712   **Supplementary Table 1.** Marmosets analyzed with snRNA-seq in this study. Colonies: NEPRC
713   - New England Primate Research Colony; CLEA - Central Institute for Experimental Animals,
714   Japan; Company A: marmosets obtained from a non-clinical contract research organization.

| ID | Tissue | Sex | Age | No. birth siblings (sex of sibling(s)) | Colony | Single-cell platform |
|---|---|---|---|---|---|---|
| CJ001 | Brain | F | Neonate | 2 (M, M) | NEPRC | Drop-seq |
| CJ006 | Brain | M | Neonate | 2 (F, unknown) | CLEA | 10X |
| CJ007 | Brain | F | Neonate | 2 (M, unknown) | CLEA | 10X |
| CJ022 | Brain | F | 2 yrs 8 mos | 1 (M) | NEPRC | Drop-seq, 10X |
| CJ023 | Brain | F | 2 yrs | 2 (F, M) | NEPRC | Drop-seq |
| CJ025 | Brain | M | 2 yrs | 1 (M) | NEPRC | Drop-seq |
| CJ026 | Brain | M | 2 yrs 8 mos | 1 (F) | NEPRC | Drop-seq |
| CJ026 | Blood | | | | | 10X |
| CJ026 | Liver | | | | | 10X |
| CJ026 | Kidney | | | | | 10X |
| CJ027 | Brain | M | 2 years | 1 (M) | CompanyA | 10X |
| CJ027 | Blood | | | | | 10X |
| CJ028 | Brain | F | 2 years | 2 (M, F) | NEPRC | 10X |
| CJ028 | Blood | | | | | 10X |
| CJ029 | Brain | M | 2 years | 1 (M) | CLEA | 10X |
| CJ102 | Brain | F | 6 mos | 1 (M) | CompanyA | Drop-seq, 10X |

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**Supplementary Table 2.** Number of microglia and macrophage cells identified in brain datasets and number of nuclei profiled in blood, liver and kidney.

| ID | Tissue | Microglia | Macrophage | Other Cell Types | Total nuclei | Percent Microglia | Percent Macrophage |
|---|---|---|---|---|---|---|---|
| CJ001 | Brain | 1,063 | 16 | 89,599 | 90,678 | 1.17% | 0.02% |
| CJ006 | Brain | 632 | 259 | 165,272 | 166,163 | 0.38% | 0.16% |
| CJ007 | Brain | 1,155 | 139 | 105,407 | 106,701 | 1.08% | 0.13% |
| CJ022 | Brain | 3,659 | 228 | 217,312 | 221,199 | 1.65% | 0.10% |
| CJ023 | Brain | 581 | 38 | 79692 | 80,311 | 0.72% | 0.05% |
| CJ025 | Brain | 1,366 | 131 | 210628 | 212,125 | 0.64% | 0.06% |
| CJ026 | Brain | 693 | 26 | 62743 | 63,462 | 1.09% | 0.04% |
| CJ027 | Brain | 8,398 | 167 | 342,419 | 350,984 | 2.39% | 0.05% |
| CJ028 | Brain | 18,185 | 172 | 478,765 | 497,333 | 3.66% | 0.03% |
| CJ029 | Brain | 11,874 | 285 | 320,000 | 332,159 | 3.57% | 0.09% |
| CJ102 | Brain | 1,124 | 43 | 56,602 | 57,769 | 1.95% | 0.07% |
|  |  |  |  |  |  |  |  |
| CJ026 | Blood | NA | NA | 1,741 | 1,741 | NA | NA |
| CJ026 | Liver | NA | NA | 10,877 | 10,877 | NA | NA |
| CJ026 | Kidney | NA | NA | 9,262 | 9,262 | NA | NA |
| CJ027 | Blood | NA | NA | 2,529 | 2,529 | NA | NA |
| CJ028 | Blood | NA | NA | 10,042 | 10,042 | NA | NA |

723 **Supplementary Table 3**. Comparison of chimerism between CJ028's two birth siblings, in blood
724 and in brain myeloid cells (microglia and macrophage). *P*-values are from a two-sided test of
725 proportions between chimerism fractions of sibling 1 and sibling 2 using the prop.test function in
726 R.

| Cell type | Total nuclei | Sibling 1 nuclei | Sibling 2 nuclei | Sibling 1 Fraction | Sibling 2 Fraction | Sibling 1 + Sibling 2 Fraction | *P*-value |
|---|---|---|---|---|---|---|---|
| microglia and macrophage | 19701 | 6922 | 2689 | 0.35 | 0.14 | 0.49 | $<2.2 \times 10^{-16}$ |
| microglia only | 19447 | 6873 | 2621 | 0.35 | 0.13 | 0.49 | $<2.2 \times 10^{-16}$ |
| macrophage only | 254 | 49 | 68 | 0.20 | 0.27 | 0.46 | $5.8 \times 10^{-2}$ |
| blood | 10042 | 1758 | 6739 | 0.18 | 0.67 | 0.85 | $<2.2 \times 10^{-16}$ |

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730 **Supplementary Table 4.** Summary of context versus genetic effects analysis, with two brain
731 regions of an animal as two contexts. The analysis described in Fig. 5D-F was repeated across
732 all animals and brain regions with at least 60 cells that are available for analysis in each context,
733 and the summary of the correlations are tabulated here. The correlations are plotted in
734 Supplementary Fig. 5. Abbreviations; STR: striatum; Thal: thalamus; Hippo: hippocampus; Hyp:
735 hypothalamus; BF: basal forebrain.

| Host ID | Sibling ID | Brain Region1 | Brain Region2 | Genetic Effects Spearman Correlation | Context Effects Spearman Correlation |
|---|---|---|---|---|---|
| CJ022 | CJ106 | Cortex | Thal | 0.1 | 0.73 |
| CJ025 | CJ104 | Cortex | STR | 0.03 | 0.2 |
| CJ027 | CJ140 | Cortex | Thal | 0.13 | 0.64 |
| CJ027 | CJ140 | Cortex | STR | 0.14 | 0.69 |
| CJ027 | CJ140 | Cortex | Hippo | 0.08 | 0.46 |
| CJ027 | CJ140 | Cortex | Hyp | 0.03 | 0.68 |
| CJ027 | CJ140 | Thal | Hippo | 0.04 | 0.56 |
| CJ027 | CJ140 | Thal | Hyp | 0.09 | 0.66 |
| CJ027 | CJ140 | STR | Hippo | 0.08 | 0.43 |
| CJ027 | CJ140 | STR | Hyp | 0.08 | 0.59 |
| CJ027 | CJ140 | Hippo | Hyp | 0.04 | 0.51 |
| CJ028 | CJ141 | Cortex | Thal | 0.1 | 0.66 |
| CJ028 | CJ142 | Cortex | Thal | 0.03 | 0.55 |
| CJ141 | CJ142 | Cortex | Thal | 0.07 | 0.59 |
| CJ028 | CJ141 | Cortex | STR | 0.13 | 0.68 |
| CJ028 | CJ142 | Cortex | STR | 0.1 | 0.58 |
| CJ141 | CJ142 | Cortex | STR | 0.09 | 0.61 |
| CJ028 | CJ141 | Cortex | Hippo | 0.06 | 0.39 |

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| CJ028 | CJ142 | Cortex | Hippo | 0 | 0.33 |
|---|---|---|---|---|---|
| CJ141 | CJ142 | Cortex | Hippo | 0.04 | 0.38 |
| CJ028 | CJ141 | Cortex | BF | 0.13 | 0.73 |
| CJ028 | CJ142 | Cortex | BF | 0.07 | 0.6 |
| CJ141 | CJ142 | Cortex | BF | 0.09 | 0.6 |
| CJ028 | CJ141 | Cortex | Hyp | 0.06 | 0.78 |
| CJ028 | CJ142 | Cortex | Hyp | 0.07 | 0.72 |
| CJ141 | CJ142 | Cortex | Hyp | 0.08 | 0.75 |
| CJ028 | CJ141 | Cortex | Amygdala | 0.14 | 0.65 |
| CJ028 | CJ142 | Cortex | Amygdala | 0.1 | 0.53 |
| CJ141 | CJ142 | Cortex | Amygdala | 0.12 | 0.57 |
| CJ028 | CJ141 | STR | Hippo | 0.06 | 0.63 |
| CJ028 | CJ142 | STR | Hippo | 0.01 | 0.56 |
| CJ141 | CJ142 | STR | Hippo | 0.03 | 0.61 |
| CJ028 | CJ141 | STR | BF | 0.14 | 0.63 |
| CJ028 | CJ142 | STR | BF | 0.06 | 0.5 |
| CJ141 | CJ142 | STR | BF | 0.05 | 0.52 |
| CJ028 | CJ141 | Hyp | Amygdala | 0.14 | 0.68 |
| CJ028 | CJ142 | Hyp | Amygdala | 0.21 | 0.65 |
| CJ141 | CJ142 | Hyp | Amygdala | 0.07 | 0.68 |
| CJ029 | CJ143 | Cortex | Thal | 0.09 | 0.61 |
| CJ029 | CJ143 | Cortex | STR | 0.06 | 0.5 |
| CJ029 | CJ143 | Cortex | Hippo | 0.05 | 0.62 |
| CJ029 | CJ143 | Cortex | BF | 0.09 | 0.79 |
| CJ029 | CJ143 | Cortex | Hyp | 0.07 | 0.78 |
| CJ029 | CJ143 | Cortex | Amygdala | 0.07 | 0.32 |
| CJ029 | CJ143 | Thal | STR | 0.09 | 0.48 |
| CJ029 | CJ143 | Thal | Hippo | 0.06 | 0.71 |
| CJ029 | CJ143 | Thal | BF | 0.14 | 0.75 |
| CJ029 | CJ143 | Thal | Hyp | 0.13 | 0.8 |
| CJ029 | CJ143 | Thal | Amygdala | 0.05 | 0.52 |
| CJ029 | CJ143 | Hippo | BF | 0.06 | 0.77 |
| CJ029 | CJ143 | Hippo | Hyp | 0.03 | 0.78 |
| CJ102 | CJ103 | Cortex | STR | 0.07 | 0.32 |

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740 **Supplementary Table 5**. Clustering parameters used to identify microglia and macrophage cell
741 types, and thresholds for identifying host-sibling doublets. The final number of microglia and
742 macrophages after the second round of clustering are in Supplementary Table 2. A cell is
743 assigned as a doublet if the Dropulation tool `DetectDoublets` assigned the highest likelihood
744 for the cell as a doublet and if the log10 of the best likelihood minus the log10 of the second-
745 best likelihood (lrt_test_stat) is greater than the doublet detection threshold (last column).

| Marmo set ID | Tissue | Resolution parameter | Nearest neighbor parameter | UMI threshold (min log-UMI per cell) | Doublet Detection Threshold (lrt_test_stat) |
|---|---|---|---|---|---|
| CJ001 | Brain | 0.8 | 10 | 1.2 | 0.0 |
| CJ006 | Brain | 0.5 | 10 | 1.2 | 5.0 |
| CJ007 | Brain | 0.5 | 20 | 1.2 | 10.0 |
| CJ022 | Brain Drop-seq | 0.5 | 20 | 1.2 | 2.0 |
| CJ022 | Brain 10X | 0.5 | 20 | 1.5 | 2.0 |
| CJ023 | Brain | 0.5 | 20 | 1.2 | 3.0 |
| CJ025 | Brain | 0.5 | 20 | 1.0 | 0.5 |
| CJ026 | Brain | 0.5 | 20 | 1.0 | 2.0 |
| CJ026 | Blood | 0.5 | 20 | 1.4 | 4.0 |
| CJ026 | Liver | 0.5 | 20 | 1.9 | 8.0 |
| CJ026 | Kidney | 0.5 | 20 | 1.9 | 8.0 |
| CJ027 | Brain Cortex A | 0.5 | 20 | 1.5 | 20.0 |
| CJ027 | Brain Cortex B | 0.5 | 20 | 1.5 | 20.0 |
| CJ027 | Brain others | 0.5 | 20 | 1.5 | 20.0 |
| CJ027 | Blood | 0.5 | 20 | 1.5 | 1.0 |
| CJ028 | Brain Cortex A | 0.5 | 20 | 1.5 | 25.0 |
| CJ028 | Brain Cortex B | 0.8 | 10 | 1.5 | 25.0 |
| CJ028 | Brain others | 0.5 | 20 | 1.5 | 25.0 |
| CJ028 | Blood | 0.5 | 20 | 1.5 | 1.0 |
| CJ029 | Brain Cortex | 0.5 | 20 | 1.5 | 20.0 |
| CJ029 | Brain others | 0.5 | 20 | 1.5 | 20.0 |
| CJ102 | Brain, Drop-seq | 0.8 | 10 | 1.2 | 3.0 |
| CJ102 | Brain, 10X | 0.5 | 20 | 1.2 | 5.0 |

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749 **Supplementary Table 6**. Whole genome sequencing datasets used in (1) donor-of-origin
750 assignment from snRNA-seq (Dropulation), and (2) estimating chimerism from blood whole
751 genome sequencing (Census-seq).

| ID | Tissue/DNA source | Sequencing coverage |
|---|---|---|
| CJ001 | Fibroblast culture | 36.4X |
| CJ119 (CJ001's sibling1) | Fibroblast culture | 39.7X |
| CJ120 (CJ001's sibling2) | Fibroblast culture | 36.7X |
| CJ006 (CJ007's sibling) | Fibroblast culture | 45.9X |
| CJ007 (CJ006's sibling) | Fibroblast culture | 55.8X |
| CJ022 | Fibroblast culture | 38.4X |
| CJ106 (CJ022's sibling) | Buccal swab | 36.0X |
| CJ023 | Fibroblast culture | 34.9X |
| CJ131 (CJ023's sibling1) | Fibroblast culture | 39.5X |
| CJ116 (CJ023's sibling2) | Fibroblast culture | 28.3X |
| CJ025 | Fibroblast culture | 72.7X |
| CJ104 (CJ025's sibling) | Buccal swab | 58.0X |
| CJ026 | Fibroblast culture | 74.1X |
| CJ105 (CJ026's sibling) | Buccal swab | 43.7X |
| CJ027 | Fibroblast culture | 47.5X |
| CJ027 | Blood | 46.9X |
| CJ140 (CJ027's sibling) | Fibroblast culture | 40.2X |
| CJ028 | Fibroblast culture | 44.6X |
| CJ028 | Blood | 52.6X |
| CJ141 (CJ028's sibling1) | Fibroblast culture | 43.6X |
| CJ142 (CJ028's sibling2) | Fibroblast culture | 41.2X |
| CJ029 | Fibroblast culture | 49.2X |
| CJ143 (CJ029's sibling) | Fibroblast culture | 40.8X |
| CJ102 | Brain | 32.4X |
| CJ103 (CJ102's sibling) | Buccal swab | 38.5X |

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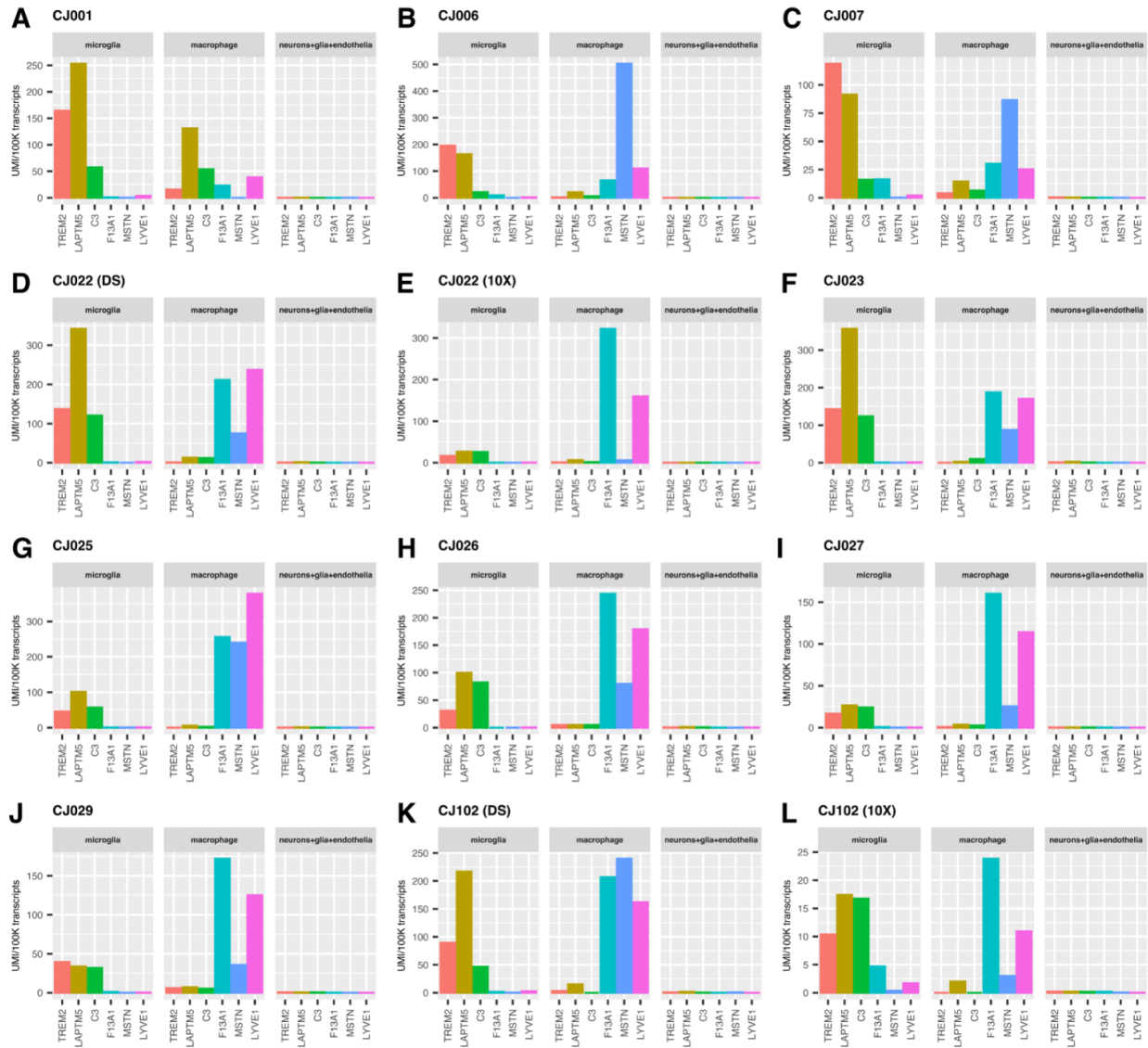
**Supplementary Figure 1. Microglia and brain macrophages can be identified in all animals**. Expression of microglia and macrophage markers in microglia (left sub-panels), macrophages (middle sub-panels) and all other cell types in the brain (right sub-panels; neurons, glia (astrocytes, oligodendrocytes, polydendrocytes, ependymal cells), and endothelial cells of each animal. Marmosets CJ022 and CJ102 were profiled using two technologies (DS: Drop-seq, 10X: 10X Chromium). y-axis: unique molecular identifier (UMI, a measure of transcript abundance) of each gene across cells, summed and normalized to 100,000 transcripts. Microglia markers: *TREM2, LAPTM5, C3*; macrophage markers: *F13A1, MSTN, LYVE1*.

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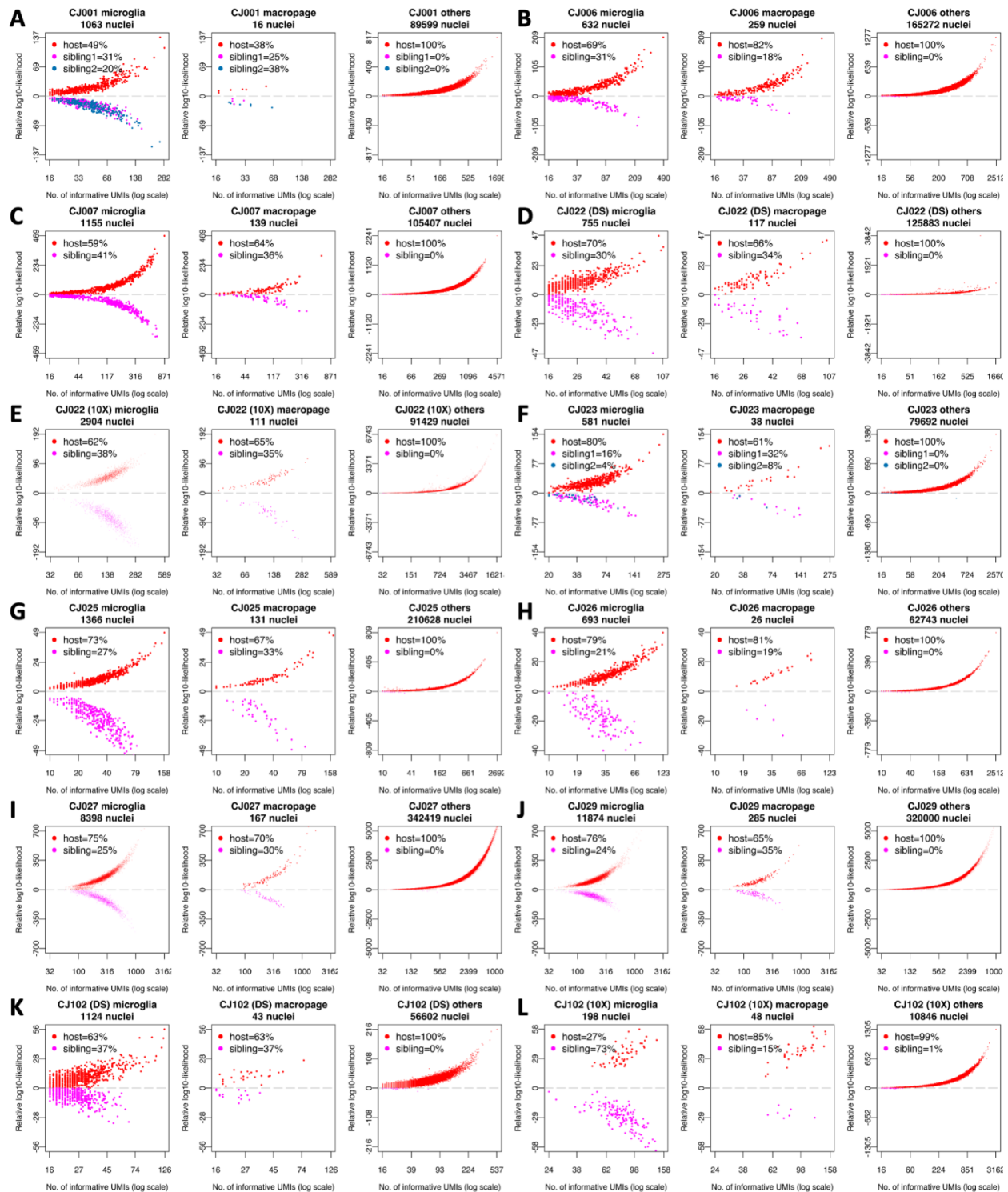
**765**

**766    Supplementary Figure 2.  Donor-of-origin assignments from brain snRNA-seq reveals**

**767    only microglia and macrophages are chimeric.  (A-L)** Donor of origin (Dropulation)

768    assignments of each nucleus from brain snRNA-seq of 10 animals.  Marmosets CJ022 and

769    CJ102 were profiled using two technologies (DS: Drop-seq, 10X: 10X Chromium). For each

770    marmoset, the snRNA-seq data are grouped into microglia, macrophage, and all other cell types

771    (others: neurons, astrocytes, oligodendrocytes, polydendrocytes, ependymal cells, endothelial

772     cells). x-axis: number of UMI that contains SNPs for which the host and sibling's genomes differ,
773     in log scale; y-axis: inferred likelihood that the cell has host genome minus likelihood that the
774     cell has sibling genome (log10).  Nuclei with positive y-values are assigned to the host and
775     those on the negative y-axes are assigned to the sibling.
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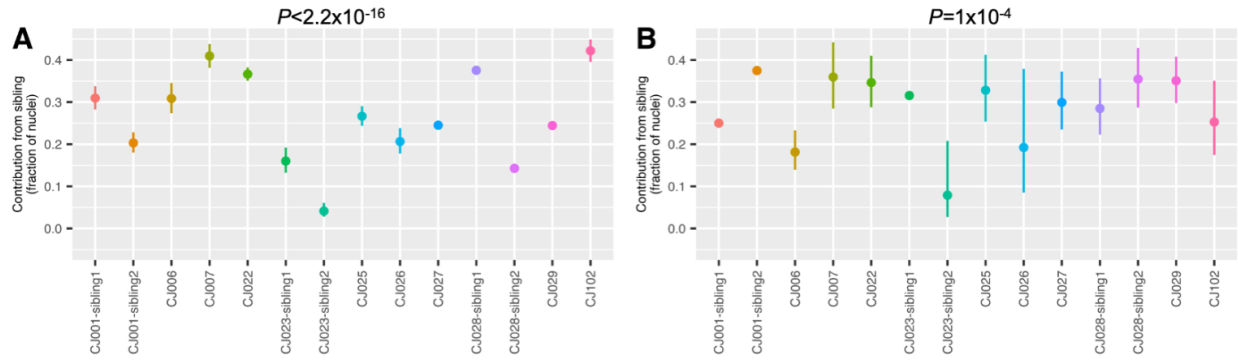
**Supplementary Figure 3. Summary of microglia (A) and macrophage (B) chimerism across animals.** y-axis: fraction of twin cells. Vertical bars: binomial confidence interval (95%). *P*-values: test of heterogeneity across animals.
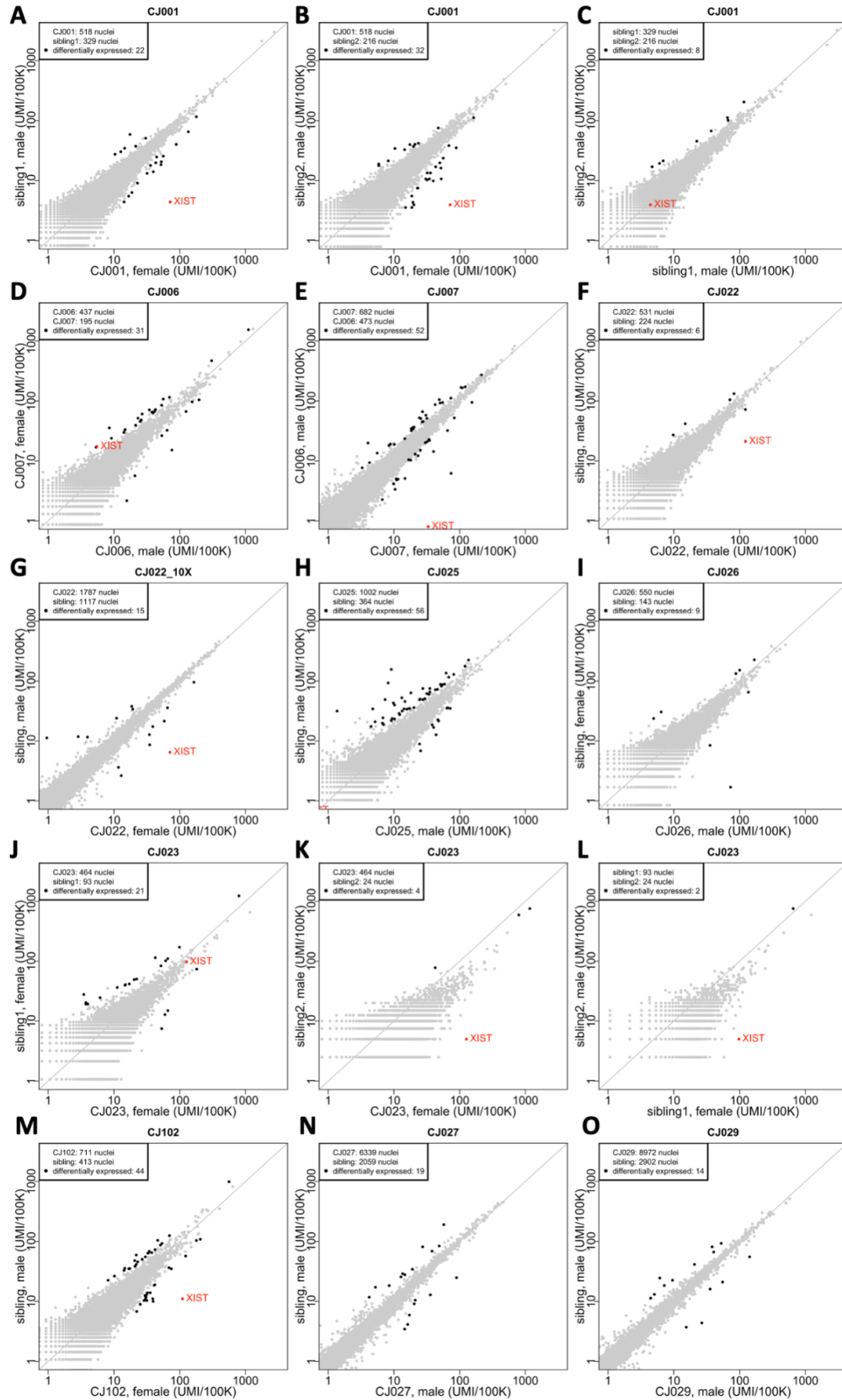
**Supplementary Figure 4. Comparison of gene expression between microglia with**

784    **different genomes in each host animal's brain.** Each point represents a gene; its location on
785    the plot represents the level of expression of that gene among microglia with two different
786    genomes in the same animal.  x- and y-axes: normalized gene expression levels (number of
787    transcripts per 100,000 transcripts). Fold-change and $P$-values were calculated using edgeR
788    and differentially expressed genes (black dots) were defined as: FDR $Q$-value<0.05 and fold-
789    change>1.5 or less than 1/1.5 and the gene must be expressed in at least 10% of one of the
790    microglia sets.
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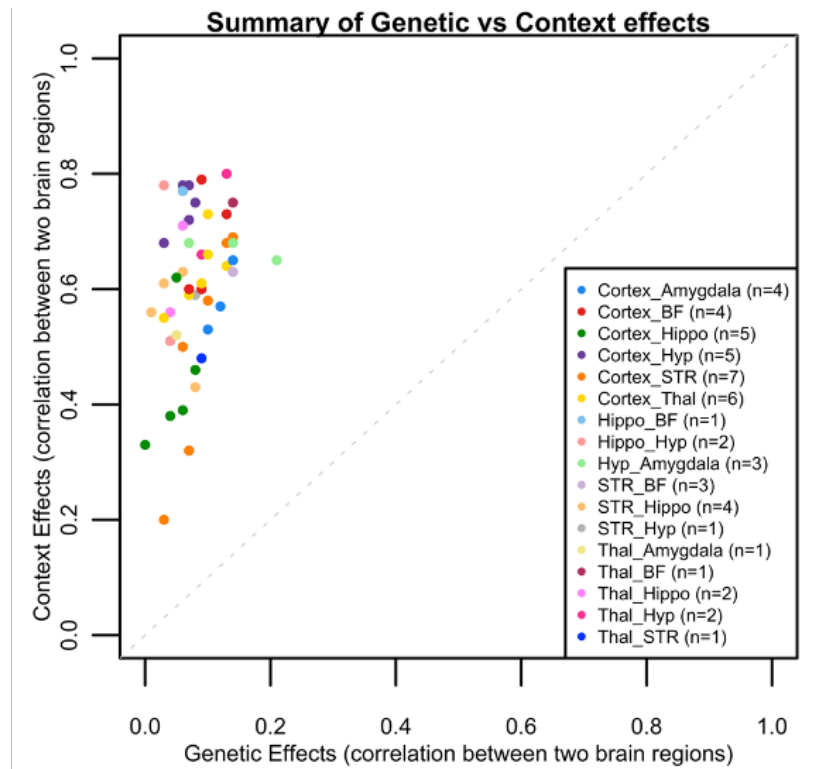


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**Supplementary Figure 5. Summary of genetic versus context effects.** This is a plot of the
correlation values from Supplementary Table 5.  Abbreviations; STR: striatum; Thal: thalamus;
Hippo: hippocampus; Hyp: hypothalamus; BF: basal forebrain

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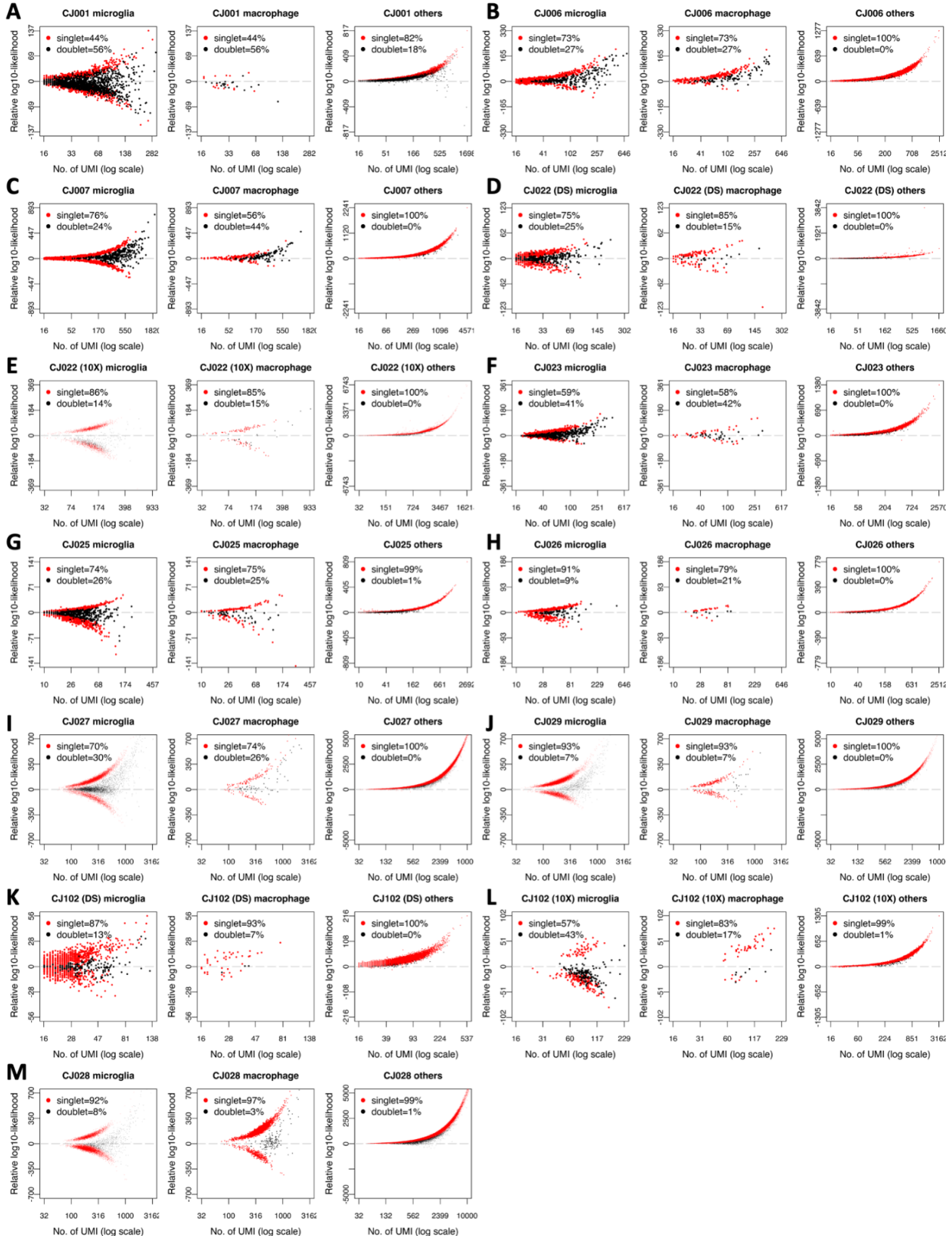
**Supplementary Figure 6. Doublet detection using host and sibling genotypes.** The axes are the same as in Supplementary Fig. 2, and each dot is a nucleus. Here, nuclei that were

805    identified as doublets and discarded in analyses were indicated (black dots).  Marmosets CJ022
806    and CJ102 were profiled using two technologies (DS: Drop-seq, 10X: 10X Chromium).
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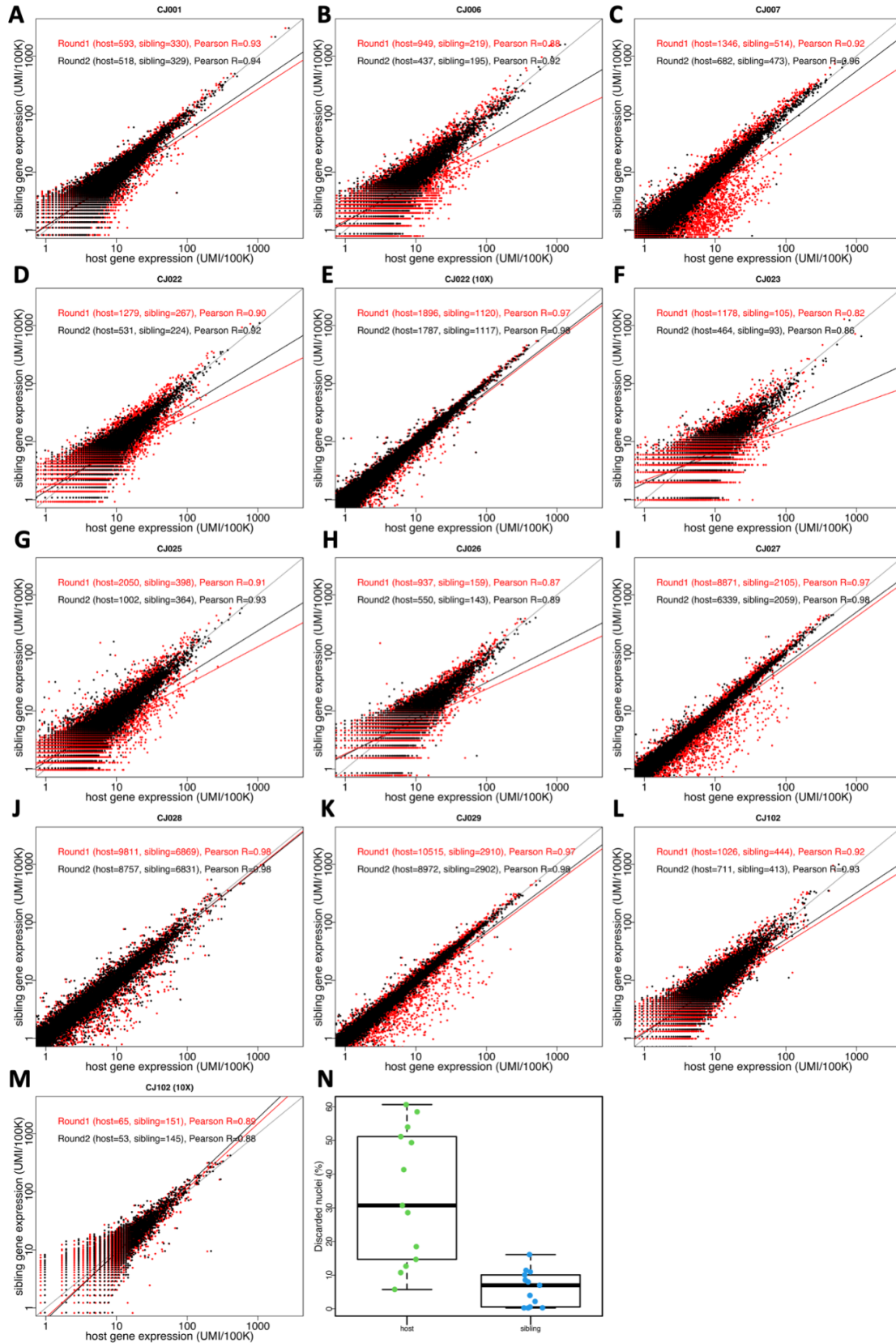
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811     **Supplementary Figure 7.  Second round clustering of microglia to discard mis-classified**

812    **cells. (A-M)** Gene expression comparison between host and sibling cells. Red dots: nuclei
813    identified as microglia from first-round of clustering, black dots: nuclei that were retained after
814    second-round clustering. For triplets, only the first sibling is included in the plots. Pearson
815    correlation as calculated for each set (before and after second round clustering) and shows an
816    improvement in correlation after discarding mis-classified cells. Marmosets CJ022 and CJ102
817    were profiled using two technologies (Drop-seq and 10X Chromium). **(N)** Summary (box plot) of
818    fraction of microglia cells discarded during second round of clustering, for host and birth sibling.
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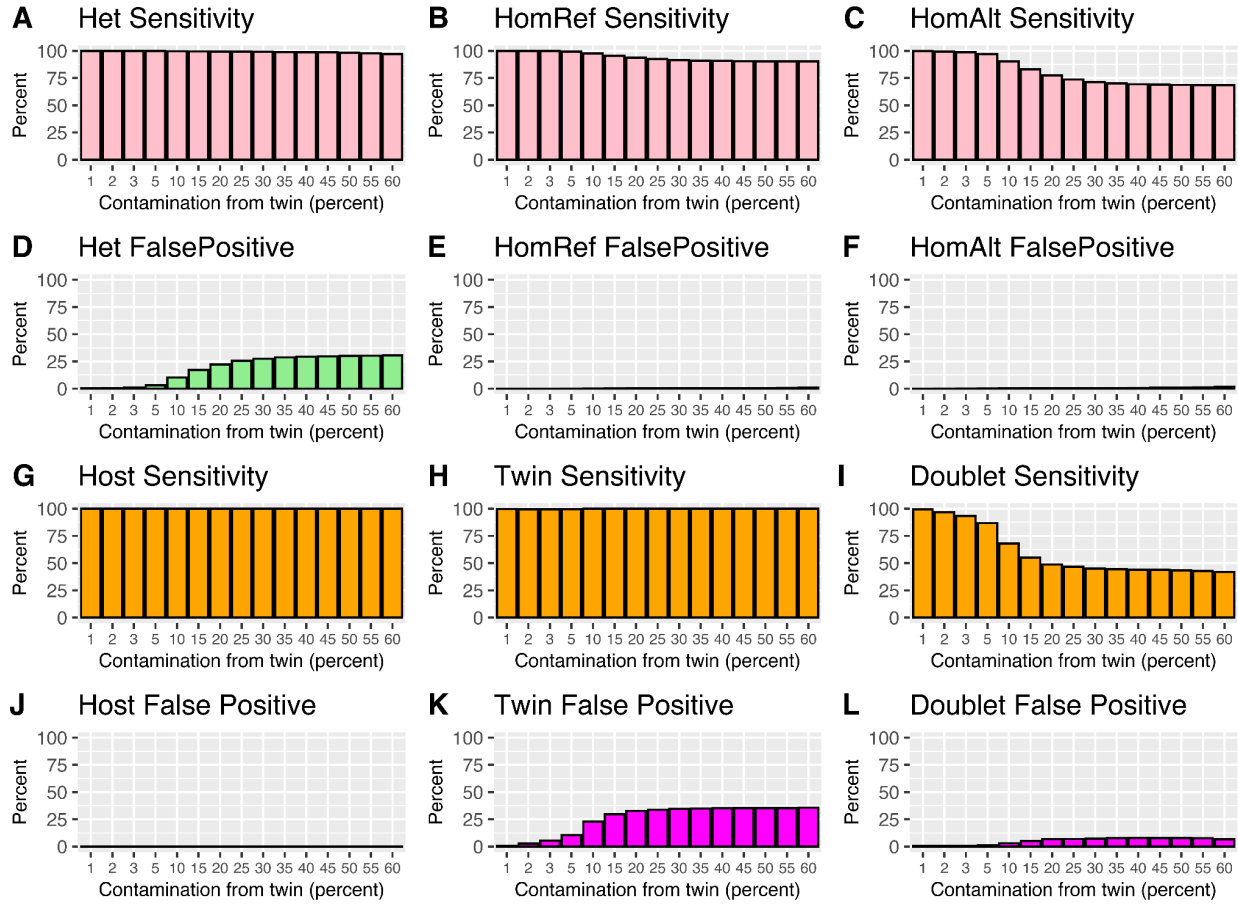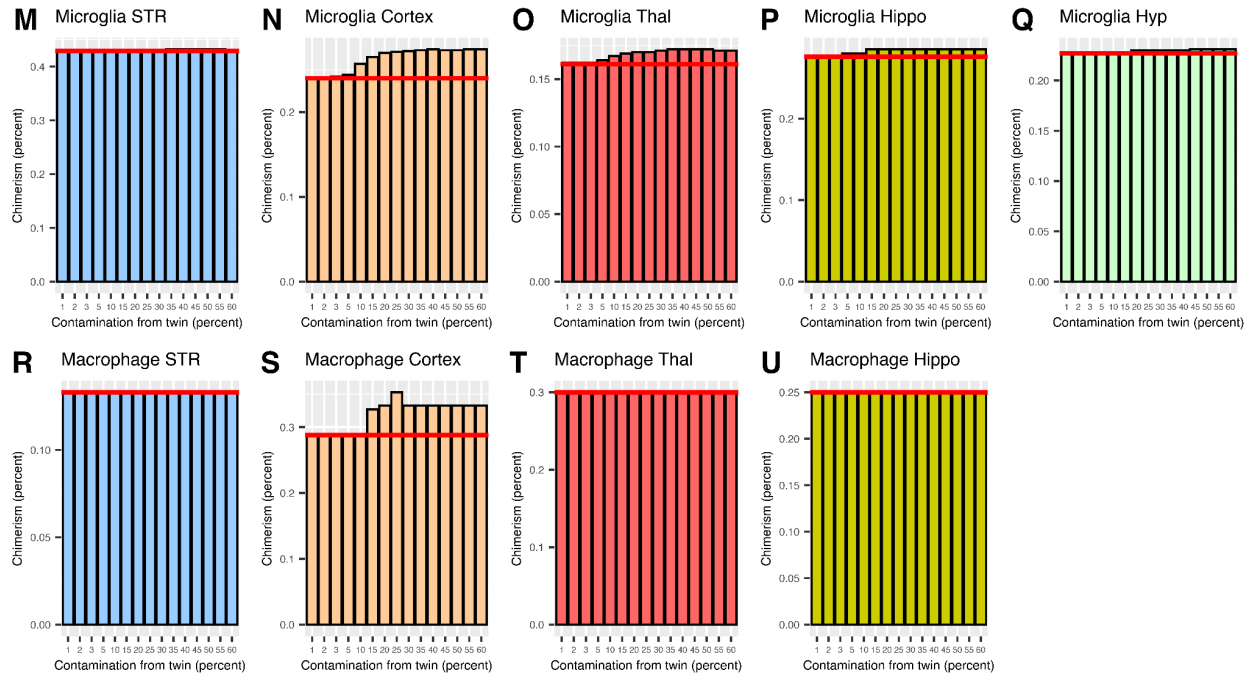
826 **Supplementary Figure 8. Analysis of genotyping and chimerism if the genotypes of the**

827 **sibling are contaminated by the hosts' DNA. (A)-(F)** Sensitivity and false positives in

828    genotyping; HomRef: homozygous reference, HomAlt: homozygous alternate allele, Het:

829    heterozygous. **(G)-(L)** Sensitivity and false positives in donor-of-origin assignment. **(M)-(Q)**

830    Microglia chimerism estimates when sibling WGS are contaminated by the hosts' DNA, for 5

831    brain regions; red horizontal line: chimerism estimates when there's no error in sibling

832    genotypes. **(R)-(U)** Macrophage chimerism estimates when sibling WGS are contaminated by

833    hosts' DNA; red horizontal line: chimerism estimates when there's no error in sibling genotypes.