Supporting Information for:

RNA-Seq from Single Nuclei

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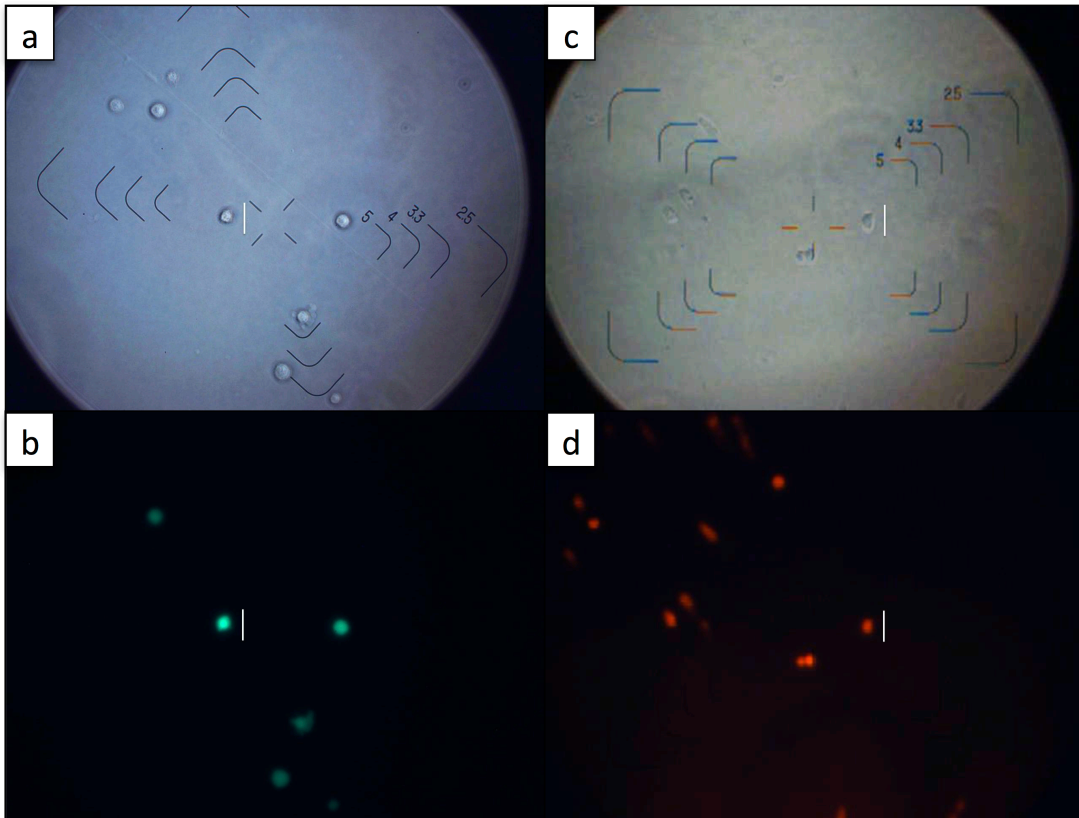> **Supporting Information Methods S1-S5**

Figures

Figure S1. Evaluation of FACS sorted single cells and single nuclei using fluorescence microscopy. Single cells and nuclei were sorted onto a slide containing 100 µl of 1X PBS. Imaging was done by phase contrast microscopy (a,c) and epifluorescence microscopy (b,d). **(a,b):** Sorted NPC cells (400X). **(c,d):** Sorted NPC nuclei (600X), stained with propidium iodide (d) (600X). White line is a 25 µm calibration ruler.
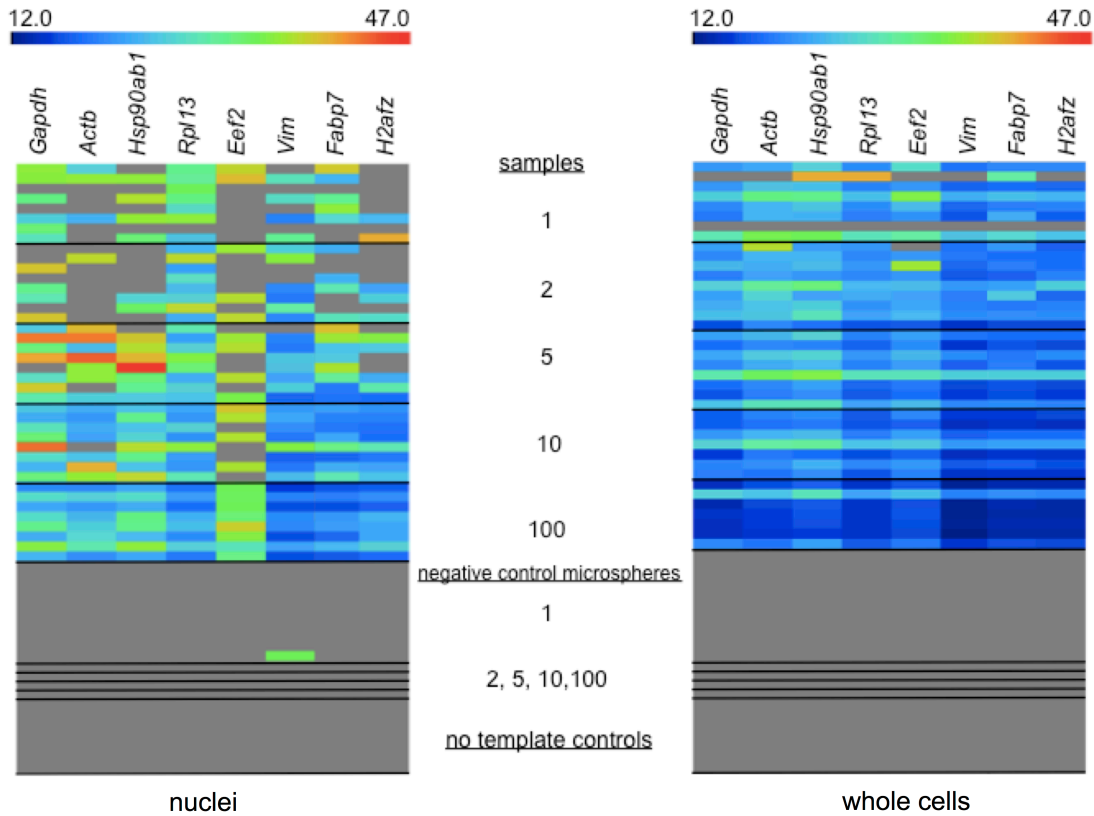
Figure S2. Heat map of TaqMan Ct values for the sorted NPC-EYFP nuclei and whole cells.
Samples were FACS sorted corresponding to (1, 2, 5, 10, 100 cells or nuclei), sorted negative microspheres of NPC-YFP whole cells and nuclei (1, 2, 5, 10, 100 beads), and non-template controls (NTC). The heat map scale ranges from 12 to 47 Ct (representing high to low expression). Gray sections in the heat map indicate no Ct detection. Eight replicates were tested for single cells or nuclei and only one sample was tested for the 2, 5, 10 and 100 cells or nuclei. A single positive event obtained from one control microsphere sort was associated with a Ct value of 39, which is a marginal value for reliable detection, and about 13 cycles later than Ct values obtained when a single cell or nucleus was sorted.
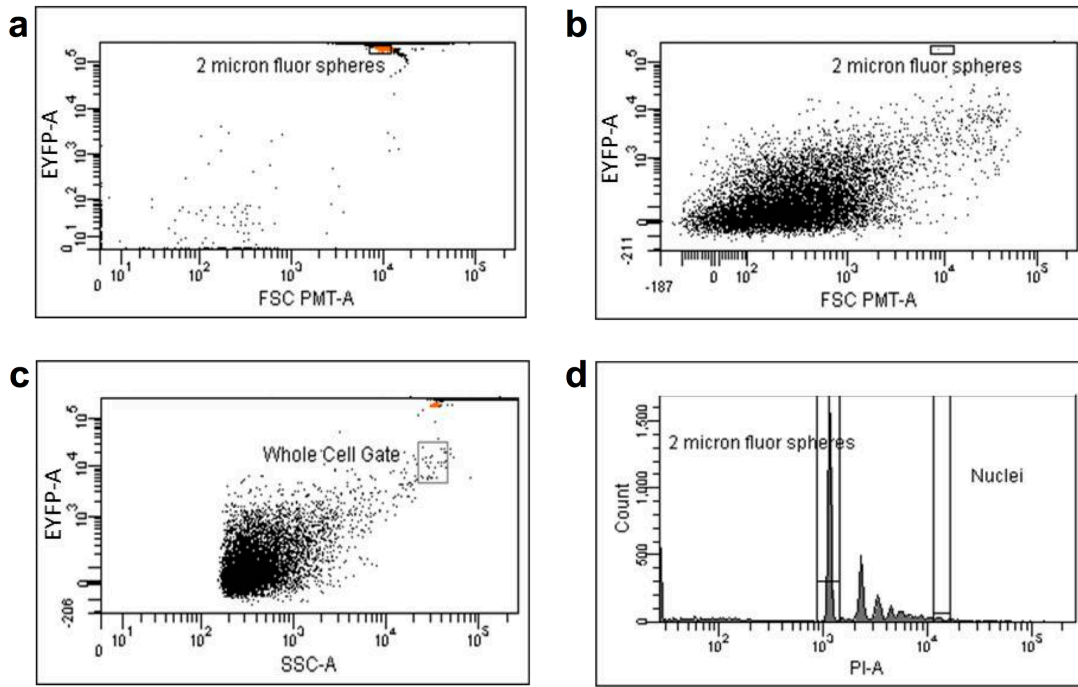
Figure S3. Absence of contaminating transcripts transmitted through flow sorting. FACS was employed to recover 2 μm fluorescent microspheres spiked into the NPC whole cells and the nuclear preparations. Biparametric flow analysis of **(a)**: a diluted sample of the fluorescent microspheres **(b)**: whole cells **(c)**: whole cells containing spiked microspheres and **(d)**: PI-stained nuclei containing spiked microspheres. The gate employed for sorting the microspheres (box) does not overlap the positions of the whole cells or the nuclei. Ten replicates were tested for single negative microspheres of cells or nuclei and only one sample was tested for the 2, 5, 10 and 100 cells or nuclei.
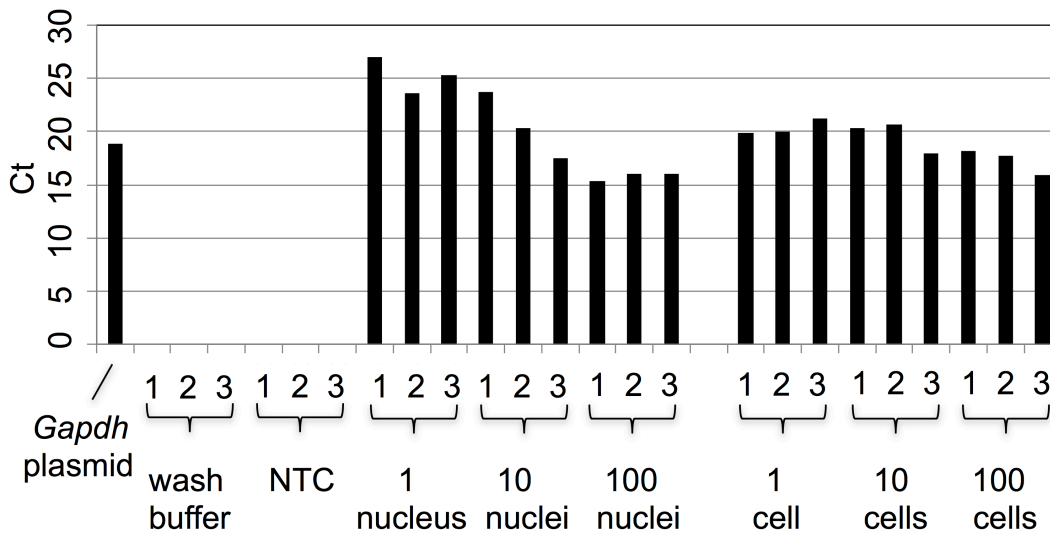
Figure S4. Confirmation of cDNA synthesis by qPCR. qPCR was employed to detect *Gapdh* transcripts within cDNA derived from biological triplicates of 1, 10 and 100 nuclei and cells. A linearized plasmid containing the *Gapdh* sequence was used as positive control. Triplicate wash buffer and triplicate qPCR no template controls (NTCs) lacked signals.
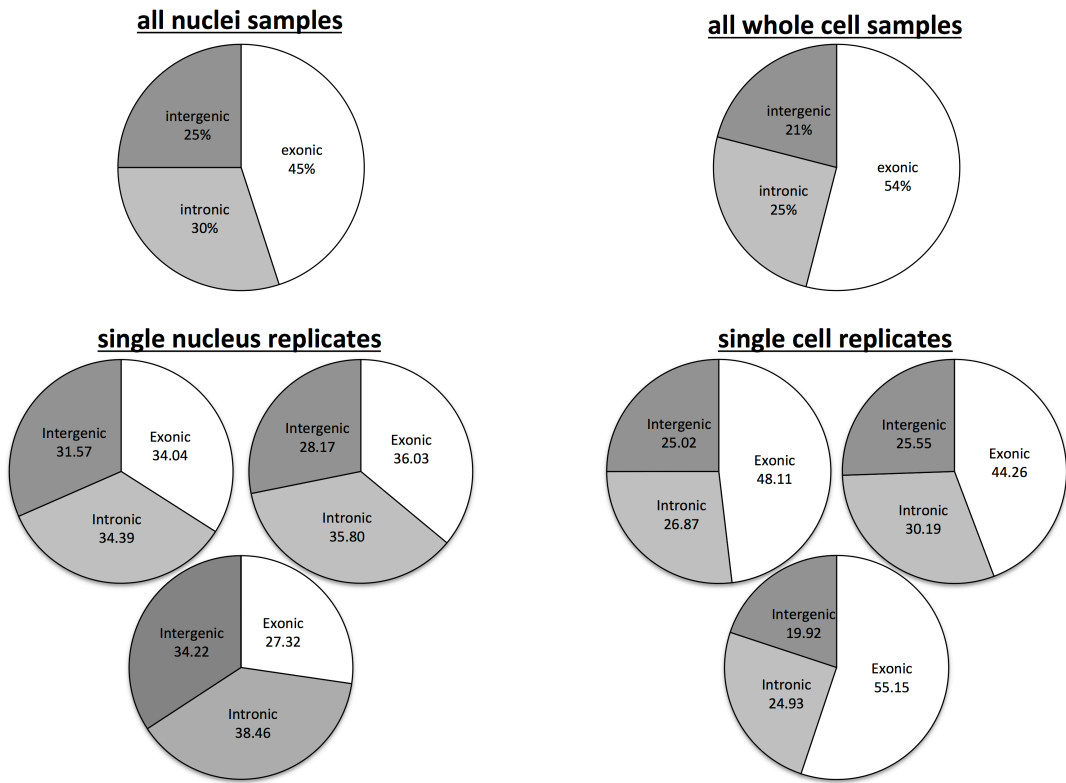
Figure S5. Unique sequencing read distributions for single cell and single nuclei replicates. All unique reads that map to the genome were counted and divided into three categories showing that the single nucleus samples have more intronic and intergenic reads than in the single cells (on average 16.7% more). A read was labeled as intronic if it mapped completely within an intron, as exonic if it was completely contained within an exon (as defined by the reference genome) and intergenic if it did not overlap a gene. All reads mapping to 5'- and 3'- untranslated regions were categorized as exonic.
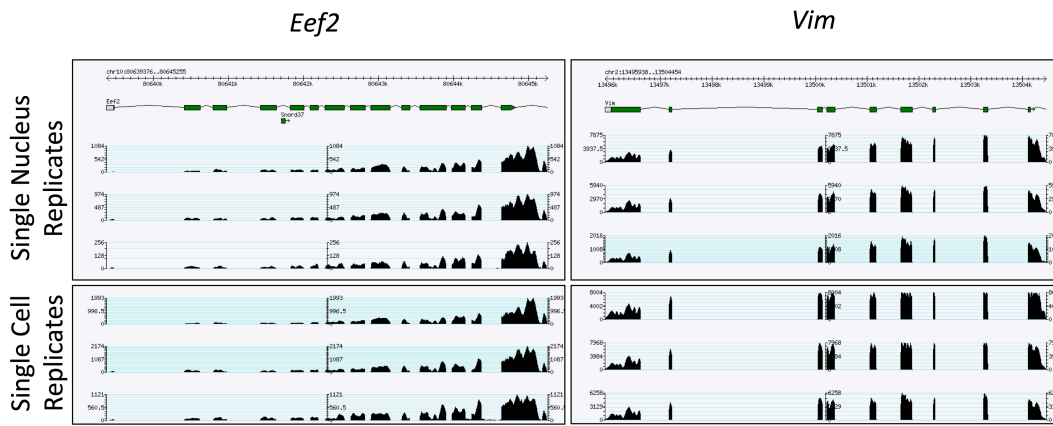
Figure S6. Exon-specific plot coverage of exemplar genes. The housekeeping gene *eukaryotic translation elongation factor 2* (*Eef2*) and the neural progenitor cell-specific gene *Vimentin* (*Vim*) are illustrated. Reads map to exons and not to introns, indicating accurate mapping of processed transcripts from single nuclei.

Read Hits Per Intron Across Mouse Genome
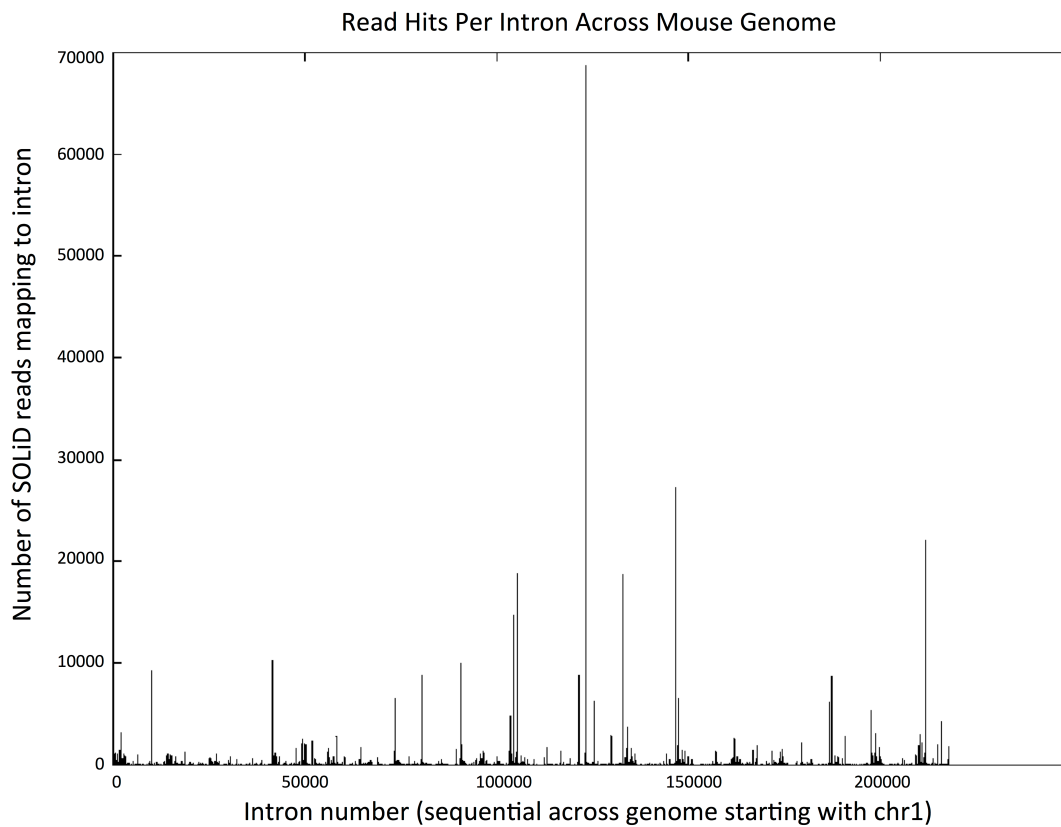
Figure S7. Intronic artifact reads are minimal and can be identified bioinformatically. Reads to annotated introns from the mouse genome (build mm9) are plotted against location of the chromosome. In this example, the 687,233 reads mapped to a single intron near a polyTC enriched island of 28 nucleotides in length (TTTGTCTTTCTCCTCTCCTCTCCTCTCC), indicating a mapping artifact. Based on all intronic reads, 95% of the introns have less than 200 reads (on average 82 reads per intron). Therefore, intronic reads arising from mapping artifacts can be identified and removed bioinformatically.

Expression of Gene Features at Various RPKM Thresholds
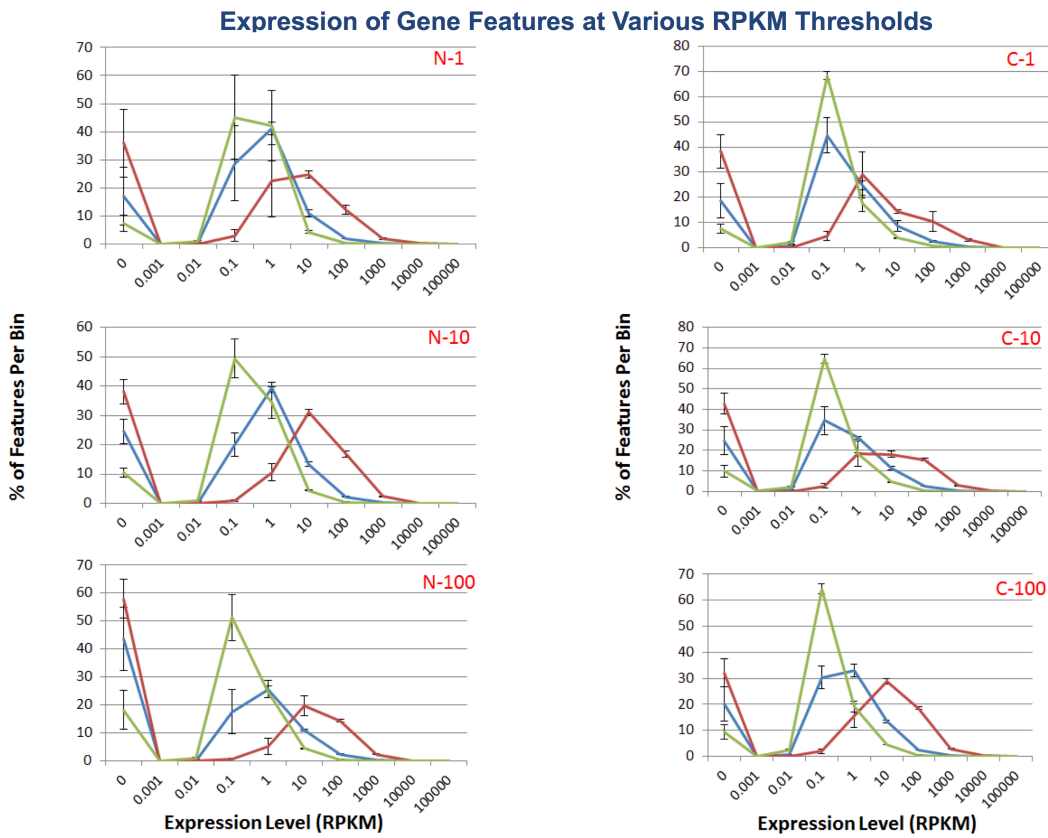
Figure S8. Expression of gene features at various RPKM thresholds. The annotated exons and introns of the transcripts and the intergenic regions from the mouse genome (build mm9) are plotted against the expression levels, over an interval starting at RPKM of 0 and ending at 100,000. Intron and intergenic reads have a peak RPKM of 0.10 (blue and green lines), which differs from exons detected at higher RPKM values (peak RPKM of 10). The intergenic regions can serve as controls for background mapping signal. Nearly all mapped exons have an RPKM value between 0.1 and 1000 confirming a dynamic range of 4 logs and a sensitivity approaching a single transcript per cell. N-1, N-10, and N-100 refer to 1, 10 and 100 nuclei respectively and C-1, C-10, and C-100 refers to 1, 10 and 100 cells respectively.
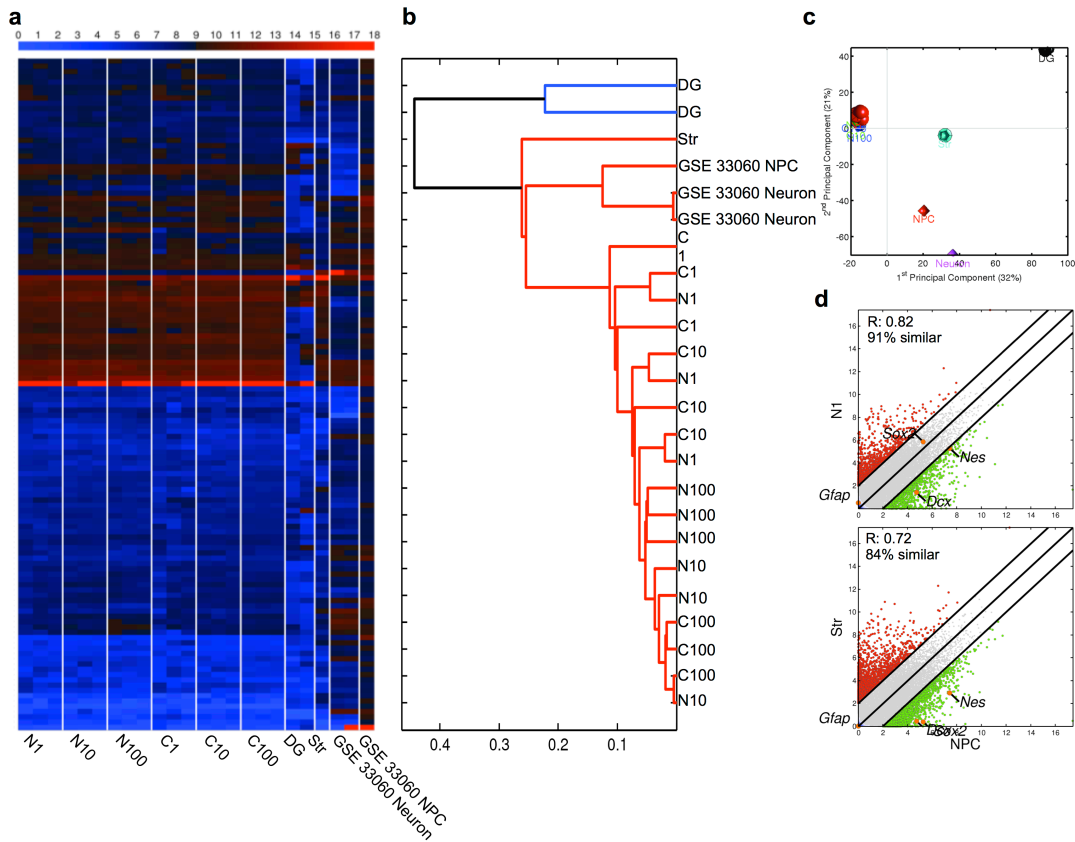
Figure S9. External confirmation of cell-type specific sequencing of NPC nuclei. Comparison of single nuclei and cell samples to external RNA-Seq comparators (GSE33060 from (1), GSM818956 (NPC), GSM818951 (Neuron biological replicate 1) and GSM818952 (Neuron biological replicate 2). (a) heat map of highly expressed genes, (b) hierarchical clustering, (c) principal component (PCA) and (d) pairwise scatter plot analysis determines that NPC single nuclei and cells are more similar to the external NPCs than to DG and Str controls. Log_2 transformation and quantile normalization of all samples was performed. Due to the differences in technical preparation between data sets, we do not expect 100% correlation of all NPC samples. However, these technical differences do not account for all of the differences as the DG (prepared as for NPC single nuclei) cluster further away from single NPCs than the GSE33060 data set.
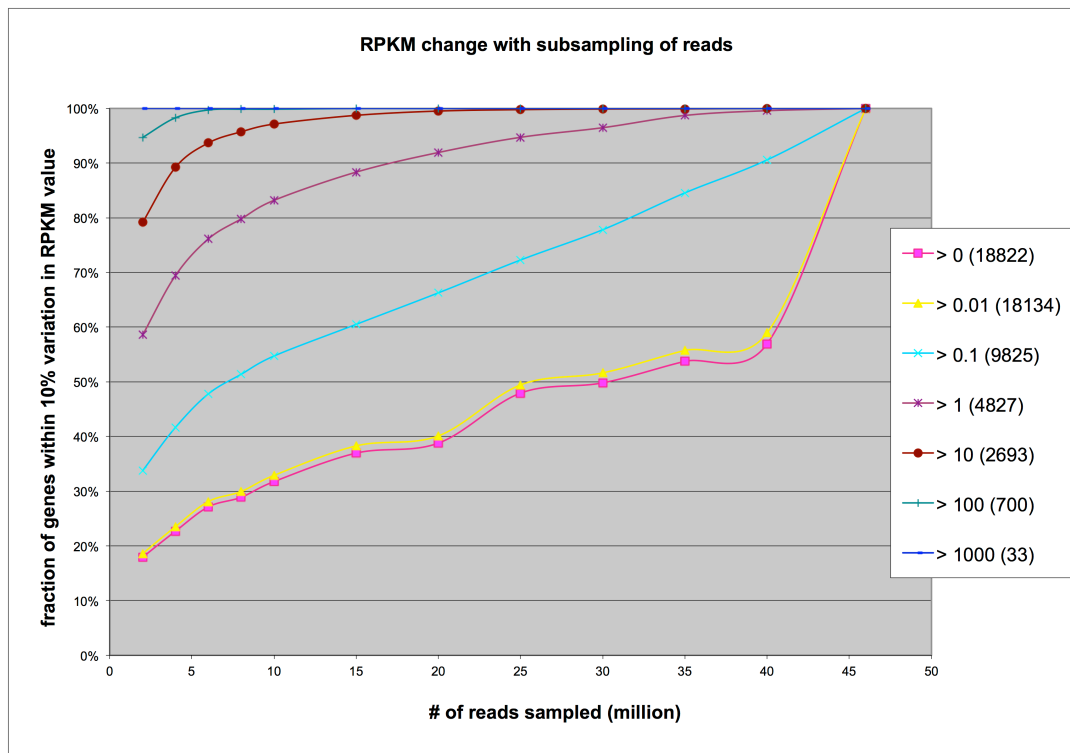
Figure S10. Transcripts with 5 or more copies are successfully interrogated. The ordinate is a term reflecting the variation of RPKM relative to the total reads. As the number of reads approaches 46 million (abscissa), the different RPKM bins (see colored lines and key) are saturated at 100% indicating that sequencing to a greater depth will not improve the confidence level. Genes with RPKM of 1 or greater (or about 5 transcripts per cell) are well addressable in this cell type under the probed conditions.
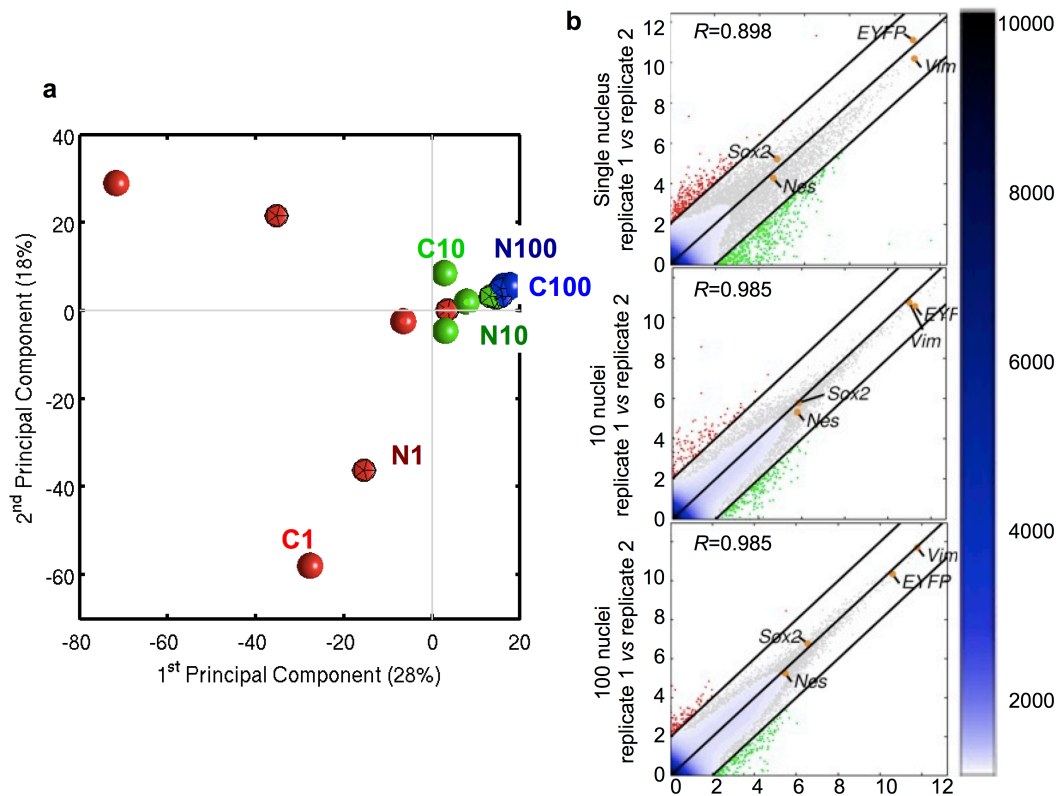
Figure S11. Single sample biological replicates display more variability than pooled replicates.
(a): Principal Component Analysis (PCA). The first principal component (PC1) captures 21% of the gene expression variability and the second principal component (PC2) captures 16% of the variability. Together these principal components account for 37% of the gene expression variability in all samples and all replicates. <u>Symbols:</u> The N1 (single nucleus) populations are depicted by red icosahedra, N10 (10 nuclei) by green icosahedra, the N100 (100 nuclei) by blue icosahedra, the C1 (1 cell) by red spheres, the C10 (10 cells) by green spheres and the C100 (100 cells) by blue spheres.
(b): Pairwise scatter plots of biological replicates within a group. The replicates represented here are a single nucleus, ten nuclei and one hundred nuclei (see Supplementary Fig. 12a and b for comparisons of all samples). Every point in a pairwise scatter plot represents the gene expression level (RPKM) of a transcript in two samples. The horizontal projection corresponds to the expression level in the first sample and the vertical projection corresponds with the expression level in the second sample. The more similar two samples are, the more points in the scatter plots group near the diagonal. Lines parallel to the diagonal indicate a 2-fold difference in expression. A $\log_2$ scale was used and the Fisher's correlation coefficient (R) was calculated with respect to the total number of transcripts (21,611) in the dataset.
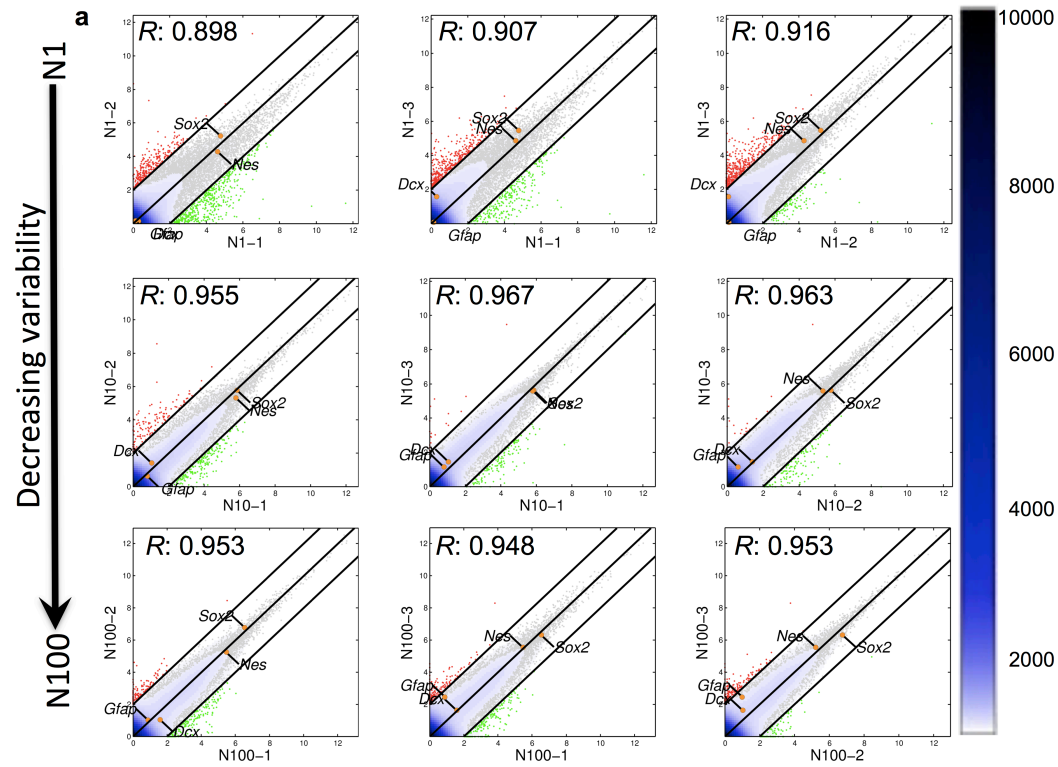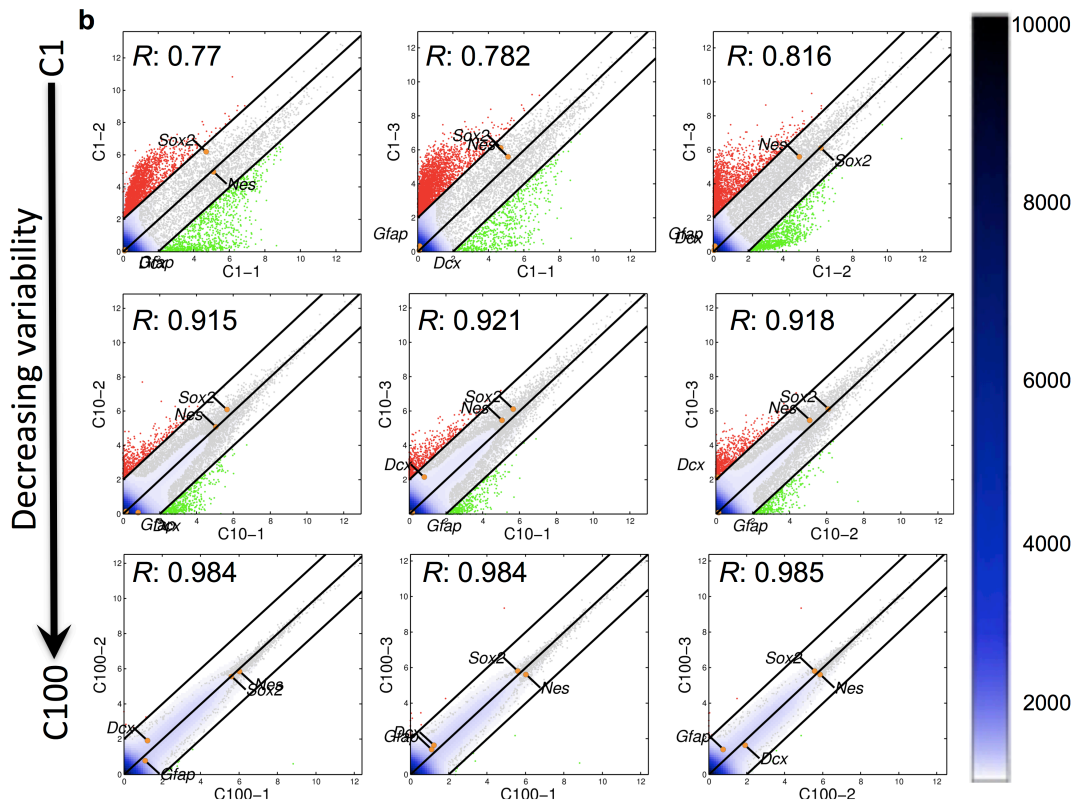
Figure S12. A decrease in variability is associated with sample pooling, as indicated by pairwise scatterplots of biological triplicates within a group. The replicates used to perform the pairwise scatter plots were: **(a):** N1-1 through -3, N10-1 through -3, N100-1 through -3, **(b):** C1-1 through -3, C10-1 through -3, C100-1 through -3. These are some (18) pairwise scatter plot comparisons within 6 sample sizes (N-1, N-10, N-100, C-1, C-10 and C-100). Every point in a pairwise scatter plot represents the gene expression level of a transcript in two samples. The horizontal projection corresponds to the expression level in the first sample and the vertical projection corresponds with the expression level in the second sample. The more similar two samples are, the more points in the scatter plots group near the diagonal. Lines parallel to the diagonal indicate a 2-fold difference in expression. A log_2 scale was used and the Fisher's correlation coefficient (R) was calculated with respect to the total number of transcripts (21,611) in the dataset.

Column scale (log2): 0 – 1 – 2 – 3 – 4 – 5 – 6 – 7 – 8 – 9 – 10 – 11

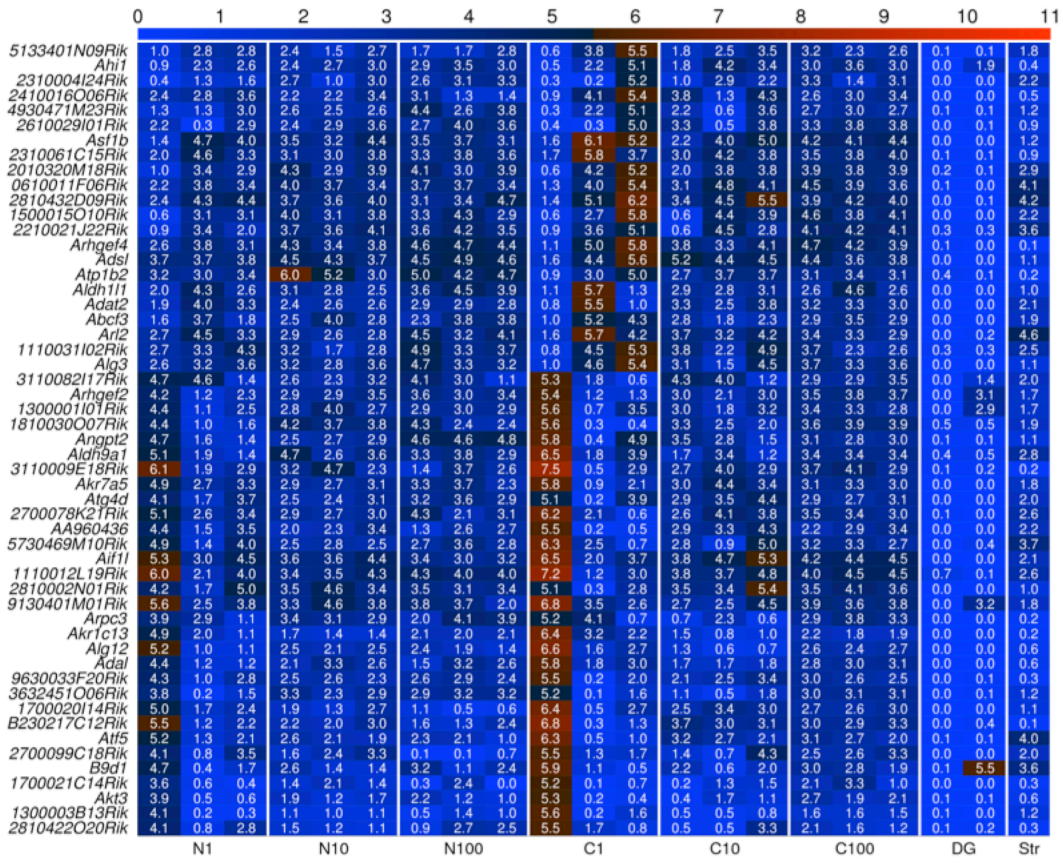| Gene	N1			N10			N100			C1			C10			C100			DG		Str
5133401N09Rik	1.0	2.8	2.8	2.4	1.5	2.7	1.7	1.7	2.8	0.6	3.8	5.5	1.8	2.5	3.5	3.2	2.3	2.6	0.1	0.1	1.8
Ahi1	0.9	2.3	2.6	2.4	2.7	3.0	2.9	3.5	3.0	0.5	2.2	5.1	1.8	4.2	3.4	3.0	3.6	3.0	0.0	1.9	0.4
2310004I24Rik	0.4	1.3	1.6	2.7	1.0	3.0	2.6	3.1	3.3	0.3	0.2	5.2	1.0	2.9	2.2	3.3	1.4	3.1	0.0	0.0	2.2
2410016O06Rik	2.4	2.8	3.6	2.2	2.2	3.4	3.1	1.3	1.4	0.9	4.1	5.4	3.8	1.3	4.3	2.6	3.0	3.4	0.0	0.0	0.5
4930471M23Rik	1.3	1.3	3.0	2.6	2.5	2.6	4.4	2.6	3.8	0.3	2.2	5.1	2.2	0.6	3.6	2.7	3.0	2.7	0.1	0.1	1.2
2610029I01Rik	2.2	0.3	2.9	2.4	2.9	3.6	2.7	4.0	3.6	0.4	0.3	5.0	3.3	0.5	3.8	3.3	3.8	3.8	0.0	0.1	0.9
Asf1b	1.4	4.7	4.0	3.5	3.2	4.4	3.5	3.7	3.1	1.6	6.1	5.2	2.2	4.0	5.0	4.2	4.1	4.4	0.0	0.0	1.2
2310061C15Rik	2.0	4.6	3.3	3.1	3.0	3.8	3.3	3.8	3.6	1.7	5.8	3.7	3.0	4.2	3.8	3.5	3.8	4.0	0.1	0.1	0.9
2010320M18Rik	1.0	3.4	2.9	4.3	2.9	3.9	4.1	3.0	3.9	0.6	4.2	5.2	2.0	3.8	3.8	3.9	3.8	3.9	0.2	0.1	2.9
0610011F06Rik	2.2	3.8	3.4	4.0	3.7	3.4	3.7	3.7	3.4	1.3	4.0	5.4	3.1	4.8	4.1	4.5	3.9	3.6	0.1	0.0	4.1
2810432D09Rik	2.4	4.3	4.4	3.7	3.6	4.0	3.1	3.4	4.7	1.4	5.1	6.2	3.4	4.5	5.5	3.9	4.2	4.0	0.0	0.1	4.2
1500015O10Rik	0.6	3.1	3.1	4.0	3.1	3.8	3.3	4.3	2.9	0.6	2.7	5.8	0.6	4.4	3.9	4.6	3.8	4.1	0.0	0.0	2.2
2210021J22Rik	0.9	3.4	2.0	3.7	3.6	4.1	3.6	4.2	3.5	0.9	3.6	5.1	0.6	4.5	2.8	4.1	4.2	4.1	0.3	0.3	3.6
Arhgef4	2.6	3.8	3.1	4.3	3.4	3.8	4.6	4.7	4.4	1.1	5.0	5.8	3.8	3.3	4.1	4.7	4.2	3.9	0.1	0.0	0.1
Adsl	3.7	3.7	3.8	4.5	4.3	3.7	4.5	4.9	4.6	1.6	4.4	5.6	5.2	4.4	4.5	4.4	3.6	3.8	0.0	0.0	1.1
Atp1b2	3.2	3.0	3.4	6.0	5.2	3.0	5.0	4.2	4.7	0.9	3.0	5.0	2.7	3.7	3.7	3.1	3.4	3.1	0.4	0.1	0.2
Aldh1l1	2.0	4.3	2.6	3.1	2.8	2.5	3.6	4.5	3.9	1.1	5.7	1.3	2.9	2.8	3.1	2.6	4.6	2.6	0.0	0.0	1.0
Adat2	1.9	4.0	3.3	2.4	2.6	2.6	2.9	2.9	2.8	0.8	5.5	1.0	3.3	2.5	3.8	3.2	3.3	3.0	0.0	0.0	2.1
Abcf3	1.6	3.7	1.8	2.5	4.0	2.8	2.3	3.8	3.8	1.0	5.2	4.3	2.8	1.8	2.3	2.9	3.5	2.9	0.0	0.0	1.9
Arl2	2.7	4.5	3.3	2.9	2.6	2.8	4.5	3.2	4.1	1.6	5.7	4.2	3.7	3.2	4.2	3.4	3.3	2.9	0.0	0.2	4.6
1110031I02Rik	2.7	3.3	4.3	3.2	1.7	2.8	4.9	3.3	3.7	0.8	4.5	5.3	3.8	2.2	4.9	3.7	2.3	2.6	0.3	0.3	2.5
Alg3	2.6	3.2	3.6	3.2	2.8	3.6	4.7	3.3	3.2	1.0	4.6	5.4	3.1	1.5	4.5	3.7	3.3	3.6	0.0	0.0	1.1
3110082I17Rik	4.7	4.6	1.4	2.6	2.3	3.2	4.1	3.0	1.1	5.3	1.8	0.6	4.3	4.0	1.2	2.9	2.9	3.5	0.0	1.4	2.0
Arhgef2	4.2	1.2	2.3	2.9	2.9	3.5	3.6	3.0	3.4	5.4	1.2	1.3	3.0	2.1	3.0	3.5	3.8	3.7	0.0	3.1	1.7
1300001I01Rik	4.4	1.1	2.5	2.8	4.0	2.7	2.9	3.0	2.9	5.6	0.7	3.5	3.0	1.8	3.2	3.4	3.3	2.8	0.0	2.9	1.7
1810030O07Rik	4.4	1.0	1.6	4.2	3.7	3.8	4.3	2.4	2.4	5.6	0.3	0.4	3.3	2.5	2.0	3.6	3.9	3.9	0.5	0.5	1.9
Angpt2	4.7	1.6	1.4	2.5	2.7	2.9	4.6	4.6	4.8	5.8	0.4	4.9	3.5	2.8	1.5	3.1	2.8	3.0	0.1	0.1	1.1
Aldh9a1	5.1	1.9	1.4	4.7	2.6	3.6	3.3	3.8	2.9	6.5	1.8	3.9	1.7	3.4	1.2	3.4	3.4	3.4	0.4	0.5	2.8
3110009E18Rik	6.1	1.9	2.9	3.2	4.7	2.3	1.4	3.7	2.6	7.5	0.5	2.9	2.7	4.0	2.9	3.7	4.1	2.9	0.1	0.2	0.2
Akr7a5	4.9	2.7	3.3	2.9	2.7	3.1	3.3	3.7	2.3	5.8	0.9	2.1	3.0	4.4	3.4	3.1	3.3	3.0	0.0	0.0	1.8
Atg4d	4.1	1.7	3.7	2.5	2.4	3.1	3.2	3.6	2.9	5.1	0.2	3.9	2.9	3.5	4.4	2.9	2.7	3.1	0.0	0.0	2.0
2700078K21Rik	5.1	2.6	3.4	2.9	2.7	3.0	4.3	2.1	3.1	6.2	2.1	0.6	2.6	4.1	3.8	3.5	3.4	3.0	0.1	0.0	2.6
AA960436	4.4	1.5	3.5	2.0	2.3	3.4	1.3	2.6	2.7	5.5	0.2	0.5	2.9	3.3	4.3	2.2	2.9	3.4	0.0	0.0	2.2
5730469M10Rik	4.9	1.4	4.0	2.5	2.8	2.5	2.7	3.6	2.8	6.3	2.5	0.7	2.8	0.9	5.0	3.2	3.3	2.7	0.0	0.4	3.7
Aif1l	5.3	3.0	4.5	3.6	3.6	4.4	3.4	3.0	3.2	6.5	2.0	3.7	3.8	4.7	5.3	4.2	4.4	4.5	0.0	0.0	2.1
1110012L19Rik	6.0	2.1	4.0	3.4	3.5	4.3	4.3	4.0	4.0	7.2	1.2	3.0	3.8	3.7	4.8	4.0	4.5	4.5	0.7	0.1	2.6
2810002N01Rik	4.2	1.7	5.0	3.5	4.6	3.4	3.5	3.1	3.4	5.1	0.3	2.8	3.5	3.4	5.4	3.5	4.1	3.6	0.0	0.0	1.0
9130401M01Rik	5.6	2.5	3.8	3.3	4.6	3.8	3.8	3.7	2.0	6.8	3.5	2.6	2.7	2.5	4.5	3.9	3.6	3.8	0.0	3.2	1.8
Arpc3	3.9	2.9	1.1	3.4	3.1	2.9	2.0	4.1	3.9	5.2	4.1	0.7	0.7	2.3	0.6	2.9	3.8	3.3	0.0	0.0	0.2
Akr1c13	4.9	2.0	1.1	1.7	1.4	1.4	2.1	2.0	2.1	6.4	3.2	2.2	1.5	0.8	1.0	2.2	1.8	1.9	0.0	0.0	0.2
Alg12	5.2	1.0	1.1	2.5	2.1	2.5	2.4	1.9	1.4	6.6	1.6	2.7	1.3	0.6	0.7	2.6	2.4	2.7	0.0	0.0	0.6
Adal	4.4	1.2	1.2	2.1	3.3	2.6	1.5	3.2	2.6	5.8	1.8	3.0	1.7	1.7	1.8	2.8	3.0	3.1	0.0	0.0	0.6
9630033F20Rik	4.3	1.0	2.8	2.5	2.6	2.3	2.6	2.9	2.4	5.5	0.2	2.0	2.1	2.5	3.4	3.0	2.6	2.5	0.0	0.1	0.3
3632451O06Rik	3.8	0.2	1.5	3.3	2.3	2.9	2.9	3.2	3.2	5.2	0.1	1.6	1.1	0.5	1.8	3.0	3.1	3.1	0.0	0.1	1.2
1700020I14Rik	5.0	1.7	2.4	1.9	1.3	2.7	1.1	0.5	0.6	6.4	0.5	2.7	2.5	3.4	3.0	2.7	2.6	3.0	0.0	0.0	1.1
B230217C12Rik	5.5	1.2	2.2	2.2	2.0	3.0	1.6	1.3	2.4	6.8	0.3	1.3	3.7	3.0	3.1	3.0	2.9	3.3	0.0	0.4	0.1
Atf5	5.2	1.3	2.1	2.6	2.1	1.9	2.3	2.1	1.0	6.3	0.5	1.0	3.2	2.7	2.1	3.1	2.7	2.0	0.1	0.1	4.0
2700099C18Rik	4.1	0.8	3.5	1.6	2.4	3.3	0.1	0.1	0.7	5.5	1.3	1.7	1.4	0.7	4.3	2.5	2.6	3.3	0.0	0.0	2.0
B9d1	4.7	0.4	1.7	2.6	1.4	1.4	3.2	1.1	2.4	5.9	1.1	0.5	2.2	0.6	2.0	3.0	2.8	1.9	0.1	5.5	3.6
1700021C14Rik	3.6	0.6	0.4	1.4	2.1	1.4	0.3	2.4	0.0	5.2	0.1	0.7	0.2	1.3	1.5	2.1	3.3	1.0	0.0	0.0	0.3
Akt3	3.9	0.5	0.6	1.9	1.2	1.7	2.2	1.2	1.0	5.3	0.2	0.4	0.4	1.7	1.1	2.7	1.9	2.1	0.1	0.1	0.6
1300003B13Rik	4.1	0.2	0.3	1.1	1.0	1.1	0.5	1.4	1.0	5.6	0.2	1.6	0.5	0.5	0.8	1.6	1.6	1.5	0.1	0.0	1.2
2810422O20Rik	4.1	0.8	2.8	1.5	1.2	1.1	0.9	2.7	2.5	5.5	1.7	0.8	0.5	0.5	3.3	2.1	1.6	1.2	0.1	0.2	0.3

Figure S13. Heat map of transcripts that are highly variable among the single cells and single nuclei. Variability decreases with pooled samples. The color bar codifies the gene expression in log2 scale. The highly expressed genes are red.
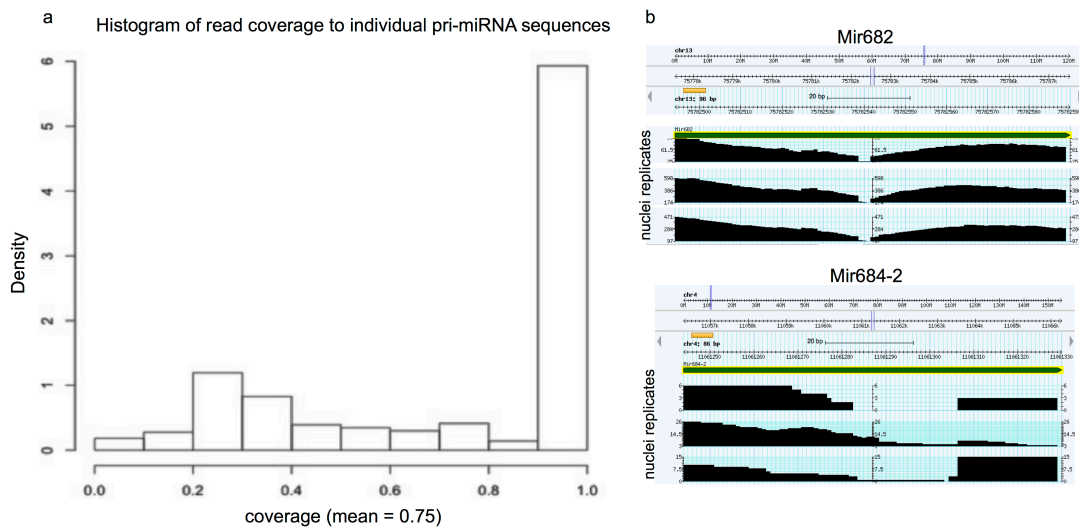
Figure S14. Coverage of pri-miRNA. Deep coverage of the 5' end of pri-miRNA demonstrates full-length cDNA synthesis (arrow). The lower coverage in the central hairpin region of the pri-miRNA is presumably an artifact of cDNA synthesis, as the polymerase pauses entering the central hairpin structure from both polarities, as it copies the first strand and then the second stand cDNA. However, we cannot formally disprove that some of the 5' reads were derived from clipped species via terminal transferase poly-A tailing enabling second strand synthesis. Possibly, if clipped species are stable, they have novel functions. They could also contribute to the analysis of processing mechanisms and rates.
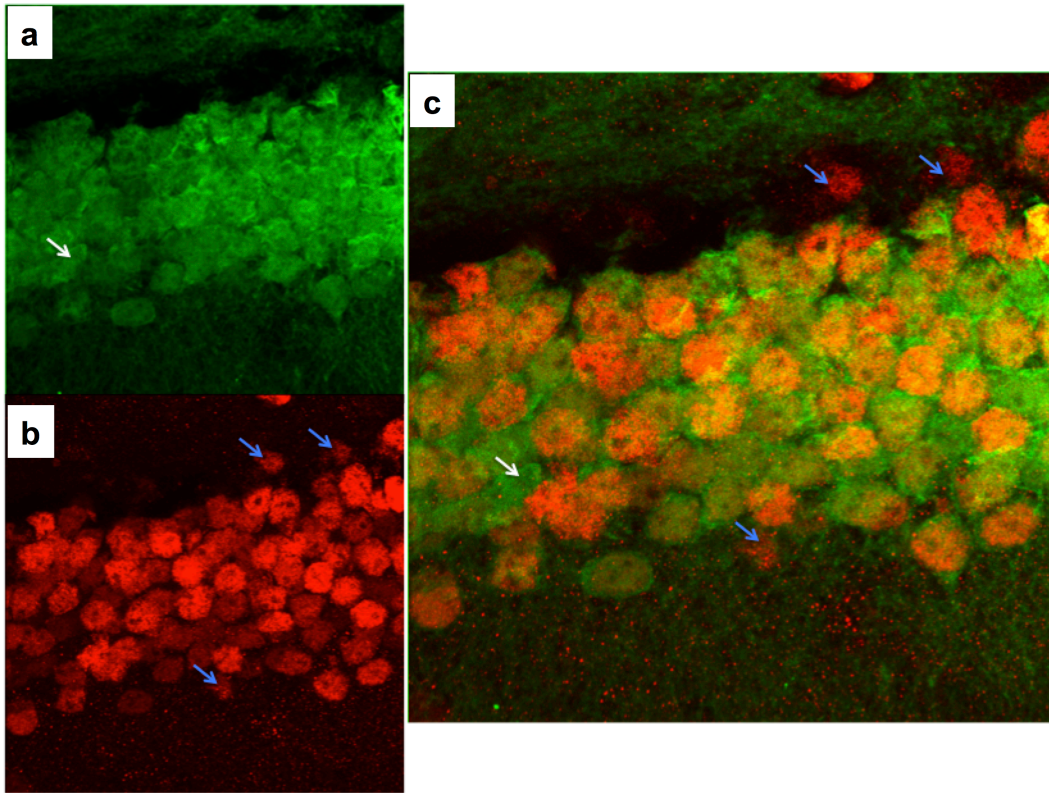
Figure S15. GFP fluorescence and Prox1 antibody co-localize in dentate gyrus cells. Dentate gyrus tissue from a transgenic mouse expressing GFP under the *Prox1* promoter **(a)** enables the observation of endogenous Prox1 protein expression **(b)** *in vivo*, (**c**)**:** merged. Images are displayed as a 60x z-stack projection.
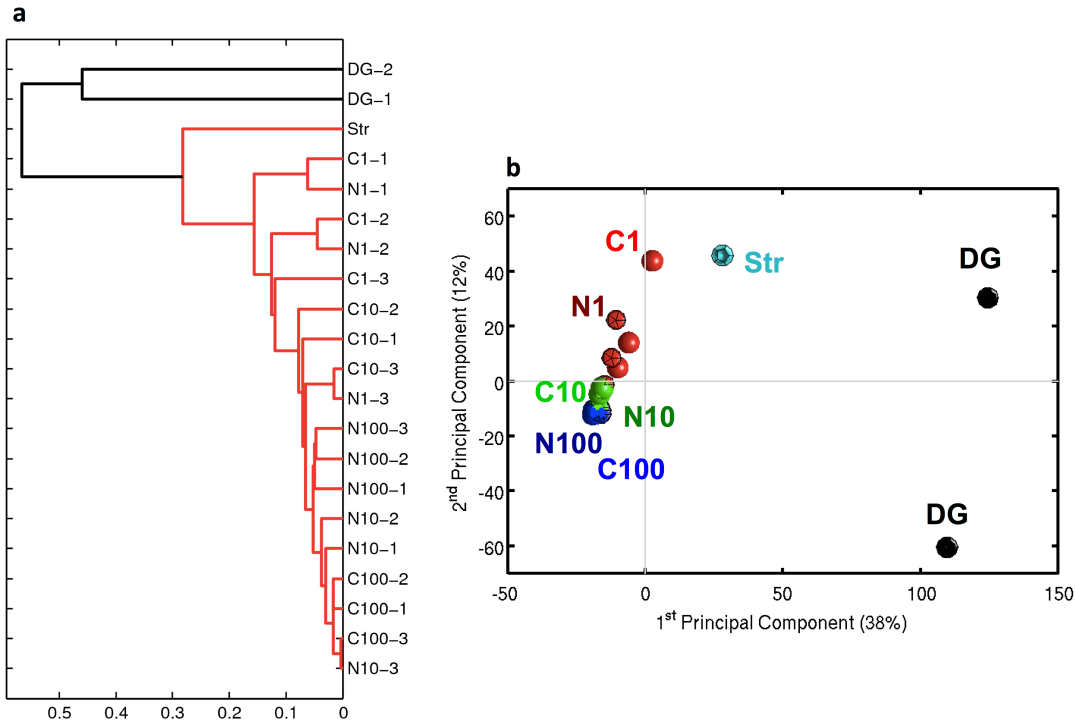
Figure S16. Identification of cell types through clustering. (a): Hierarchical clustering indicates that replicates with 10 or more cells or nuclei tend to cluster, whereas single cells and nuclei do not. This implies local variation in transcriptional profiles within single cells and nuclei. Clustering of samples was performed using the correlation metric and the average linkage method. Shorter horizontal links connecting two branches indicate closer similarities between the populations. **(b):** PCA analysis of all samples. The first principal component (PC1) captures 38% of the gene expression variability, and the second principal component (PC2) captures 12% of the variability. The first principal separates between **N1**, **N10**, **N100**, **C1**, **C10**, **C100** samples (negative coordinates) and **dentate gyrus (DG)**, **stromal (Str)** samples (positive coordinates). The second principal separates between **N10**, **N100**, **C10**, **C100**, **DG** samples (negative coordinates) and **N1**, **C1**, **Str** samples (positive coordinates). <u>Symbols</u>: The **N1** populations are depicted by red icosahedra, the **N10** by green icosahedra, the **N100** by blue icosahedra, the **C1** by red spheres, the **C10** by green spheres, the **C100** by blue spheres, the **DG** by black dodecahedra, and the **Str** by cyan dodecahedra.

Tables

Table S1. Absence of contaminating transcripts from FACS sorted spike-in microsphere controls in whole cell and nuclei samples, based on qPCR.

Ct Values - Nuclei-Microsphere Controls

	1	1	1	1	1	1	1	1	2	5	10	100
ActB	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Hsp90ab	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Eef2	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Rpl13	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Vim	ND	ND	ND	ND	ND	ND	38.1	ND	ND	ND	ND	ND
Fabp7	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
H2afz	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
GAPDH	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

Ct values - Whole Cell-Microsphere Controls

	1	1	1	1	1	1	1	1	2	5	10	100
ActB	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Hsp90ab	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Eef2	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Rpl13	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Vim	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
Fabp7	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
H2afz	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND
GAPDH	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND	ND

Table S2. Sequencing read distribution of each sample.

	Total	Mapped	%	Not mapped	%	Filtered	%
NPC cells							
1 cell -1	88,997,195	46,364,183	52.10	39,799,020	44.72	2,833,992	3.18
1 cell -2	130,341,634	52,390,968	40.20	76,793,663	58.92	1,157,003	0.89
1 cell -3	47,845,402	21,737,512	45.43	25,440,448	53.17	667,442	1.39
10 cells -1	57,571,578	30,500,820	52.98	26,267,024	45.62	803,734	1.40
10 cells -2	48,498,112	30,645,411	63.19	17,382,824	35.84	469,877	0.97
10 cells -3	29,458,542	11,842,450	40.20	17,268,045	58.62	348,047	1.18
100 cells -1	37,701,354	21,960,024	58.25	15,467,146	41.03	274,184	0.73
100 cells -2	20,756,129	13,614,385	65.59	6,976,694	33.61	165,050	0.80
100 cells -3	59,111,226	34,141,121	57.76	24,530,651	41.50	439,454	0.74
NPC nuclei							
1 nucleus -1	103,775,925	40,046,520	38.59	60,537,577	58.33	3,191,828	3.08
1 nucleus -2	161,855,470	47,637,824	29.43	112,932,010	69.77	1,285,636	0.79
1 nucleus -3	33,789,450	7,515,379	22.24	25,791,447	76.33	482,624	1.43
10 nuclei -1	39,045,664	12,602,634	32.28	14,012,036	35.89	12,430,994	31.84
10 nuclei -2	23,692,971	7,668,648	32.37	15,711,450	66.31	312,873	1.32
10 nuclei -3	26,683,050	12,904,655	48.36	13,577,879	50.89	200,516	0.75
100 nuclei -1	13,850,974	8,977,623	64.82	4,594,622	33.17	278,729	2.01
100 nuclei -2	14,663,334	7,796,708	53.17	6,558,245	44.73	308,381	2.10
100 nuclei -3	4,557,367	2,363,315	51.86	2,084,839	45.75	109,213	2.40
DG nuclei							
1 nucleus -1	37,303,022	30,934,184	82.93	6,051,810	16.22	317,028	0.85
1 nucleus -2	86,092,621	70,274,129	81.63	15,102,771	17.54	715,721	0.83
control	45,676,405	34,547,610	75.64	10,925,111	23.92	203,684	0.45

Table S3. Neural progenitor cell markers and housekeeping genes with non-intronic (exon specific) reads.

Gene name	Full gene name	MGI ID
Actb	actin, beta	MGI:87904
Aldoc	aldolase C, fructose-bisphosphate	MGI:101863
Apoe	apolipoprotein E	MGI:88057
Ascl1	achaete-scute complex homolog 1	MGI:96919
Atp1a1	ATPase, Na+/K+ transporting, alpha 1 polypeptide	MGI:88105
Bex2	brain expressed X-linked 2	MGI:1338017
Ccnd1	cyclin D1	MGI:88313
Cct3	chaperonin containing Tcp1, subunit 3 (gamma)	MGI:104708
Cct5	chaperonin containing Tcp1, subunit 5 (epsilon)	MGI:107185
Cct7	chaperonin containing Tcp1, subunit 7 (eta)	MGI:107184
CD15	fucosyltransferase 4	MGI:95594
CD81	CD81 antigen	MGI:1096398
CD9	CD9 antigen	MGI:88348
Chmp2a	charged multivesicular body protein 2A	MGI:1916203
Dbi	diazepam binding inhibitor	MGI:94865
Eef1a1	eukaryotic translation elongation factor 1 alpha 1	MGI:1096881
Eef2	eukaryotic translation elongation factor 2	MGI:95288
Fabp7	fatty acid binding protein 7, brain	MGI:101916
Fos	FBJ osteosarcoma oncogene	MGI:95574
FoxG1	forkhead box G1	MGI:1347464
Fut4	fucosyltransferase 4	MGI:95594
H2afz	H2A histone family, member Z	MGI:1888388
Hist1h1c	histone cluster 1, H1c	MGI:1931526
Hist1h1e	histone cluster 1, H1e	MGI:1931527
Hist1h4i	histone cluster 1, H4i	MGI:2448432
Hsp90ab1	heat shock protein 90 alpha (cytosolic), class B member 1	MGI:96247
Hspa8	heat shock protein 8	MGI:105384
Id1	inhibitor of DNA binding 1	MGI:96396
Id2	inhibitor of DNA binding 2	MGI:96397
Ldhb	lactate dehydrogenase B	MGI:96763
Nestin	nestin	MGI:101784
Olig2	oligodendrocyte transcription factor 2	MGI:1355331
Pa2g4	proliferation-associated 2G4	MGI:894684
Pou3f2	POU domain, class 3, transcription factor 2	MGI:101895
Pou3f4	POU domain, class 3, transcription factor 4	MGI:101894
PPIA	peptidylprolyl isomerase A	MGI:97749
Rpl13	ribosomal protein L13	MGI:105922
Rpl14	ribosomal protein L14	MGI:1914365
Rps2	ribosomal protein S2	MGI:105110
Rps3	ribosomal protein S3	MGI:1350917
Rpsa	ribosomal protein SA	MGI:105381
Sfpq	splicing factor proline/glutamine rich	MGI:1918764
Sox1	SRY-box containing gene 1	MGI:98357

Sox11	SRY-box containing gene 11	MGI:98359
Sox2	SRY-box containing gene 2	MGI:98364
Sox21	SRY-box containing gene 21	MGI:2654070
Sox3	SRY-box containing gene 3	MGI:98365
Strap	serine/threonine kinase receptor associated protein	MGI:1329037
Tomm22	translocase of outer mitochondrial membrane 22 homolog	MGI:2450248
Vim	vimentin	MGI:98932

Table S4. Differential accumulation of transcripts between nuclei and whole cells.

Column ID	Gene Symbol	Transcript	p-value(Nuclei vs. Whole cells)	FoldChange (Nuclei vs. Whole cells)	FoldChange (Nuclei vs. Whole cells)
NM_207261>Kcnk18	Kcnk18	NM_207261	0.0259213	32.9303	Nuclei up vs Whole cells
NM_001080553>Gsg1	Gsg1	NM_001080553	0.00767106	31.5359	Nuclei up vs Whole cells
NM_010352>Gsg1	Gsg1	NM_010352	0.00767109	31.5359	Nuclei up vs Whole cells
NM_001038590>Cldn19	Cldn19	NM_001038590	0.0185929	30.5443	Nuclei up vs Whole cells
NM_028092>Slc39a5	Slc39a5	NM_028092	0.0279075	30.1003	Nuclei up vs Whole cells
NM_053110>Gpnmb	Gpnmb	NM_053110	0.0122546	29.2083	Nuclei up vs Whole cells
NM_029326>1700018L24Rik	1700018L24Rik	NM_029326	0.0456587	28.7776	Nuclei up vs Whole cells
NM_016873>Wisp2	Wisp2	NM_016873	0.0329411	27.0517	Nuclei up vs Whole cells
NM_172776>D630002G06Rik	D630002G06Rik	NM_172776	0.0334497	24.3775	Nuclei up vs Whole cells
NM_001037800>Cd209b	Cd209b	NM_001037800	0.0237352	23.0353	Nuclei up vs Whole cells
NM_009880>Cdx1	Cdx1	NM_009880	0.0433389	22.0012	Nuclei up vs Whole cells
NM_147073>Olfr33	Olfr33	NM_147073	0.0370179	21.9078	Nuclei up vs Whole cells
NR_027137>Gm10565	Gm10565	NR_027137	1.24E-08	18.4231	Nuclei up vs Whole cells
NM_172944>Itgae	Itgae	NM_172944	0.0316746	17.887	Nuclei up vs Whole cells
NM_001159275>Slc25a2	Slc25a2	NM_001159275	0.0302349	17.8153	Nuclei up vs Whole cells
NM_027072>Plac8l1	Plac8l1	NM_027072	0.0120059	16.956	Nuclei up vs Whole cells
NR_033588>AY512931	AY512931	NR_033588	0.000937218	16.8646	Nuclei up vs Whole cells
NM_008438>Kera	Kera	NM_008438	0.00292894	16.6684	Nuclei up vs Whole cells
NM_010611>Kcnq2	Kcnq2	NM_010611	0.0330587	16.0979	Nuclei up vs Whole cells
NM_001079865>Ces2f	Ces2f	NM_001079865	0.0325815	15.745	Nuclei up vs Whole cells
NR_003248>Foxl2os	Foxl2os	NR_003248	0.0212267	15.2969	Nuclei up vs Whole cells
NM_147080>Olfr615	Olfr615	NM_147080	0.0160466	14.8496	Nuclei up vs Whole cells
NM_001145015>Arhgap40	Arhgap40	NM_001145015	0.00604643	14.7046	Nuclei up vs Whole cells
NM_001170851>Klra2	Klra2	NM_001170851	0.0327288	14.5646	Nuclei up vs Whole cells
NM_001034851>Fam134b	Fam134b	NM_001034851	0.0342995	14.0756	Nuclei up vs Whole cells
NM_008006>Fgf2	Fgf2	NM_008006	0.0423801	13.9405	Nuclei up vs Whole cells
NM_001166638_dup3>Gm4303_dup3	Gm4303_dup3	NM_001166638_dup3	0.0432971	13.7245	Nuclei up vs Whole cells
NM_001166639_dup3>Gm4305_dup3	Gm4305_dup3	NM_001166639_dup3	0.0432971	13.7245	Nuclei up vs Whole cells
NM_001166641_dup3>Gm4307_dup3	Gm4307_dup3	NM_001166641_dup3	0.0432971	13.7245	Nuclei up vs Whole cells
NM_001009548>4930529F22Rik	4930529F22Rik	NM_001009548	0.0198921	12.9524	Nuclei up vs Whole cells

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NM_008293>Hsd3b1	Hsd3b1	NM_008293	0.0373183	12.8473	Nuclei up vs Whole cells
NM_194069>Ifi27l1	Ifi27l1	NM_194069	0.00280294	12.7908	Nuclei up vs Whole cells
NM_173779>Ankrd58	Ankrd58	NM_173779	0.0424858	12.6388	Nuclei up vs Whole cells
NM_139301>Catsper1	Catsper1	NM_139301	0.00334878	12.5615	Nuclei up vs Whole cells
NM_001003952>Sval3	Sval3	NM_001003952	0.00886078	12.2222	Nuclei up vs Whole cells
NM_022014>Fn3k	Fn3k	NM_022014	0.00464704	12.0932	Nuclei up vs Whole cells
NM_001008426>Gm5531	Gm5531	NM_001008426	0.000423572	12.0269	Nuclei up vs Whole cells
NM_011872>Klk7	Klk7	NM_011872	0.00438833	11.7867	Nuclei up vs Whole cells
NM_018792>Hils1	Hils1	NM_018792	0.0249981	11.6674	Nuclei up vs Whole cells
NM_001033206>Pwwp2b	Pwwp2b	NM_001033206	0.0298047	11.4168	Nuclei up vs Whole cells
NM_199013>Irgc1	Irgc1	NM_199013	0.0421075	11.2067	Nuclei up vs Whole cells
NM_001113391>Cd247	Cd247	NM_001113391	0.031263	10.964	Nuclei up vs Whole cells
NR_028591>Gm14005	Gm14005	NR_028591	0.0179678	10.857	Nuclei up vs Whole cells
NM_029061>Ccdc7	Ccdc7	NM_029061	0.0426827	10.7846	Nuclei up vs Whole cells
NR_029414>Gsdmcl-ps	Gsdmcl-ps	NR_029414	0.0345501	10.6806	Nuclei up vs Whole cells
NM_001195258>Gm14378	Gm14378	NM_001195258	0.0342597	10.5989	Nuclei up vs Whole cells
NM_001099688>Fbxo39	Fbxo39	NM_001099688	0.0174352	10.548	Nuclei up vs Whole cells
NM_198415>Ckmt2	Ckmt2	NM_198415	0.0234437	10.283	Nuclei up vs Whole cells
NM_001172481>Aspn	Aspn	NM_001172481	0.0433687	9.56592	Nuclei up vs Whole cells
NM_178738>Prss35	Prss35	NM_178738	0.0253698	9.49154	Nuclei up vs Whole cells
NM_011286>Rph3a	Rph3a	NM_011286	0.0166845	9.33287	Nuclei up vs Whole cells
NM_030596>Dsg3	Dsg3	NM_030596	0.00196315	9.15125	Nuclei up vs Whole cells
NM_001037166>Gm4925	Gm4925	NM_001037166	0.0168733	8.95151	Nuclei up vs Whole cells
NM_001081106>Cytl1	Cytl1	NM_001081106	0.0160729	8.90225	Nuclei up vs Whole cells
NM_178257>Il22ra1	Il22ra1	NM_178257	0.0351971	8.84032	Nuclei up vs Whole cells
NM_011477>Sprr2k	Sprr2k	NM_011477	0.034149	8.68925	Nuclei up vs Whole cells
NM_001110267>Vegfa	Vegfa	NM_001110267	0.0238397	8.67245	Nuclei up vs Whole cells
NM_001110268>Vegfa	Vegfa	NM_001110268	0.0238395	8.67244	Nuclei up vs Whole cells
NM_001110266>Vegfa	Vegfa	NM_001110266	0.0238395	8.67243	Nuclei up vs Whole cells
NM_145831>Dmrt2	Dmrt2	NM_145831	0.0414498	8.6041	Nuclei up vs Whole cells
NM_017372>Lyz2	Lyz2	NM_017372	0.0118585	8.59227	Nuclei up vs Whole cells
NM_027600>4921504E06Rik	4921504E06Rik	NM_027600	0.0265725	8.56998	Nuclei up vs Whole cells
NR_001570>Xist	Xist	NR_001570	0.0396399	8.53533	Nuclei up vs Whole cells
NM_175476>Arhgap25	Arhgap25	NM_175476	0.0349165	8.30042	Nuclei up vs Whole cells
NM_177676>4931409K22Rik	4931409K22Rik	NM_177676	0.00534009	8.21177	Nuclei up vs Whole cells

NM_145845>Vmn1r192	Vmn1r192	NM_145845	0.0479842	8.16903	Nuclei up vs Whole cells
NM_028737>4931406B18Rik	4931406B18Rik	NM_028737	0.0171372	8.13054	Nuclei up vs Whole cells
NM_001045526>A430084P05Rik	A430084P05Rik	NM_001045526	0.0161973	8.04145	Nuclei up vs Whole cells
NM_030710>Slamf6	Slamf6	NM_030710	0.0428082	8.02463	Nuclei up vs Whole cells
NM_008109>Gdf5	Gdf5	NM_008109	0.00782624	8.02408	Nuclei up vs Whole cells
NM_010045>Darc	Darc	NM_010045	0.0161304	7.99827	Nuclei up vs Whole cells
NM_001122736>Igf2	Igf2	NM_001122736	0.0277919	7.99344	Nuclei up vs Whole cells
NM_010558>Il5	Il5	NM_010558	0.0458584	7.78246	Nuclei up vs Whole cells
NM_028654>4930404H21Rik	4930404H21Rik	NM_028654	0.000217552	7.51968	Nuclei up vs Whole cells
NM_019506>Gdf2	Gdf2	NM_019506	0.00553465	7.5095	Nuclei up vs Whole cells
NM_001004184>Slc28a1	Slc28a1	NM_001004184	0.00217449	7.46534	Nuclei up vs Whole cells
NM_172142>Nfkbid	Nfkbid	NM_172142	0.0315665	7.44135	Nuclei up vs Whole cells
NM_008092>Gata4	Gata4	NM_008092	1.01E-05	7.32932	Nuclei up vs Whole cells
NM_020577>As3mt	As3mt	NM_020577	0.0174042	7.24199	Nuclei up vs Whole cells
NM_001177756>Pfkfb3	Pfkfb3	NM_001177756	0.0298474	7.11594	Nuclei up vs Whole cells
NM_001177753>Pfkfb3	Pfkfb3	NM_001177753	0.0298484	7.11548	Nuclei up vs Whole cells
NM_153795>Fermt3	Fermt3	NM_153795	0.019649	7.08292	Nuclei up vs Whole cells
NM_183193>Foxi2	Foxi2	NM_183193	0.0139603	7.03085	Nuclei up vs Whole cells
NM_001177755>Pfkfb3	Pfkfb3	NM_001177755	0.0301947	7.01076	Nuclei up vs Whole cells
NM_001164804>Coro2a	Coro2a	NM_001164804	0.0268896	6.96116	Nuclei up vs Whole cells
NM_001142960>Bcl2l15	Bcl2l15	NM_001142960	0.0156664	6.93665	Nuclei up vs Whole cells
NM_010741>Ly6c1	Ly6c1	NM_010741	0.0230316	6.9216	Nuclei up vs Whole cells
NM_001146351>Ephb6	Ephb6	NM_001146351	0.0172309	6.89613	Nuclei up vs Whole cells
NM_007680>Ephb6	Ephb6	NM_007680	0.017231	6.89612	Nuclei up vs Whole cells
NM_001097977_dup1>Gm14151_dup1	Gm14151_dup1	NM_001097977_dup1	0.0292118	6.86337	Nuclei up vs Whole cells
NM_172815>Rspo2	Rspo2	NM_172815	0.0325743	6.85351	Nuclei up vs Whole cells
NM_007887>Dub1	Dub1	NM_007887	0.00572311	6.83837	Nuclei up vs Whole cells
NM_001011812>Olfr951	Olfr951	NM_001011812	0.0483078	6.74582	Nuclei up vs Whole cells
NM_019784>Tex21	Tex21	NM_019784	0.042456	6.68585	Nuclei up vs Whole cells
NM_008318>Ibsp	Ibsp	NM_008318	0.0212626	6.67522	Nuclei up vs Whole cells
NM_019549>Plek	Plek	NM_019549	0.0231236	6.63543	Nuclei up vs Whole cells
NM_001039720>9030619P08Rik	9030619P08Rik	NM_001039720	0.017819	6.57481	Nuclei up vs Whole cells
NM_021508>Myoz1	Myoz1	NM_021508	0.0187761	6.51622	Nuclei up vs Whole cells
NM_177686>Clec12a	Clec12a	NM_177686	0.0488787	6.50617	Nuclei up vs Whole cells
NM_021609>Ccbp2	Ccbp2	NM_021609	0.0121685	6.49224	Nuclei up vs Whole cells
NR_033433>2900079G21Rik	2900079G21Rik	NR_033433	0.0316663	6.48121	Nuclei up vs Whole cells

NM_016704>C6	C6	NM_016704	0.0039169	6.46163	Nuclei up vs Whole cells
NM_026290>49305 11I11Rik	4930511I11Rik	NM_026290	0.026612	6.31005	Nuclei up vs Whole cells
NM_007651>Cd53	Cd53	NM_007651	0.0095559 9	6.3002	Nuclei up vs Whole cells
NM_198096>Arap1	Arap1	NM_198096	0.0211743	6.27331	Nuclei up vs Whole cells
NM_201608>H2-M10.3	H2-M10.3	NM_201608	0.03795	6.27	Nuclei up vs Whole cells
NM_023907>Foxi1	Foxi1	NM_023907	0.0405673	6.23746	Nuclei up vs Whole cells
NM_010250>Gabra 1	Gabra1	NM_010250	0.0028762 5	6.21055	Nuclei up vs Whole cells
NM_027220>Prss32	Prss32	NM_027220	0.0322237	6.20369	Nuclei up vs Whole cells
NM_027572>Slc22a 16	Slc22a16	NM_027572	0.0454912	6.1977	Nuclei up vs Whole cells
NM_001172207>Lrt m2	Lrtm2	NM_00117220 7	0.0012475 4	6.19644	Nuclei up vs Whole cells
NM_146978>Olfr12 58	Olfr1258	NM_146978	0.0349401	6.1166	Nuclei up vs Whole cells
NM_170673>Cpne9	Cpne9	NM_170673	0.0036028 3	6.0776	Nuclei up vs Whole cells
NM_001177897>98 30107B12Rik	9830107B12Rik	NM_00117789 7	0.0417668	6.06758	Nuclei up vs Whole cells
NM_198642>50314 14D18Rik	5031414D18Rik	NM_198642	6.38E-05	6.0036	Nuclei up vs Whole cells
NM_001085419>G m13102	Gm13102	NM_00108541 9	0.0069875 9	5.92878	Nuclei up vs Whole cells
NM_146077>Trim3 1	Trim31	NM_146077	0.0099838 2	5.9131	Nuclei up vs Whole cells
NM_008685>Nfe2	Nfe2	NM_008685	0.0131159	5.90672	Nuclei up vs Whole cells
NM_001164229>Nrf 1	Nrf1	NM_00116422 9	0.0375182	5.81975	Nuclei up vs Whole cells
NM_011724>Xirp1	Xirp1	NM_011724	0.0123851	5.81227	Nuclei up vs Whole cells
NM_011067>Per3	Per3	NM_011067	0.0016832 6	5.81188	Nuclei up vs Whole cells
NM_178669>Clrn3	Clrn3	NM_178669	0.0231537	5.67265	Nuclei up vs Whole cells
NM_001077705>Pt pn6	Ptpn6	NM_00107770 5	0.0483223	5.67008	Nuclei up vs Whole cells
NM_053079>Slc15a 1	Slc15a1	NM_053079	0.0073102 6	5.59742	Nuclei up vs Whole cells
NM_010596>Kcna7	Kcna7	NM_010596	0.0050849 9	5.58035	Nuclei up vs Whole cells
NM_001109753>Sv 2b	Sv2b	NM_00110975 3	0.0041479 2	5.56641	Nuclei up vs Whole cells
NM_199473>Col8a2	Col8a2	NM_199473	0.0002666 56	5.52074	Nuclei up vs Whole cells
NM_001081663>Bt nl7	Btnl7	NM_00108166 3	0.0280777	5.4975	Nuclei up vs Whole cells
NR_033472>Gm107 68	Gm10768	NR_033472	0.0009871 05	5.48074	Nuclei up vs Whole cells
NM_178747>Gulo	Gulo	NM_178747	0.0333997	5.46703	Nuclei up vs Whole cells
NM_146849>Olfr11 57	Olfr1157	NM_146849	0.0148258	5.45135	Nuclei up vs Whole cells
NM_010149>Epor	Epor	NM_010149	0.0154369	5.43651	Nuclei up vs Whole cells
NM_170730>Ank3	Ank3	NM_170730	0.0351953	5.39619	Nuclei up vs Whole cells
NR_033543>Gm162 87	Gm16287	NR_033543	0.0455593	5.36784	Nuclei up vs Whole cells
NM_009307>Syt2	Syt2	NM_009307	0.0465264	5.31749	Nuclei up vs Whole cells
NR_033556>A63001 0A05Rik	A630010A05Rik	NR_033556	0.0434043	5.25633	Nuclei up vs Whole cells

NM_178767>Tmem195	Tmem195	NM_178767	0.0310538	5.24047	Nuclei up vs Whole cells
NM_001163498>Rundc2a	Rundc2a	NM_001163498	0.0386938	5.23843	Nuclei up vs Whole cells
NM_173031>BC066135	BC066135	NM_173031	0.0437084	5.20013	Nuclei up vs Whole cells
NM_177638>Crb3	Crb3	NM_177638	0.0373266	5.18924	Nuclei up vs Whole cells
NM_178036>Lcn10	Lcn10	NM_178036	0.0312151	5.18779	Nuclei up vs Whole cells
NM_172887>Fry	Fry	NM_172887	0.015197	5.10664	Nuclei up vs Whole cells
NM_013731>Sgk2	Sgk2	NM_013731	0.0200449	5.10575	Nuclei up vs Whole cells
NM_183222>Fcrl5	Fcrl5	NM_183222	0.00905035	5.10286	Nuclei up vs Whole cells
NM_001001714>Sohlh1	Sohlh1	NM_001001714	0.0461846	5.05325	Nuclei up vs Whole cells
NM_001160268>Plekha6	Plekha6	NM_001160268	0.00720961	5.03858	Nuclei up vs Whole cells
NR_033207>2010016I18Rik	2010016I18Rik	NR_033207	0.0143607	5.02758	Nuclei up vs Whole cells
NM_199154>Tas2r107	Tas2r107	NM_199154	0.0459807	5.01125	Nuclei up vs Whole cells
NR_033616>Pldi	Pldi	NR_033616	0.0194964	5.00535	Nuclei up vs Whole cells
NM_016911>Srpx	Srpx	NM_016911	0.0401532	5.00023	Nuclei up vs Whole cells
NM_001145096>Hhla1	Hhla1	NM_001145096	0.00983134	4.99336	Nuclei up vs Whole cells
NM_023653>Wnt2	Wnt2	NM_023653	0.0192982	4.99215	Nuclei up vs Whole cells
NM_027770>Col24a1	Col24a1	NM_027770	0.0013306	4.98628	Nuclei up vs Whole cells
NM_009578>Ikzf1	Ikzf1	NM_009578	0.0257547	4.97489	Nuclei up vs Whole cells
NM_183015>Ccnb3	Ccnb3	NM_183015	0.0310704	4.97337	Nuclei up vs Whole cells
NM_030728>9930013L23Rik	9930013L23Rik	NM_030728	0.0213917	4.96949	Nuclei up vs Whole cells
NM_008026>Fli1	Fli1	NM_008026	0.0068206	4.96308	Nuclei up vs Whole cells
NM_013811>Dnahc8	Dnahc8	NM_013811	0.030975	4.94225	Nuclei up vs Whole cells
NM_173029>Adcy10	Adcy10	NM_173029	0.0174529	4.93766	Nuclei up vs Whole cells
NM_008091>Gata3	Gata3	NM_008091	0.000261554	4.93522	Nuclei up vs Whole cells
NM_177076>Fbxl13	Fbxl13	NM_177076	0.00890098	4.88594	Nuclei up vs Whole cells
NR_036630>Gm1082	Gm1082	NR_036630	0.0482847	4.84621	Nuclei up vs Whole cells
NM_028772>Dmgdh	Dmgdh	NM_028772	0.0124709	4.83315	Nuclei up vs Whole cells
NM_025276>Evpl	Evpl	NM_025276	0.0354202	4.82927	Nuclei up vs Whole cells
NM_022995>Pmepa1	Pmepa1	NM_022995	0.000655478	4.79457	Nuclei up vs Whole cells
NM_008090>Gata2	Gata2	NM_008090	0.00996804	4.78947	Nuclei up vs Whole cells
NM_011318>Apcs	Apcs	NM_011318	0.00917897	4.78801	Nuclei up vs Whole cells
NM_019992>Stap1	Stap1	NM_019992	0.0136753	4.77481	Nuclei up vs Whole cells
NM_009821>Runx1	Runx1	NM_009821	5.33E-05	4.75382	Nuclei up vs Whole cells
NM_153062>Slc37a1	Slc37a1	NM_153062	0.0111562	4.74738	Nuclei up vs Whole cells
NM_175448>Clvs2	Clvs2	NM_175448	0.0450876	4.74168	Nuclei up vs Whole cells
NM_010278>Gfi1	Gfi1	NM_010278	0.0297163	4.6982	Nuclei up vs Whole cells

NM_008498>Lhx1	Lhx1	NM_008498	6.73E-05	4.69455	Nuclei up vs Whole cells
NM_153541>Zbtb8b	Zbtb8b	NM_153541	0.0173955	4.68923	Nuclei up vs Whole cells
NM_001013390>Scn4b	Scn4b	NM_001013390	0.00214846	4.66839	Nuclei up vs Whole cells
NM_001008230>Rtp2	Rtp2	NM_001008230	0.0427621	4.6602	Nuclei up vs Whole cells
NM_153105>Cldn19	Cldn19	NM_153105	0.00884977	4.63905	Nuclei up vs Whole cells
NM_001081254>Fam186b	Fam186b	NM_001081254	0.0296634	4.6377	Nuclei up vs Whole cells
NM_176942>Gabra5	Gabra5	NM_176942	0.0338321	4.63728	Nuclei up vs Whole cells
NM_013660>Sema4d	Sema4d	NM_013660	0.00646704	4.63064	Nuclei up vs Whole cells
NM_001001489>BC021785	BC021785	NM_001001489	0.00702075	4.59825	Nuclei up vs Whole cells
NR_015571>4930471G03Rik	4930471G03Rik	NR_015571	0.0235436	4.58923	Nuclei up vs Whole cells
NM_010226>Foxs1	Foxs1	NM_010226	0.03708	4.58877	Nuclei up vs Whole cells
NM_201370>Wee2	Wee2	NM_201370	0.0355595	4.56445	Nuclei up vs Whole cells
NM_010130>Emr1	Emr1	NM_010130	0.0373065	4.56396	Nuclei up vs Whole cells
NM_001037937>Depdc6	Depdc6	NM_001037937	0.00399151	4.54455	Nuclei up vs Whole cells
NM_172508>Dse	Dse	NM_172508	0.0447869	4.49143	Nuclei up vs Whole cells
NM_001039214>Mex3c	Mex3c	NM_001039214	0.0369534	4.47659	Nuclei up vs Whole cells
NM_009308>Syt4	Syt4	NM_009308	0.0351425	4.44649	Nuclei up vs Whole cells
NM_001013755>5730409E04Rik	5730409E04Rik	NM_001013755	0.00721073	4.43919	Nuclei up vs Whole cells
NM_001145950>5730409E04Rik	5730409E04Rik	NM_001145950	0.00721073	4.43919	Nuclei up vs Whole cells
NM_008425>Kcnj2	Kcnj2	NM_008425	0.00192711	4.43509	Nuclei up vs Whole cells
NM_011704>Vnn1	Vnn1	NM_011704	0.0194034	4.39625	Nuclei up vs Whole cells
NM_177431>Adamts20	Adamts20	NM_177431	0.0437042	4.39294	Nuclei up vs Whole cells
NM_001033531>Klhl32	Klhl32	NM_001033531	0.0270713	4.37583	Nuclei up vs Whole cells
NM_018754>Sfn	Sfn	NM_018754	0.0432357	4.36993	Nuclei up vs Whole cells
NM_010686>Laptm5	Laptm5	NM_010686	0.0121067	4.35278	Nuclei up vs Whole cells
NM_139200>Cytip	Cytip	NM_139200	0.0490818	4.34626	Nuclei up vs Whole cells
NM_028075>Tnfrsf13c	Tnfrsf13c	NM_028075	1.92E-05	4.34491	Nuclei up vs Whole cells
NM_028343>Tmem135	Tmem135	NM_028343	0.016982	4.32606	Nuclei up vs Whole cells
NM_001170954>A4galt	A4galt	NM_001170954	0.000722318	4.32384	Nuclei up vs Whole cells
NM_008082>Galr1	Galr1	NM_008082	0.0486485	4.31636	Nuclei up vs Whole cells
NM_008873>Plau	Plau	NM_008873	0.00796218	4.29196	Nuclei up vs Whole cells
NM_026862>Cd177	Cd177	NM_026862	0.0422918	4.28245	Nuclei up vs Whole cells
NM_010932>Pnoc	Pnoc	NM_010932	0.00142649	4.27056	Nuclei up vs Whole cells
NR_033532>B230206H07Rik	B230206H07Rik	NR_033532	0.0183886	4.26954	Nuclei up vs Whole cells
NM_001109873>Cbfa2t3	Cbfa2t3	NM_001109873	0.000249546	4.25997	Nuclei up vs Whole cells

NM_177289>Cbfa2t3	Cbfa2t3	NM_177289	0.000249549	4.25997	Nuclei up vs Whole cells
NM_181072>Myo1e	Myo1e	NM_181072	0.0305234	4.24747	Nuclei up vs Whole cells
NM_001161413>Slc3a2	Slc3a2	NM_001161413	0.035037	4.23982	Nuclei up vs Whole cells
NR_033398>Gm9159	Gm9159	NR_033398	0.000284621	4.23244	Nuclei up vs Whole cells
NM_001081052>Nhs	Nhs	NM_001081052	0.0362923	4.22133	Nuclei up vs Whole cells
NM_001190406>Gas2l1	Gas2l1	NM_001190406	0.0366568	4.21	Nuclei up vs Whole cells
NM_173749>Pamr1	Pamr1	NM_173749	0.00303327	4.19254	Nuclei up vs Whole cells
NM_175342_dup1>Cphx_dup1	Cphx_dup1	NM_175342_dup1	0.0119937	4.16963	Nuclei up vs Whole cells
NM_001037909>C130026I21Rik	C130026I21Rik	NM_001037909	0.0352156	4.15699	Nuclei up vs Whole cells
NM_175219>C130026I21Rik	C130026I21Rik	NM_175219	0.0352156	4.15699	Nuclei up vs Whole cells
NM_023887>Gcnt2	Gcnt2	NM_023887	0.0392181	4.14987	Nuclei up vs Whole cells
NM_001159538>Fgd2	Fgd2	NM_001159538	0.0416497	4.14857	Nuclei up vs Whole cells
NM_013710>Fgd2	Fgd2	NM_013710	0.0416497	4.14857	Nuclei up vs Whole cells
NM_008213>Hand1	Hand1	NM_008213	0.0495461	4.08572	Nuclei up vs Whole cells
NM_001126487>Gm1027	Gm1027	NM_001126487	0.0413552	4.04348	Nuclei up vs Whole cells
NM_007807>Cybb	Cybb	NM_007807	0.043819	3.97422	Nuclei up vs Whole cells
NM_008550>Man2b2	Man2b2	NM_008550	0.0278977	3.9379	Nuclei up vs Whole cells
NM_011077>Phex	Phex	NM_011077	0.00172077	3.93516	Nuclei up vs Whole cells
NM_001110163>Pde4dip	Pde4dip	NM_001110163	0.0485885	3.9334	Nuclei up vs Whole cells
NM_008239>Foxq1	Foxq1	NM_008239	0.0285887	3.90165	Nuclei up vs Whole cells
NM_146734>Olfr478	Olfr478	NM_146734	0.0300762	3.89321	Nuclei up vs Whole cells
NM_207210>Dyrk4	Dyrk4	NM_207210	0.0454084	3.88809	Nuclei up vs Whole cells
NM_028623>Cst6	Cst6	NM_028623	0.00749022	3.88741	Nuclei up vs Whole cells
NM_001039187>Ceacam1	Ceacam1	NM_001039187	0.0214607	3.8863	Nuclei up vs Whole cells
NM_177709>Tusc5	Tusc5	NM_177709	0.0160145	3.88607	Nuclei up vs Whole cells
NM_194064>Nanos2	Nanos2	NM_194064	0.0193511	3.88504	Nuclei up vs Whole cells
NM_001081348>Hecw1	Hecw1	NM_001081348	7.24E-05	3.88218	Nuclei up vs Whole cells
NM_008599>Cxcl9	Cxcl9	NM_008599	0.00534745	3.87246	Nuclei up vs Whole cells
NM_019753>Cdh17	Cdh17	NM_019753	0.04787	3.86726	Nuclei up vs Whole cells
NM_025763>4933436I01Rik	4933436I01Rik	NM_025763	0.0469292	3.86688	Nuclei up vs Whole cells
NM_177123>Spef2	Spef2	NM_177123	0.0417809	3.85869	Nuclei up vs Whole cells
NM_001168510>Ffar2	Ffar2	NM_001168510	0.0363798	3.8576	Nuclei up vs Whole cells
NM_144943>Cd207	Cd207	NM_144943	0.0345845	3.85702	Nuclei up vs Whole cells
NM_001146198>Nkx2-1	Nkx2-1	NM_001146198	0.0347061	3.85601	Nuclei up vs Whole cells
NM_011109>Pla2g2d	Pla2g2d	NM_011109	0.0133866	3.83723	Nuclei up vs Whole cells

NM_008002>Fgf10	Fgf10	NM_008002	0.0168744	3.8314	Nuclei up vs Whole cells
NM_001039146>Vmn1r90	Vmn1r90	NM_001039146	0.0369416	3.82455	Nuclei up vs Whole cells
NM_001037923>Lekr1	Lekr1	NM_001037923	0.0428099	3.82336	Nuclei up vs Whole cells
NM_028721>Nphp3	Nphp3	NM_028721	0.00279607	3.82306	Nuclei up vs Whole cells
NR_033456>Gm4710	Gm4710	NR_033456	0.0477874	3.81875	Nuclei up vs Whole cells
NM_021541>Cryba2	Cryba2	NM_021541	0.0398934	3.79228	Nuclei up vs Whole cells
NM_177054>Casc4	Casc4	NM_177054	0.0456436	3.77095	Nuclei up vs Whole cells
NM_144803>Chrna2	Chrna2	NM_144803	0.00304606	3.74055	Nuclei up vs Whole cells
NM_001038607>Kcnh1	Kcnh1	NM_001038607	0.0022302	3.73567	Nuclei up vs Whole cells
NM_001163816>Vav1	Vav1	NM_001163816	0.0255311	3.72379	Nuclei up vs Whole cells
NM_001163386>4930579F01Rik	4930579F01Rik	NM_001163386	0.0467671	3.71744	Nuclei up vs Whole cells
NM_178877>Nhedc2	Nhedc2	NM_178877	0.0427693	3.70719	Nuclei up vs Whole cells
NM_178673>Fstl5	Fstl5	NM_178673	0.0303172	3.65906	Nuclei up vs Whole cells
NM_007873>Doc2b	Doc2b	NM_007873	0.045567	3.65746	Nuclei up vs Whole cells
NM_001085421>Tspyl5	Tspyl5	NM_001085421	0.0233135	3.65567	Nuclei up vs Whole cells
NM_183139>Pld6	Pld6	NM_183139	0.0331996	3.65239	Nuclei up vs Whole cells
NM_001195097>3425401B19Rik	3425401B19Rik	NM_001195097	0.0183732	3.63956	Nuclei up vs Whole cells
NM_172444>Thsd4	Thsd4	NM_172444	0.0415086	3.63813	Nuclei up vs Whole cells
NM_177039>A530016L24Rik	A530016L24Rik	NM_177039	0.0207886	3.63246	Nuclei up vs Whole cells
NM_001034859>Gm4841	Gm4841	NM_001034859	0.0157037	3.6149	Nuclei up vs Whole cells
NM_001159532>Tex21	Tex21	NM_001159532	0.0281809	3.59758	Nuclei up vs Whole cells
NM_017394>Slc7a10	Slc7a10	NM_017394	0.0300168	3.58777	Nuclei up vs Whole cells
NM_010054>Dlx2	Dlx2	NM_010054	0.0231757	3.57968	Nuclei up vs Whole cells
NM_001033795>Zcchc16	Zcchc16	NM_001033795	0.0112874	3.56306	Nuclei up vs Whole cells
NM_008402>Itgav	Itgav	NM_008402	0.0279642	3.55822	Nuclei up vs Whole cells
NM_011998>Chst4	Chst4	NM_011998	0.0157403	3.55604	Nuclei up vs Whole cells
NM_025973>Pgc	Pgc	NM_025973	0.0405279	3.54237	Nuclei up vs Whole cells
NM_010289>Gja10	Gja10	NM_010289	0.04527	3.53342	Nuclei up vs Whole cells
NM_001033304>5330417C22Rik	5330417C22Rik	NM_001033304	0.045189	3.51917	Nuclei up vs Whole cells
NM_001025067>Lrig2	Lrig2	NM_001025067	2.51E-05	3.51901	Nuclei up vs Whole cells
NM_001164787_dup1>Sprr2a2_dup1	Sprr2a2_dup1	NM_001164787_dup1	0.00253234	3.51301	Nuclei up vs Whole cells
NM_011468_dup1>Sprr2a1_dup1	Sprr2a1_dup1	NM_011468_dup1	0.00253234	3.51301	Nuclei up vs Whole cells
NM_172861>Slc7a14	Slc7a14	NM_172861	0.000470135	3.50659	Nuclei up vs Whole cells
NM_172564>Tns4	Tns4	NM_172564	0.0283971	3.50137	Nuclei up vs Whole cells
NM_010683>Lamc1	Lamc1	NM_010683	0.0197939	3.49422	Nuclei up vs Whole cells
NM_023709>Capn9	Capn9	NM_023709	0.0236392	3.47254	Nuclei up vs Whole cells

NM_153559>Qsox2	Qsox2	NM_153559	0.0200056	3.46793	Nuclei up vs Whole cells
NM_001161355>Timd2	Timd2	NM_001161355	0.0441534	3.4665	Nuclei up vs Whole cells
NM_001177579>Gm10471	Gm10471	NM_001177579	0.00916907	3.46323	Nuclei up vs Whole cells
NM_001174047>Cacna2d2	Cacna2d2	NM_001174047	0.00989755	3.46041	Nuclei up vs Whole cells
NM_001174048>Cacna2d2	Cacna2d2	NM_001174048	0.00989756	3.46041	Nuclei up vs Whole cells
NM_001174049>Cacna2d2	Cacna2d2	NM_001174049	0.00989756	3.46041	Nuclei up vs Whole cells
NM_001174050>Cacna2d2	Cacna2d2	NM_001174050	0.00989756	3.46041	Nuclei up vs Whole cells
NM_020263>Cacna2d2	Cacna2d2	NM_020263	0.00989756	3.46041	Nuclei up vs Whole cells
NM_001126322>Gm11595	Gm11595	NM_001126322	0.0495075	3.45743	Nuclei up vs Whole cells
NM_146028>Stac2	Stac2	NM_146028	0.000277826	3.454	Nuclei up vs Whole cells
NR_024257>4930412O13Rik	4930412O13Rik	NR_024257	0.0312299	3.45286	Nuclei up vs Whole cells
NM_015826>Dmrt1	Dmrt1	NM_015826	0.000318659	3.4375	Nuclei up vs Whole cells
NR_027858>Nlrp1c-ps	Nlrp1c-ps	NR_027858	0.0289108	3.396	Nuclei up vs Whole cells
NM_001004150>A4galt	A4galt	NM_001004150	0.00155606	3.39192	Nuclei up vs Whole cells
NM_177086>Zmat4	Zmat4	NM_177086	0.0364836	3.39062	Nuclei up vs Whole cells
NM_145136>Myocd	Myocd	NM_145136	0.0477561	3.3874	Nuclei up vs Whole cells
NM_172521>Nut	Nut	NM_172521	0.00232199	3.38407	Nuclei up vs Whole cells
NM_009421>Traf1	Traf1	NM_009421	0.0459212	3.37438	Nuclei up vs Whole cells
NR_015593>D130009I18Rik	D130009I18Rik	NR_015593	0.013378	3.35635	Nuclei up vs Whole cells
NM_010456>Hoxa9	Hoxa9	NM_010456	0.0361866	3.34416	Nuclei up vs Whole cells
NM_001024727>Gm16387	Gm16387	NM_001024727	0.00514048	3.33949	Nuclei up vs Whole cells
NM_173385>Cilp	Cilp	NM_173385	0.017037	3.33086	Nuclei up vs Whole cells
NM_027937>Caskin1	Caskin1	NM_027937	0.0393128	3.33072	Nuclei up vs Whole cells
NM_001167832>Zfp764	Zfp764	NM_001167832	0.0229346	3.31341	Nuclei up vs Whole cells
NM_146203>Zfp764	Zfp764	NM_146203	0.0229347	3.31341	Nuclei up vs Whole cells
NM_001102563>Prrt2	Prrt2	NM_001102563	0.0257805	3.30376	Nuclei up vs Whole cells
NM_001079932>Trim72	Trim72	NM_001079932	0.0145404	3.30254	Nuclei up vs Whole cells
NM_001127177>Ptpn2	Ptpn2	NM_001127177	0.00109725	3.30097	Nuclei up vs Whole cells
NM_172486>Zfp677	Zfp677	NM_172486	0.0259954	3.29973	Nuclei up vs Whole cells
NM_018873>Srcin1	Srcin1	NM_018873	0.0492297	3.29457	Nuclei up vs Whole cells
NM_145592>Dkk4	Dkk4	NM_145592	0.0147257	3.29406	Nuclei up vs Whole cells
NR_027651>Meg3	Meg3	NR_027651	0.00516322	3.29376	Nuclei up vs Whole cells
NM_001145978>Parp4	Parp4	NM_001145978	0.0400015	3.28839	Nuclei up vs Whole cells
NM_206958>Ltbp1	Ltbp1	NM_206958	0.0375915	3.287	Nuclei up vs Whole cells
NM_133690>Atp1b4	Atp1b4	NM_133690	0.000390955	3.27338	Nuclei up vs Whole cells

NM_207298>Cercam	Cercam	NM_207298	0.0409793	3.27037	Nuclei up vs Whole cells
NR_033491>Gm10466	Gm10466	NR_033491	0.0114894	3.26599	Nuclei up vs Whole cells
NM_009675>Aoc3	Aoc3	NM_009675	0.00299178	3.2616	Nuclei up vs Whole cells
NM_133191>Eps8l2	Eps8l2	NM_133191	0.031332	3.25486	Nuclei up vs Whole cells
NM_001145927>C530028O21Rik	C530028O21Rik	NM_001145927	0.0322913	3.2539	Nuclei up vs Whole cells
NM_001104638>Vmn2r23	Vmn2r23	NM_001104638	0.0266353	3.24864	Nuclei up vs Whole cells
NM_007735>Col4a4	Col4a4	NM_007735	0.0244636	3.24057	Nuclei up vs Whole cells
NM_001164724>Il33	Il33	NM_001164724	0.0412384	3.23711	Nuclei up vs Whole cells
NM_178685>Pcdh20	Pcdh20	NM_178685	0.00992449	3.23413	Nuclei up vs Whole cells
NM_012045>Pla2g2f	Pla2g2f	NM_012045	0.0178663	3.22653	Nuclei up vs Whole cells
NM_010466>Hoxc8	Hoxc8	NM_010466	0.00772116	3.22101	Nuclei up vs Whole cells
NM_029698>Ttc18	Ttc18	NM_029698	0.0148221	3.21102	Nuclei up vs Whole cells
NM_001195672>Gm221	Gm221	NM_001195672	0.0318773	3.2038	Nuclei up vs Whole cells
NM_138750>Prom2	Prom2	NM_138750	0.000684577	3.2014	Nuclei up vs Whole cells
NM_178047>Prom2	Prom2	NM_178047	0.000684578	3.2014	Nuclei up vs Whole cells
NM_001037859>Csf1r	Csf1r	NM_001037859	0.00186891	3.19546	Nuclei up vs Whole cells
NM_011204>Ptpn13	Ptpn13	NM_011204	0.0229828	3.19187	Nuclei up vs Whole cells
NM_001110240>Slc24a2	Slc24a2	NM_001110240	0.0223882	3.17858	Nuclei up vs Whole cells
NM_011859>Osr1	Osr1	NM_011859	0.0228279	3.16607	Nuclei up vs Whole cells
NR_030692>A930011G23Rik	A930011G23Rik	NR_030692	0.0155406	3.1649	Nuclei up vs Whole cells
NM_177278>L3mbtl4	L3mbtl4	NM_177278	0.0042952	3.13005	Nuclei up vs Whole cells
NM_172485>Thsd7b	Thsd7b	NM_172485	0.0236392	3.12015	Nuclei up vs Whole cells
NM_153508>Clstn3	Clstn3	NM_153508	0.011319	3.11808	Nuclei up vs Whole cells
NM_028085>Anks4b	Anks4b	NM_028085	0.0199275	3.10689	Nuclei up vs Whole cells
NM_173734>Tmem87a	Tmem87a	NM_173734	0.0307979	3.09705	Nuclei up vs Whole cells
NM_007739>Col8a1	Col8a1	NM_007739	0.00167962	3.08325	Nuclei up vs Whole cells
NM_001146268>Pdgfrb	Pdgfrb	NM_001146268	0.000128259	3.05599	Nuclei up vs Whole cells
NM_008809>Pdgfrb	Pdgfrb	NM_008809	0.000128261	3.05599	Nuclei up vs Whole cells
NM_001113393>Cd247	Cd247	NM_001113393	0.00316347	3.03565	Nuclei up vs Whole cells
NM_001113394>Cd247	Cd247	NM_001113394	0.00316347	3.03565	Nuclei up vs Whole cells
NM_001085540>Pramef17	Pramef17	NM_001085540	0.0353828	3.03166	Nuclei up vs Whole cells
NM_019969>Plag1	Plag1	NM_019969	0.0108907	3.0285	Nuclei up vs Whole cells
NM_011772>Ikzf4	Ikzf4	NM_011772	0.0274504	3.02639	Nuclei up vs Whole cells
NM_009707>Arhga	Arhgap6	NM_009707	0.0356864	3.01173	Nuclei up vs Whole cells

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NM_001039149>Cd226	Cd226	NM_001039149	0.0488657	3.00708	Nuclei up vs Whole cells
NM_010074>Dpp4	Dpp4	NM_010074	0.0408543	3.00059	Nuclei up vs Whole cells
NM_016766>Mcrs1	Mcrs1	NM_016766	0.001993	-3.1206	Nuclei down vs Whole cells
NM_134002>Csnk1g2	Csnk1g2	NM_134002	0.0199871	-3.12415	Nuclei down vs Whole cells
NM_001033819>9130409I23Rik	9130409I23Rik	NM_001033819	0.010026	-3.29095	Nuclei down vs Whole cells
NM_001099349_dup3>Gm14308_dup3	Gm14308_dup3	NM_001099349_dup3	0.0197868	-3.29889	Nuclei down vs Whole cells
NM_010758>Mag	Mag	NM_010758	0.0411256	-3.3354	Nuclei down vs Whole cells
NR_033220>BC039771	BC039771	NR_033220	0.0269799	-3.3733	Nuclei down vs Whole cells
NR_003639>1700013N18Rik	1700013N18Rik	NR_003639	0.000102133	-3.47506	Nuclei down vs Whole cells
NM_001039391>Pkig	Pkig	NM_001039391	0.0453363	-3.51501	Nuclei down vs Whole cells
NM_001042725>Calcr	Calcr	NM_001042725	0.0480252	-3.58088	Nuclei down vs Whole cells
NM_007588>Calcr	Calcr	NM_007588	0.0480252	-3.58088	Nuclei down vs Whole cells
NM_177887>Tmem150b	Tmem150b	NM_177887	0.0279536	-3.6307	Nuclei down vs Whole cells
NM_001177406_dup3>Gm14431_dup3	Gm14431_dup3	NM_001177406_dup3	0.0101731	-3.65331	Nuclei down vs Whole cells
NM_001177407_dup3>Gm8898_dup3	Gm8898_dup3	NM_001177407_dup3	0.0101731	-3.65331	Nuclei down vs Whole cells
NM_175249>Psapl1	Psapl1	NM_175249	0.0257171	-3.699	Nuclei down vs Whole cells
NR_033550>Gm10248	Gm10248	NR_033550	0.0192265	-3.77634	Nuclei down vs Whole cells
NM_177382>Cyp2r1	Cyp2r1	NM_177382	0.0448083	-3.92774	Nuclei down vs Whole cells
NM_033268>Actn2	Actn2	NM_033268	0.0457634	-4.00766	Nuclei down vs Whole cells
NM_175519>Kctd8	Kctd8	NM_175519	0.0186554	-4.02592	Nuclei down vs Whole cells
NM_172923>AI118078	AI118078	NM_172923	0.0449712	-4.29708	Nuclei down vs Whole cells
NM_178203>Hist1h3b	Hist1h3b	NM_178203	0.0424376	-4.46837	Nuclei down vs Whole cells
NM_001126489>Zfp735	Zfp735	NM_001126489	0.0489386	-4.85045	Nuclei down vs Whole cells
NM_030703>Cpn1	Cpn1	NM_030703	0.0256042	-5.01338	Nuclei down vs Whole cells
NM_031867>Tas1r1	Tas1r1	NM_031867	0.00125648	-5.03614	Nuclei down vs Whole cells
NM_001001327>Vkorc1l1	Vkorc1l1	NM_001001327	0.00636324	-5.11608	Nuclei down vs Whole cells
NR_015488>A930003A15Rik	A930003A15Rik	NR_015488	0.0482706	-5.22585	Nuclei down vs Whole cells
NM_001134660>Prr23a	Prr23a	NM_001134660	0.0289154	-5.30456	Nuclei down vs Whole cells
NR_033121_dup2>Gm8348_dup2	Gm8348_dup2	NR_033121_dup2	0.0410417	-5.37492	Nuclei down vs Whole cells
NM_001145806>Capn8	Capn8	NM_001145806	0.0369749	-5.60523	Nuclei down vs Whole cells
NM_027650>Speer3	Speer3	NM_027650	0.0114941	-5.64153	Nuclei down vs Whole cells
NM_183158>Cyp2ab1	Cyp2ab1	NM_183158	0.00212559	-5.65339	Nuclei down vs Whole cells
NM_029946>Efcab6	Efcab6	NM_029946	0.0243017	-5.75752	Nuclei down vs Whole cells
NM_009611>Actl7a	Actl7a	NM_009611	0.0476764	-5.82649	Nuclei down vs Whole cells

NM_033601>Bcl3	Bcl3	NM_033601	0.0244082	-5.89593	Nuclei down vs Whole cells
NM_001085534>Gm5938	Gm5938	NM_001085534	0.047917	-5.92387	Nuclei down vs Whole cells
NM_198419>Phactr1	Phactr1	NM_198419	0.0347575	-5.99857	Nuclei down vs Whole cells
NM_008039>Fpr2	Fpr2	NM_008039	0.00320578	-6.39629	Nuclei down vs Whole cells
NM_134170>Vmn1r32	Vmn1r32	NM_134170	0.0367088	-6.41742	Nuclei down vs Whole cells
NM_144821>AI317395	AI317395	NM_144821	0.0241932	-6.81518	Nuclei down vs Whole cells
NM_021325>Cd200r1	Cd200r1	NM_021325	0.0304908	-7.00704	Nuclei down vs Whole cells
NM_025769>Efcab1	Efcab1	NM_025769	0.0222441	-7.33025	Nuclei down vs Whole cells
NM_001166627_dup4>Dynlt1f_dup4	Dynlt1f_dup4	NM_001166627_dup4	0.00434293	-7.34359	Nuclei down vs Whole cells
NM_013486>Cd2	Cd2	NM_013486	0.0459818	-7.36452	Nuclei down vs Whole cells
NM_175525>D630042P16Rik	D630042P16Rik	NM_175525	0.0348087	-7.85203	Nuclei down vs Whole cells
NM_020503>Tas2r119	Tas2r119	NM_020503	0.0443585	-7.95372	Nuclei down vs Whole cells
NM_133193>Il1rl2	Il1rl2	NM_133193	0.00827209	-8.04354	Nuclei down vs Whole cells
NM_001104547>Vmn2r96	Vmn2r96	NM_001104547	0.0421371	-8.44227	Nuclei down vs Whole cells
NM_001034101>Gm13119	Gm13119	NM_001034101	0.0379931	-8.48303	Nuclei down vs Whole cells
NM_001048196>Krtap4-1	Krtap4-1	NM_001048196	0.0478059	-8.68869	Nuclei down vs Whole cells
NM_001039653>Lhx3	Lhx3	NM_001039653	0.000294468	-8.78365	Nuclei down vs Whole cells
NM_023729>Asz1	Asz1	NM_023729	0.00857558	-8.93075	Nuclei down vs Whole cells
NM_013596>Mc5r	Mc5r	NM_013596	0.0489222	-9.19794	Nuclei down vs Whole cells
NM_021483>Pex5l	Pex5l	NM_021483	0.0214987	-9.21198	Nuclei down vs Whole cells
NM_007967>Evx2	Evx2	NM_007967	0.0402564	-9.70061	Nuclei down vs Whole cells
NM_001018087>Ldoc1	Ldoc1	NM_001018087	0.0212415	-9.98858	Nuclei down vs Whole cells
NM_153096>Zfp353	Zfp353	NM_153096	0.0227177	-10.0516	Nuclei down vs Whole cells
NM_146783>Olfr26	Olfr26	NM_146783	0.0441297	-10.1988	Nuclei down vs Whole cells
NM_177923>H2-M10.2	H2-M10.2	NM_177923	0.0284159	-10.4289	Nuclei down vs Whole cells
NM_009317>Tal2	Tal2	NM_009317	0.0087421	-10.626	Nuclei down vs Whole cells
NM_001111059>Cd34	Cd34	NM_001111059	0.0269535	-10.7477	Nuclei down vs Whole cells
NM_029067>Spata17	Spata17	NM_029067	0.0444364	-10.9112	Nuclei down vs Whole cells
NM_001081283>Tmem28	Tmem28	NM_001081283	0.0362378	-10.9293	Nuclei down vs Whole cells
NM_001003951>Ces5a	Ces5a	NM_001003951	0.0340595	-12.4363	Nuclei down vs Whole cells
NM_178215>Hist2h3b	Hist2h3b	NM_178215	0.00229243	-12.5105	Nuclei down vs Whole cells
NM_199225>Cd300c	Cd300c	NM_199225	0.0257218	-12.7242	Nuclei down vs Whole cells
NM_026593>D730048I06Rik	D730048I06Rik	NM_026593	0.04276	-12.902	Nuclei down vs Whole cells
NM_018866>Cxcl13	Cxcl13	NM_018866	0.046067	-13.1631	Nuclei down vs Whole cells
NM_013542>Gzmb	Gzmb	NM_013542	0.0180082	-13.229	Nuclei down vs Whole cells

			0.0046630		
NM_009654>Alb	Alb	NM_009654	5	-14.7251	Nuclei down vs Whole cells
NM_001011759>Olfr1031	Olfr1031	NM_00101175 9	0.0050020 8	-16.4963	Nuclei down vs Whole cells
NM_134201>Vmn1r 236	Vmn1r236	NM_134201	1.96E-05	-17.5803	Nuclei down vs Whole cells
NM_001159617>Pig p	Pigp	NM_00115961 7	0.0264643	-17.9118	Nuclei down vs Whole cells
NM_010662>Krt13	Krt13	NM_010662	0.0127378	-22.7554	Nuclei down vs Whole cells
NR_030705>Snord2	Snord2	NR_030705	0.0438372	-24.8022	Nuclei down vs Whole cells
NM_001161769>Lm o4	Lmo4	NM_00116176 9	0.0010660 7	-25.1349	Nuclei down vs Whole cells

Table S5. Gene ontology results of genes enriched in nuclei as compared to cells.

Biological Processes

Category	Term	Count	%	PValue
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	32	10.03134796	0.015191102
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	32	10.03134796	0.018575851
GOTERM_BP_FAT	GO:0007155~cell adhesion	22	6.896551724	4.86E-05
GOTERM_BP_FAT	GO:0022610~biological adhesion	22	6.896551724	4.99E-05
GOTERM_BP_FAT	GO:0006811~ion transport	19	5.956112853	0.012737724
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	18	5.642633229	0.001476793
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	18	5.642633229	0.002268093
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	18	5.642633229	0.002490561
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	18	5.642633229	0.008807094
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	16	5.015673981	0.003229158
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	16	5.015673981	0.004148375
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	16	5.015673981	0.00618514
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	16	5.015673981	0.008122409
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	15	4.702194357	0.002490023
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	15	4.702194357	0.002657817

GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	15	4.702194357	0.056220821
GOTERM_BP_FAT	GO:0006812~cation transport	14	4.388714734	0.032321934
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	13	4.07523511	0.005151355
GOTERM_BP_FAT	GO:0030001~metal ion transport	13	4.07523511	0.024062749
GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	13	4.07523511	0.082085763
GOTERM_BP_FAT	GO:0051094~positive regulation of developmental process	11	3.448275862	9.72E-04
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	11	3.448275862	0.005736057
GOTERM_BP_FAT	GO:0045597~positive regulation of cell differentiation	10	3.134796238	8.88E-04
GOTERM_BP_FAT	GO:0048568~embryonic organ development	10	3.134796238	0.007593387

Table S6. Categories and numbers of noncoding RNAs identified in nuclei and whole cell sample.

category	antisense	lincRNA	miRNA	misc RNA	noncoding	processed transcript	retained intron	snRNA	snoRNA	total
*All Nuclei	3	146	86	5	2	76	10	1	64	**393**
Nuclei Average	3	138	51	4	2	71	10	1	43	**323**
N10 group	3	135	47	4	2	71	9	1	44	**316**
N100 group	2	120	30	0	2	65	8	0	28	**255**
N1-1	2	122	34	3	2	67	8	1	23	**262**
N1-2	3	130	27	2	2	68	9	1	20	**262**
N1-3	2	86	17	1	2	51	6	0	20	**185**
N10-1	2	111	24	1	2	58	7	1	19	**225**
N10-2	1	105	20	0	2	58	6	1	22	**215**
N10-3	2	122	24	3	2	67	8	0	31	**259**
N100-1	1	88	20	0	2	52	6	0	19	**188**
N100-2	2	96	13	0	2	53	8	0	15	**189**
N100-3	1	76	11	0	1	43	5	0	16	**153**
*All Whole Cells	3	147	103	2	2	77	10	2	71	**417**
Whole Cells Average	2	138	48	1	2	72	8	1	27	**299**
C10 group	3	133	31	1	2	71	9	1	45	**296**
C100 group	3	138	56	2	2	74	10	1	62	**348**
C1A	2	118	24	0	2	61	6	1	18	**232**
C1B	2	118	24	1	2	64	6	1	10	**228**
C1C	2	101	15	0	2	55	6	0	15	**196**
C10A	2	109	19	1	2	58	6	0	20	**217**
C10B	2	119	13	0	2	66	8	0	20	**230**
C10C	2	98	14	0	2	55	6	1	28	**206**
C100A	3	119	24	0	2	65	8	0	34	**255**
C100B	1	107	22	1	2	62	7	0	35	**237**
C100C	3	129	39	2	2	67	10	1	49	**302**
DG group	1	120	22	1	2	62	6	1	11	**226**
DG 1-1	1	113	19	0	2	59	4	1	7	**206**
DG 1-2	0	100	13	1	2	50	6	0	8	**180**
fetal stromal bulk	1	115	20	3	2	62	8	1	17	**229**

* = values represent non-redundant union of all 3 groups (n1,n10,n100 or c1,c10,c100).

group = values represent non-redundant union of 3 replicates within each of 3 groups of nuclei or cells (eg: N1-1,N1-2, N1-3, etc.).
        Or 2 replicates in case of DG nuclei

antisense: transcripts overlapping the genomic extent of one or more coding loci on the opposite strand

lincRNA: long intergenic non-coding RNA. Transcripts do not overlap protein-coding locus on same or opposite strand.

miRNA: microRNA precursors

misc RNA: miscellaneous other RNA

noncoding: known transcripts with non-coding function confirmed by literature or experiments

processed transcript: does not contain an open reading frame (ORF) which can be unambiguously assigned as a CDS

retained intron: has retained intronic sequence compared to a reference variant

snRNA: small nuclear RNA

snoRNA: small nucleolar RNA

Methods

S1 *Micromanipulation of single cells and nuclei*

Following isolation of NP cells and purification of nuclei, each sample was diluted to 1,000 objects (cells, nuclei) per microliter with cold phosphate buffered saline (PBS) (ultrapure-grade phosphate buffers and saline solutions, 1X concentration is 137 mM NaCl, 2.7 mM KCl, 8 mM Na_2HPO_4 and 2 mM KH_2PO_4 (Ambion)). An aliquot (50 µl) of the diluted sample was transferred onto a cold glass slide and viewed with an IX70 Olympus microscope under phase contrast and fluorescence illumination. Cells or nuclei were individually aspirated using a glass micropipette having a 15 µm inner diameter (Eppendorf) connected to a CellTram® Oil Transferman® (Eppendorf), and serially expelled and washed three times in cold, nuclease free PBS. The individual cell or nucleus was then expelled from the micropipette into a 0.2 ml thin-walled PCR tube containing a droplet (1.0 µl) of cold lysis buffer solution. Each sample was immediately either lysed for cDNA synthesis or flash-frozen in liquid nitrogen and stored at -80° C.

S2 *cDNA synthesis, amplification and TaqMan analysis*

cDNA synthesis and PCR amplification was done according to previous methods (2, 3). Briefly, samples were lysed with heat, and mRNA was reverse-transcribed using a poly(dT) primer. First strand cDNA was polyadenylated with terminal transferase and second-strand cDNA synthesis was done with a second poly(dT) primer. Double stranded cDNA was amplified, limiting the rounds of PCR to preserve relative expression levels. The products of the first round of PCR (18 cycles for the NPCs and 22 cycles for the DGs) were then screened for genes of interest by qPCR.

TaqMan loci (Applied Biosystems) qPCR employed a 1:10 dilution of the first round PCR products. An aliquot (0.5 µl) of TaqMan gene expression assay mixed with 5.0 µl of 1x PerfeCTa™ qPCR FastMix™ (Quanta Biosciences) and brought to a final volume of 10 µl with nuclease-free water

(Ambion). Real-time thermal cycling conditions were: $95^{\circ}C$ for 2 minutes, followed by 50 cycles of $95^{\circ}C$ for 10 seconds and $60^{\circ}C$ for 30 seconds.

S3 *SOLiD sequencing, mapping, and error correction*

Fragment libraries were constructed following published protocols for the SOLiD platform (3). In a single-end, 50 base pair read run, multiplexed samples were sequenced on each of two slides. The SOLiD Accuracy Enhancement Tool (SAET) and the transcriptome pipelines in the Bioscope™ Software were used for error correction and high accuracy mapping against the *Mus musculus* genome assembly MGSCv37 (mm9) to which the EYFP transgene transcript sequence was added. The DG nuclei and stromal control were sequenced later with improved protocols (for example in library production and increased bead density on the sequencing plate), which can account for the increase in mapping efficiency (SI Appendix, Table S2).

S4 *Bioinformatics analysis*

Gene expression was quantified using RPKM values (4). Variance was stabilized by $\log_2$ scaling. Data post-processing and graphics production was done using Matlab functions developed in-house. Hierarchical clustering of gene expression and samples was performed with one minus correlation metric and the unweighted average distance (UPGMA; also known as group average) linkage method (5).

Variation of the replicates of each type of sample was quantified using the coefficient of variation (CV): first, for each group of samples corresponding to the same biological entity, the variation of each gene was calculated as the CV of its $\log_2$ RKPM expression across all the replicates of the group. Second, the variation of all the genes of the group was summarized using the mean values. Thus, the variation in a group is defined as the mean $\mu(CV)$ of the coefficient of variation of each gene expression across all the replicates.

S5 *Gene ontology analysis*

Transcripts enriched in the nuclei were calculated using one-way ANOVA with a *P*-value ≤ 0.05. The list of 352 transcripts (SI Appendix, Table S4) was submitted for functional analysis to the Database for Annotation, Visualization and Integrated Discovery (DAVID; (6)) to identify categories that were overrepresented. The functional annotations were retrieved, and a threshold of a minimum of ten genes per category was set.

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