

Supplementary information (SI) for:

## *Ribosome fingerprinting with a solid-state nanopore*

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# Equal contribution

## Additional Figures

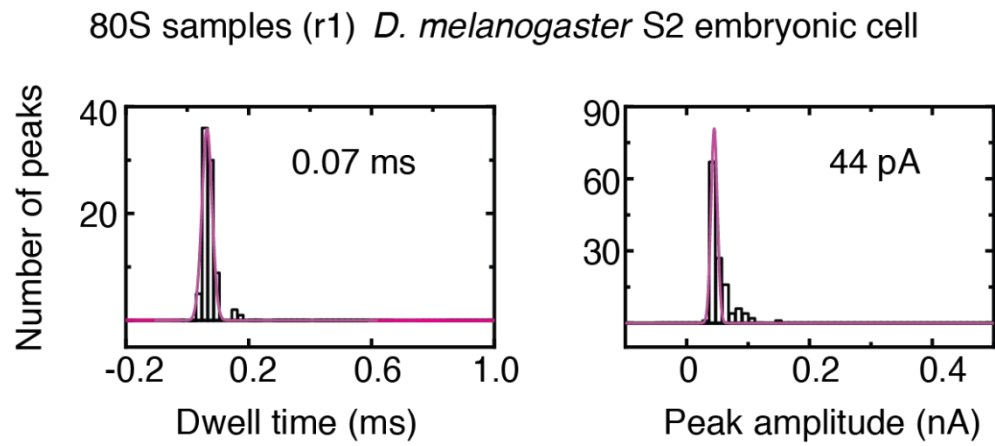


Figure S1 Dwell time and peak amplitude histogram for 80S ribosome samples (r1) from *D. melanogaster* S2 embryonic cell line.

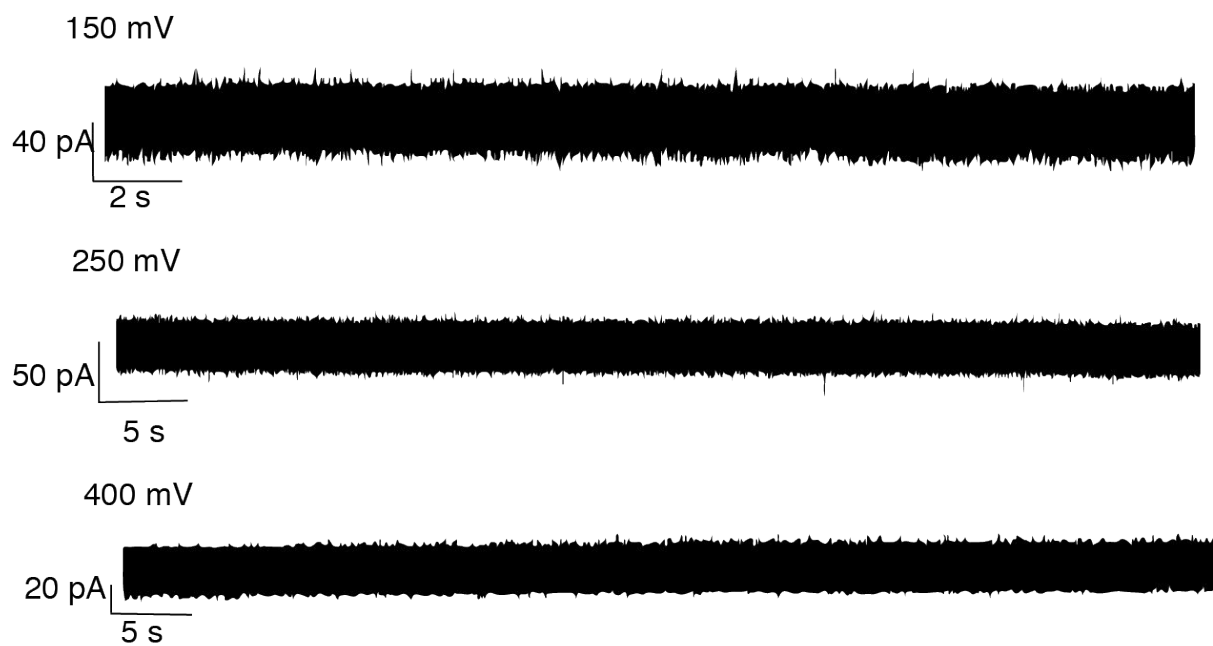


Figure S2 Ion current traces obtained at different voltages (150 mV, 250 mV and 400mV) with 40S samples from *D. melanogaster* S2 embryonic cell line. No events were observed.

*D. melanogaster* S2 embryonic cell line

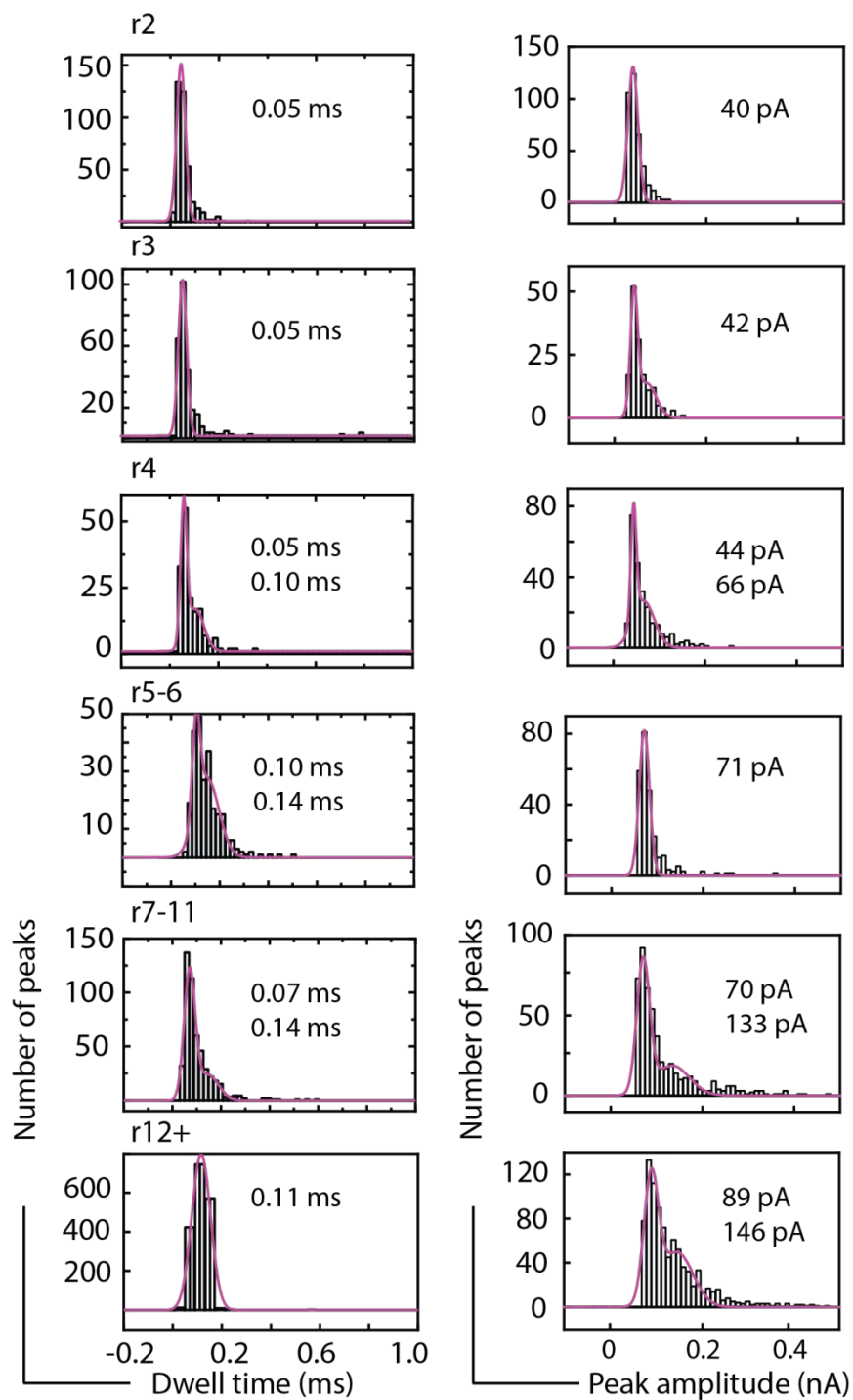


Figure S3 Individual histograms of dwell time and peak amplitude observed for the different polysome samples extracted from *D. melanogaster* S2 embryonic cells. The pink line follows the gaussian fit.

*D.melanogaster* embryonic cell line

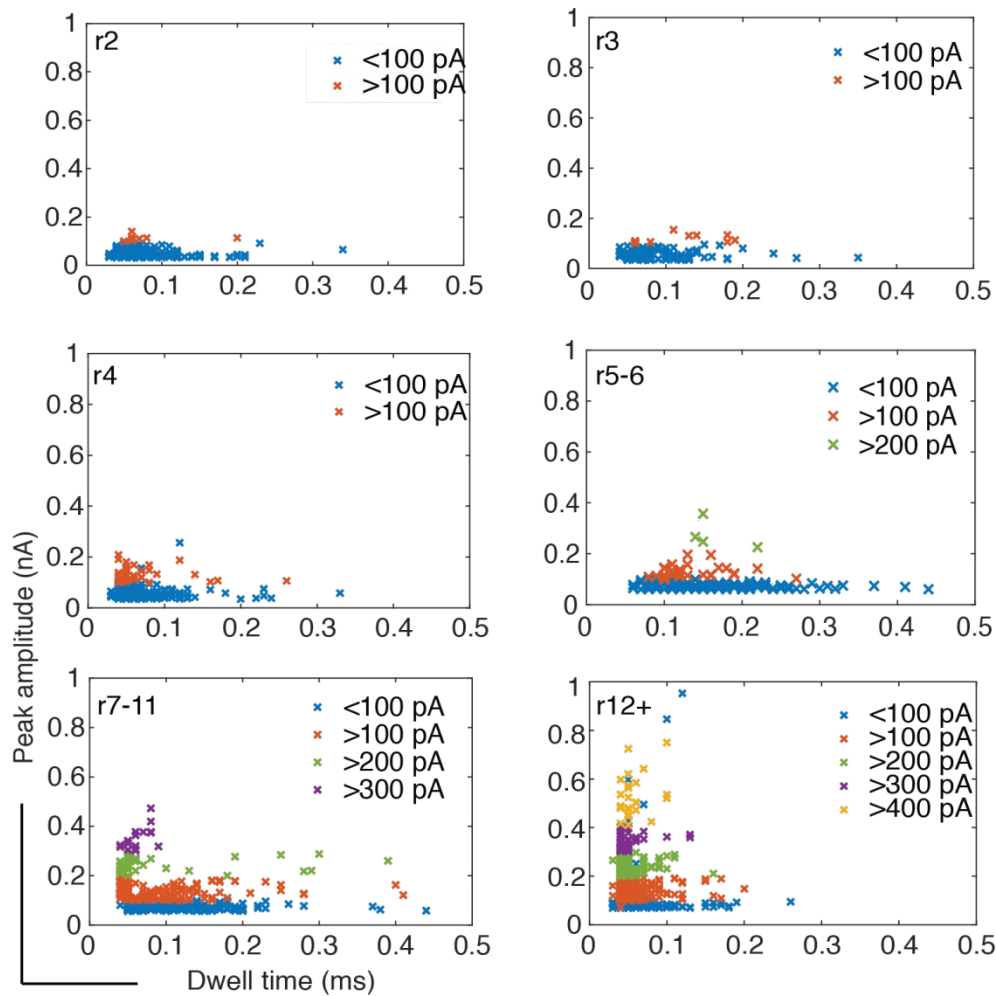


Figure S4 Scatter plots of peak amplitude plotted against dwell time for the *D. melanogaster* S2 cell samples. The events are colour-coded every 100 pA to highlight the increase in peak amplitudes.

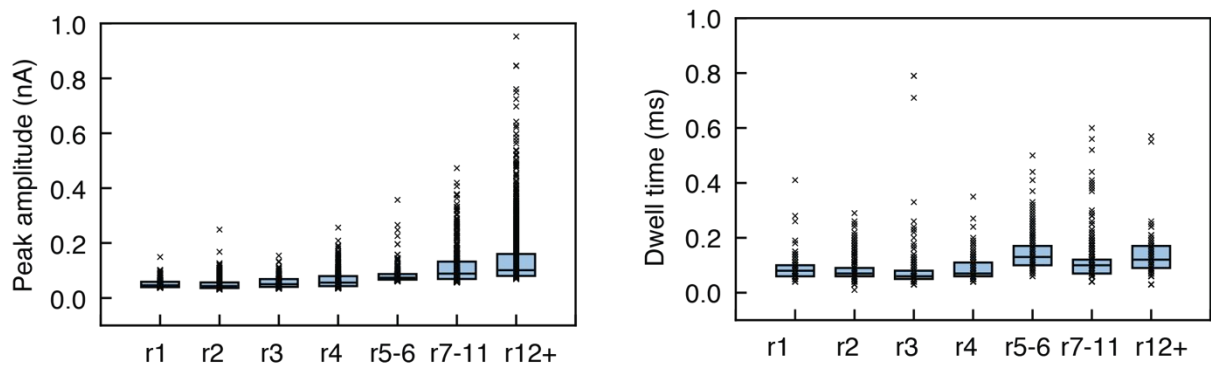
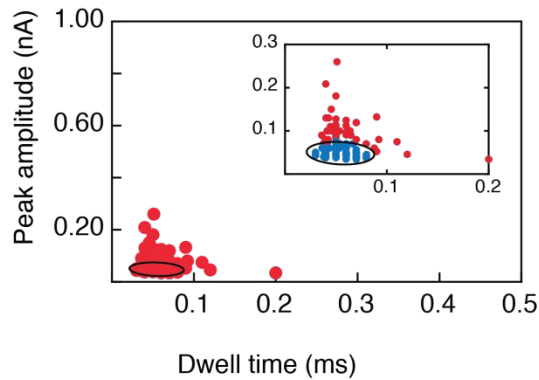


Figure S5 Peak amplitude and dwell time data for the 80S ribosome (r1) and various polysome samples (r2, r3, r4, r5-6, r7-11, r12+) of *D. melanogaster* S2 cells. The data represent >100 events for each sample. Error bars indicate standard deviation of the sample mean.

a) 80S (r1) and r2, r3, r4 mix



b) 80S (r1) and polysome mix (r2, r3, r4, r5-6, r7-11, r12+)

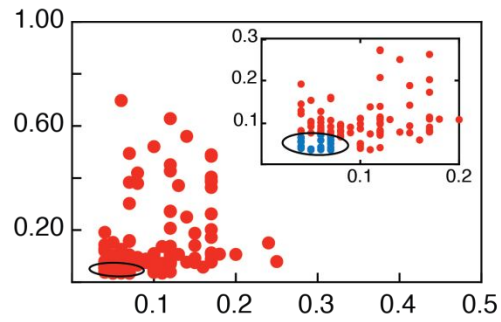


Figure S6 Scatter plots of peak amplitude plotted against dwell time for ribosome (r1) and polysome mixtures from S2 cells, the data contains >100 events for each sample. The 95% confidence ellipse fitted for individual r1 data is used as boundary to differentiate r1 from the mixture.

#### *D. melanogaster* ovaries

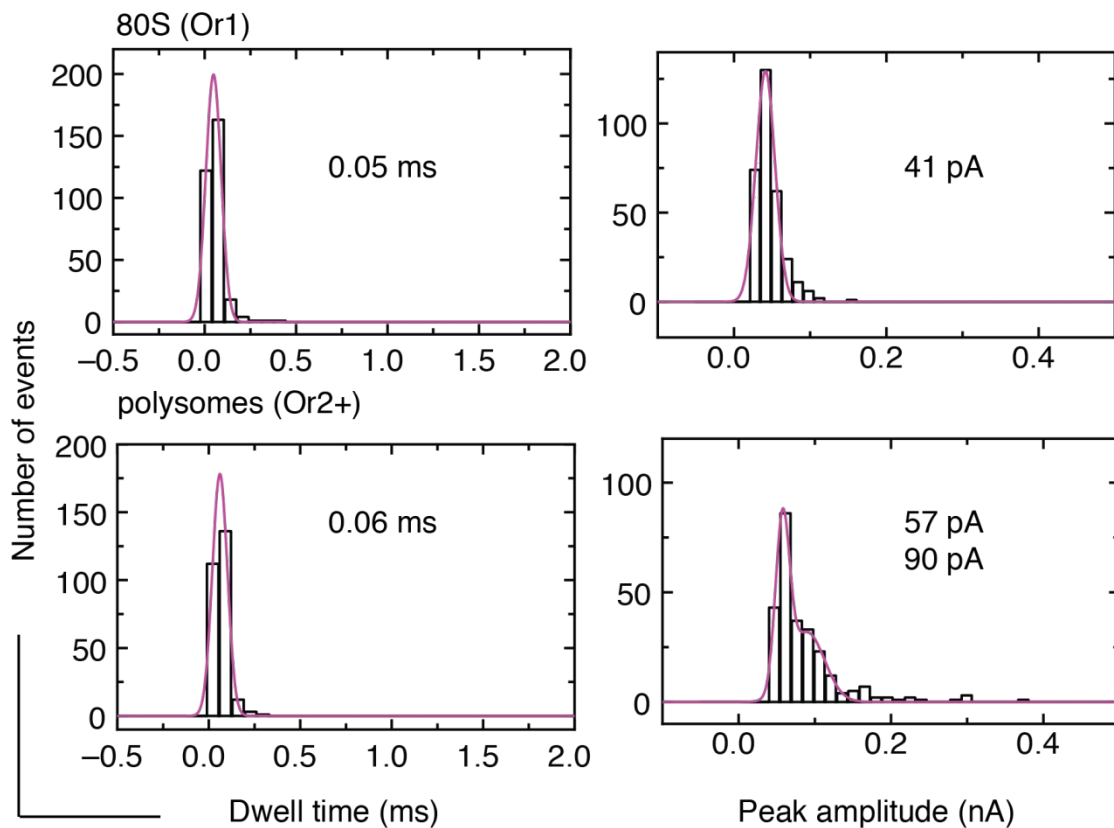


Figure S7 Histograms of peak amplitude and dwell times observed for 80S (Or1) and polysome samples (Or2+) extracted from *D. melanogaster* ovaries. The pink line follows the gaussian fit.

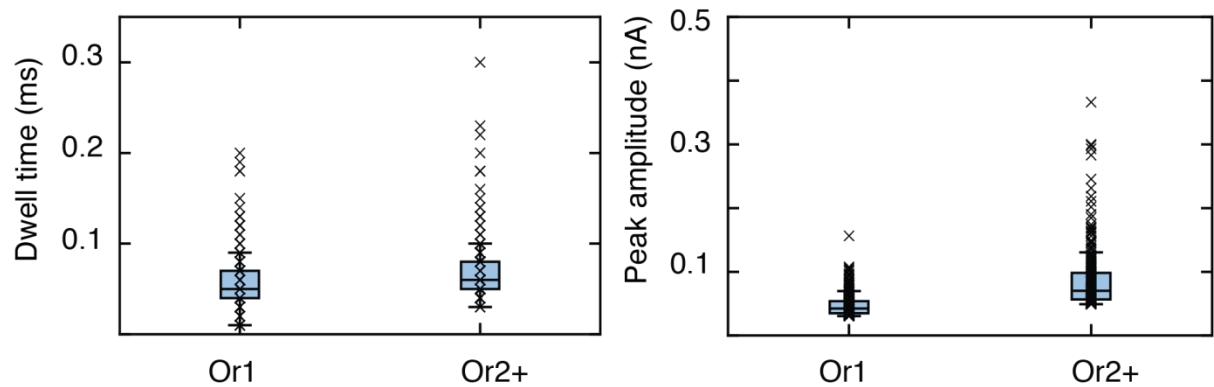


Figure S8 Individual dwell time and peak amplitude data plot for *D. melanogaster* ovaries samples (80S ribosome Or1 and polysomes Or2+), the data represents >100 events from a 2 minute ion current trace for each sample. The error bars indicate the standard deviation of the sample mean.

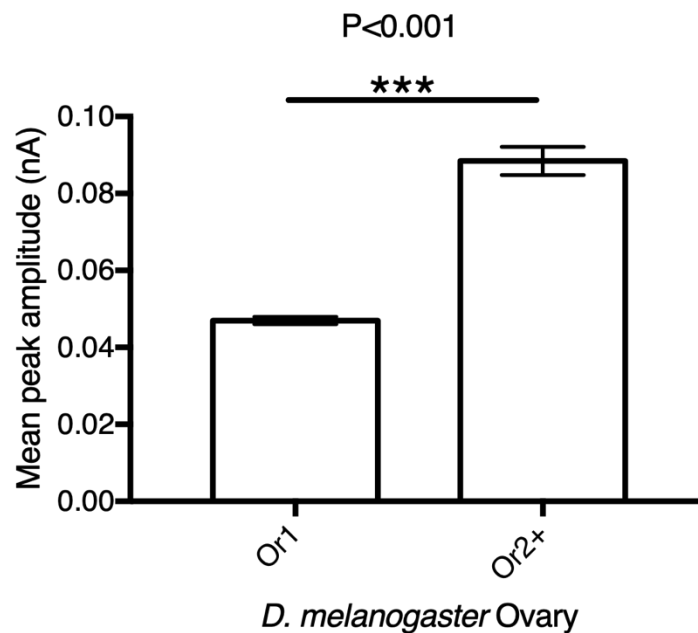


Figure S9 Mean peak amplitude data for *D. melanogaster* ovaries samples Or1 and Or2+ exhibiting a significant difference with  $p < 0.001$  represented with \*\*\*. Mann Whitney t-test was used for this data and the error bars represent standard error of mean.

Human neuronal cell lines

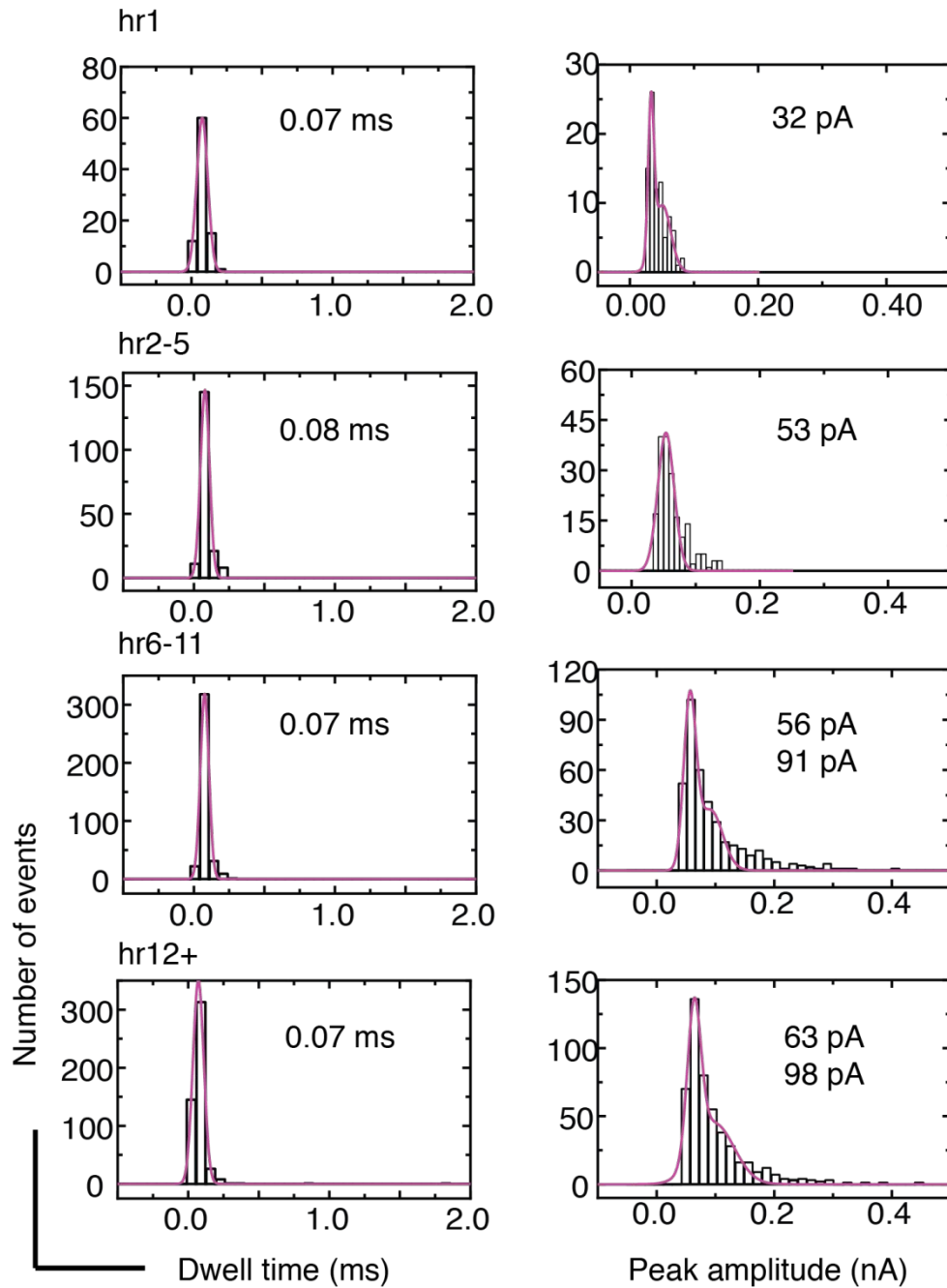
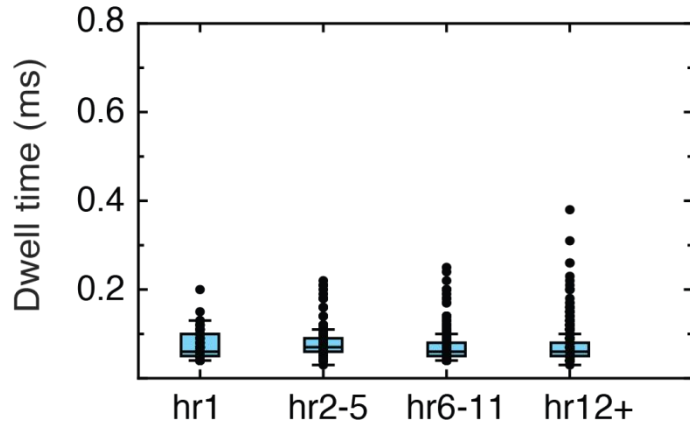


Figure S10 Individual dwell time and peak amplitude histogram data for single ribosome and polysome samples obtained from human SH-SY5Y cells. The pink line follows the gaussian fit.



SH-SY5Y cells

Figure S11 Dwell time data for human SH-SY5Y cells 80S ribosome and polysome samples, the plot consists of >100 events for each sample.

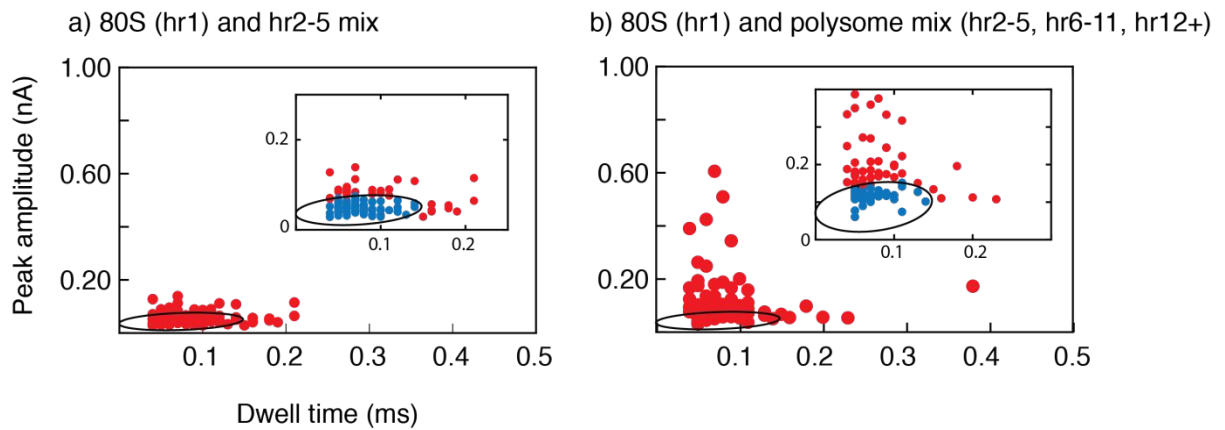


Figure S8 Scatter plots of peak amplitude plotted against dwell time for ribosome and polysome mixture from human SH-SY5Y cells, the data contains >100 events for each sample. The 95% confidence ellipse fitted for individual hr1 data is used as boundary to differentiate them from the mixture.



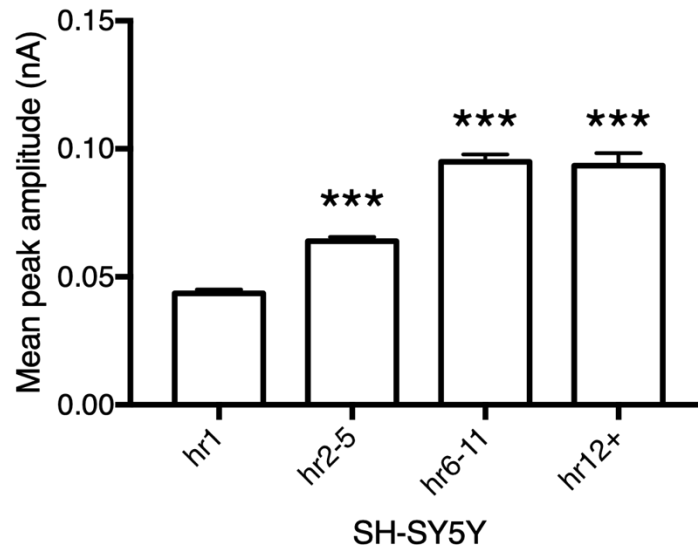


Figure S9 Human neuronal cell line samples. Mean peak amplitude data of SH-SY5Y polysomes compared with 80S samples (hr1) exhibit a significant difference of  $p < 0.001$  represented by \*\*\*. Kruskal-Wallis test was performed for this data and the error bars indicate the standard error of mean.