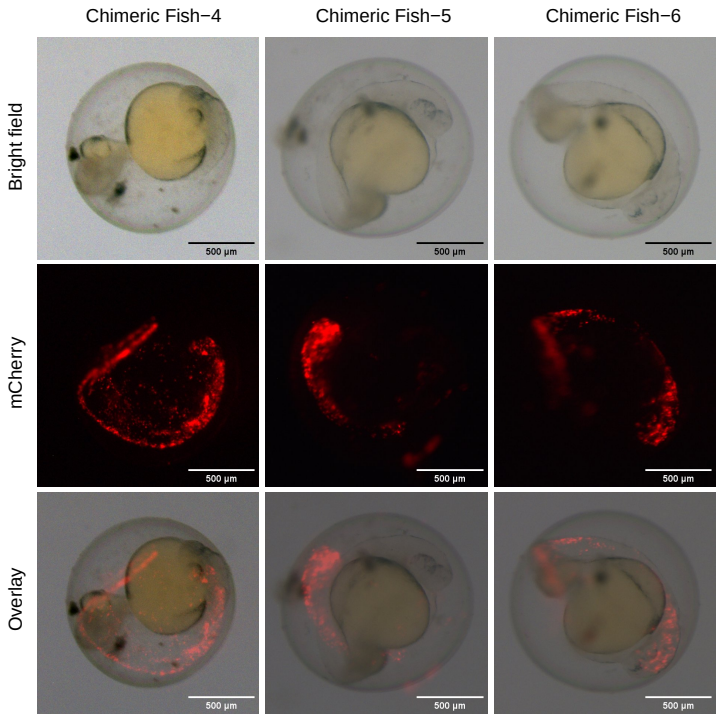
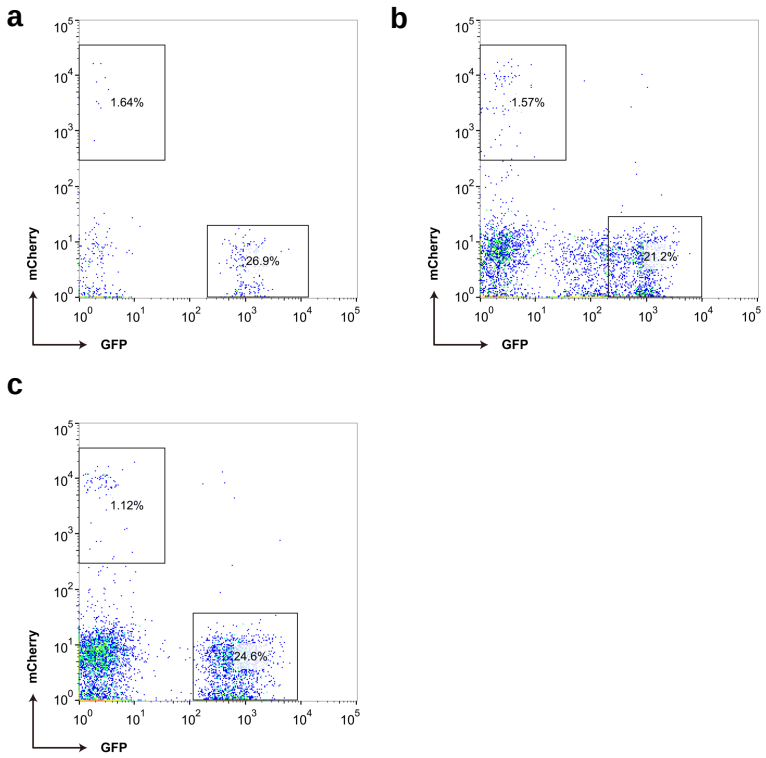
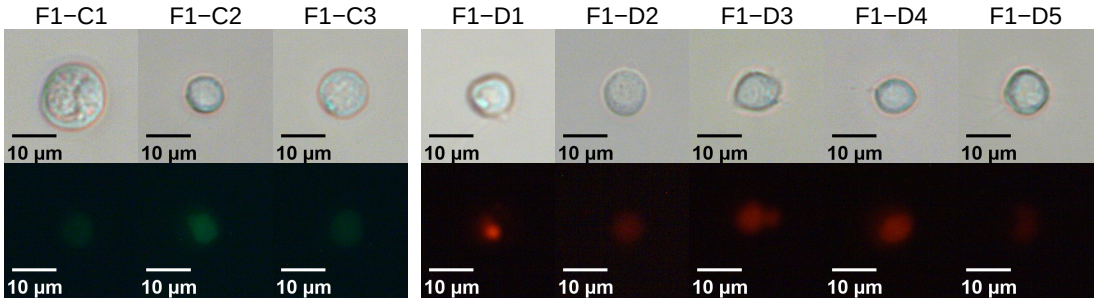



**Supplementary Figure 1. Images of chimeric zebrafish embryos at 24 hpf.** The rest individuals are shown, including Chimera Fish-4, Chimera Fish-5, and Chimera Fish-6. Donor cells originating from the TL line were labeled with mCherry fluorescence. Note that Chimera Fish-5 moved during imaging, resulting in visible skewing in the bright field and mCherry channels.

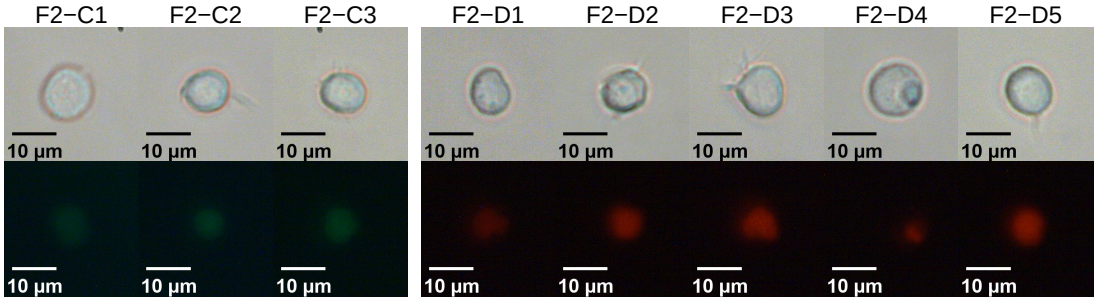



**Supplementary Figure 2. Flow Cytometry Analysis of chimeric fish. a-c.** The scatter plot showing the fluorescence intensity of EGFP (x-axis) and mCherry (y-axis) isolated from the representative chimeric embryos. Each point represents a single cell. The percentage within each gate indicates the proportion of cells within that population. The three panels represent Chimeric Fish-4, Chimeric Fish-5 and Chimeric Fish-6, respectively.

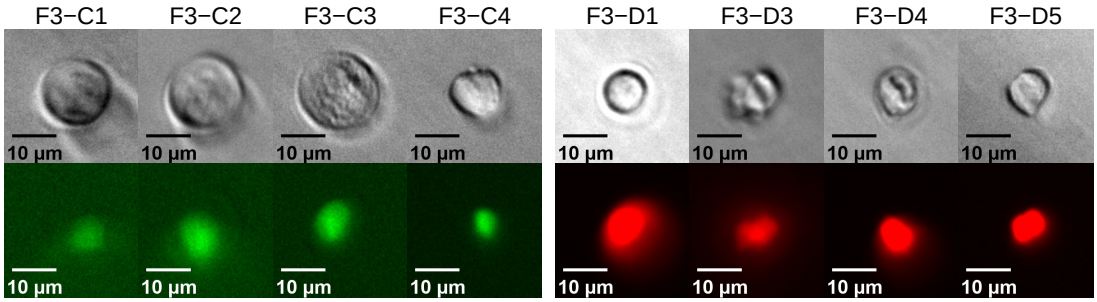
Chimeric Fish−1 (F1):



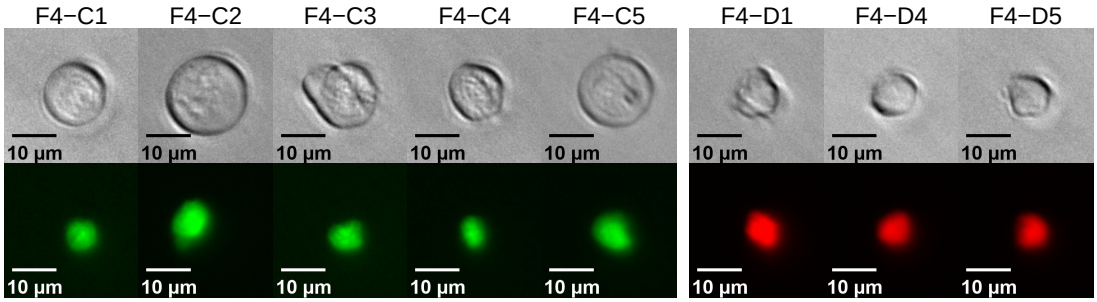

Chimeric Fish−2 (F2):



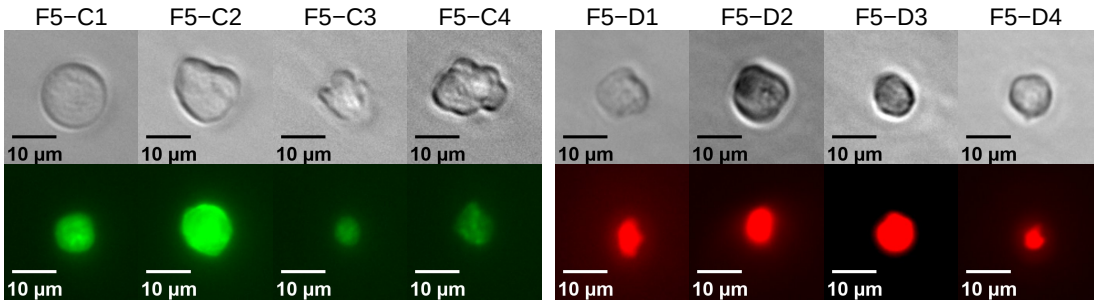

Chimeric Fish−3 (F3):



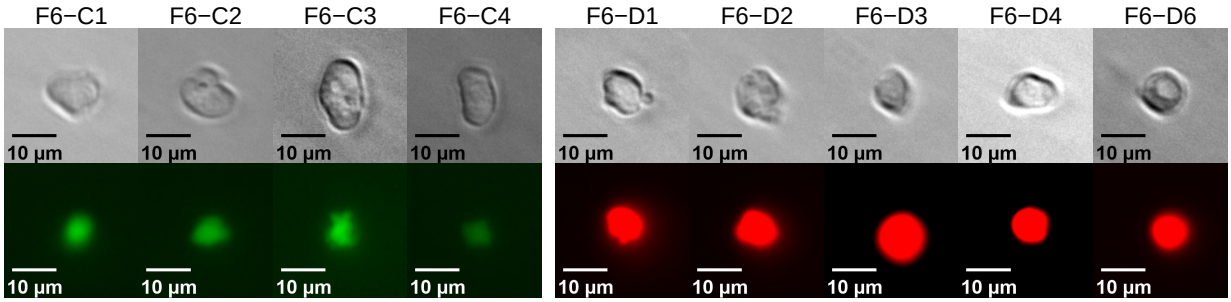

Chimeric Fish−4 (F4):



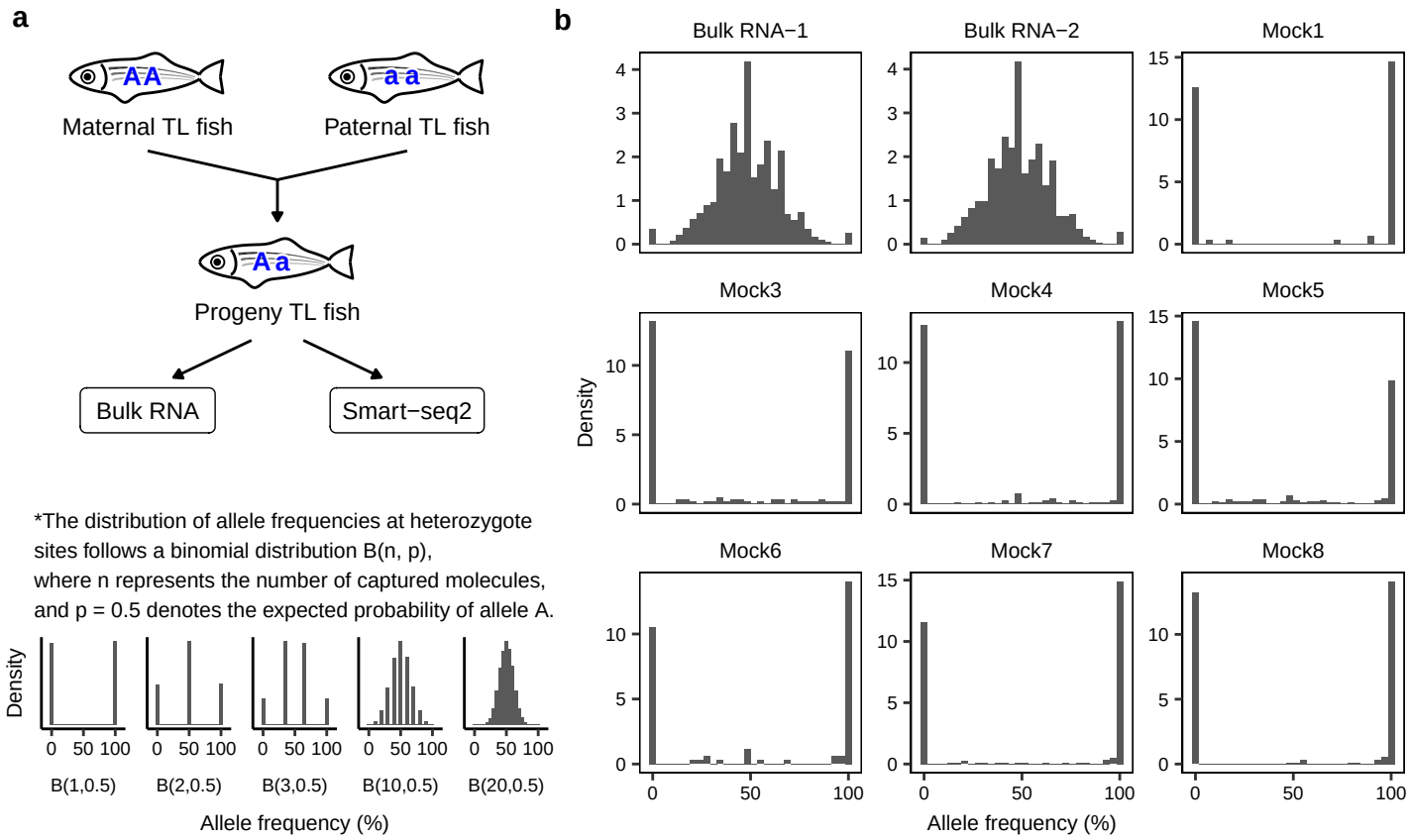

Chimeric Fish−5 (F5):



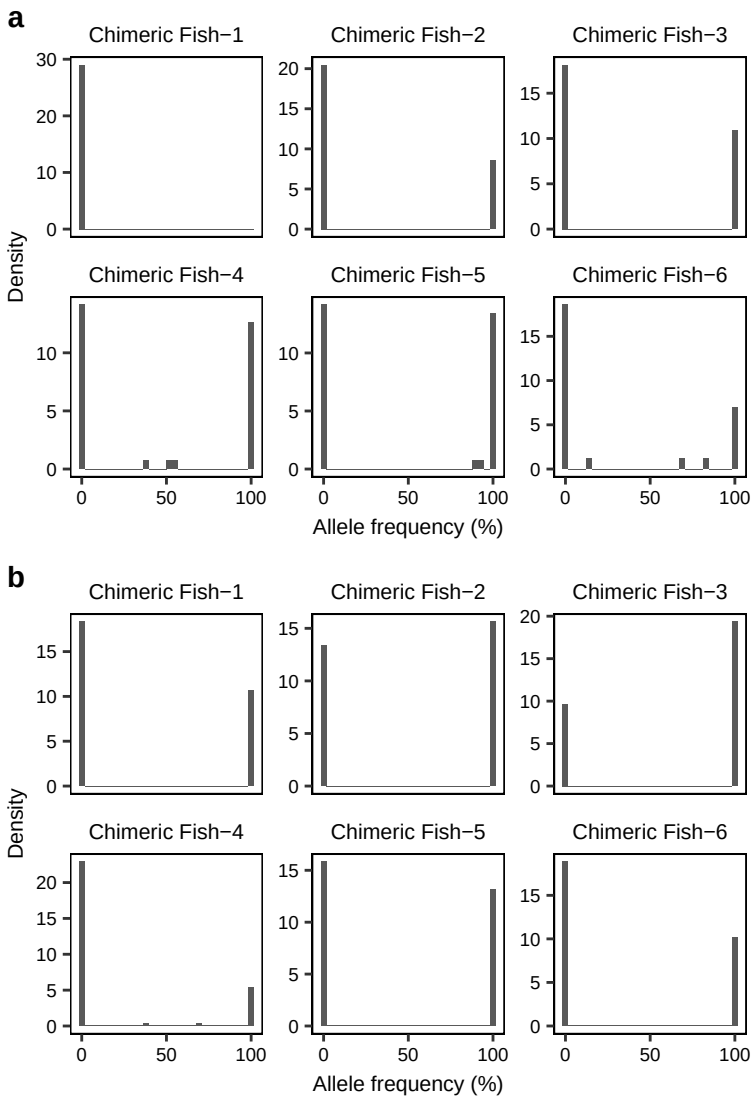

Chimeric Fish−6 (F6):



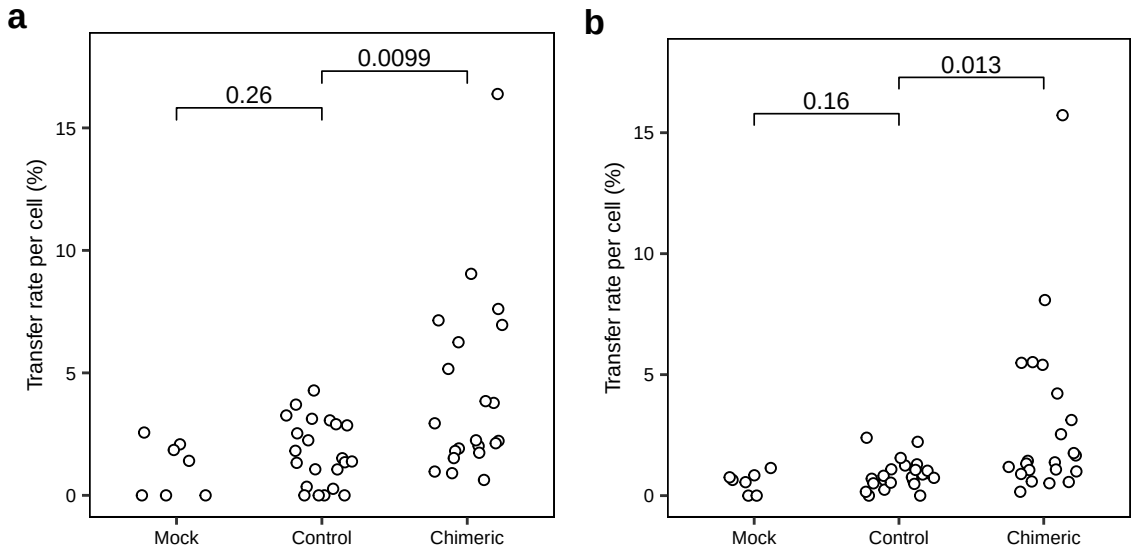
**Supplementary Figure 3. Microscopy images of isolated cells. Each panel shows a single cell.** Three channels are shown, including bright field, EGFP and mCherry, respectively. Chimeric Fish-1 and Chimeric Fish-2 were captured using a ZEISS Axio Observer A1 microscope, while the remaining four fish were captured using a ZEISS Axio Observer D1 microscope.



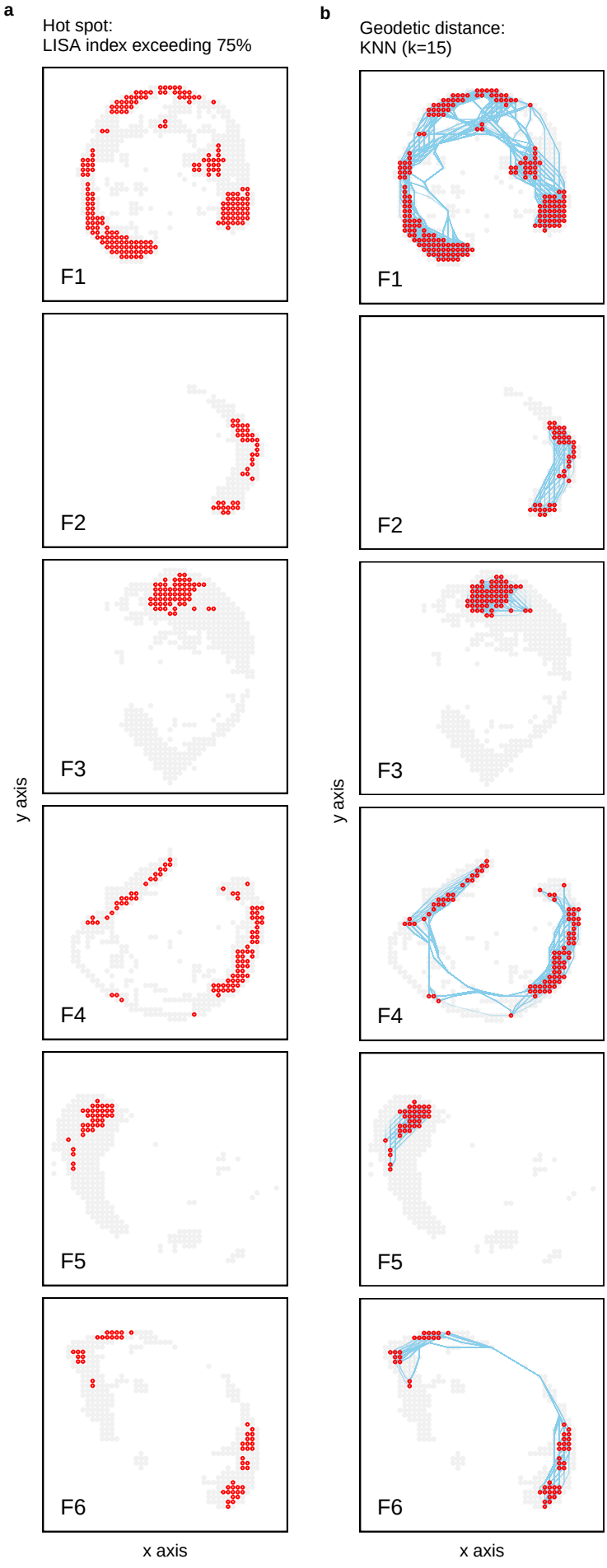

**Supplementary Figure 4. Dichotomic expression of two alleles at heterozygous sites in mock cells.** **a.** Schematic shows how the sample size can influence the allele frequency spectrum at heterozygous sites. **b.** The observed allele frequency spectrum at heterozygous sites in the TL line. Each panel shows the spectrum for a different sample, with two from bulk RNA and seven from smart-seq2 RNA sequencing.



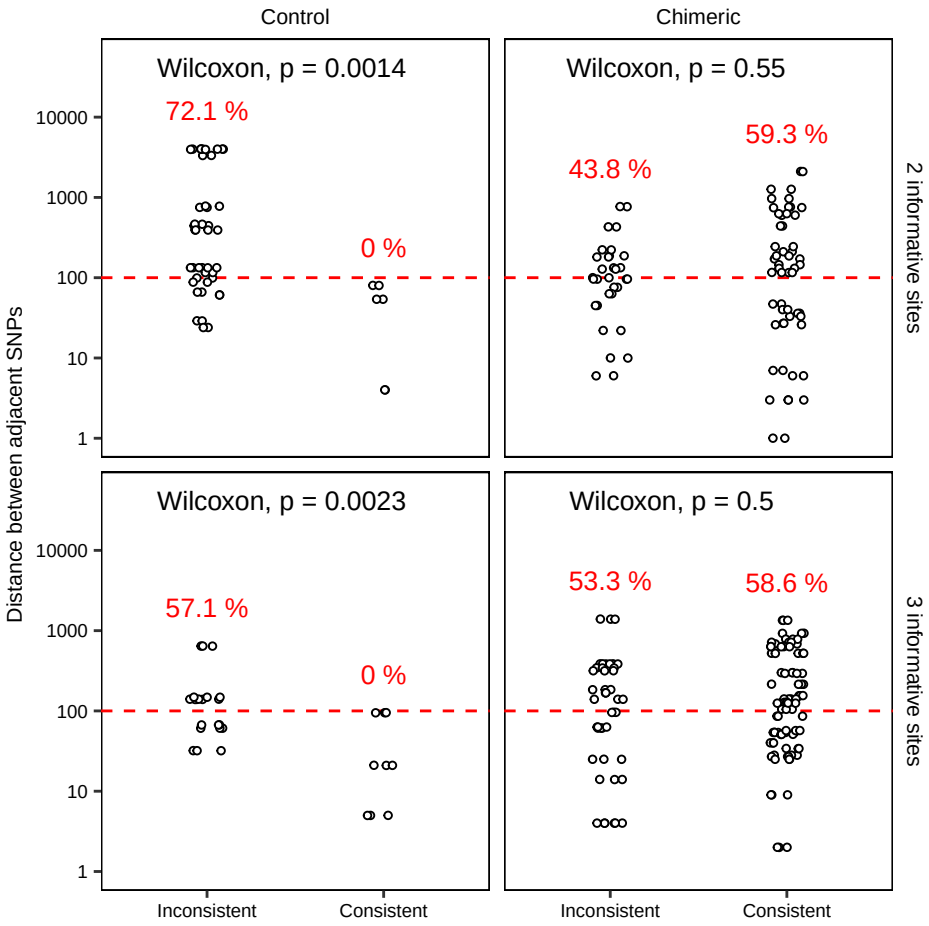

**Supplementary Figure 5. Dichotomic expression of two alleles at heterozygous sites in control and chimeric cells. a.** The observed allele frequency spectrum at heterozygous sites in the control group. **b.** The observed allele frequency spectrum at heterozygous sites in the chimeric group.



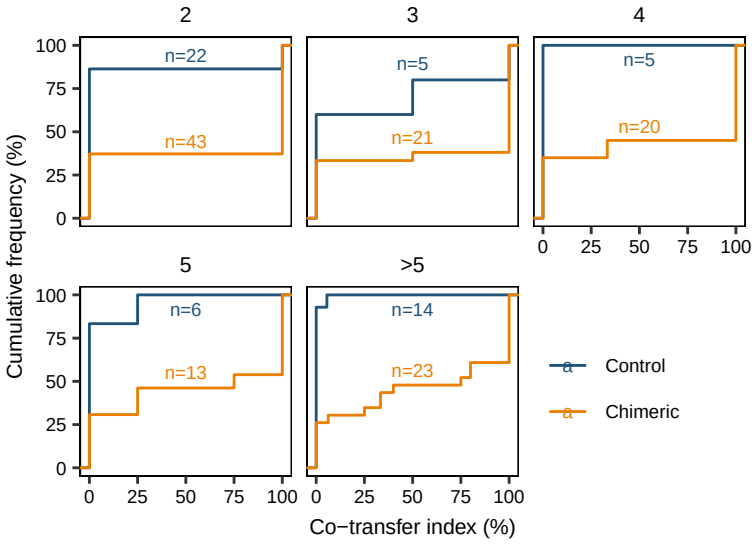

**Supplementary Figure 6. Comparative Analysis of Intercellular mRNA Transfer Rates. a.** The scatter plot illustrating the mRNA transfer rate per cell using indel-only identity-informative sites. Each dot represents the transfer rate calculated for an individual cell. P values obtained from Wilcoxon test are shown on the top. **b.** Analysis excluding potential RNA editing signals, including C>T/G>A signal for APOBEC and A>G/T>C signal for ADAR.



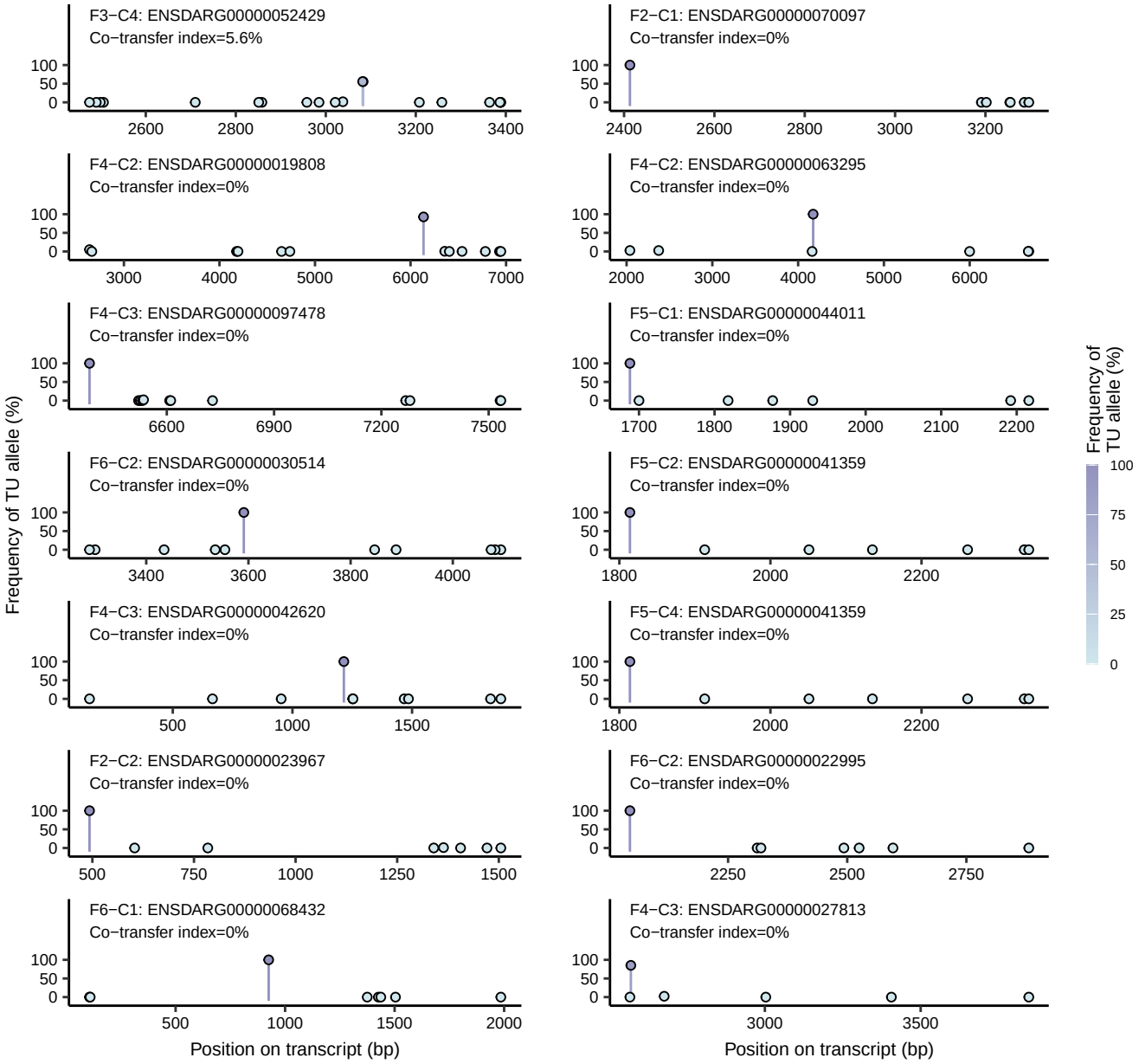

**Supplementary Figure 7. Spatial pattern analysis of donor-derived cells in chimeric zebrafish. a.** Distribution of defined hot spots obtained from Local Moran's I analysis. Dots represent a bin with 10x10 pixels, colored by hot spots (red) and non-significant regions (grey). **b.** Geodetic distance calculated with KNN network. Dots represent a bin with 10x10 pixels, colored by hot spots (red) and non-significant regions (grey). Lines (blue) indicate the shortest path between pairwise hot spots.



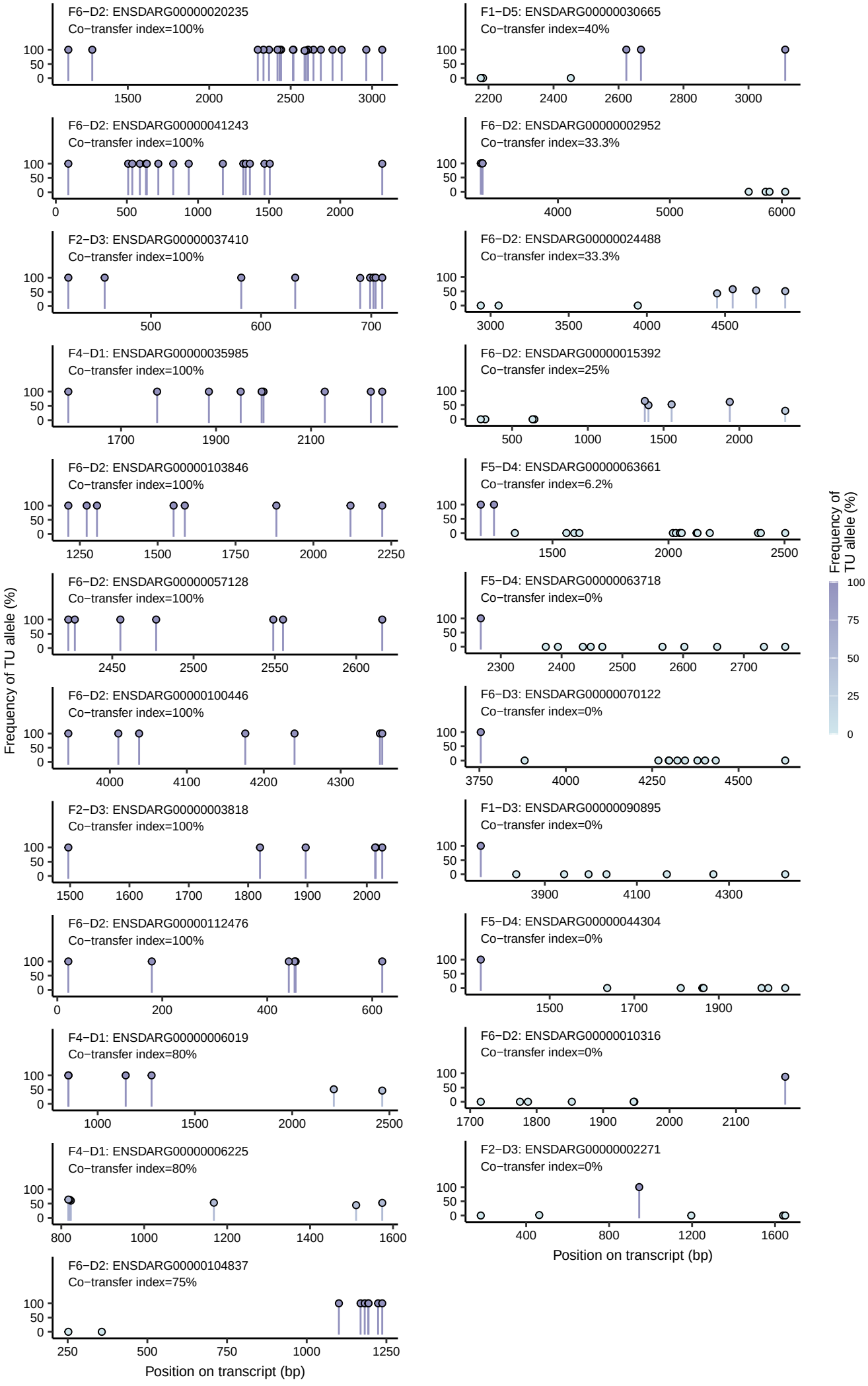

**Supplementary Figure 8. Distance analysis of adjacent informative sites.** Each panel represents data from a specific experimental group (Control or Chimeric) and genes containing a particular number of informative sites (two or three sites). Each point represents a pair of adjacent SNPs within the same gene. The X-axis categorizes these pairs based on the consistency of their transfer signal, and the Y-axis represents the distance between these adjacent sites on a log scale (bp, base pairs). The red dashed line indicates a threshold of 100 bp. The percentages shown indicate the proportion of site pairs with distances above the 100 bp threshold. The p-value from a Wilcoxon rank-sum test comparing the distances of inconsistent and consistent site pairs is indicated within each panel.



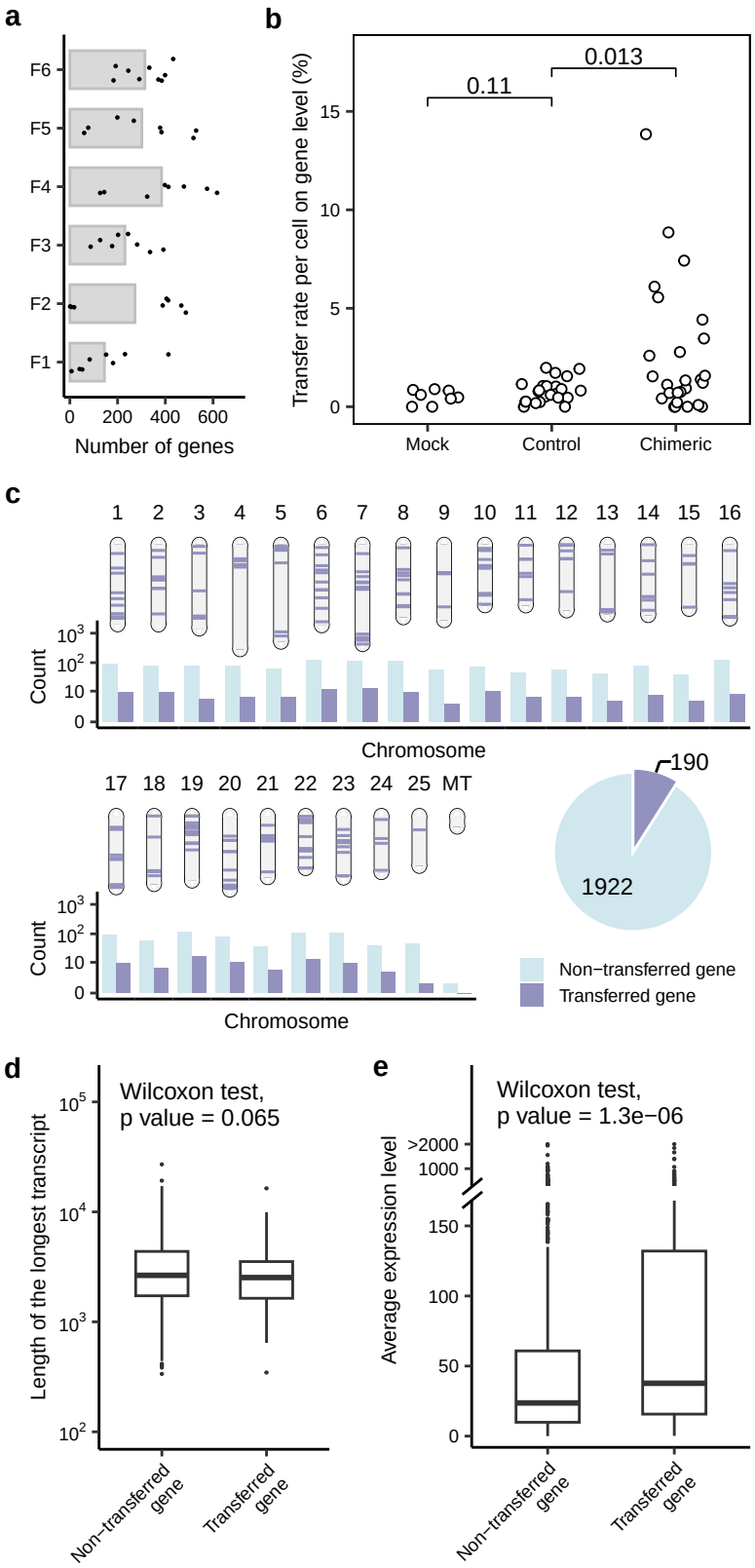

**Supplementary Figure 9. Cumulative distribution of the co-transfer index.** Each panel displays the cumulative distribution of the co-transfer index for a set of genes containing a specific number of informative sites. Two curves are shown in each panel, representing the cumulative distribution for the control group (blue) and the chimeric group (orange). The number of genes included in each group for that specific number of informative sites is indicated near the corresponding curve.




**Supplementary Figure 10. Allele frequency profiles for the control group.** Each panel displays the frequency of the TU allele (%) for individual informative sites within a specific gene (with >5 sites), plotted according to their position on the transcript. Dots represent individual informative sites and are colored by the TU allele frequency. The subtitle above each panel provides the cell identifier, the Ensembl gene identifier, and the co-transfer index for that case.

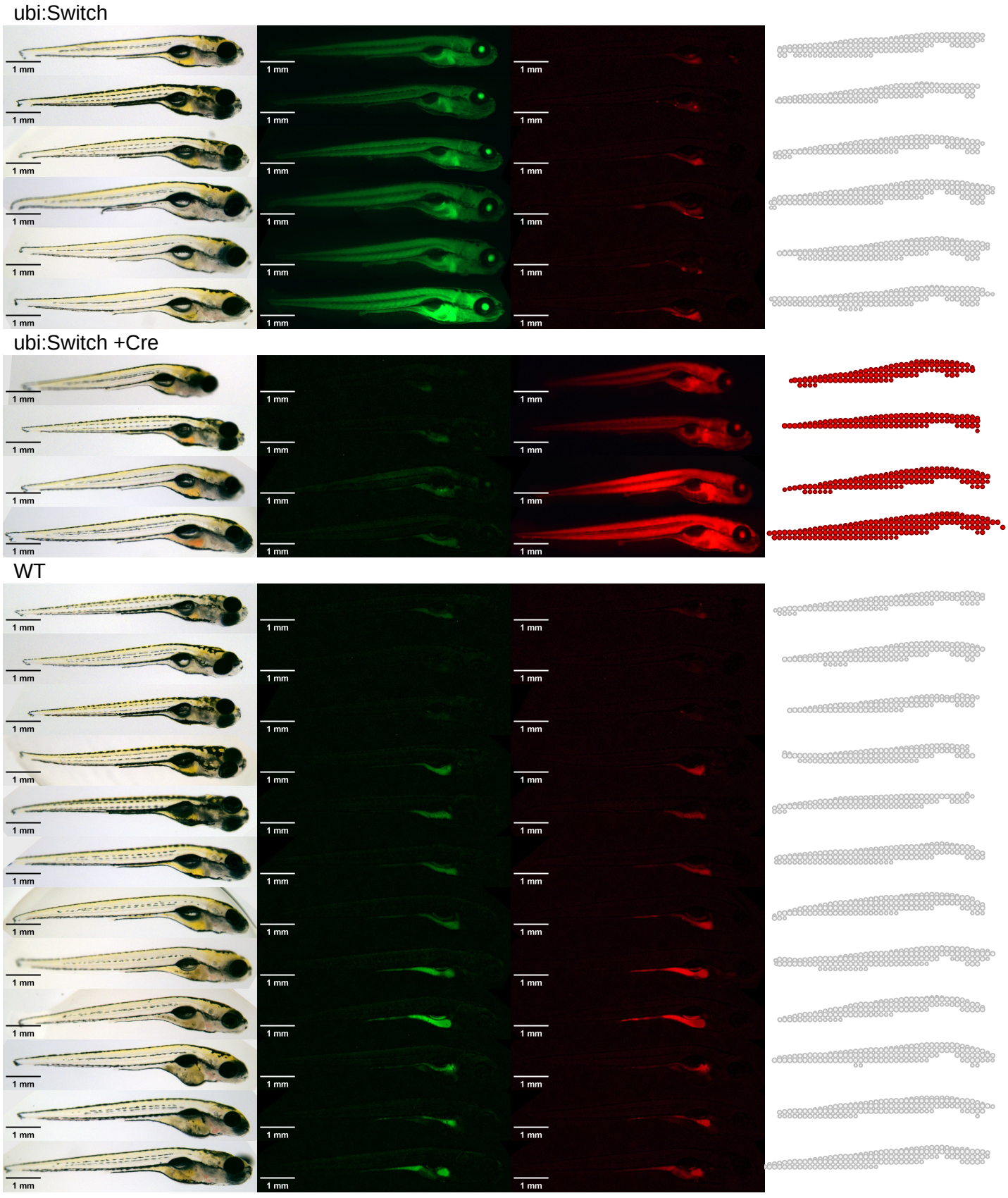

F6−D2: ENSDARG00000020235
Co−transfer index=100%
F1−D5: ENSDARG00000030665
Co−transfer index=40%
F6−D2: ENSDARG00000041243
Co−transfer index=100%
F6−D2: ENSDARG00000002952
Co−transfer index=33.3%
F2−D3: ENSDARG00000037410
Co−transfer index=100%
F6−D2: ENSDARG00000024488
Co−transfer index=33.3%
F4−D1: ENSDARG00000035985
Co−transfer index=100%
F6−D2: ENSDARG00000015392
Co−transfer index=25%
F6−D2: ENSDARG00000103846
Co−transfer index=100%
F5−D4: ENSDARG00000063661
Co−transfer index=6.2%
F6−D2: ENSDARG00000057128
Co−transfer index=100%
F5−D4: ENSDARG00000063718
Co−transfer index=0%
F6−D2: ENSDARG00000100446
Co−transfer index=100%
F6−D3: ENSDARG00000070122
Co−transfer index=0%
F2−D3: ENSDARG00000003818
Co−transfer index=100%
F1−D3: ENSDARG00000090895
Co−transfer index=0%
F6−D2: ENSDARG00000112476
Co−transfer index=100%
F5−D4: ENSDARG00000044304
Co−transfer index=0%
F4−D1: ENSDARG00000006019
Co−transfer index=80%
F6−D2: ENSDARG00000010316
Co−transfer index=0%
F4−D1: ENSDARG00000006225
Co−transfer index=80%
F2−D3: ENSDARG00000002271
Co−transfer index=0%
F6−D2: ENSDARG00000104837
Co−transfer index=75%
Frequency of TU allele (%)
Position on transcript (bp)
Frequency of TU allele (%)
100
75
50
25
0

**Supplementary Figure 11. Allele frequency profiles for the chimeric group.** Each panel displays the frequency of the TU allele (%) for individual informative sites within a specific gene (with >5 sites), plotted according to their position on the transcript. Dots represent individual informative sites and are colored by the TU allele frequency. The subtitle above each panel provides the cell identifier, the Ensembl gene identifier, and the co-transfer index for that case.

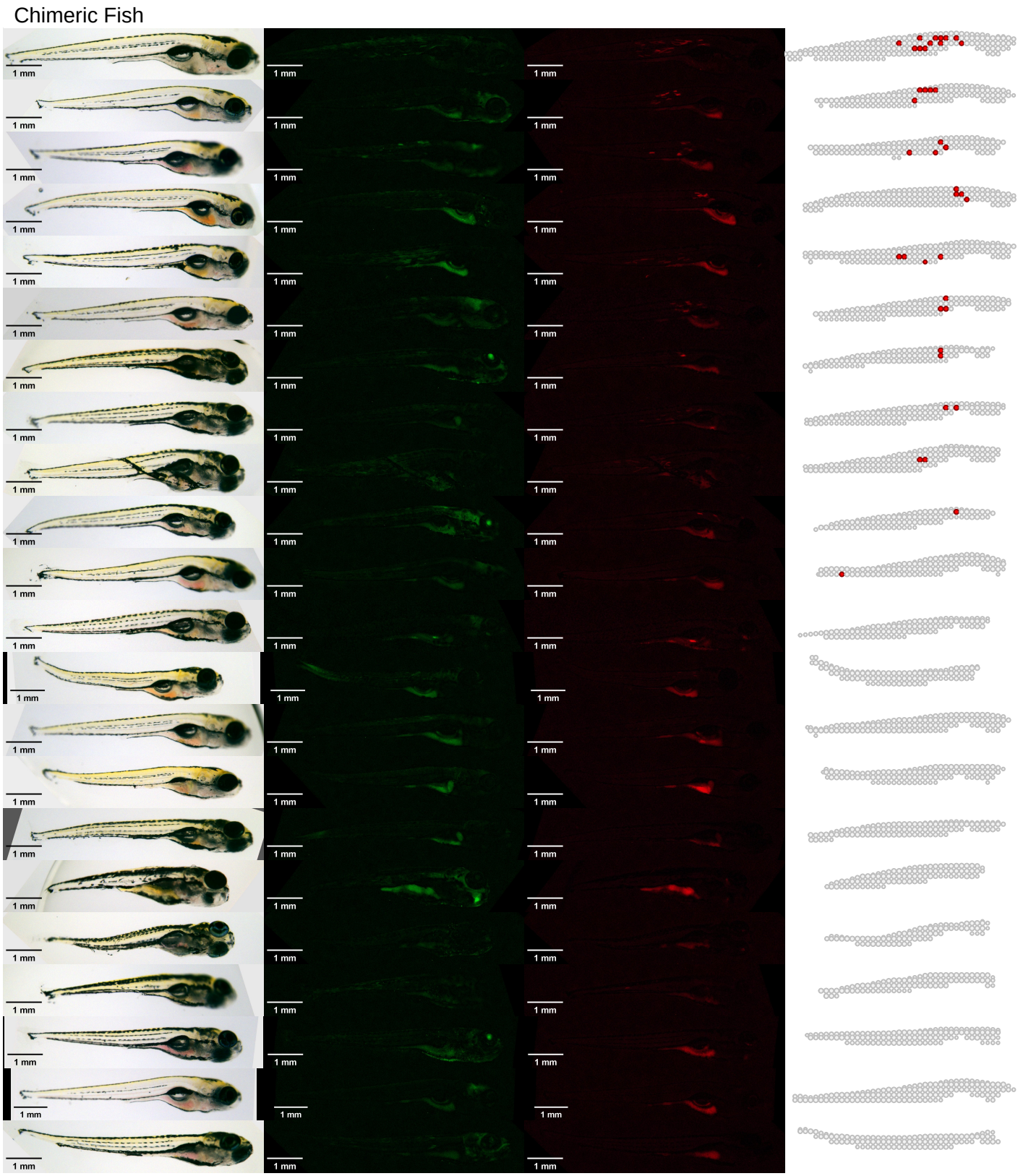



**Supplementary Figure 12. Analysis of intercellular mRNA transfer at the gene level. a.** Number of genes with at least one informative identity-informative sites detected in each individual chimeric zebrafish embryo. **b.** Gene-level mRNA transfer rates per cell. Each dot represents the estimated average transfer rate across all informative identity-informative sites for a given TL cell, separated by mock, control, and chimeric groups, respectively. P values from Wilcoxon tests comparing between groups are indicated above the respective groups. **c.** Chromosomal distribution of genes exhibiting intercellular mRNA transfer. The bar plot shows the number of genes classified as either "transferred" (at least one transferred identity-informative site detected) or "non-transferred" across the zebrafish chromosomes. The pie chart shows the overall proportion of transferred and non-transferred genes. **d.** Length of the longest transcript for transferred and non-transferred genes. The box plot shows the distribution of the longest transcript lengths for genes classified as either

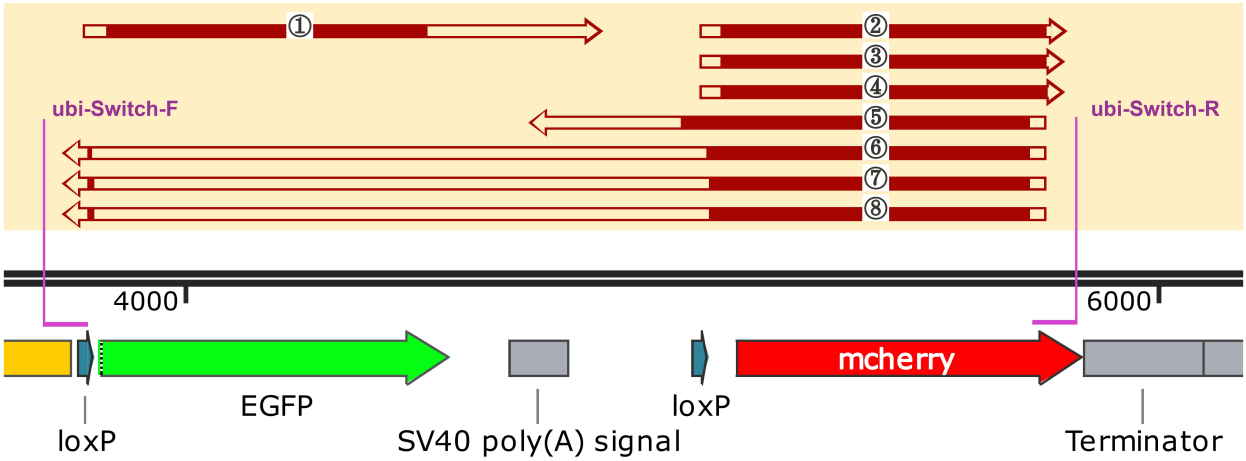
transferred or not transferred. The p value from the Wilcoxon test is indicated above the plots. **e.** Expression levels of transferred and non-transferred genes. The box plot shows the distribution of expression levels in transcript per million (TPM) for genes classified as either transferred or not transferred. The p value from the Wilcoxon test is indicated above the plots.




**Supplementary Figure 13. Fluorescence imaging and semi-quantification of control zebrafish.** Three control groups of zebrafish are shown, including ubi:Switch zebrafish (negative control), Cre mRNA-injected (positive control) and WT (mock control). Bright field, EGFP and mCherry channels are shown. The fourth column displays semi-quantitative mCherry intensity analysis using ImageJ. Red dots represent bins exhibiting significantly elevated mCherry intensity compared to background, while grey dots indicate bins with non-significant mCherry intensity.

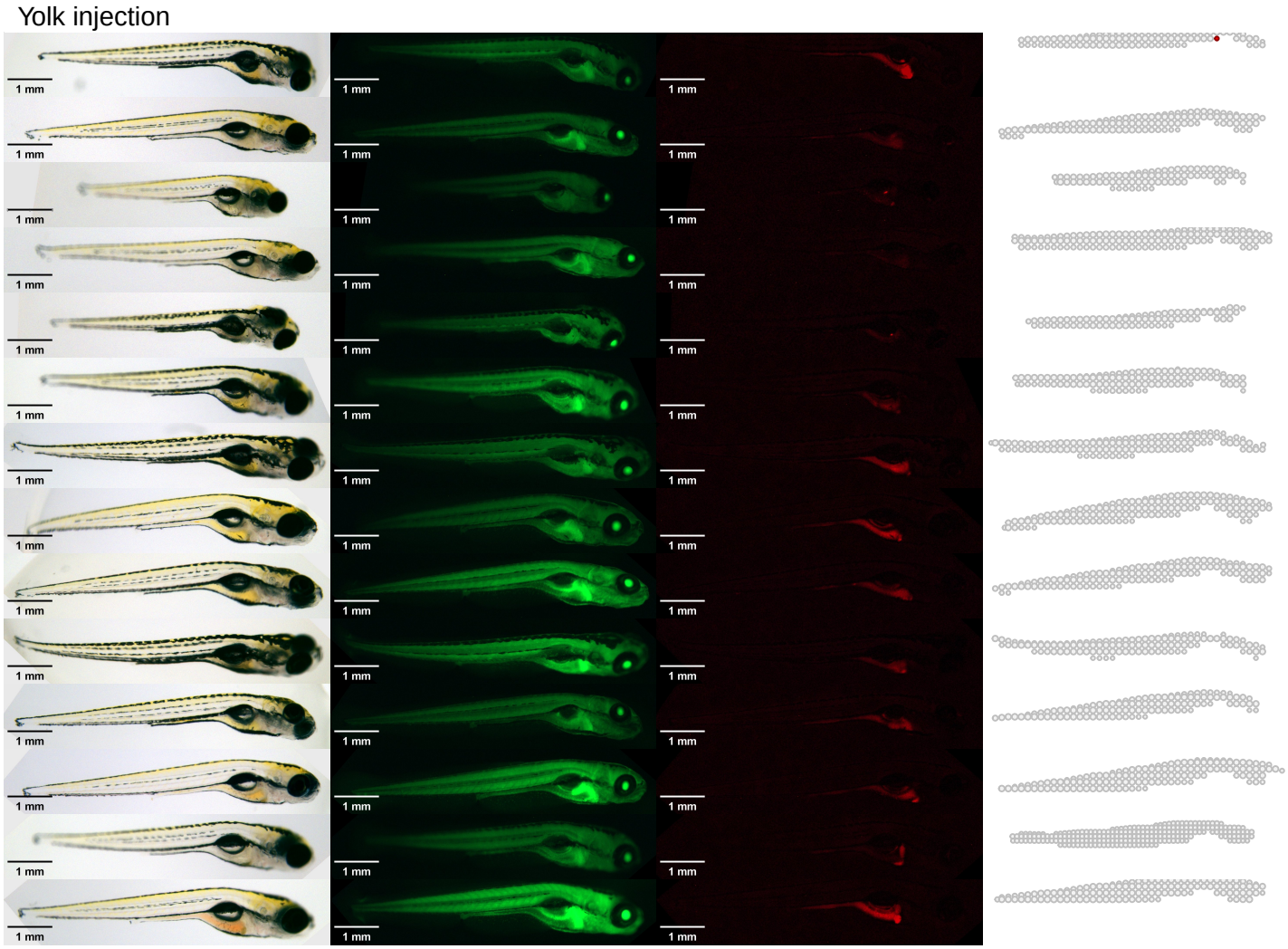



**Supplementary Figure 14. Fluorescence imaging and semi-quantification of chimeric zebrafish.** The chimeric zebrafish are shown. Bright field, EGFP and mCherry channels are shown. The fourth column displays semi-quantitative mCherry intensity analysis using ImageJ. Red dots represent bins exhibiting significantly elevated mCherry intensity compared to background, while grey dots indicate bins with non-significant mCherry intensity.

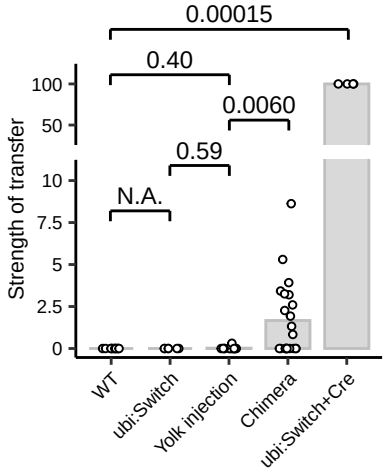



| ID | Sample | Sequencing primer |
|---|---|---|
| ① | ubi:switch | ubi-Switch-F |
| ② | ubi:switch+cre | ubi-Switch-F |
| ③ | chimera group 1 | ubi-Switch-F |
| ④ | chimera group 2 | ubi-Switch-F |
| ⑤ | ubi:switch | ubi-Switch-R |
| ⑥ | ubi:switch+cre | ubi-Switch-R |
| ⑦ | chimera group 1 | ubi-Switch-R |
| ⑧ | chimera group 2 | ubi-Switch-R |

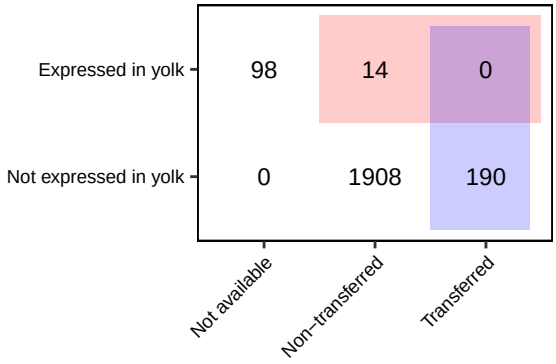
**Supplementary Figure 15. Confirmation of Cre induced recombination via Sanger sequencing.** Arrows indicate individual Sanger sequencing reads. The table lists sample names and sequencing primers used for each read.



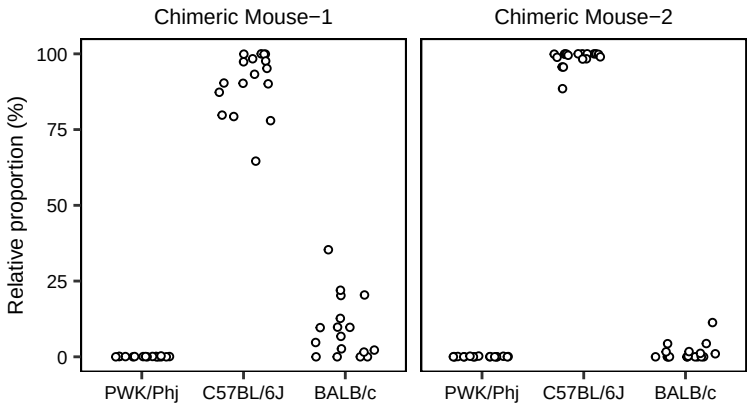

**Supplementary Figure 16. Fluorescence imaging and semi-quantification of yolk-injected Cre zebrafish.** The yolk-injected Cre ubi:Switch zebrafish are shown. Bright field, EGFP and mCherry channels are shown. The fourth column displays semi-quantitative mCherry intensity analysis using ImageJ. Red dots represent bins exhibiting significantly elevated mCherry intensity compared to background, while grey dots indicate bins with non-significant mCherry intensity.



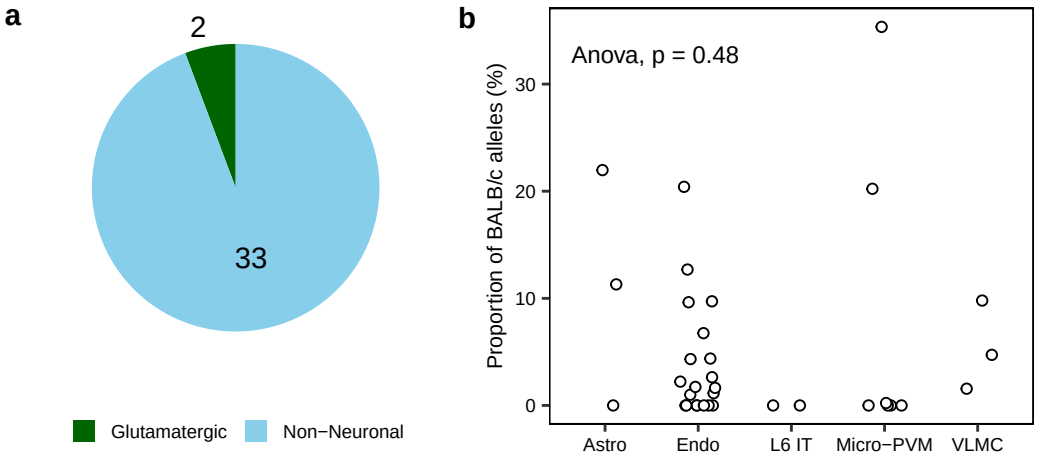

**Supplementary Figure 17. Quantification of functional mRNA transfer in yolk-injected Cre zebrafish.** The bar plot shows the percentage of mCherry-positive area per fish in the WT, negative control, Cre mRNA-injected, and yolk-injected Cre groups. Each dot represents an individual fish. P values from Wilcoxon tests comparing between groups are indicated above the respective groups.




**Supplementary Figure 18. Comparing between transferred genes and yolk-expressed genes.** The number denotes the number of genes in each group. The shadow in red highlights the genes expressed in yolk and the shadow in blue shows the transferred genes.




**Supplementary Figure 19. Relative proportions of strain-specific identity-informative sites in chimeric mice.** Scatter plots show the relative proportion of transcripts originating from the C57BL/6J, BALB/c, and PWK/Phj mouse strains for each chimeric mouse. Each dot represents a single cell.




**Supplementary Figure 20. Relative proportions of BALB/c-specific identity-informative sites across cell types. a.** Pie plot shows the number of glutamatergic and non-neuronal cells. **b.** Scatter plots show the relative proportion of transcripts originating from the BALB/c strain for each cell type, including astrocytes (Astro), endothelial cells (Endo), Layer 6 intratelencephalic neurons (L6 IT), microglia-perivascular macrophages (Micro-PVM) and vascular leptomeningeal cells (VLMC). Each dot represents a single cell.