Supplementary Information

Differential Nucleosome Spacing in Neurons and Glia

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CONTENTS

Table S1. Summary of paired-end data: MNase-seq and RNA-seq.

MNase-seq (millions of paired reads)					
Astrocytes		DRG		OPC	
Rep. 1	Rep. 2	Rep. 1	Rep. 2	Rep. 1	Rep. 2
701.3	487.4	747.5	594.3	742.7	458.8

RNA-seq (millions of paired reads)								
Astrocytes			DRG			OPC		
Rep. 1	Rep. 2	Rep. 3	Rep. 1	Rep. 2	Rep. 3	Rep. 1	Rep. 2	Rep. 3
67.9	53.8	46.5	44.4	77.5	63.4	65.5	66.1	56.4

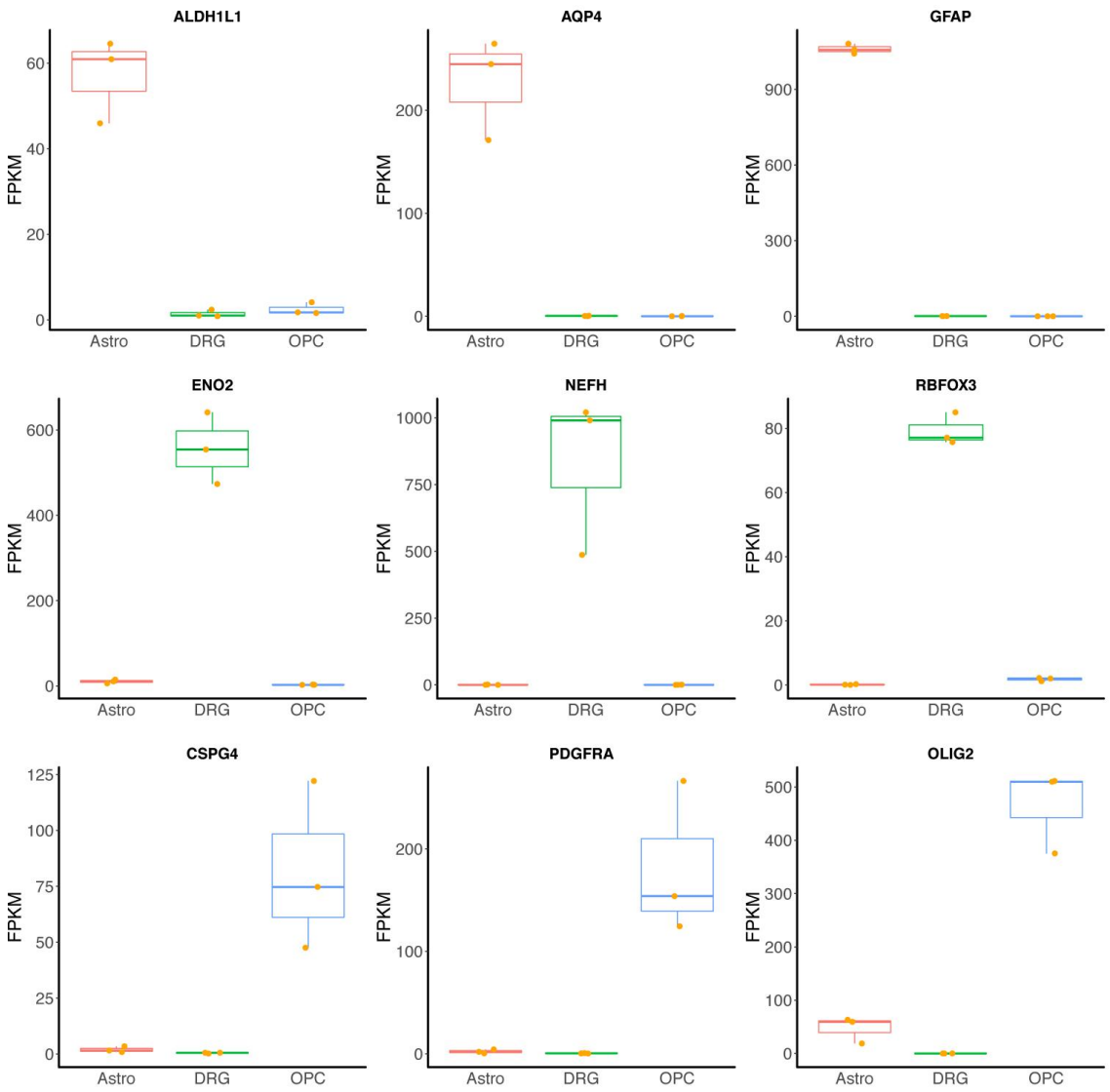

Fig. S1. Purity of primary cell cultures determined using RNA-seq data for OPCs, DRG neurons and astrocyte cultures. Gene expression levels (in FKPM) for three cell type-specific genes for each cell type. These data are consistent with immunostaining for all three cell types.

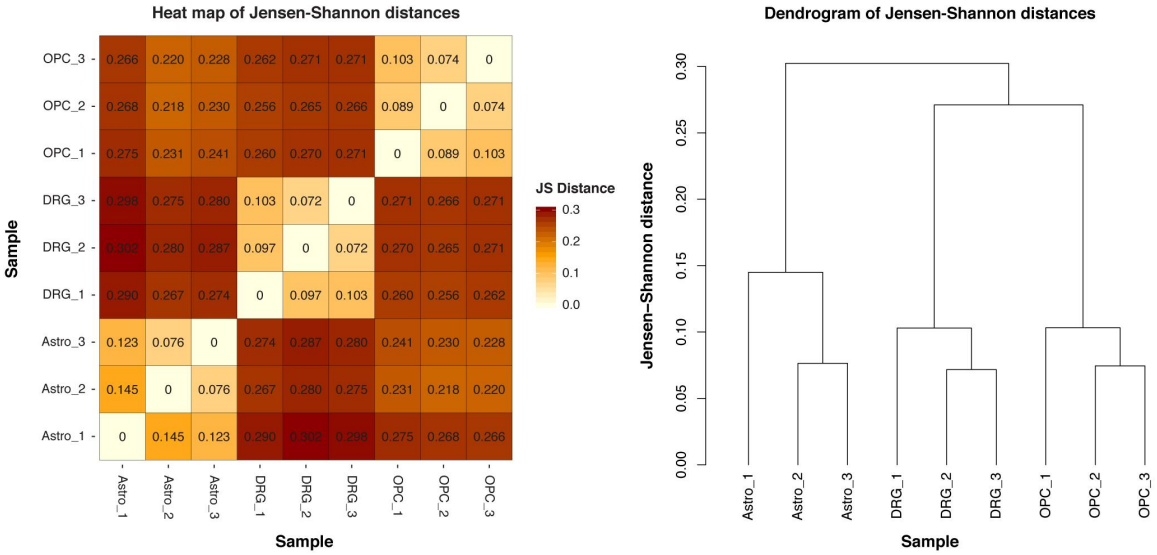

Fig. S2. Comparison of RNA-seq experiments using the Jensen-Shannon distance between all pairs of samples. Three biological replicate experiments were performed for each cell type. Left panel: heat map. Right panel: dendrogram. As expected, the replicate experiments form three clusters corresponding to the three distinct cell types.

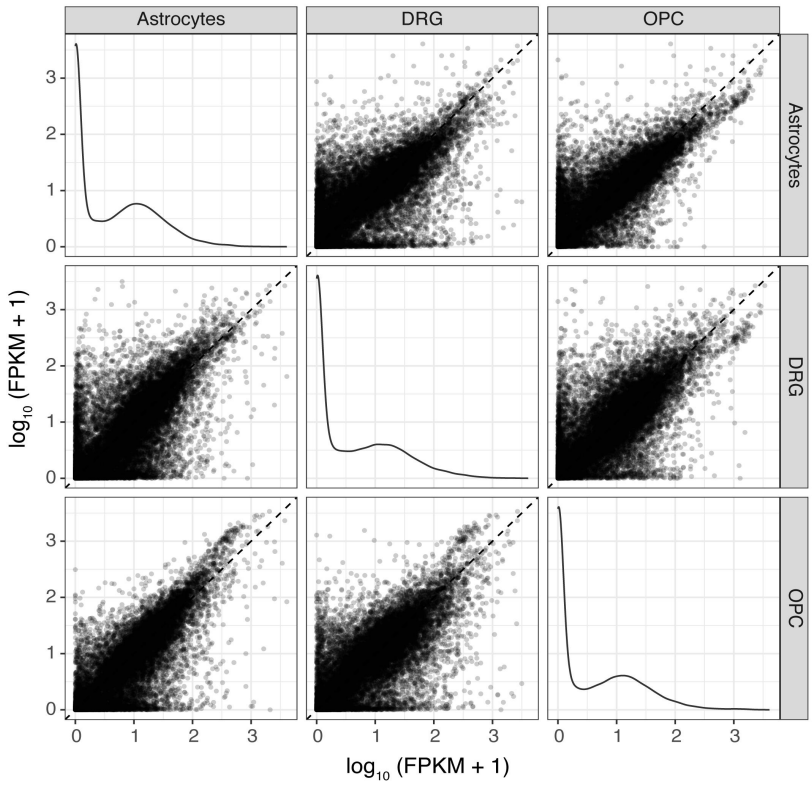

Fig. S3. Comparison of gene expression patterns in DRG neurons, OPCs and astrocytes. Panels along the main diagonal beginning at top left: histograms showing relative expression levels (FPKM) of genes in each cell type. Panels off the main diagonal: scatter plots showing pairwise comparisons of RNA-seq data for the three cell types.

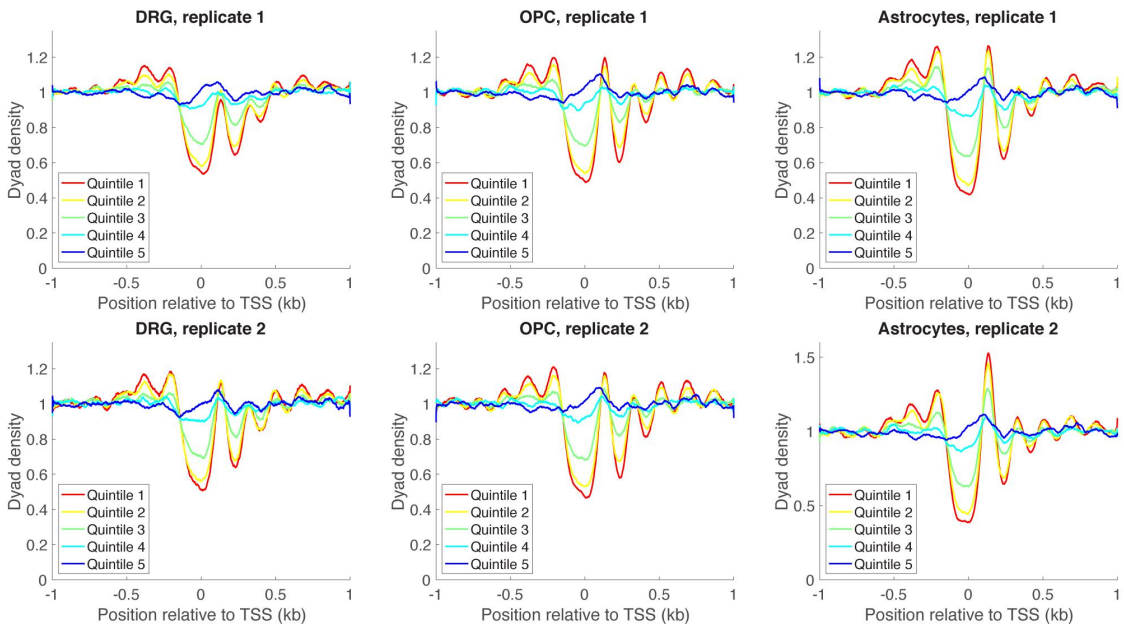

Fig. S4. Average dyad density for genes grouped into five quintiles according to their expression levels in DRG neurons, OPCs and astrocytes (two replicate experiments). Quintile 1 contains the most expressed genes. The promoters of the most active genes are nucleosome depleted and flanked by phased nucleosomes (Fig. 2A).

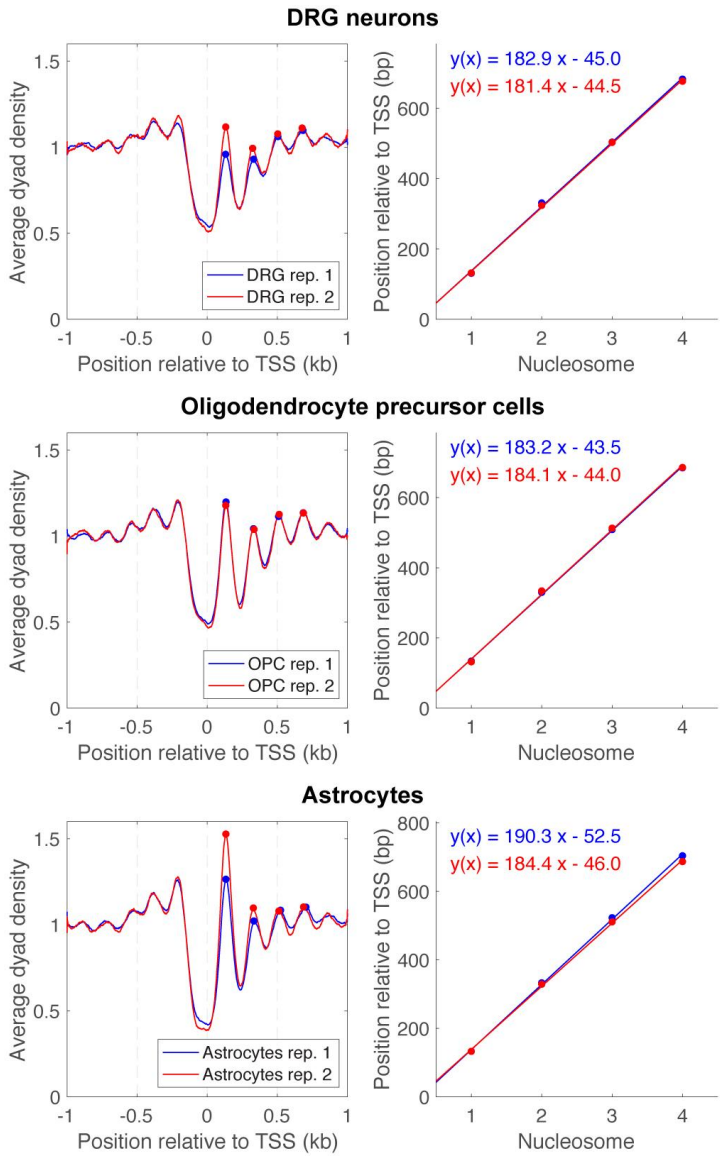

Fig. S5. Measurement of average nucleosome spacing relative to the transcription start site (TSS) for the most active gene promoters (quintile 1; Fig. 2A) in DRG neurons, OPCs and astrocytes. Left panels: Phasing plots of average nucleosome dyad (center) density vs. distance for the TSS in kb. Biological replicate experiments 1 (blue line) and 2 (red line). Right panels: Regression analyses of the distance of each nucleosome peak in base pairs from the TSS *vs*. the nucleosome peak number (data from left panels). The average spacing is given by the slope.