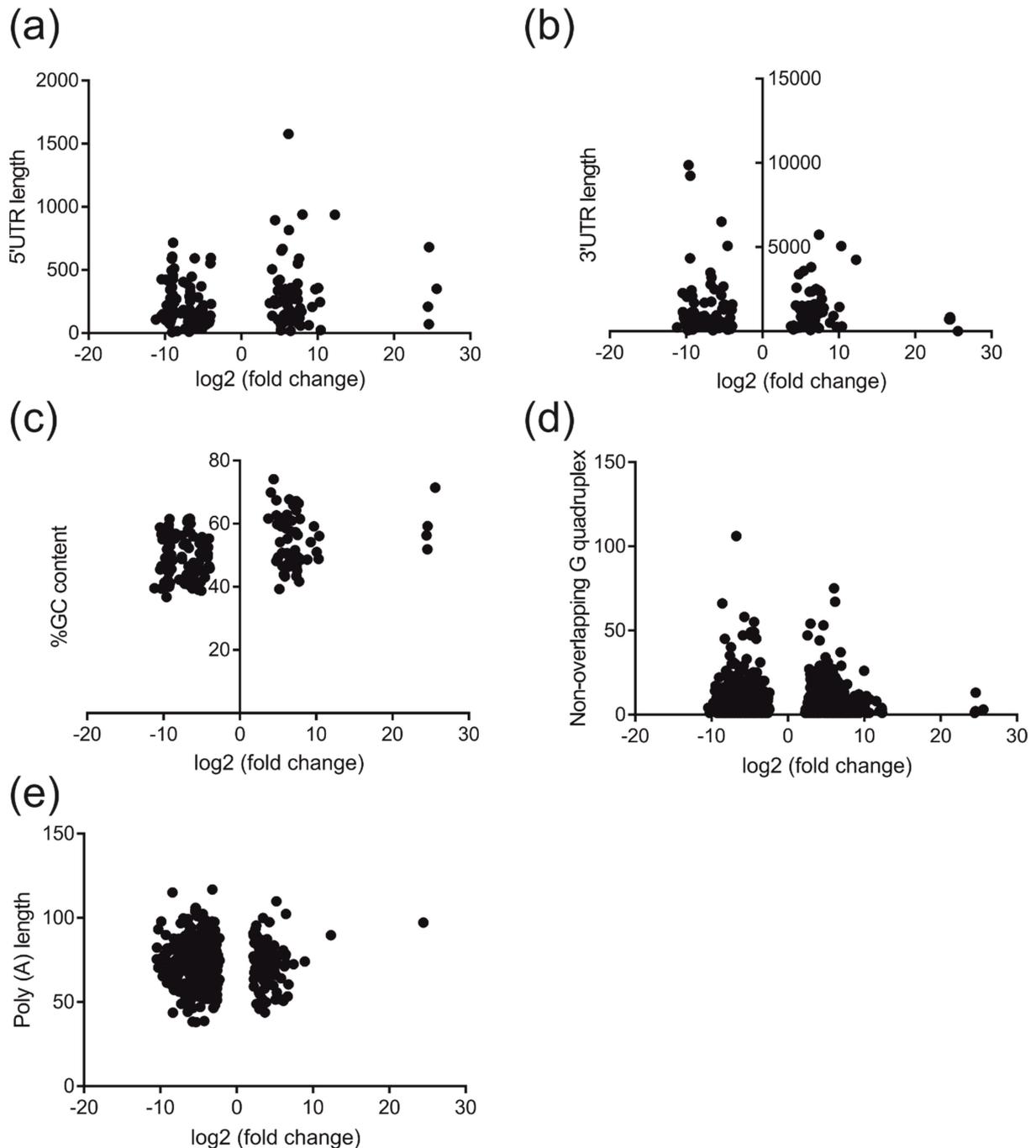
**Supplementary figure 1 Differentiation of iPSCs to neurons**

iPSCs were cultured as described in Experimental Procedures and differentiated to neurons fixed and immunocytochemistry performed using an antibody against the neuronal marker  $\beta$ III tubulin and the nuclear stain DAPI. Scale bar = 200 $\mu$ m.



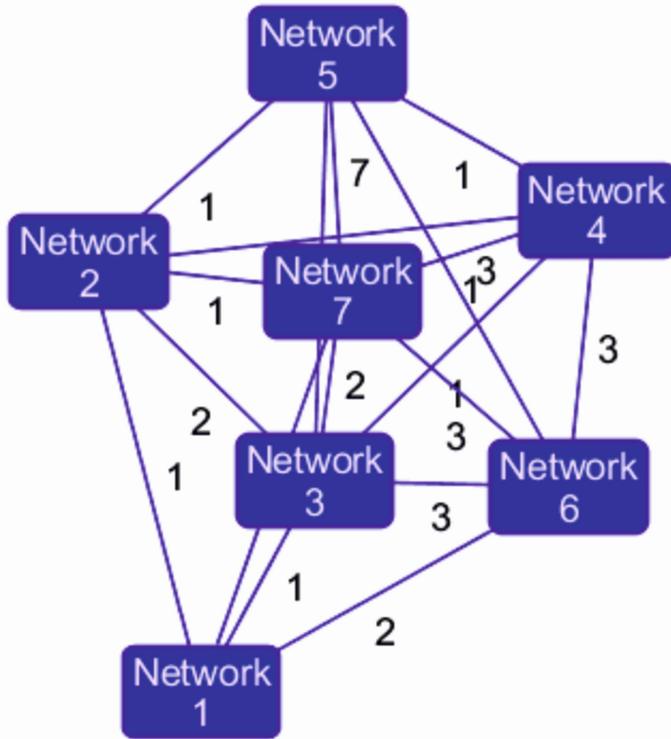
**Supplementary figure 2 Bulk protein elutes in non-vesicular SEC fractions**

EVs were isolated from iPSC-derived neurons as described by SEC and 0.5 ml fractions collected after elution of the column void volume. These fractions were subjected to SDS-PAGE alongside the cell lysate (CL) and the gels stained using Coomassie Blue. Gels were subsequently destained and imaged.



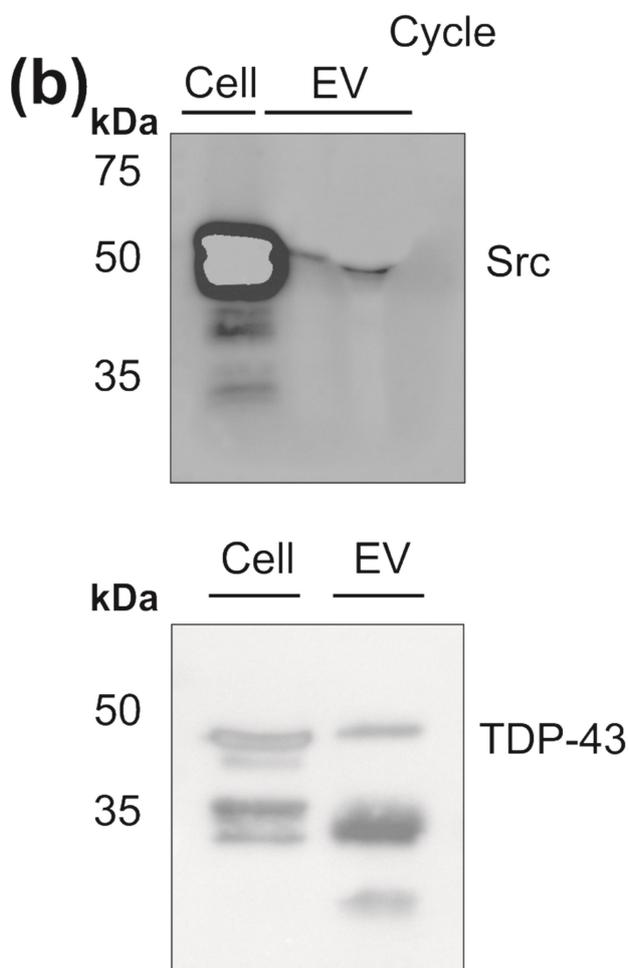
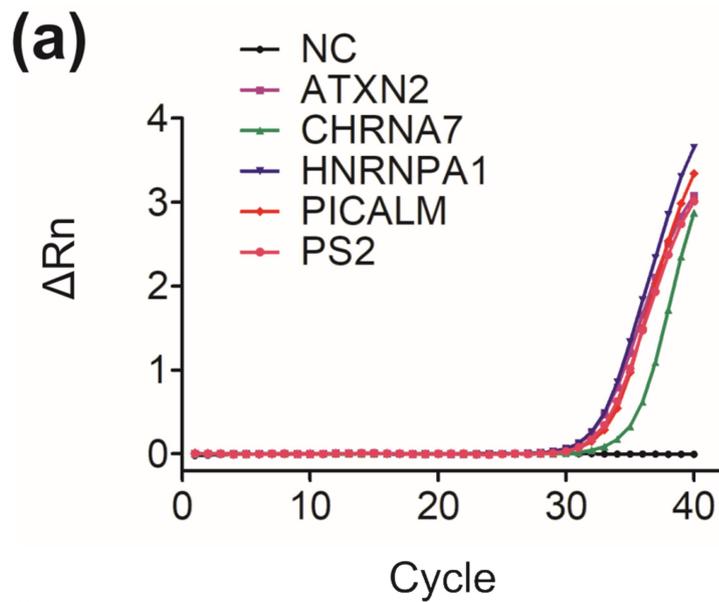
**Supplementary figure 3 EV-enriched RNA has a significantly increased GC content**

Genes identified by RNA seq were cross-referenced against databases to establish (a) 5'UTR length (Spearman  $r = 0.12$ ;  $p = 0.15$ ) (b) 3'UTR length (Spearman  $r = 0.09$ ;  $p = 0.28$ ) (c) %GC content (Spearman  $r = 0.19$ ;  $p < 0.0001$ ) (d) predicted non-overlapping G quadruplexes (Spearman  $r = 0.03$ ;  $p = 0.13$ ) and (e) poly (A) tail length (Spearman  $r = -0.02$ ;  $p = 0.30$ ). Datasets were assessed for Gaussian distribution by D'Agostino Pearson test and correlation by Spearman's rank correlation. Only a subset of the total data for (c) 150/ 18104 total and (d) 500/ 3863 total are displayed.



**Supplementary figure 4 Transcriptomic IPA networks are predominantly non-overlapping**

Transcriptomic IPA networks were displayed to identify gene interrelationships, with common network genes enumerated and shown on inter-network connecting lines.



**Supplementary figure 5 RNA seq and proteomics data can be validated by qPCR and immunoblot**

**(a)** EV mRNA was isolated as described and the presence of target transcripts assessed by gene-specific primers for ATXN2, CHRNA7, HNRNPA1, PICALM and PSEN2. NC is negative control, with reverse transcriptase omitted from the cDNA synthesis reaction. **(b)** EVs were isolated as described and the vesicular fractions

pooled. Cell and EV samples were separated by SDS-PAGE followed by immunoblotting with antibodies targeting Src and TDP-43.