

Supplementary Figures

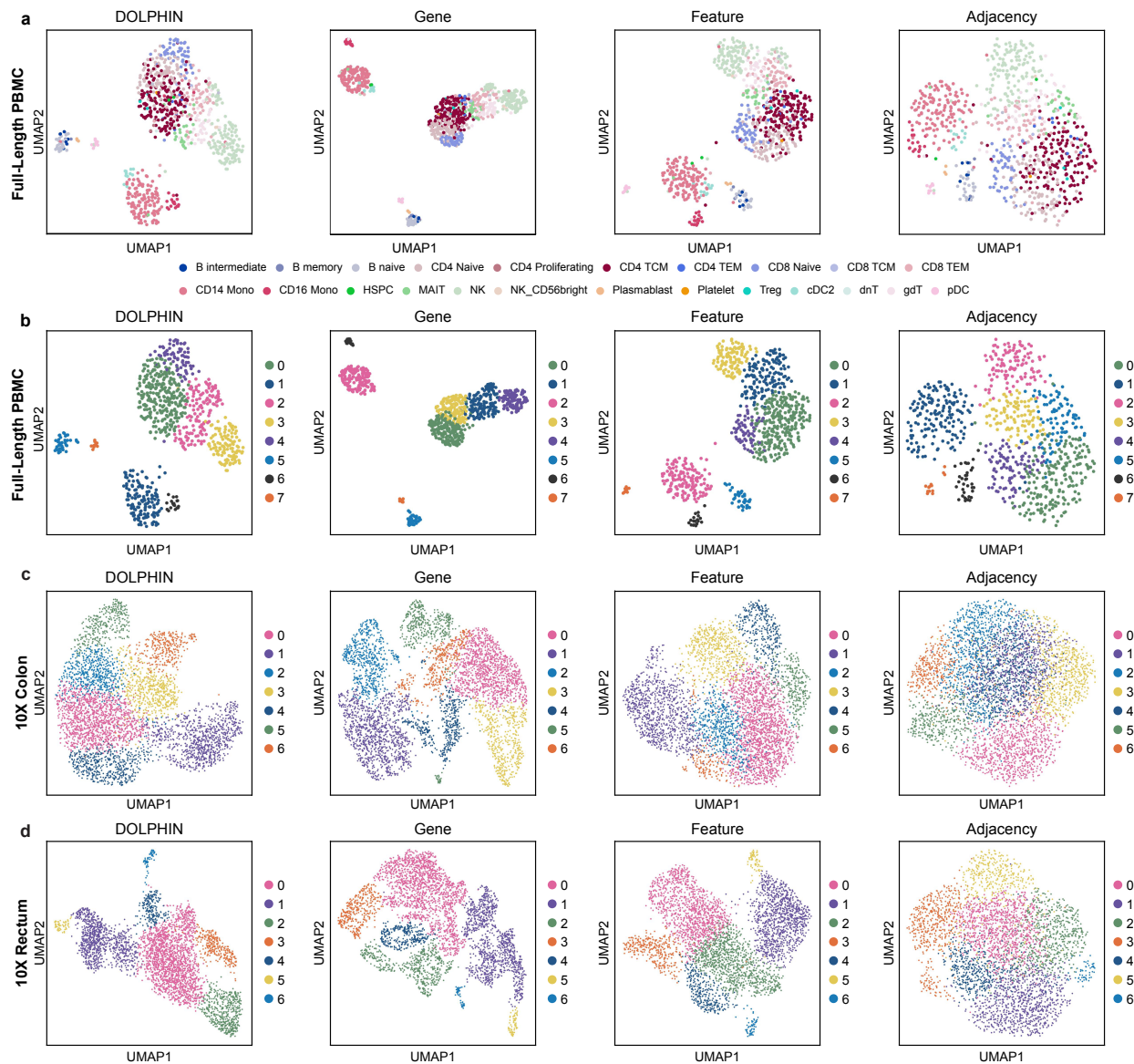


Fig. S1 UMAP visualizations of cell embeddings generated using different methods. UMAP plots compare cell embeddings from DOLPHIN, conventional gene count table, feature matrix only and adjacency matrix only. Panels show embeddings for **a**, Full-length PBMC labeled by sub-cell type, **b**, Full-length PBMC labeled by Leiden clusters, **c**, 10X Colon labeled by Leiden clusters, and **d**, 10X Rectum labeled by Leiden clusters.

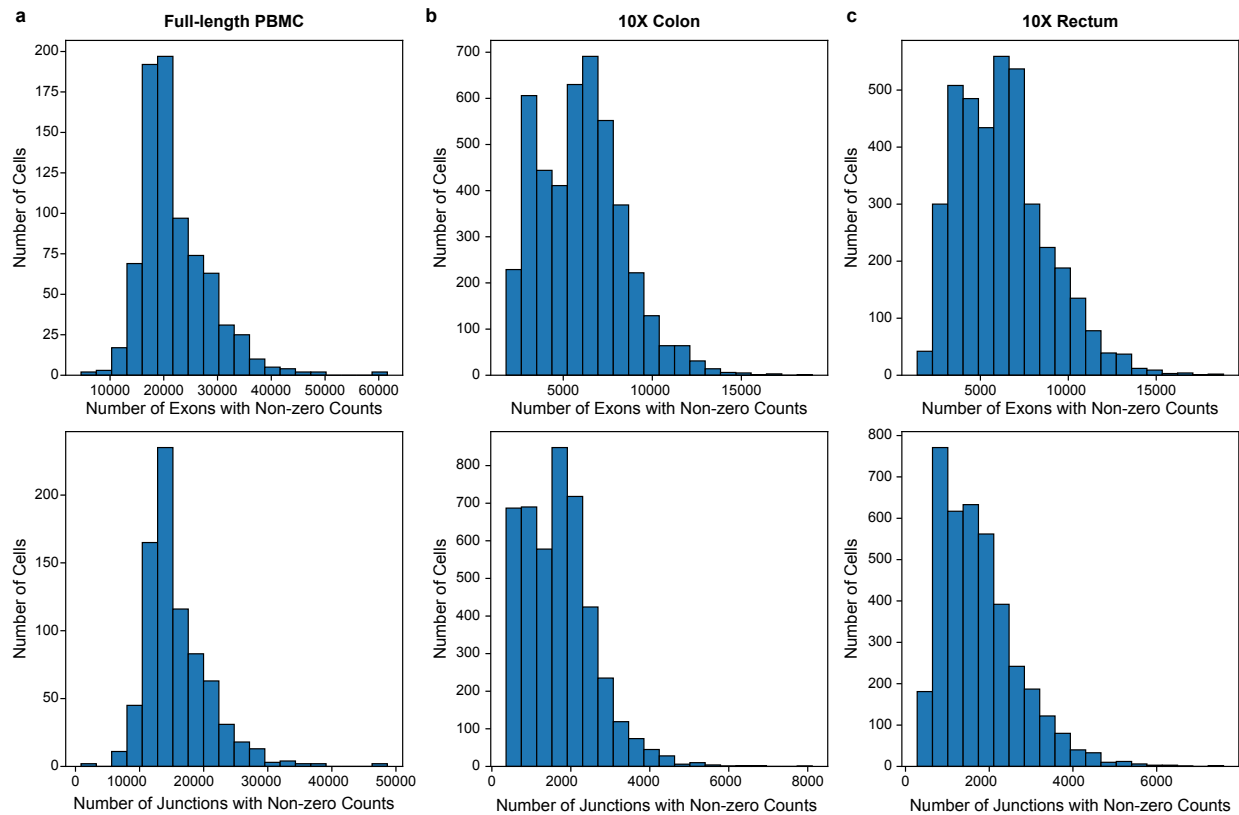


Fig. S2 Histogram of non-zero exon and junction counts across cells. This figure presents the distribution of exons and junctions with non-zero counts per cell, providing an overview of exon and junction coverage within each dataset. The x-axis represents the count of non-zero exons or junctions, while the y-axis indicates the number of cells. **a**, Full-length PBMC dataset, **b**, 10X Colon dataset, and **c**, 10X Rectum dataset. Source data are provided as a Source Data file.

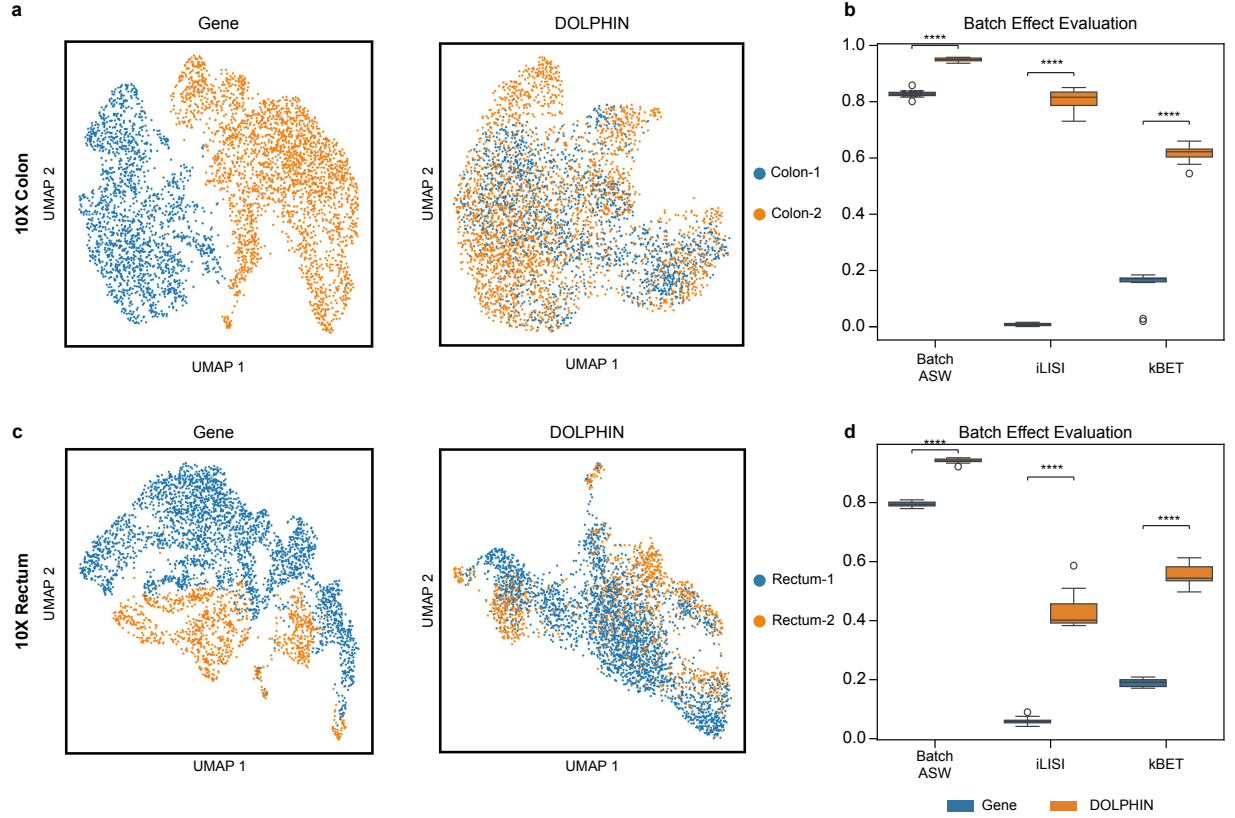


Fig. S3 Comparison of batch effects in cell embeddings generated using the gene count table method and DOLPHIN on the 10X dataset. **a**, Cell embeddings of the 10X colon dataset, colored by batch. **b**, Batch effect evaluation metrics for the 10X colon dataset, comparing the gene count table method and DOLPHIN. **c**, Cell embeddings of the 10X rectum dataset, colored by batch. **d**, Batch effect evaluation metrics for the 10X rectum dataset, comparing the gene count table method and DOLPHIN. Each score is based on $N = 10$ bootstrapping replicates using different random seeds (technical replicates). Boxes indicate the interquartile range (IQR, 25th to 75th percentile), with the line inside each box representing the median. Whiskers extend to the most extreme data points within 1.5 times the IQR from the quartiles. P -values from one-sided Student's t -tests: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$. Exact P -values are provided in the source data. Source data are provided as a Source Data file.

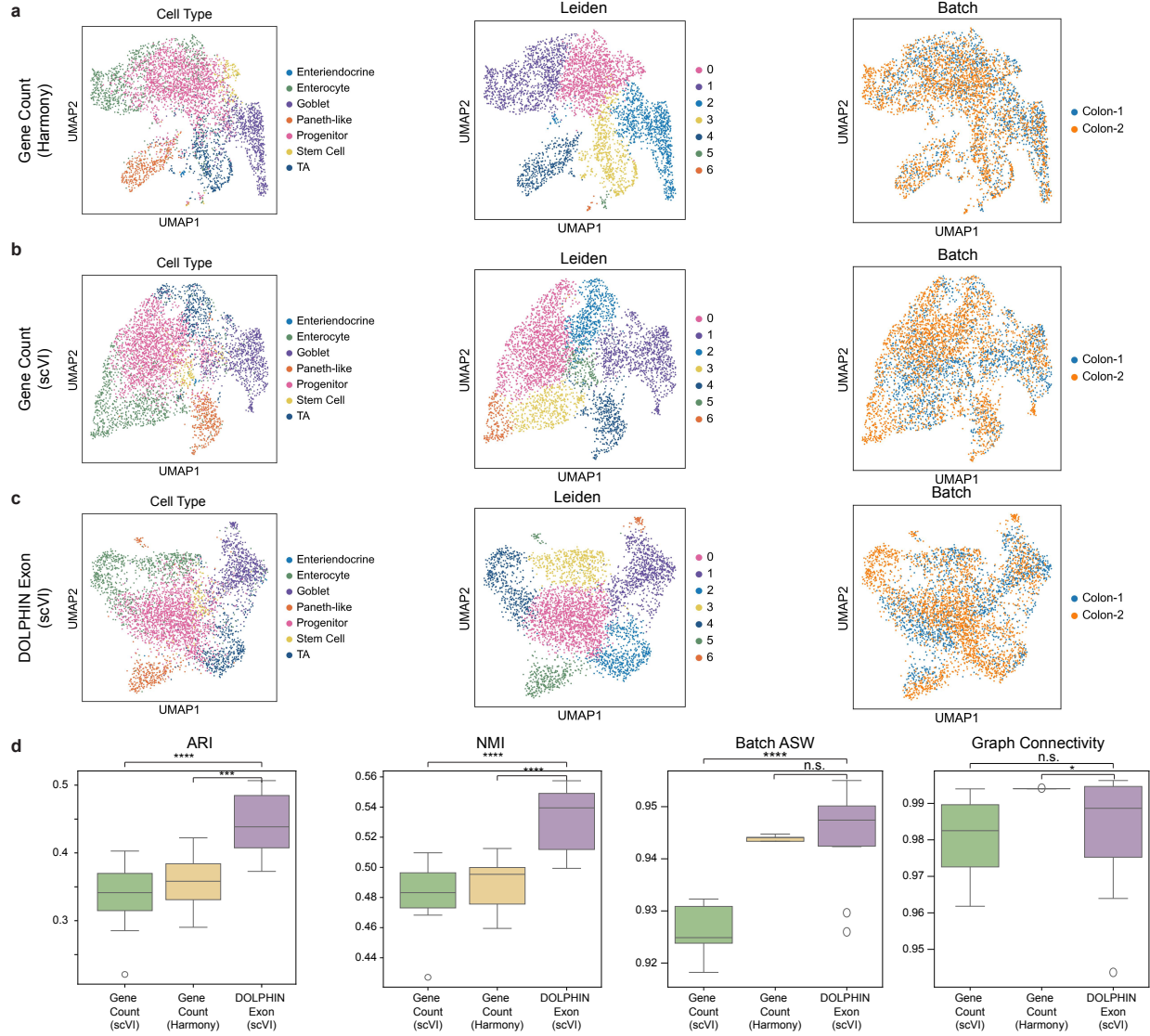


Fig. S4 Batch correction of the 10X colon dataset using gene expression and exon-level approaches, highlighting DOLPHIN's ability to reduce batch effects. UMAP visualizations show cell embeddings after batch correction using three different methods. In panels a, b, and c, each row contains cells colored by cell type, Leiden cluster, and batch origin (Colon-1 and Colon-2). Batch correction was performed using **a**, Harmony applied to normalized gene expression, **b**, scVI applied to normalized gene expression, and **c**, exon-level feature matrix batch-corrected with scVI, which served as input to the DOLPHIN model. **d**, Summary of biological conservation (ARI and NMI) and batch correction metrics (Batch ASW and Graph Connectivity) for the three methods. Each score is based on $N = 10$ bootstrapping replicates using different random seeds (technical replicates). Boxes indicate the interquartile range (IQR, 25th to 75th percentile), with the line inside each box representing the median. Whiskers extend to the most extreme data points within 1.5 times the IQR from the quartiles. P -values from one-sided Student's t -tests: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$; n.s., not significant. Exact P -values are provided in the source data. Source data are provided as a Source Data file.

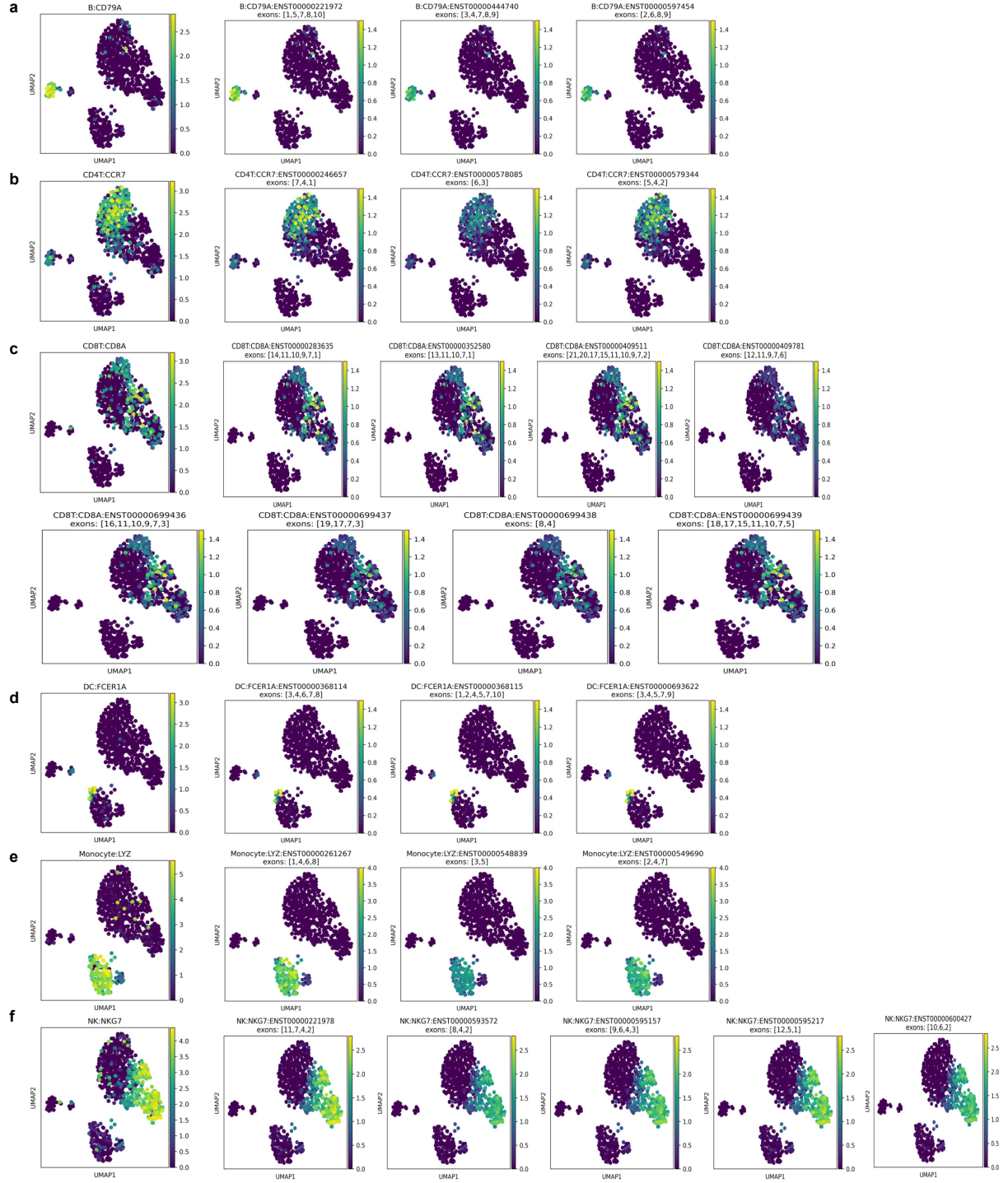


Fig. S5 Isoform-level expression patterns of canonical marker genes in the full-length PBMC dataset. UMAP visualizations of gene-level and isoform-level expression for selected canonical marker genes corresponding to major cell types: **a**, B cells; **b**, CD4 T cells; **c**, CD8 T cells; **d**, dendritic cells (DC); **e**, monocytes; **f**, NK cells. In each panel, the first plot displays the expression of the canonical marker gene (titles follow the format: “cell type: gene name”), followed by UMAPs of its associated isoforms (titles follow the format: “cell type: gene name: isoform name: exon composition”), where exon composition lists the indices of exons forming each isoform.

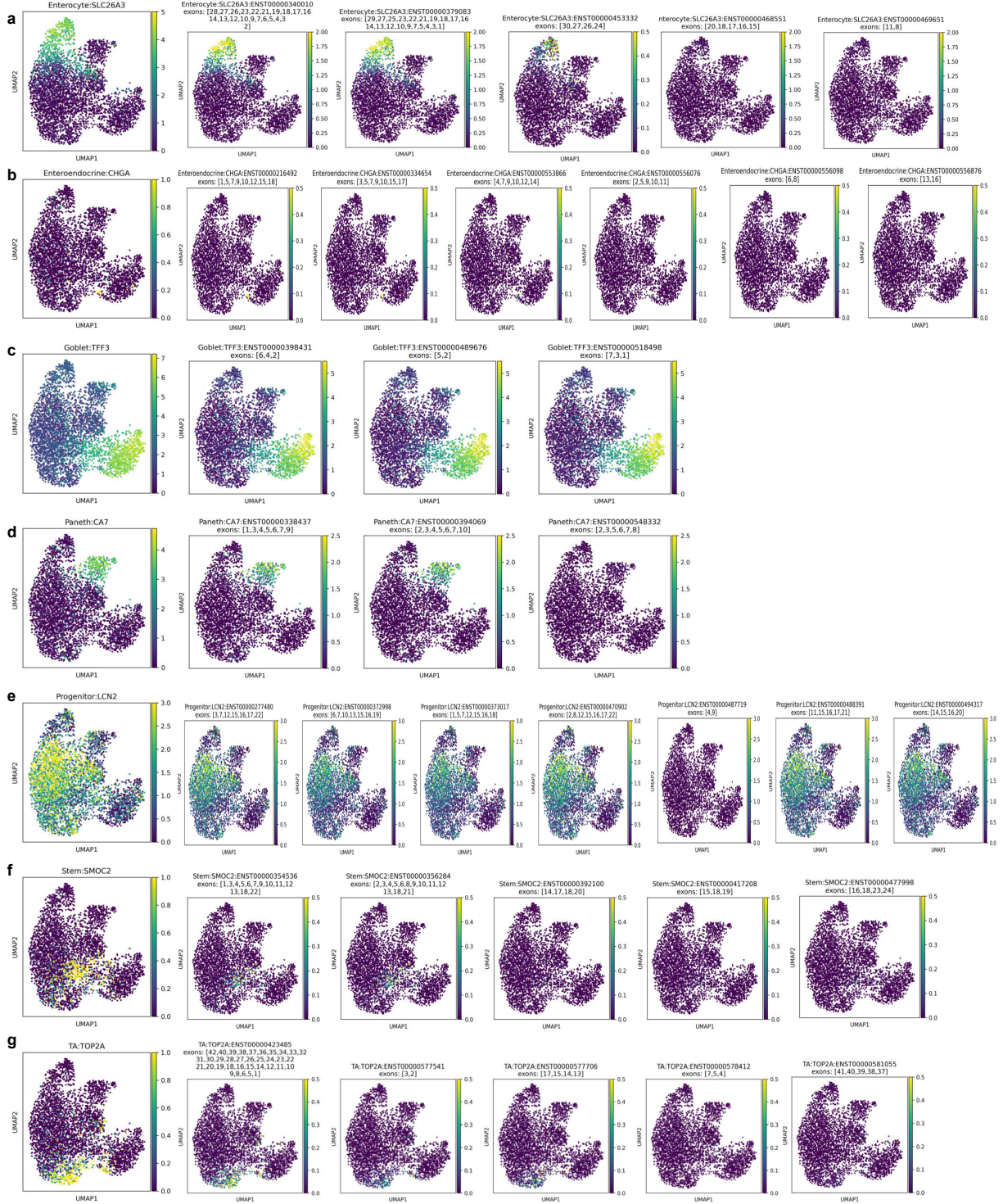


Fig. S6 Isoform-level expression patterns of canonical marker genes in the 10X colon dataset. UMAP visualizations of gene-level and isoform-level expression for selected canonical marker genes corresponding to cell types: **a**, enterocyte cells; **b**, enteroendocrine cells; **c**, goblet cells; **d**, paneth-like cells; **e**, progenitor; **f**, stem cells; **g**, transient amplifying (TA) cells. In each panel, the first plot displays the expression of the canonical marker gene (titles follow the format: “cell type: gene name”), followed by UMAPs of its associated isoforms (titles follow the format: “cell type: gene name: isoform name: exon composition”), where exon composition lists the indices of exons forming each isoform.

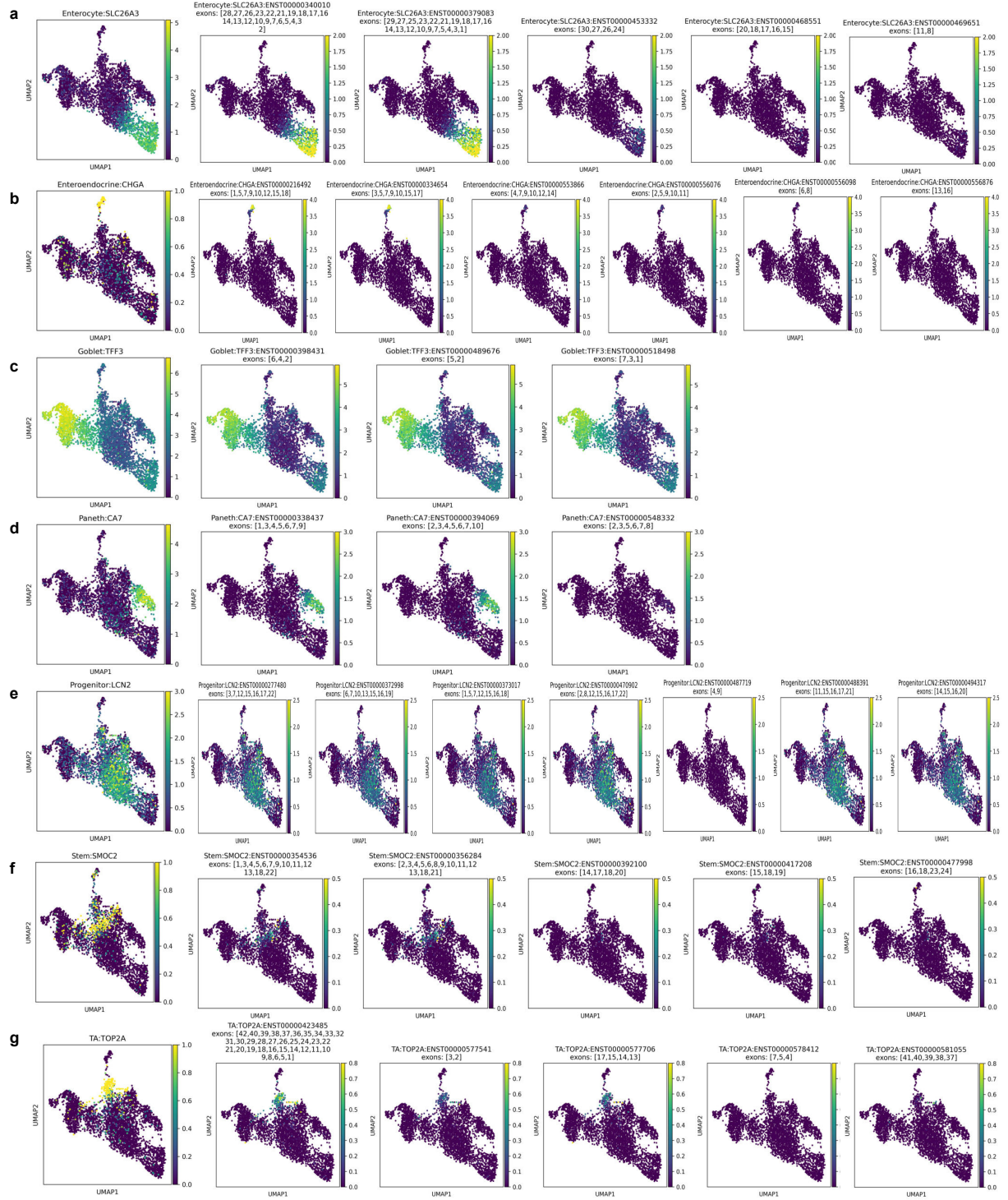


Fig. S7 Isoform-level expression patterns of canonical marker genes in the 10X rectum dataset. UMAP visualizations of gene-level and isoform-level expression for selected canonical marker genes corresponding to cell types: **a**, enterocyte cells; **b**, enteroendocrine cells; **c**, goblet cells; **d**, paneth-like cells; **e**, progenitor; **f**, stem cells; **g**, transient amplifying (TA) cells. In each panel, the first plot displays the expression of the canonical marker gene (titles follow the format: “cell type: gene name”), followed by UMAPs of its associated isoforms (titles follow the format: “cell type: gene name: isoform name: exon composition”), where exon composition lists the indices of exons forming each isoform.

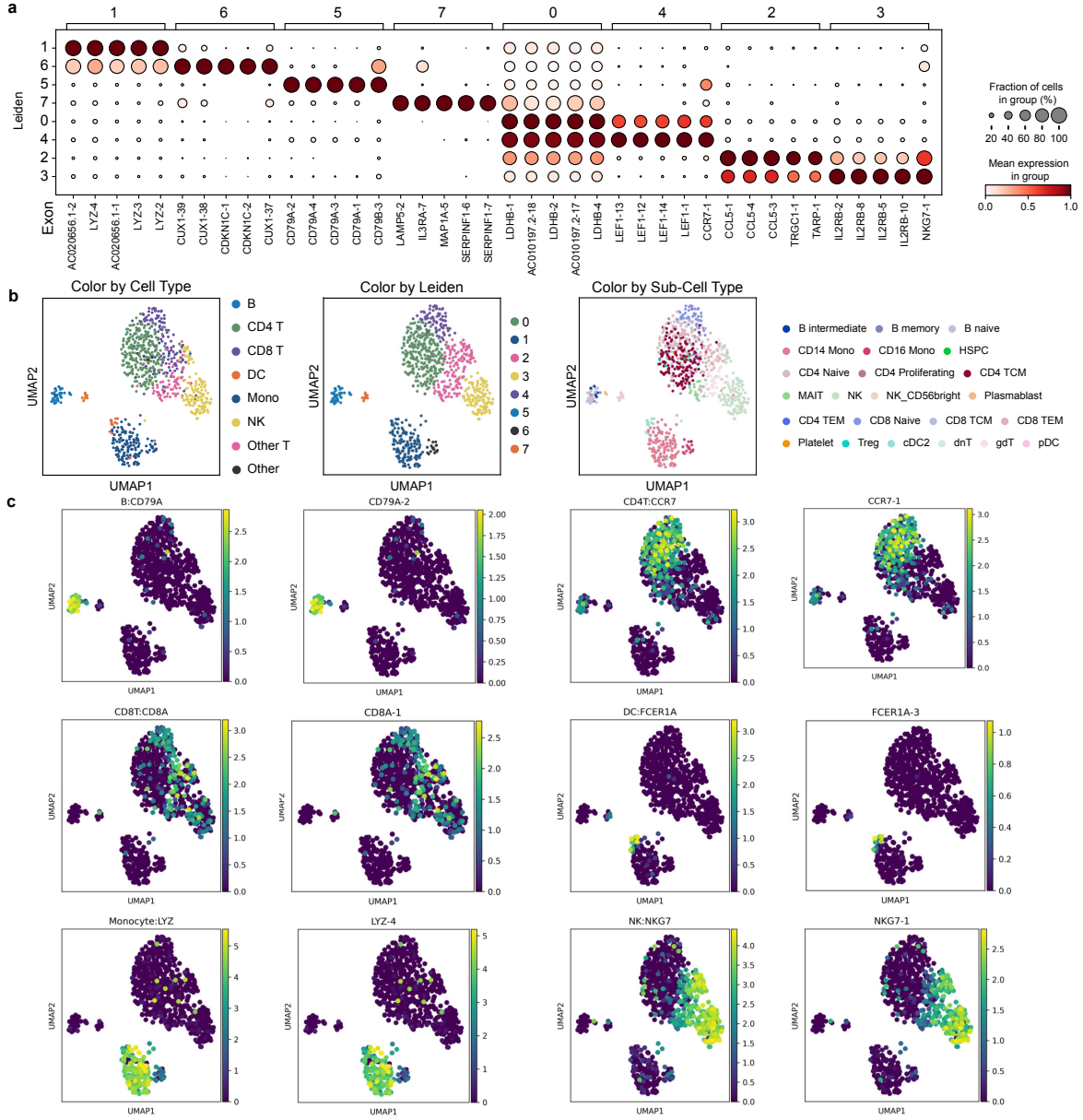


Fig. S8 Exon-level cell type identification in the full-length PBMC dataset using DOLPHIN. a, Dot plot of the top 5 differentially expressed exons per cell type, with exon labels in the format "gene name-exon number". **b**, UMAP of cell clusters identified by DOLPHIN, labeled by cell types, Leiden clusters and sub-cell types. **c**, UMAPs showing expression of selected canonical marker genes (one per cell type; titles follow the format: "cell type: gene") alongside the expression of a representative exon from the same gene (titles follow the format: "gene name-exon number").

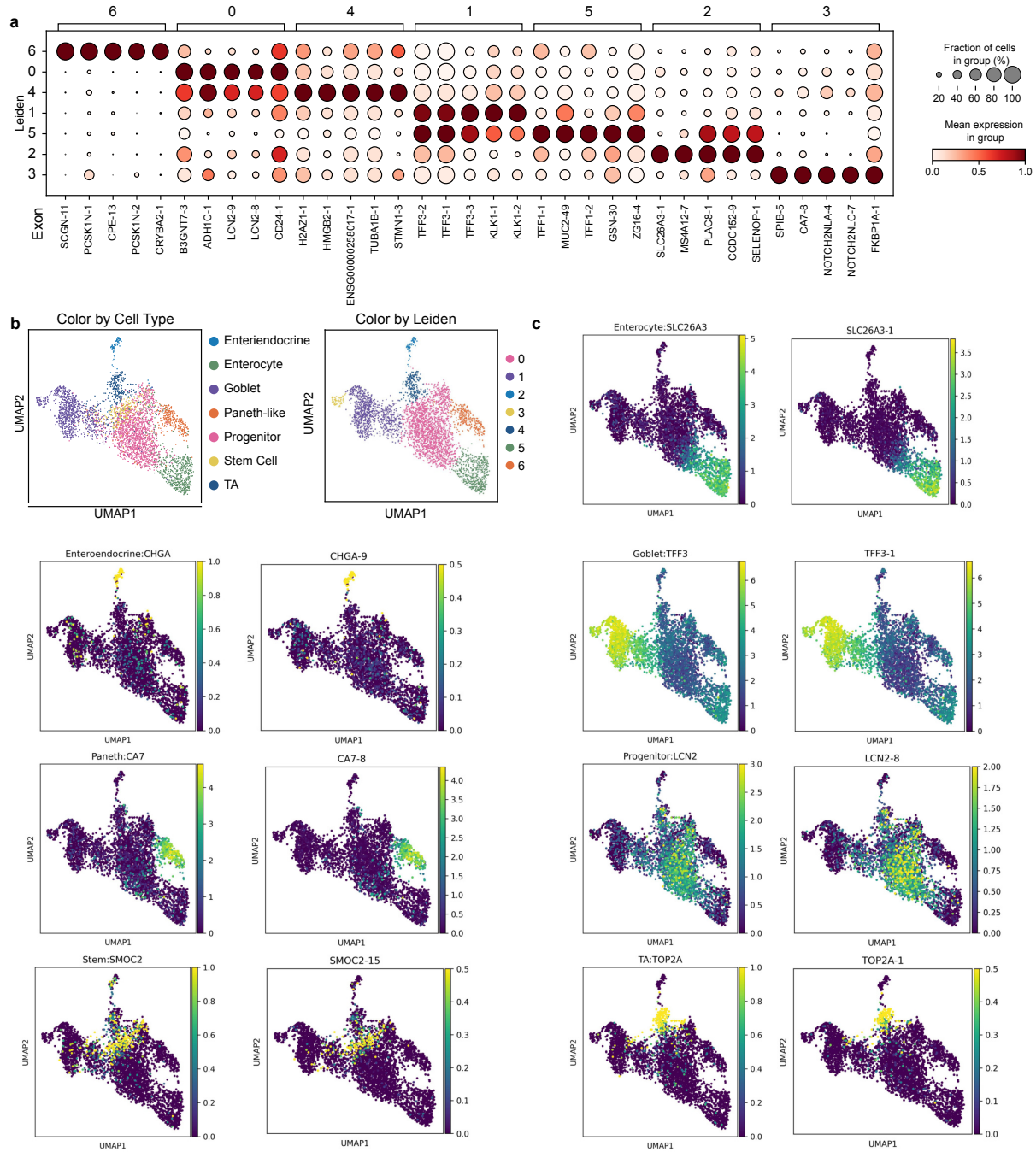


Fig. S10 Exon-level cell type identification in the 10X rectum dataset using DOLPHIN. **a**, Dot plot of the top 5 differentially expressed exons per cell type, with exon labels in the format “gene name-exon number”. **b**, UMAP of cell clusters identified by DOLPHIN, labeled by cell types and Leiden clusters. **c**, UMAPs showing expression of selected canonical marker genes (one per cell type; titles follow the format: “cell type: gene”) alongside the expression of a representative exon from the same gene (titles follow the format: “gene name-exon number”).

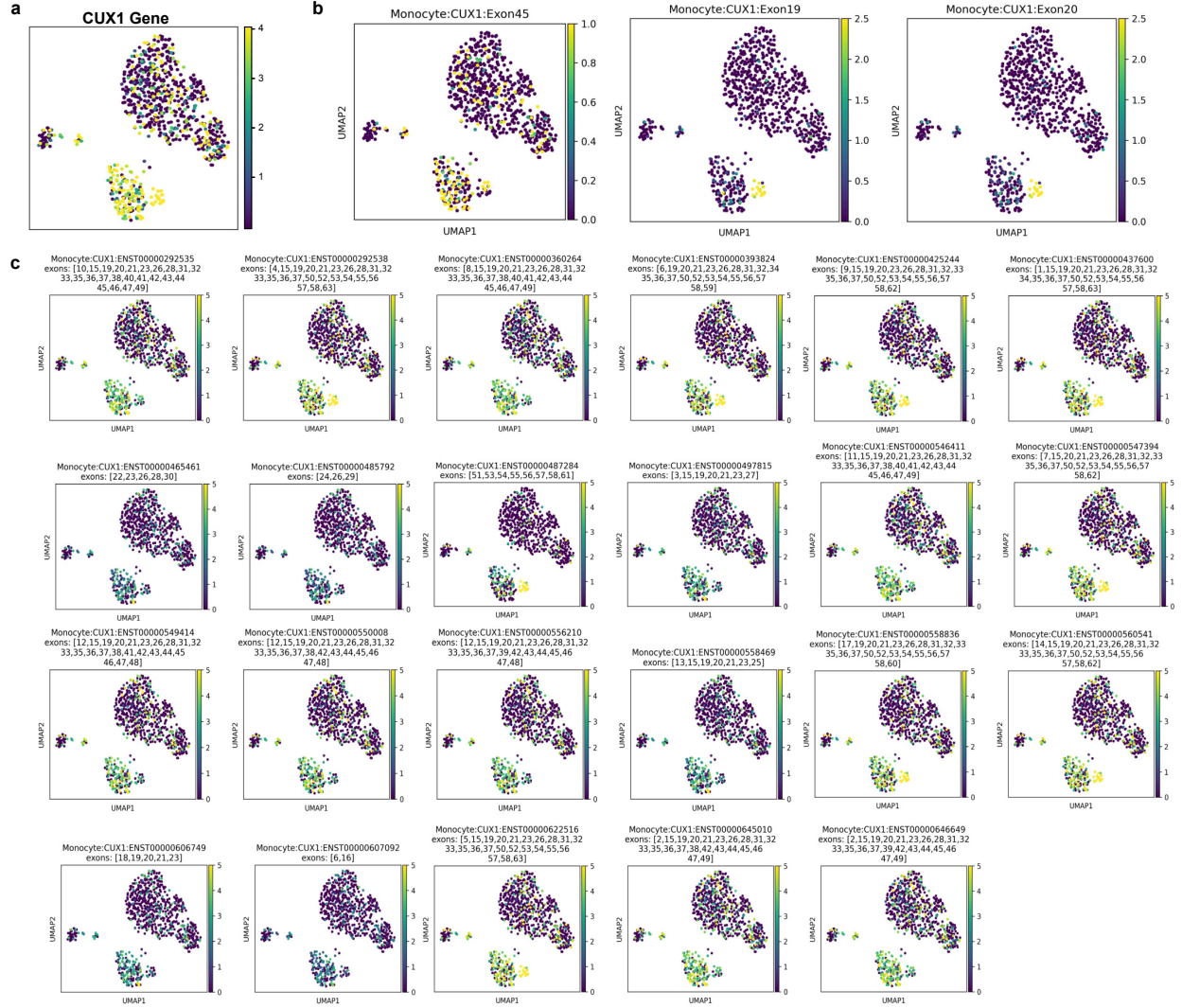


Fig. S11 Visualization of CUX1 expression in the full-length PBMC dataset. **a**, Gene-level expression pattern. **b**, Exon-level expression pattern highlighting finer substructure (titles follow the format: “cell type: gene name: exon number”). **c**, Isoform-level expression pattern showing additional resolution beyond gene-level aggregation (titles follow the format: “cell type: gene name: isoform name: exon composition”).

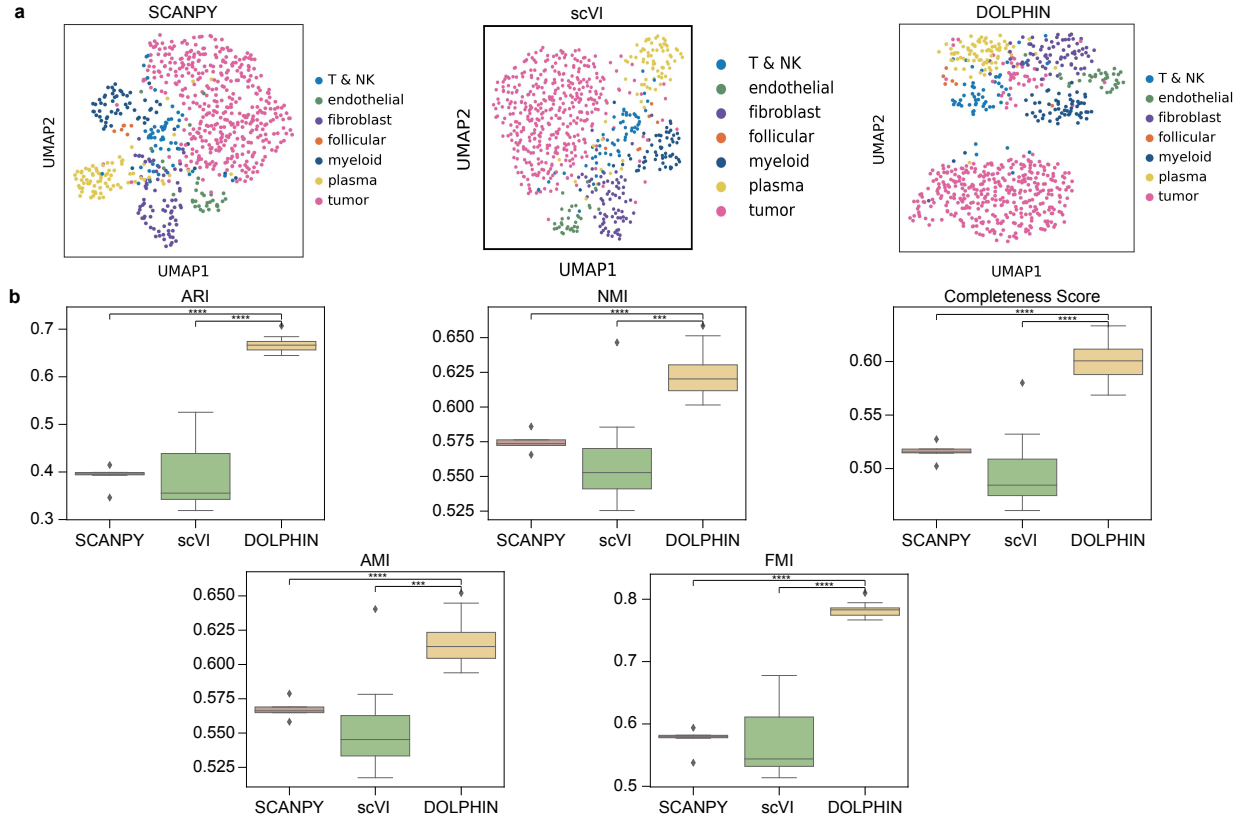


Fig. S12 Application of DOLPHIN to single-cell long-read RNA-seq data generated with nanopore technology. **a**, UMAP visualization of cell embeddings generated by transcript count-based methods (SCANPY and scVI) and exon-level embeddings from DOLPHIN. **b**, Clustering performance metrics comparing the three methods on the same dataset, demonstrating their relative performance when applied to long-read single-cell data. Each score is based on $N = 10$ bootstrapping replicates using different random seeds (technical replicates). Boxes indicate the interquartile range (IQR, 25th to 75th percentile), with the line inside each box representing the median. Whiskers extend to the most extreme data points within 1.5 times the IQR from the quartiles. P -values from one-sided Student's t -tests: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$. Exact P -values are provided in the source data. Source data are provided as a Source Data file.

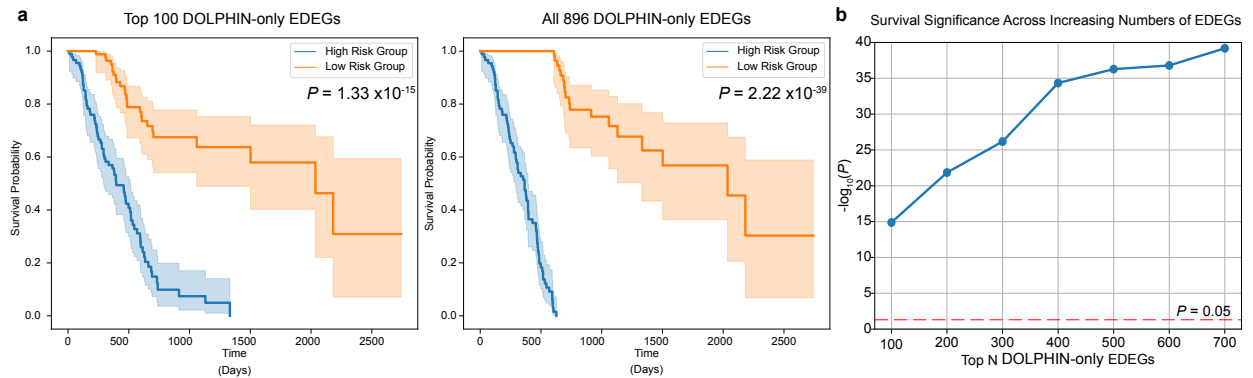


Fig. S13 Survival analysis of 896 DOLPHIN-only EDEGs. **a**, Kaplan-Meier survival curves comparing high-risk and low-risk groups stratified by expression of top 100 and all 896 DOLPHIN-only EDEGs. **b**, Line plot showing the significance of survival associations across varying numbers of top-ranked DOLPHIN-only EDEGs. The P values were determined by the two-tailed log-rank sum test. Source data are provided as a Source Data file.

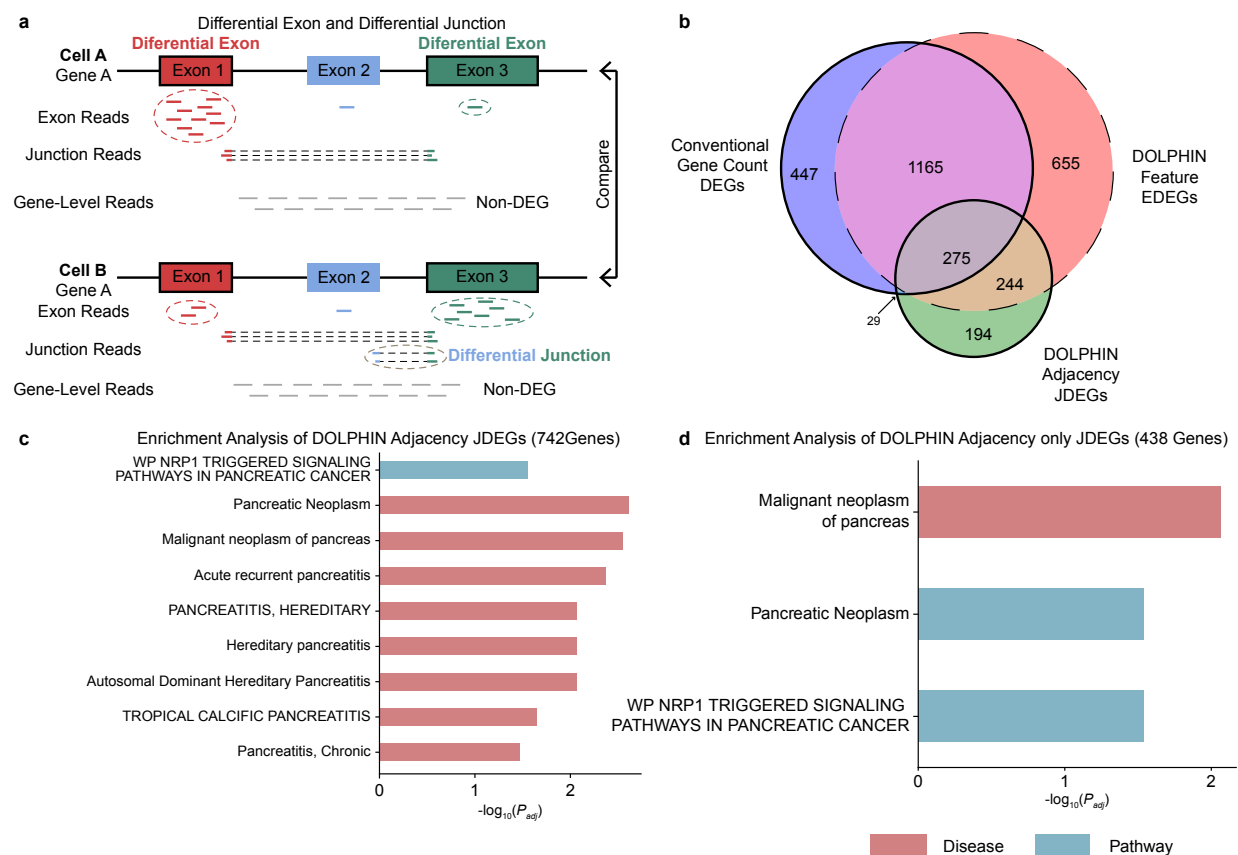


Fig. S14 Differentially expressed junction-related genes (JDEGs) identification using DOLPHIN with an adjacency matrix. **a**, A schematic diagram illustrating the identification of differential exons and junctions by comparing two cells for the same gene A. In this example, exons 1 and 3 are detected as differential exons, while the junction between exons 2 and 3 is identified as a differential junction. These identified differential exons and junctions form the basis for detecting EDEGs and JDEGs by integrating this information at the gene level. Notably, both cells show a total read count of 15 for gene A, which does not qualify as a DEG. **b**, Venn diagram showing EDEGs identified by DOLPHIN using the feature matrix, JDEGs identified by DOLPHIN using the adjacency matrix, and the DEGs using conventional gene count table method. **c**, Enrichment analysis of the 742 JDEGs identified using the DOLPHIN adjacency matrix. **d**, Enrichment analysis of JDEGs unique to DOLPHIN with the adjacency matrix (438 JDEGs are not identified as DEGs). Adjusted P -values for each enrichment term were calculated using one-sided hypergeometric tests, followed by multiple testing correction using the Benjamini–Hochberg (BH) method. Source data are provided as a Source Data file.

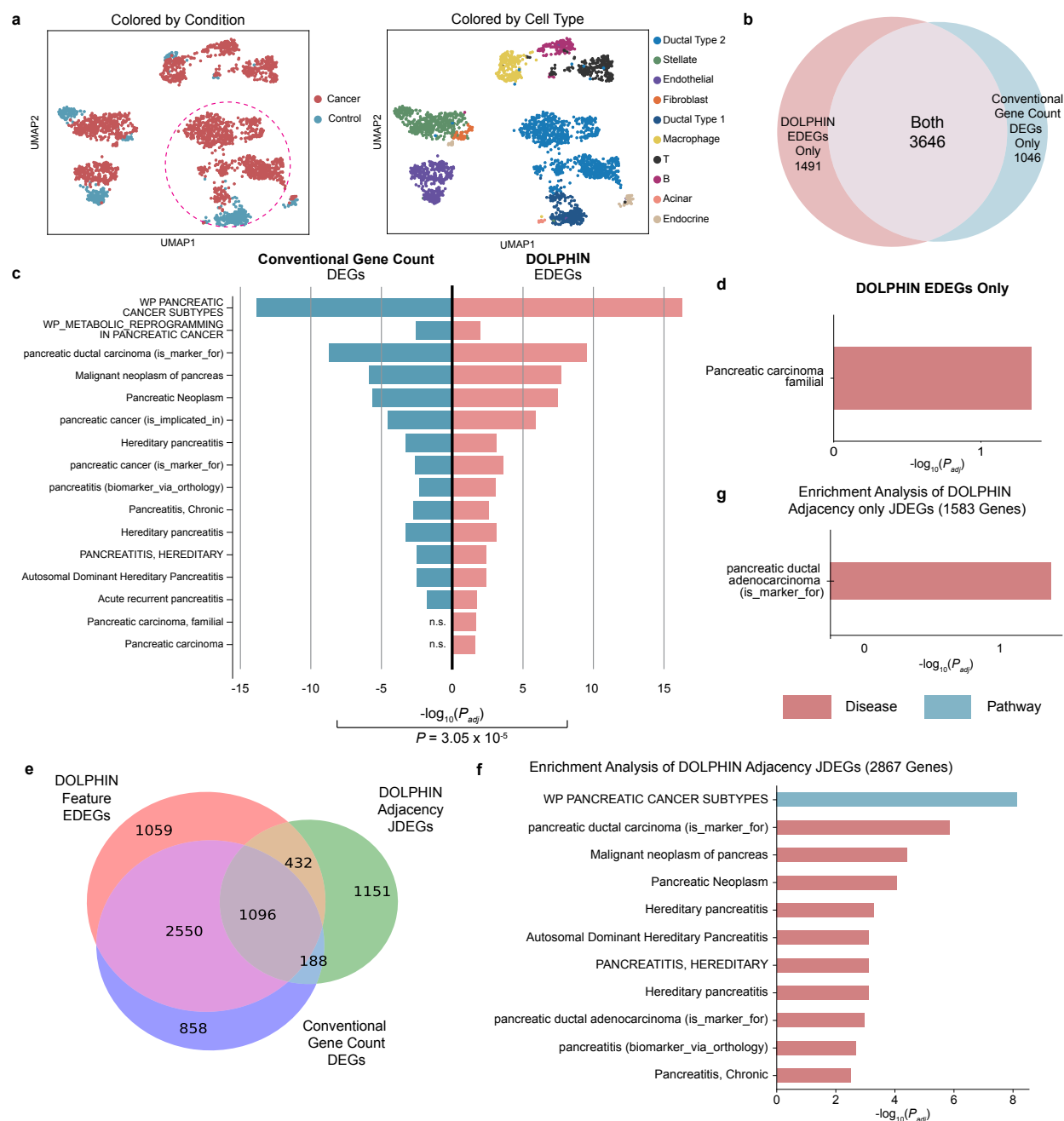


Fig. S15 DOLPHIN identifies differential exon- and junction-level markers in PDAC ductal cells. **a**, UMAP embedding of the PDAC dataset generated by DOLPHIN, colored by condition (cancer vs. control, left) and by annotated cell types (right). Ductal cell clusters (highlighted in pink) were selected for downstream differential analysis. **b**, Venn diagram showing the overlap between DEGs identified using the conventional gene count table and EDEGs identified by DOLPHIN. **c**, Enrichment analysis comparing DEGs (gene count) and EDEGs (DOLPHIN). P -value from one-sided Wilcoxon test. **d**, Enrichment analysis using the 1491 DOLPHIN-only EDEGs revealed significant pancreatic cancer-related term. Results from the 1046 DEGs identified only by gene count-based method did not reveal significant enrichment for pancreatic cancer-related terms. **e**, Venn diagram comparing DEGs (gene count), EDEGs (DOLPHIN), and JDEGs (DOLPHIN). **f**, Enrichment analysis of the 2867 JDEGs identified from DOLPHIN's junction adjacency graph. **g**, Enrichment analysis using the 1583 JDEGs that were not detected as DEGs, revealing PDAC-related term. Adjusted P -values for each enrichment term were calculated using one-sided hypergeometric tests, followed by multiple testing correction using the Benjamini-Hochberg (BH) method. Source data are provided as a Source Data file.

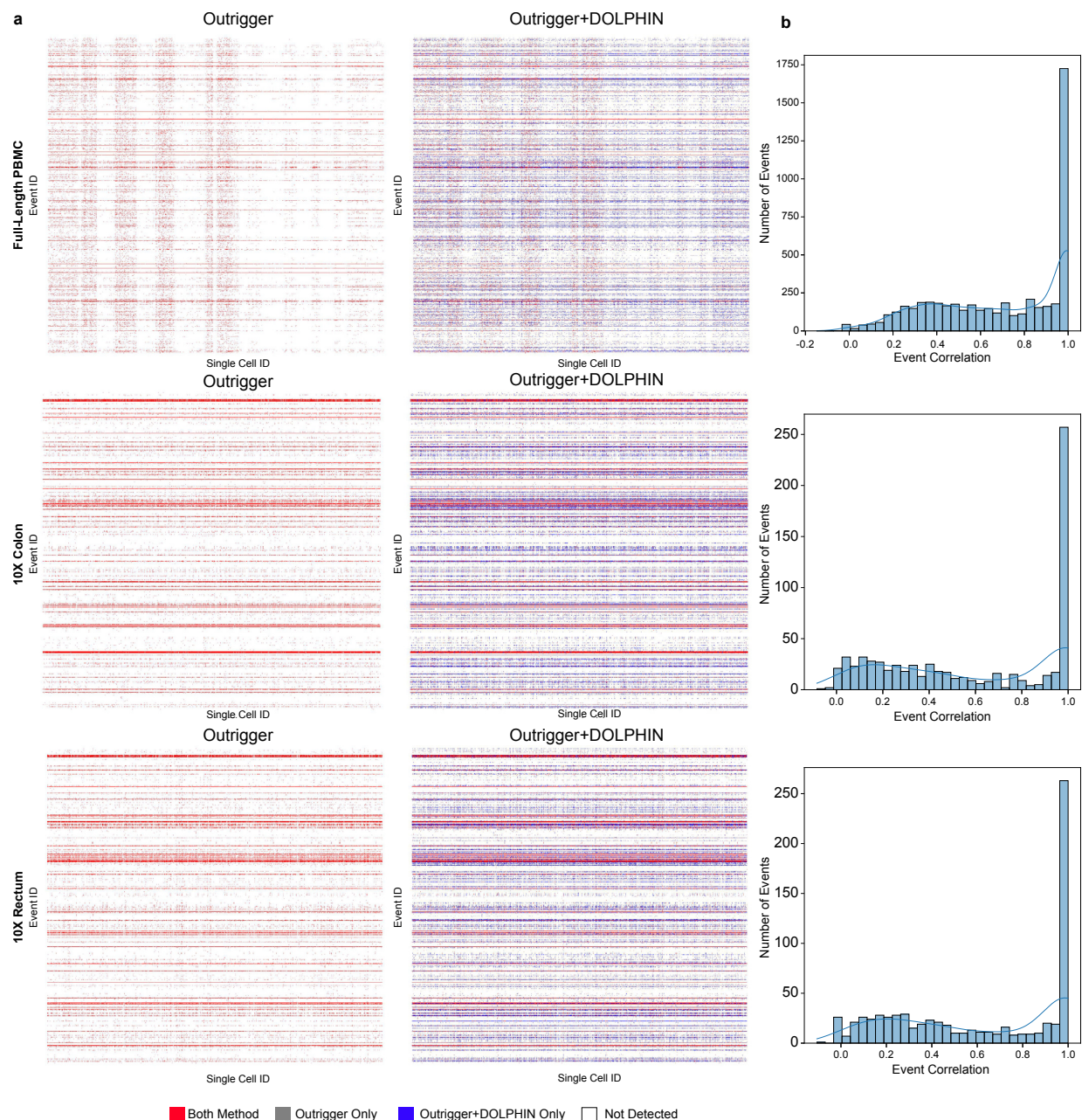


Fig. S16 Concordance of AS events detected using Outtrigger alone versus Outtrigger with DOLPHIN-based cell aggregation. **a**, Heatmaps showing the detection of overlapping AS events across cells for three datasets: full-length PBMC, 10X colon, and 10X rectum. Each panel compares Outtrigger (left) and Outtrigger+DOLPHIN (right) on a common set of events, with colors indicating cell-level detection status across methods. **b**, Histogram showing the distribution of Pearson correlation coefficients for overlapping AS events in panel (a), measuring cell-level detection similarity between Outtrigger and Outtrigger+DOLPHIN. Each bar represents the number of events whose correlation falls within a specific range, illustrating overall concordance between the two methods across shared events.

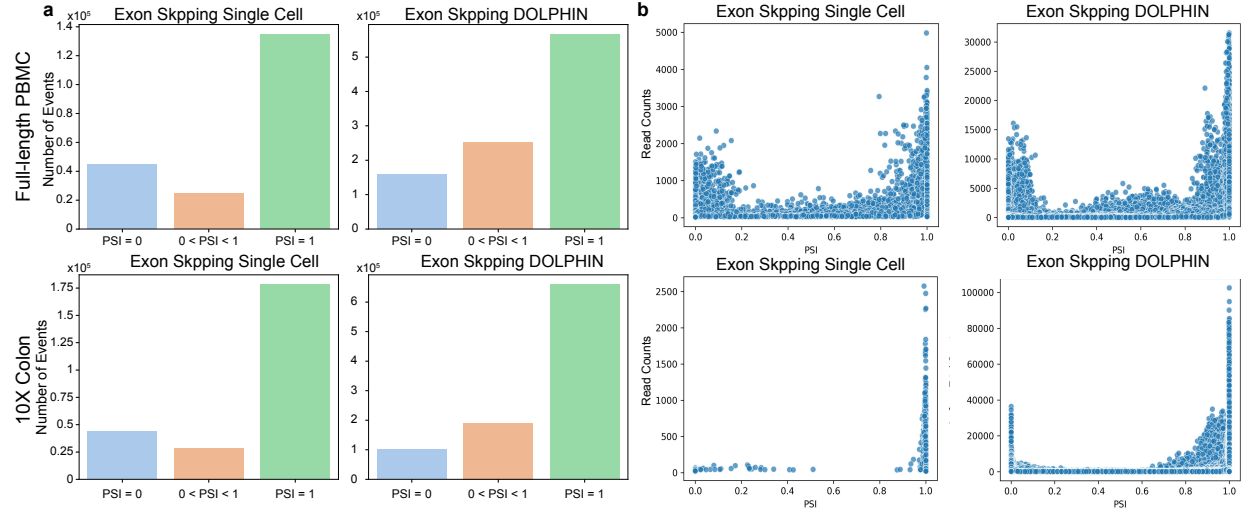


Fig. S17 Distribution of exon skipping events across PSI ranges and corresponding read support. **a**, Number of exon skipping events assigned to three PSI ranges (PSI = 0, 0 < PSI < 1, PSI = 1) using original single-cell input (left) and DOLPHIN-enhanced input (right). **b**, Scatter plot of exon skipping events, with each dot representing one event in one cell, plotted by its PSI value (x-axis) and the number of supporting junction reads (y-axis). **a** and **b** upper panel are full-length PBMC dataset and lower panel are 10X colon dataset. Source data are provided as a Source Data file.

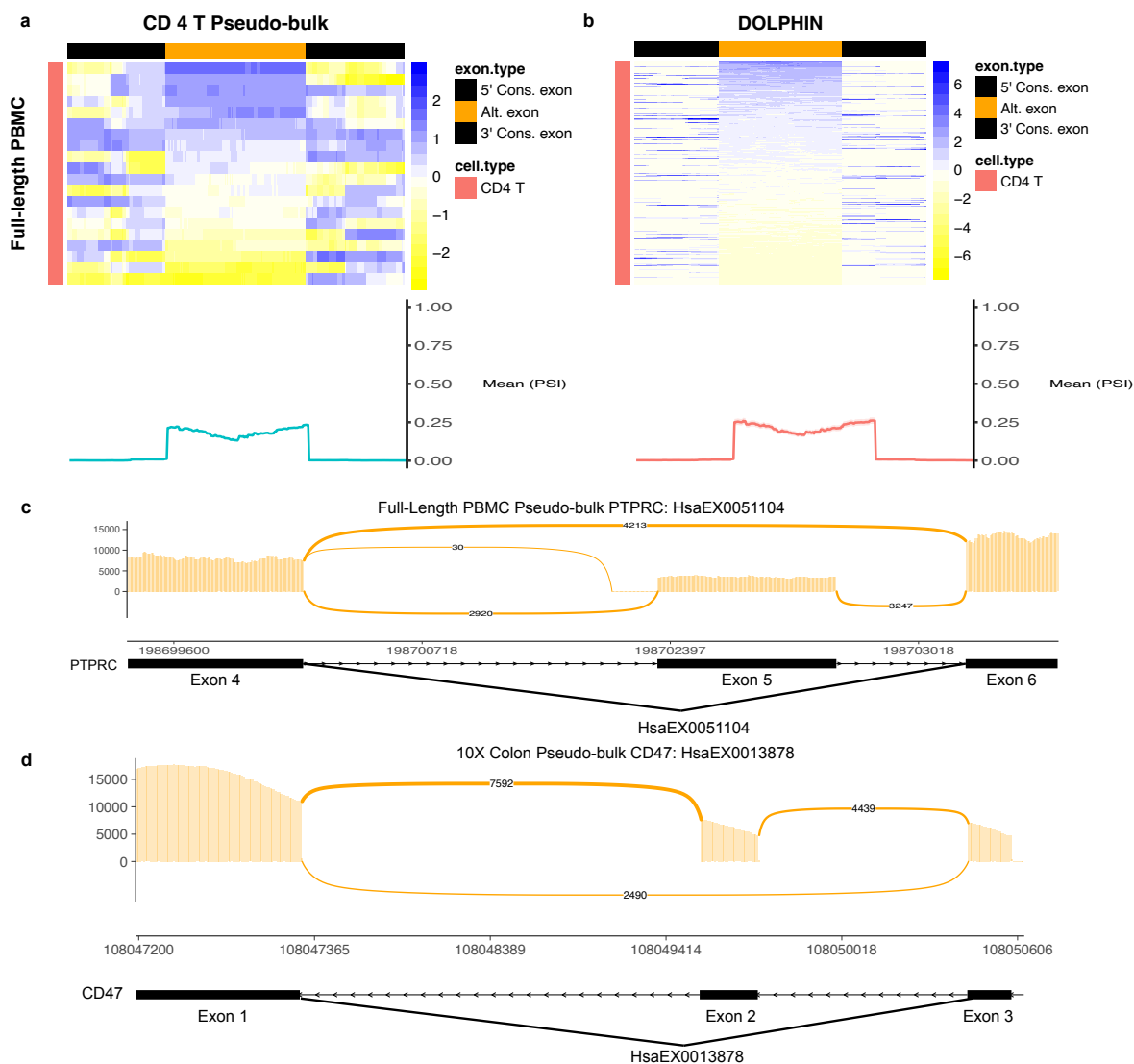


Fig. S18 In silico validation of alternative splicing events detected by DOLPHIN using VALERIE and ggsashimi. **a**, VALERIE output showing the PSI profile of the alternative exon HsaEX0051104 in *PTPRC*, based on pseudo-bulk analysis of CD4 T cells from the full-length PBMC dataset. **b**, DOLPHIN-inferred single-cell PSI values for the same exon in CD4 T cells, showing its presence in this cell type. **c**, Sashimi plot based on pseudo-bulk analysis of CD4 T cells (full-length PBMC), supporting the presence of the alternative exon HsaEX0051104 in *PTPRC* at the read level. **d**, Pseudo-bulk sashimi plot of *CD47* (HsaEX0013878) in the 10X colon dataset.

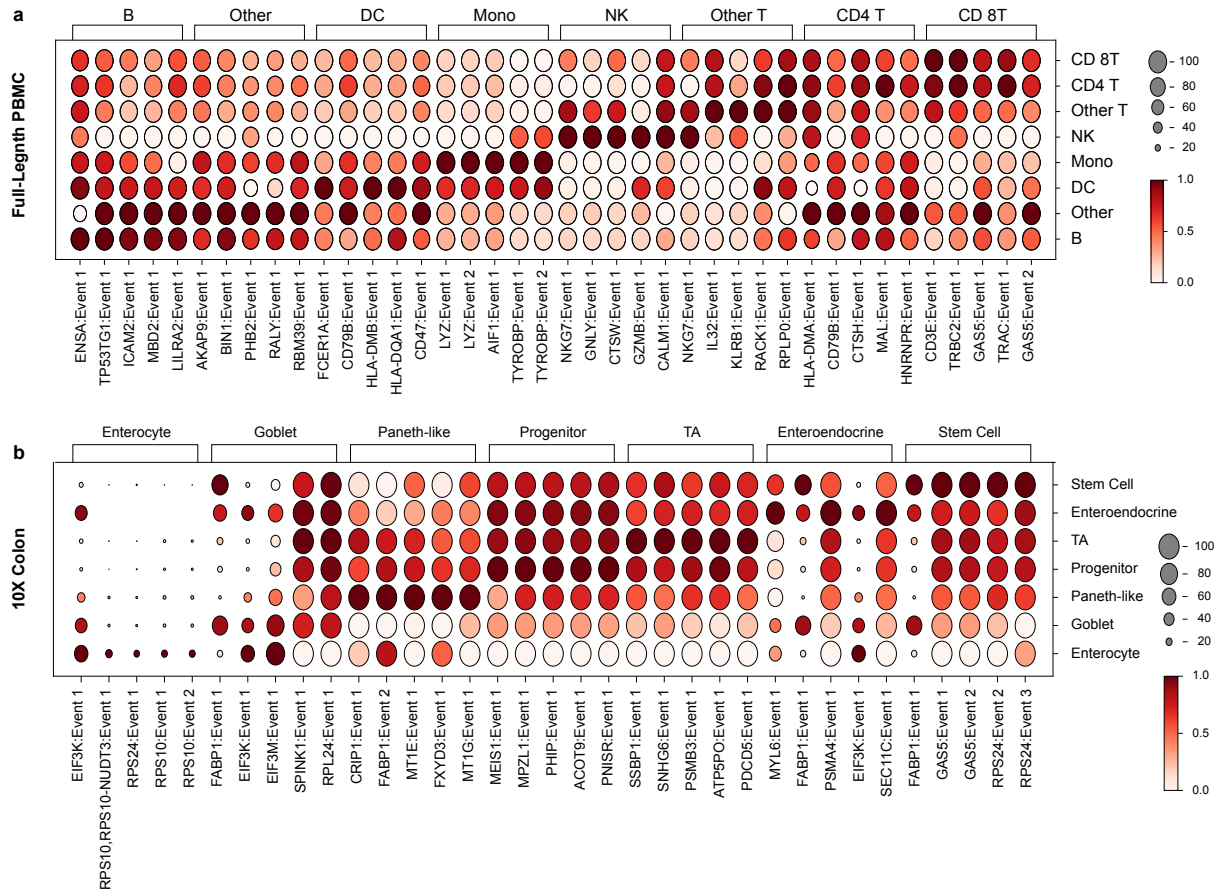


Fig. S19 Top 5 differentially spliced events across cell types using analysis on single cell without aggregation. The average PSI values per cell type are shown for the top 5 differentially spliced events identified using single cell RNA-seq data. **a**, full-length PBMC dataset **b**, tag-based 10X colon dataset. Detailed information for each event is provided in Supplementary [Table S3](#).

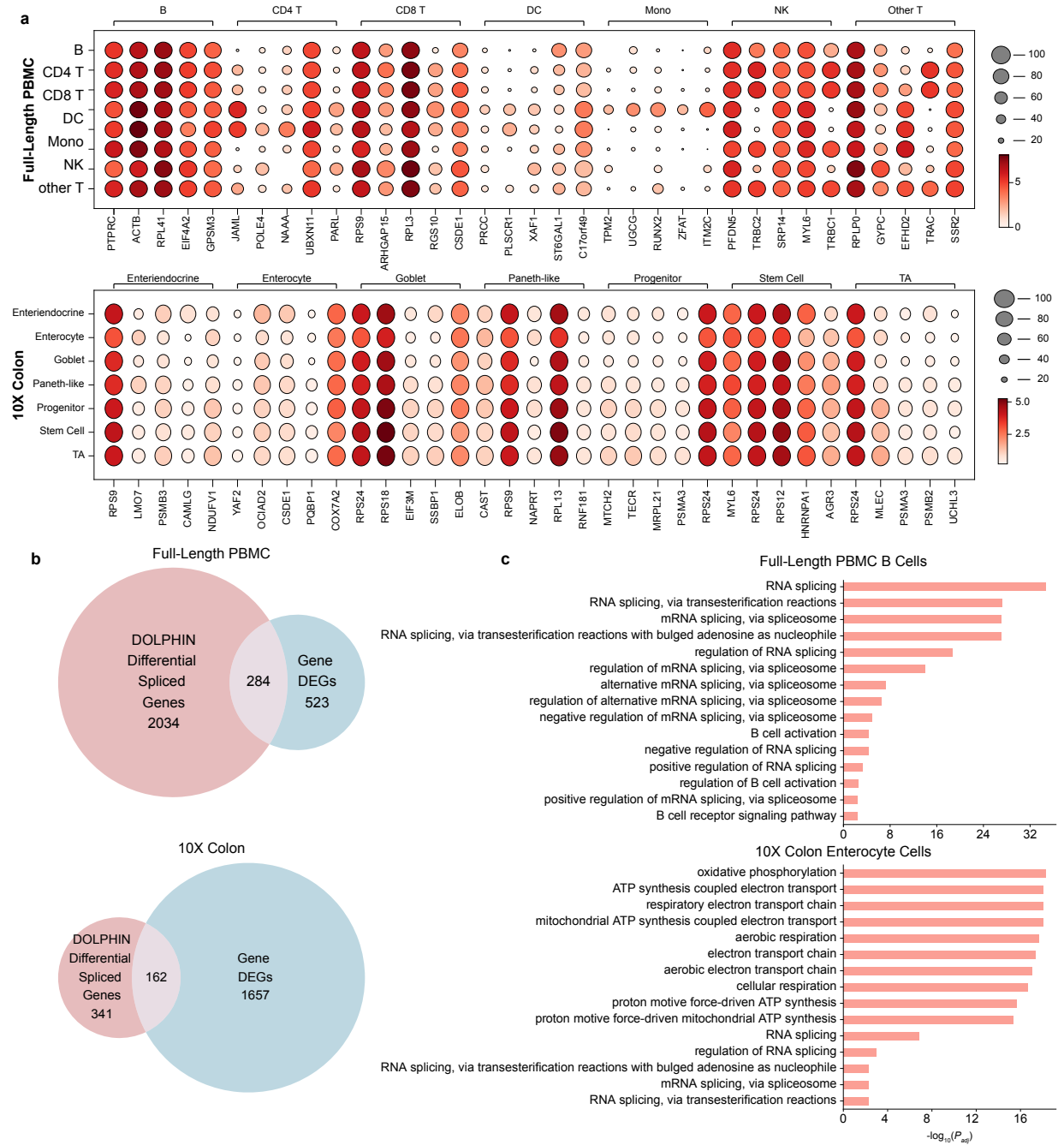


Fig. S20 Differentially spliced genes uniquely detected by DOLPHIN, which were not identified using conventional gene count tables. **a**, Differentially spliced genes identified by DOLPHIN that are not classified as DEGs across cell types. **b**, Venn diagram illustrating the overlap between differentially spliced genes detected by DOLPHIN and DEGs identified using the conventional gene count table. **c**, GOBP enrichment analysis based on differentially spliced genes, excluding those that overlap with DEGs. Adjusted P -values for each enrichment term were calculated using one-sided hypergeometric tests, followed by multiple testing correction using the Benjamini–Hochberg (BH) method. Source data are provided as a Source Data file.

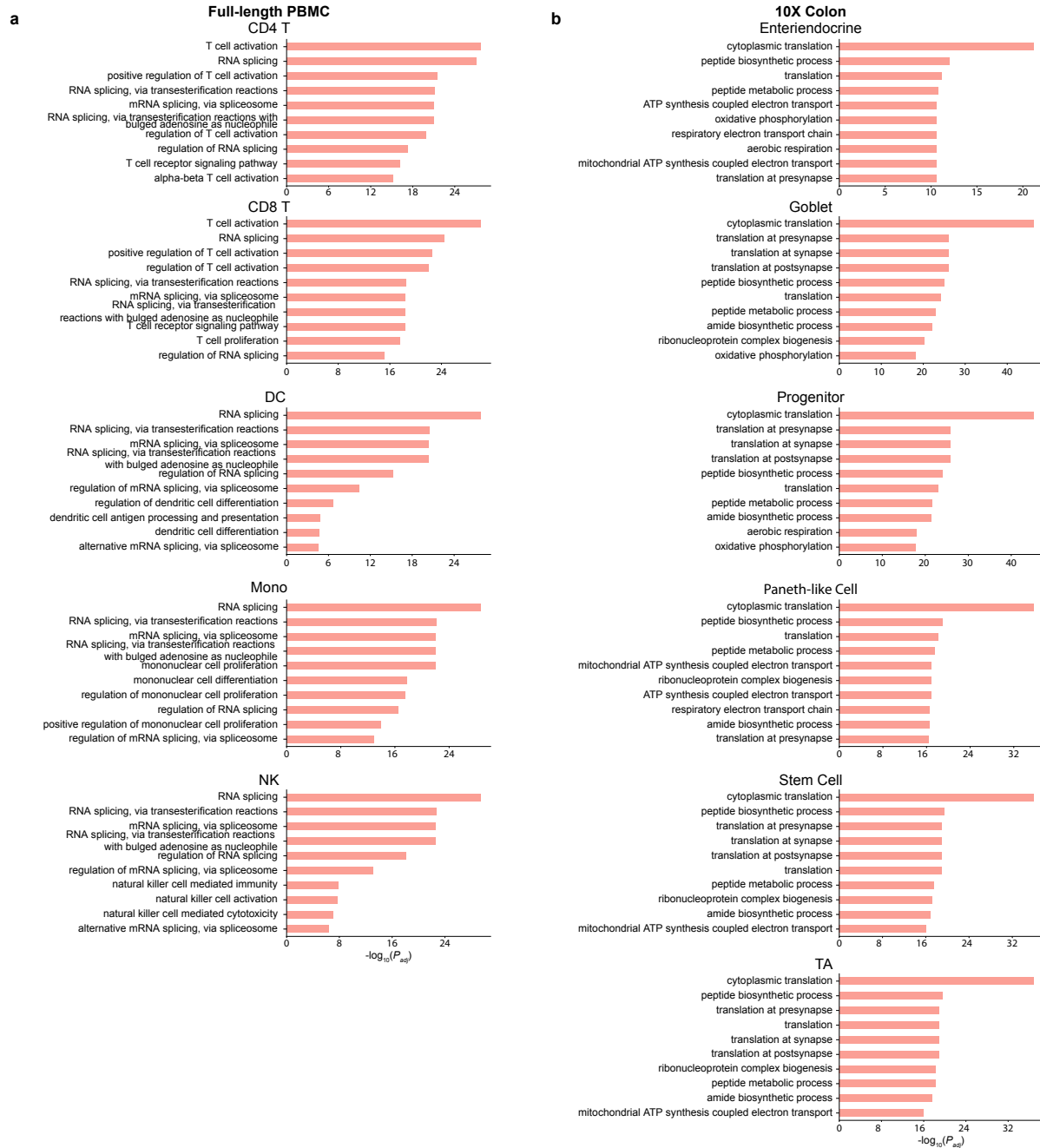


Fig. S21 GOBP enrichment results demonstrate biological processes associated with differentially spliced genes for additional cell types. GOBP terms are shown for differentially spliced genes across various cell types, with **a**, Full-length PBMC and **b**, 10X Colon datasets. Adjusted P -values for each enrichment term were calculated using one-sided hypergeometric tests, followed by multiple testing correction using the Benjamini–Hochberg (BH) method. Source data are provided as a Source Data file.

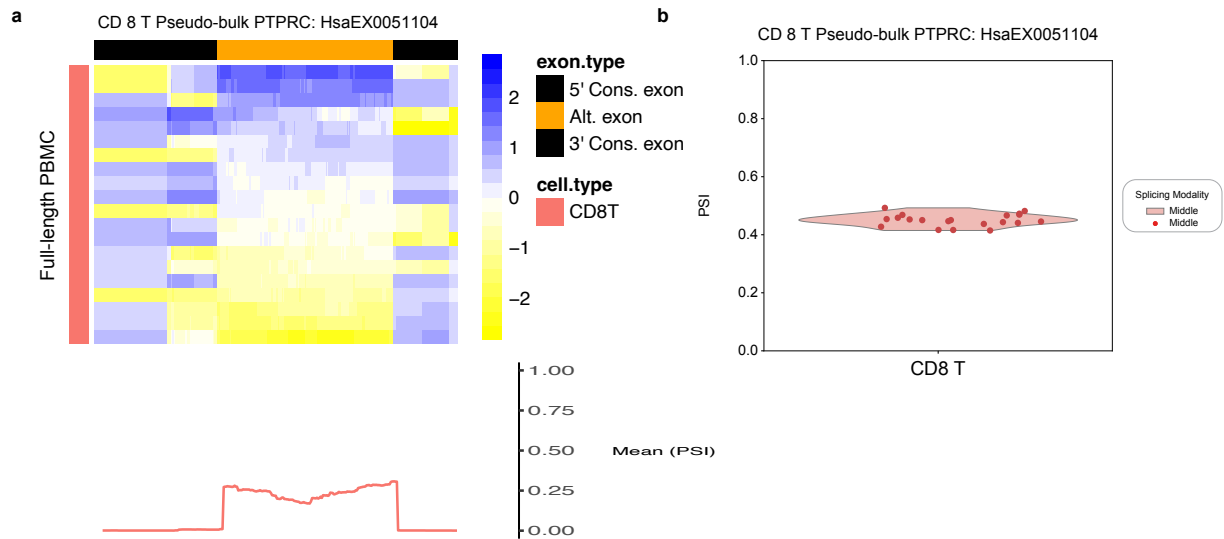


Fig. S22 In silico validation of the CD8 T alternative splicing event (*PTPRC*, HsaEX0051104) detected by DOLPHIN. **a**, VALERIE pseudo-bulk visualization of read coverage and junction usage across the *PTPRC* locus in CD8 T cells, showing clear support for the skipped exon event. **b**, Modality assignment of the same event in pseudo-bulk CD8 T cells, confirming a middle distribution of PSI values centered around 0.5.

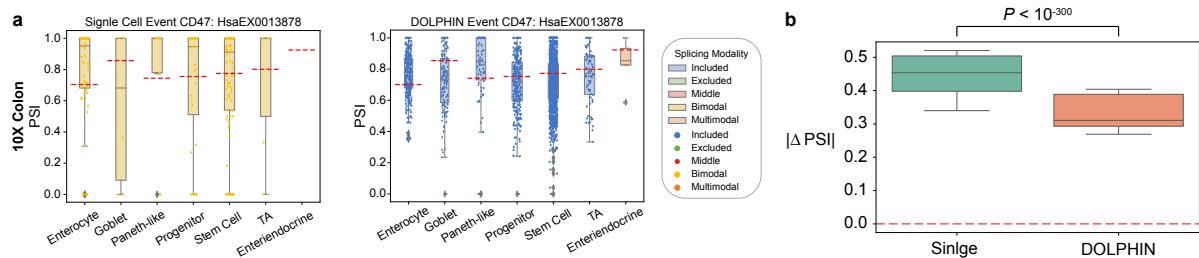


Fig. S23 Distribution of PSI for the CD45 exon-skipping event (HsaEX0013878) across cell types in the 10X colon dataset. **a**, Each dot represents the PSI value in a single cell. Red dashed lines indicate exon inclusion probabilities estimated from pseudo-bulk transcript abundance using kallisto, serving as a reference estimate of exon inclusion probability for each cell type. **b**, Absolute differences ($|\Delta\text{PSI}|$) between method-specific median PSI values and pseudo-bulk estimates across cell types. $|\Delta\text{PSI}|$ values were computed using a bootstrapping procedure in which 80% of all cells were randomly sampled in each iteration ($N = 1000$). Within each bootstrap replicate, cells were stratified by cell type, and the median PSI was calculated for each group. The absolute difference between this value and the corresponding pseudo-bulk estimate was then computed per cell type. Boxes indicate the interquartile range (IQR, 25th to 75th percentile), with the line inside each box representing the median. Whiskers extend to the most extreme data points within 1.5 times the IQR from the quartiles. Statistical significance was assessed using a one-sided Student's t-test. Source data are provided as a Source Data file.

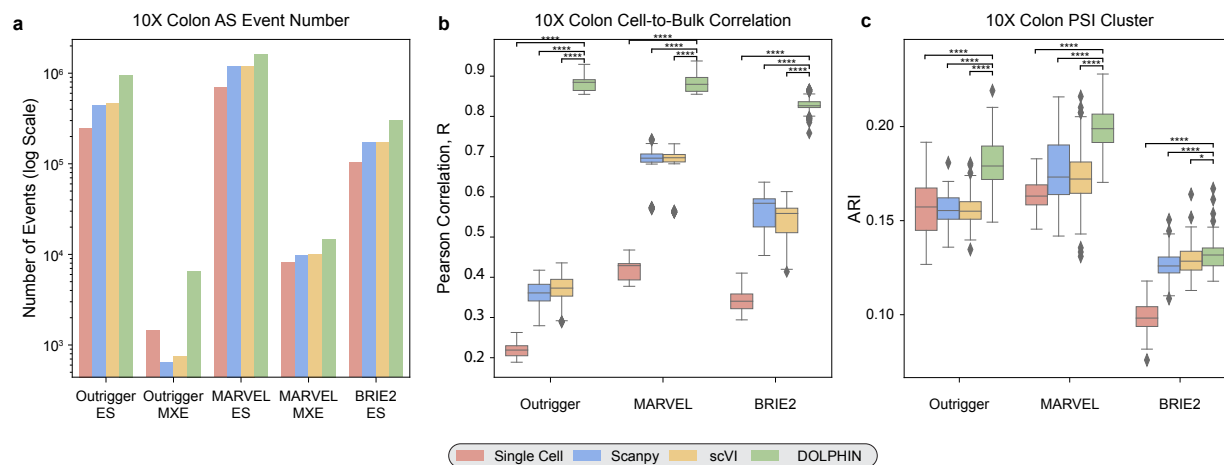


Fig. S24 Benchmarking DOLPHIN for Enhanced Sensitivity and Accuracy in Alternative Splicing Detection on the 10X Colon Dataset. DOLPHIN was compared against SCANPY, scVI, Outtrigger, MARVEL, and BRIE2. By leveraging exon-level information, DOLPHIN consistently outperformed these methods in terms of both sensitivity and accuracy. **a**, DOLPHIN identifies more AS events, including exon skipping (ES) and mutually exclusive exons (MXE), than all other methods. **b**, Higher Pearson correlations between single-cell and pseudo-bulk datasets indicate DOLPHIN's improved splicing quantification, based on $N = 70$ bootstrapping replicates (10 per cell type across 7 cell types, using different random seeds; technical replicates). **c**, Higher Adjusted Rand Index (ARI) scores for cell clustering based on Percent Spliced-In (PSI) values reflect DOLPHIN's ability to capture biologically meaningful splicing patterns, based on $N = 100$ bootstrapping replicates using different random seeds (technical replicates). Boxes indicate the interquartile range (IQR, 25th to 75th percentile), with the line inside each box representing the median. Whiskers extend to the most extreme data points within 1.5 times the IQR from the quartiles. P -values from one-sided Student's t -tests: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$. Exact P -values are provided in the source data. Source data are provided as a Source Data file.

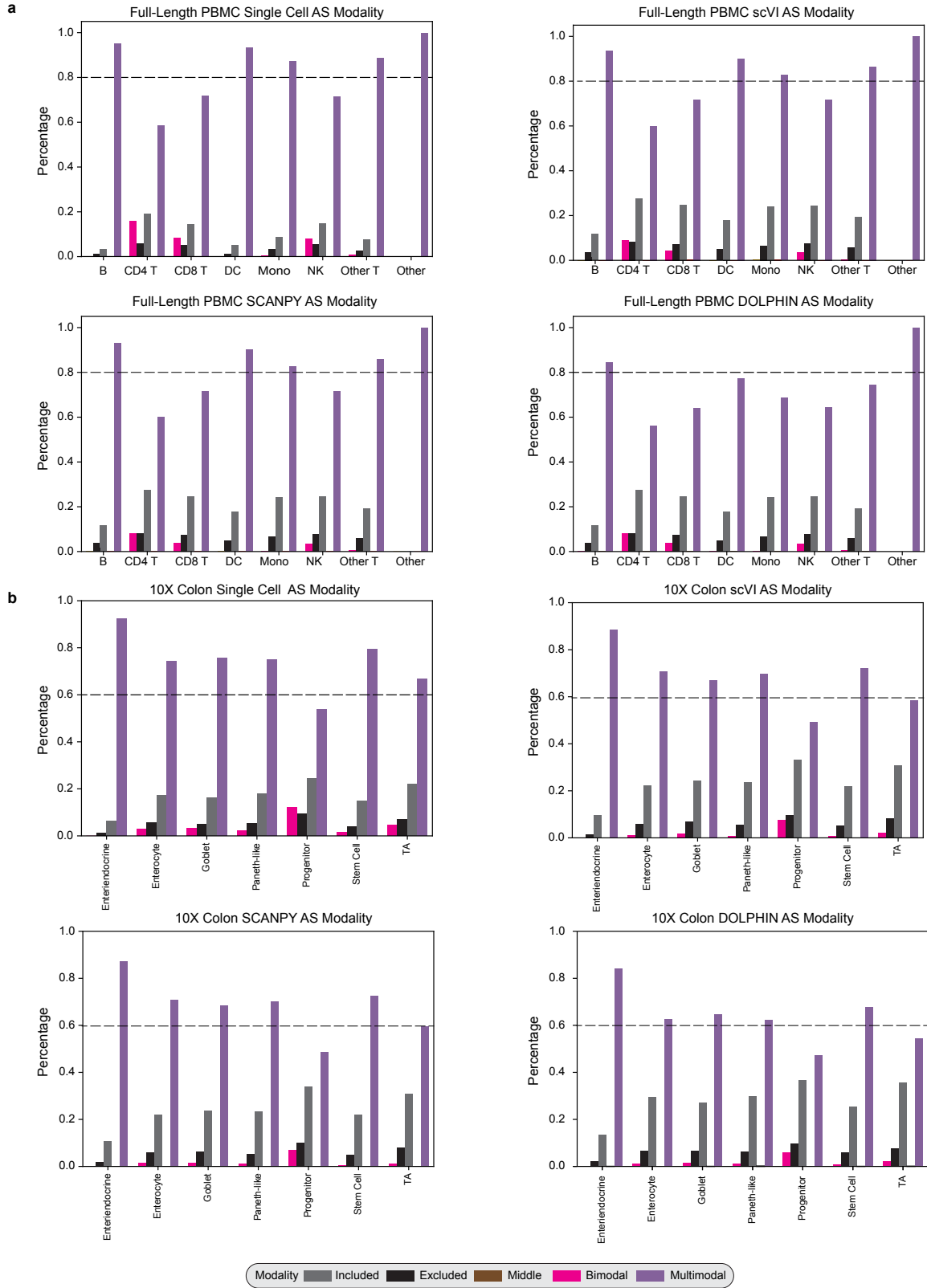


Fig. S25 Alternative splicing modality analysis across cell types. The percentage of each splicing modality within each cell type is shown for single-cell, SCANPY, scVI, and DOLPHIN analyses on **a**, Full-length PBMC and **b**, 10X Colon datasets, highlighting differences in splicing modality distributions across both cell types and analytical methods. Source data are provided as a Source Data file.

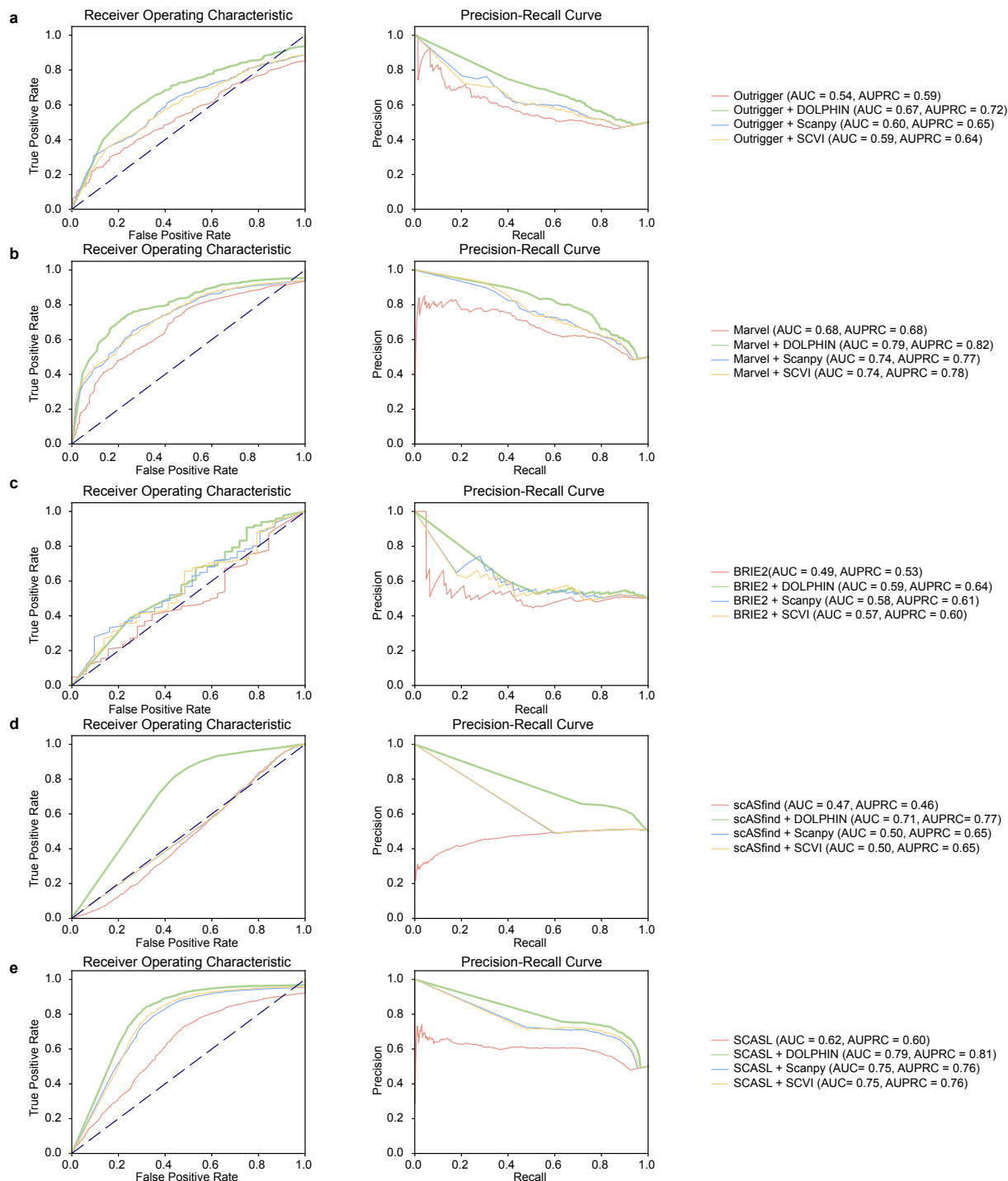


Fig. S26 Extended benchmarking of DOLPHIN for AS detection using simulated single-cell datasets with known ground truth. This figure complements Fig. 7f, g by providing a more extensive comparison across aggregation strategies. **a–e**, display Receiver Operating Characteristic (ROC) curves (left) and Precision-Recall (PR) curves (right) for five AS detection tools: **a**, Outtrigger; **b**, MARVEL; **c**, BRIE2; **d**, scASfind; **e**, SCASL. Each method was evaluated under four input settings: unaggregated single-cell data, SCANPY-based aggregation, scVI-based aggregation, and DOLPHIN-based exon-informed aggregation. Source data are provided as a Source Data file.

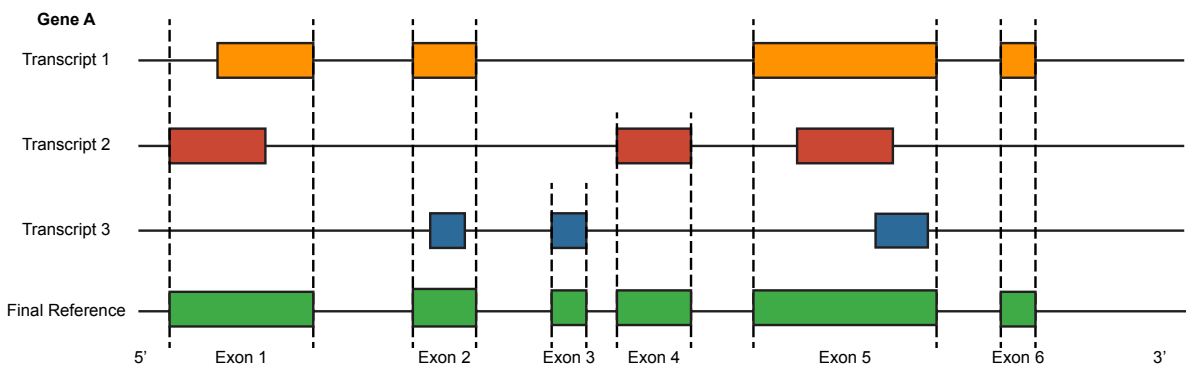


Fig. S27 Generation of the reference GTF file for exon and junction identification. The diagram illustrates the process of creating a reference GTF file designed to accurately identify exon counts and junction counts, addressing cases where multiple transcripts of the same gene contain overlapping exons.

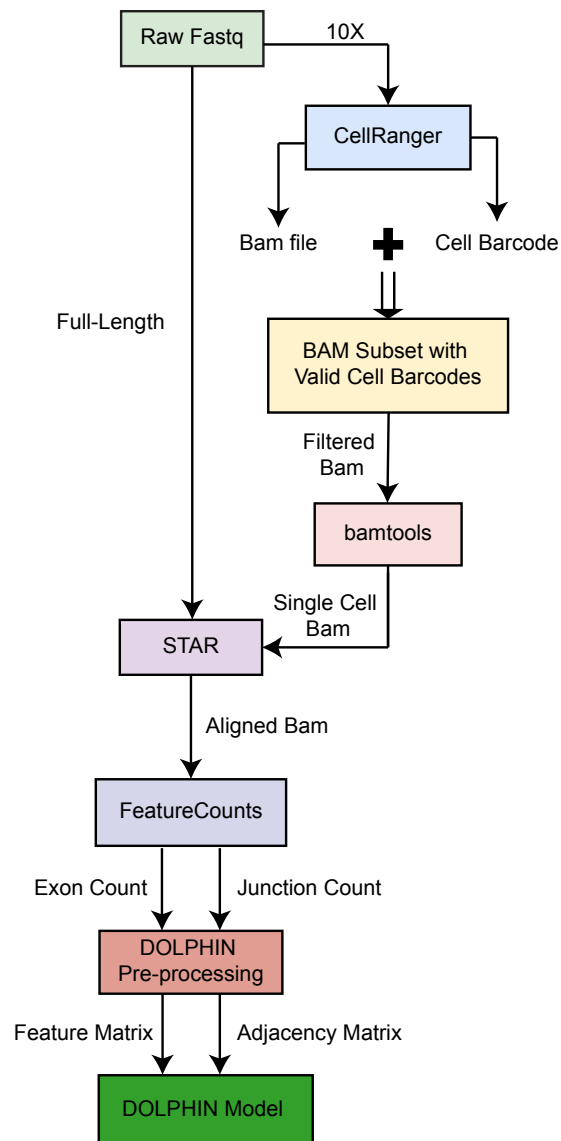


Fig. S28 Preprocessing pipeline from raw data to feature and adjacency matrices for full-length scRNA-seq and 10X Genomics data. The flowchart illustrates the preprocessing steps, beginning with raw data (Fastq files) and progressing through alignment, filtering, and counting, ultimately generating the feature matrix and adjacency matrix required for DOLPHIN analysis. Separate workflows are shown for full-length scRNA-seq and 10X Genomics data.

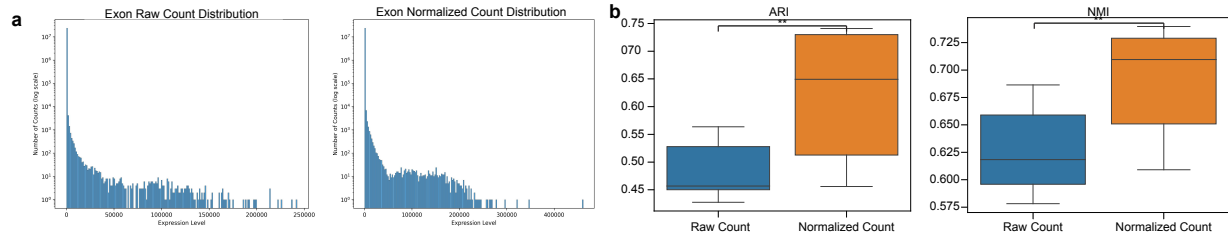


Fig. S29 Comparison of exon count distributions and model performance across different data normalization methods using the full-length PBMC dataset. **a**, Distribution of exon-level counts. Left panel: raw counts directly derived from sequencing reads. Right panel: counts after library-size normalization and rounding to the nearest integer to preserve discreteness for downstream modeling. **b**, Clustering evaluation metrics (ARI and NMI) obtained from the embeddings generated using the inputs from panel a, processed by the DOLPHIN model. Each score is based on $N = 10$ bootstrapping replicates using different random seeds (technical replicates). Boxes indicate the interquartile range (IQR, 25th to 75th percentile), with the line inside each box representing the median. Whiskers extend to the most extreme data points within 1.5 times the IQR from the quartiles. P -values from one-sided Student's t -tests: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$. Exact P -values are provided in the source data. Source data are provided as a Source Data file.

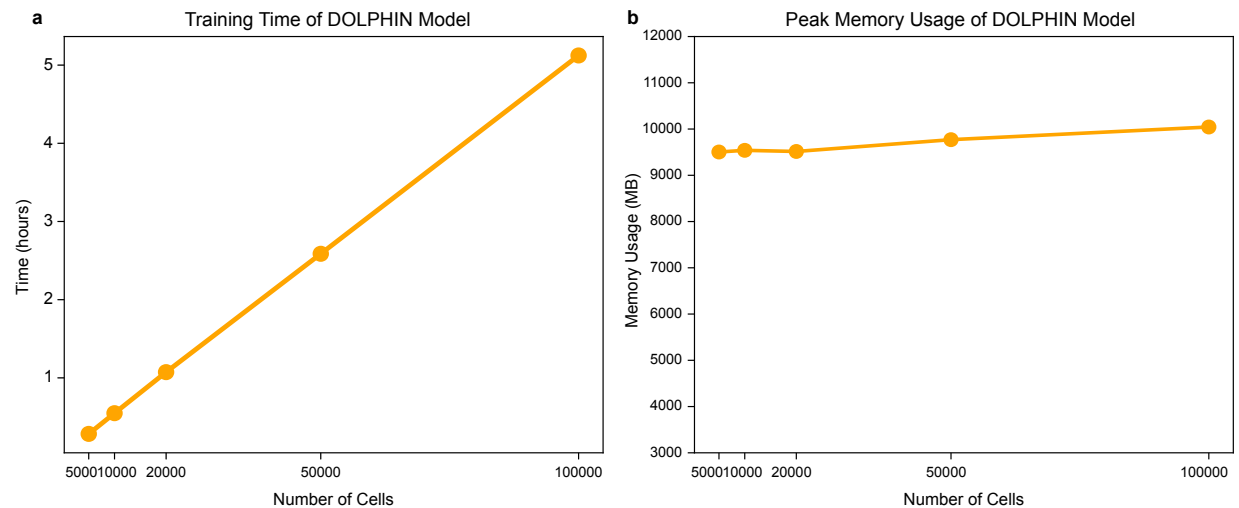


Fig. S30 Model training time and peak memory usage of the DOLPHIN model. **a**, Training time of the DOLPHIN model on Compute Canada's cloud environment using an NVIDIA A100 GPU with the default setting of 200 epochs. The x-axis represents the number of cells, while the y-axis indicates the training time in hours. **b**, Peak memory usage of the DOLPHIN model, with the x-axis showing the number of cells and the y-axis displaying peak memory usage in megabytes (MB).

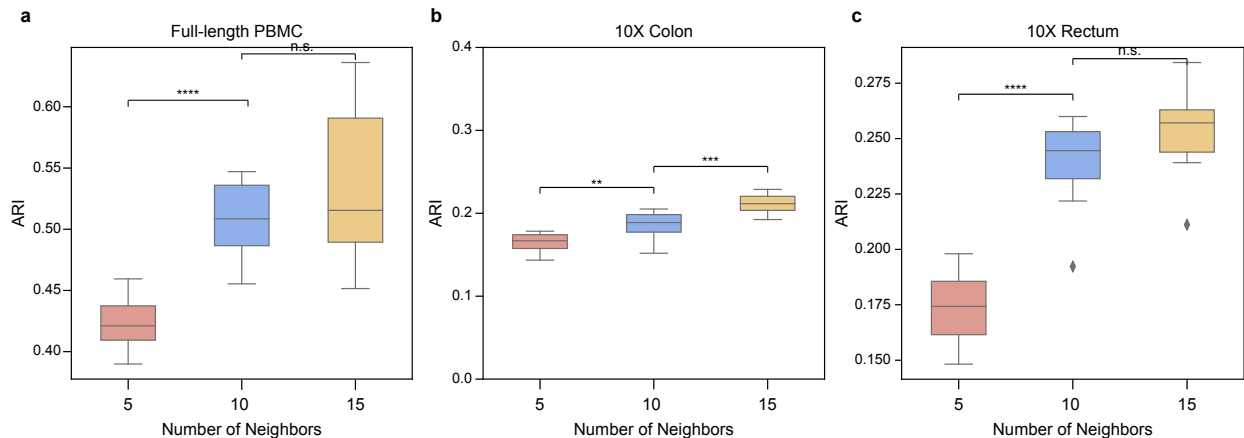


Fig. S31 Benchmarking neighbor selection for KNN-based cell aggregation in evaluating alternative splicing. This figure evaluates the effect of varying neighbor counts (K) in the KNN-based cell aggregation method on alternative splicing accuracy. After aggregating cells, alternative splicing is assessed by computing PSI values, followed by cell clustering. Clustering results are compared to ground truth cell types using ARI scores. **a**, Full-length PBMC dataset, **b**, 10X Colon dataset, and **c**, 10X Rectum dataset show ARI scores (y-axis) across different neighbor counts (x-axis), demonstrating the impact of neighbor selection on alternative splicing assessment across datasets. Each score is based on $N = 10$ bootstrapping replicates using different random seeds (technical replicates). Boxes indicate the interquartile range (IQR, 25th to 75th percentile), with the line inside each box representing the median. Whiskers extend to the most extreme data points within 1.5 times the IQR from the quartiles. P -values from one-sided Student's t -tests: * $P < 0.05$, ** $P < 0.01$, *** $P < 0.001$, **** $P < 0.0001$. Exact P -values are provided in the source data. Source data are provided as a Source Data file.

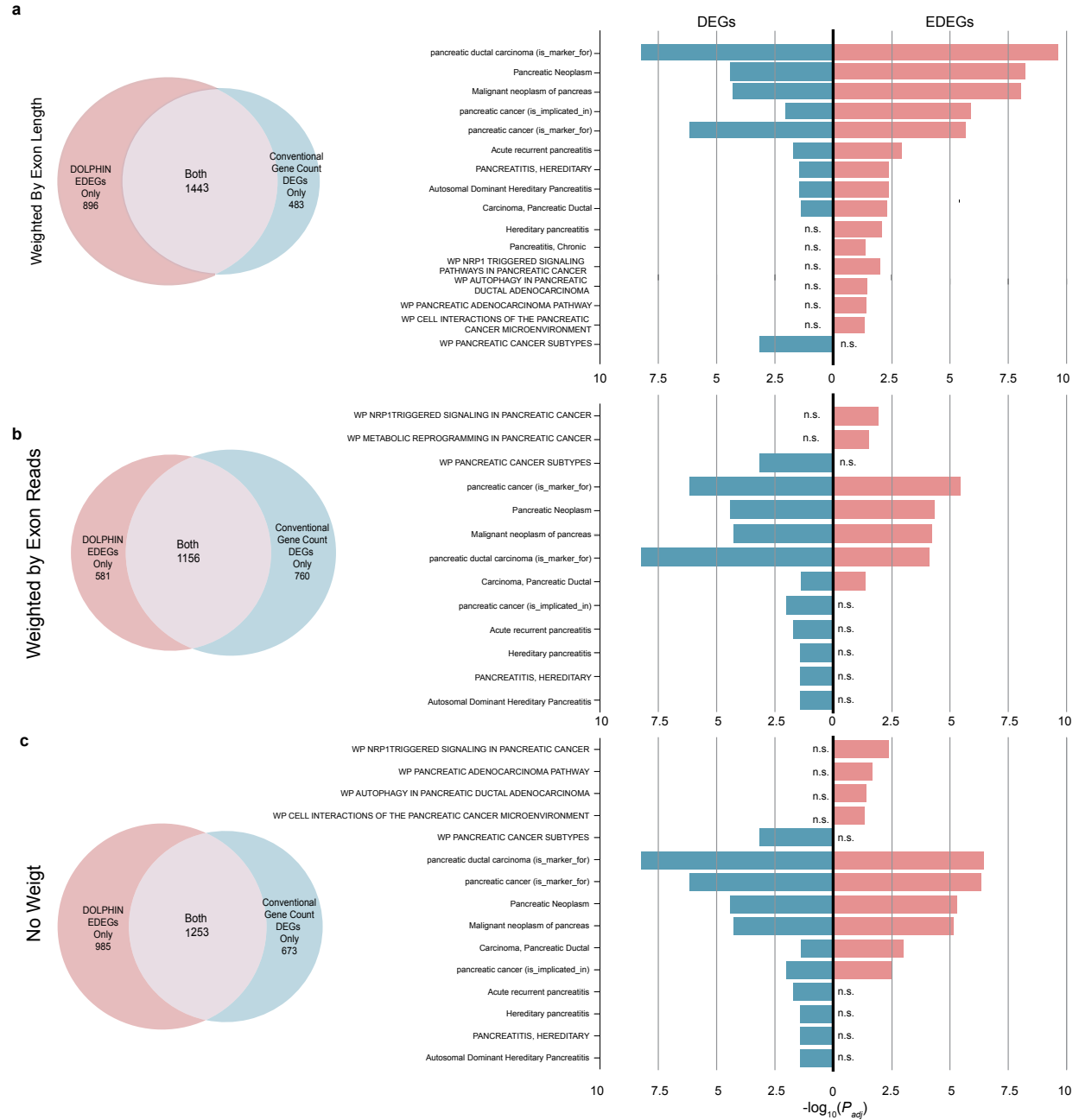


Fig. S32 Comparison of exon-level P -value aggregation weighting strategies for identifying DOLPHIN-specific EDEGs. Three different weighting schemes were applied when aggregating exon-level P -values using Stouffer's method: **a**, weighted by exon length (the default strategy used in DOLPHIN), **b**, weighted by exon-level read counts, **c**, no weighting (equal weight for all exons). For each strategy, the left panel shows the overlap between EDEGs (identified by DOLPHIN) and DEGs (identified by conventional gene counts) using a Venn diagram, while the right panel displays pathway enrichment results for both EDEGs and DEGs. Adjusted P -values for each enrichment term were calculated using one-sided hypergeometric tests, followed by multiple testing correction using the Benjamini–Hochberg (BH) method. Source data are provided as a Source Data file.

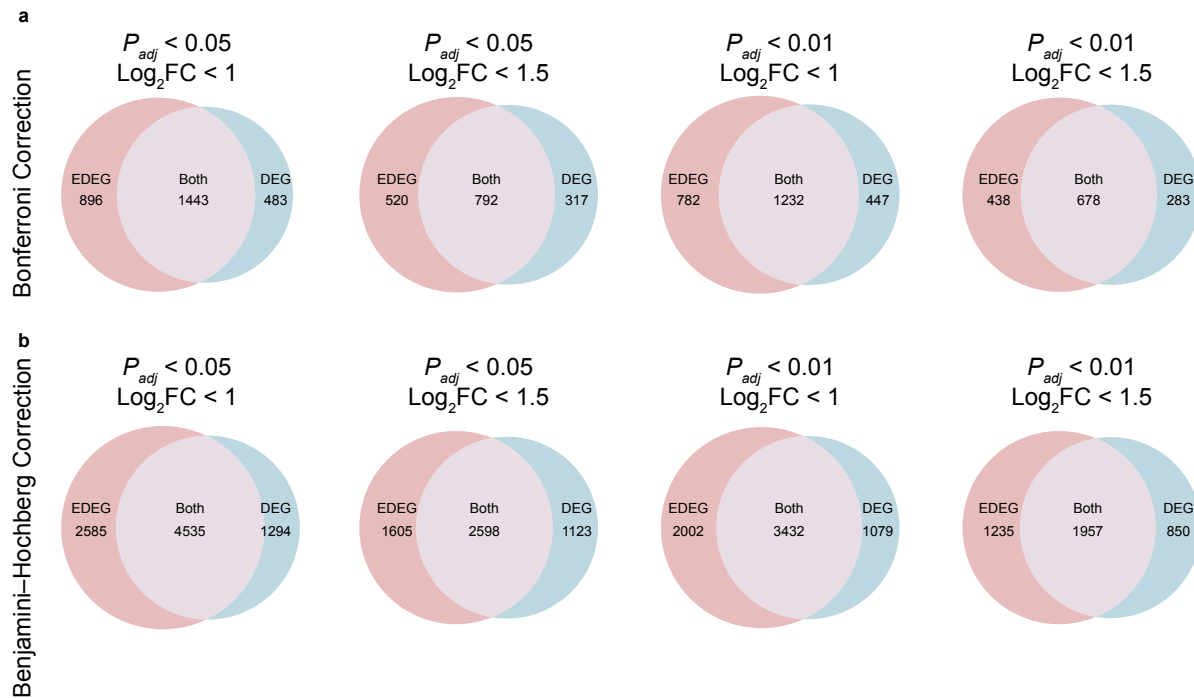


Fig. S33 Comparison of EDEGs and DEGs under different multiple testing correction strategies and statistical thresholds. Each panel shows the overlap between EDEGs and DEGs under varying combinations of adjusted P -values and $\log_2$ fold-change thresholds, as indicated in the panel headers. **a**, Venn diagrams using Bonferroni correction. **b**, Venn diagrams using Benjamini-Hochberg (FDR) correction.

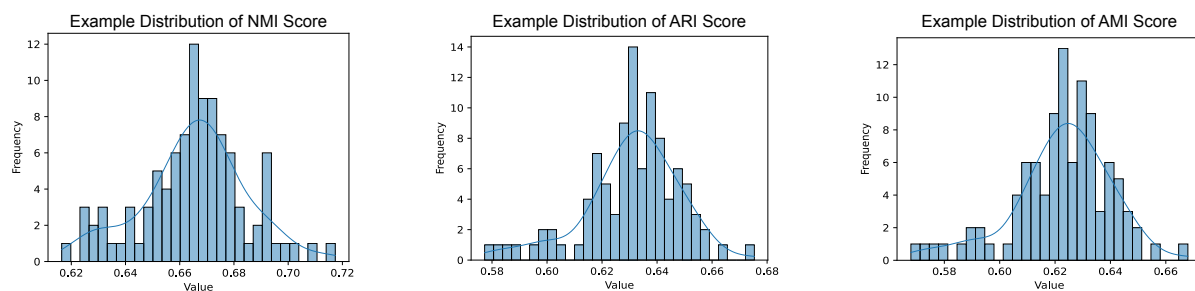


Fig. S34 Distributions of benchmarking scores. Examples of benchmarking scores show approximately Gaussian distributions, supporting the use of one-sided Student's t -tests in significance analyses presented in benchmarking results.

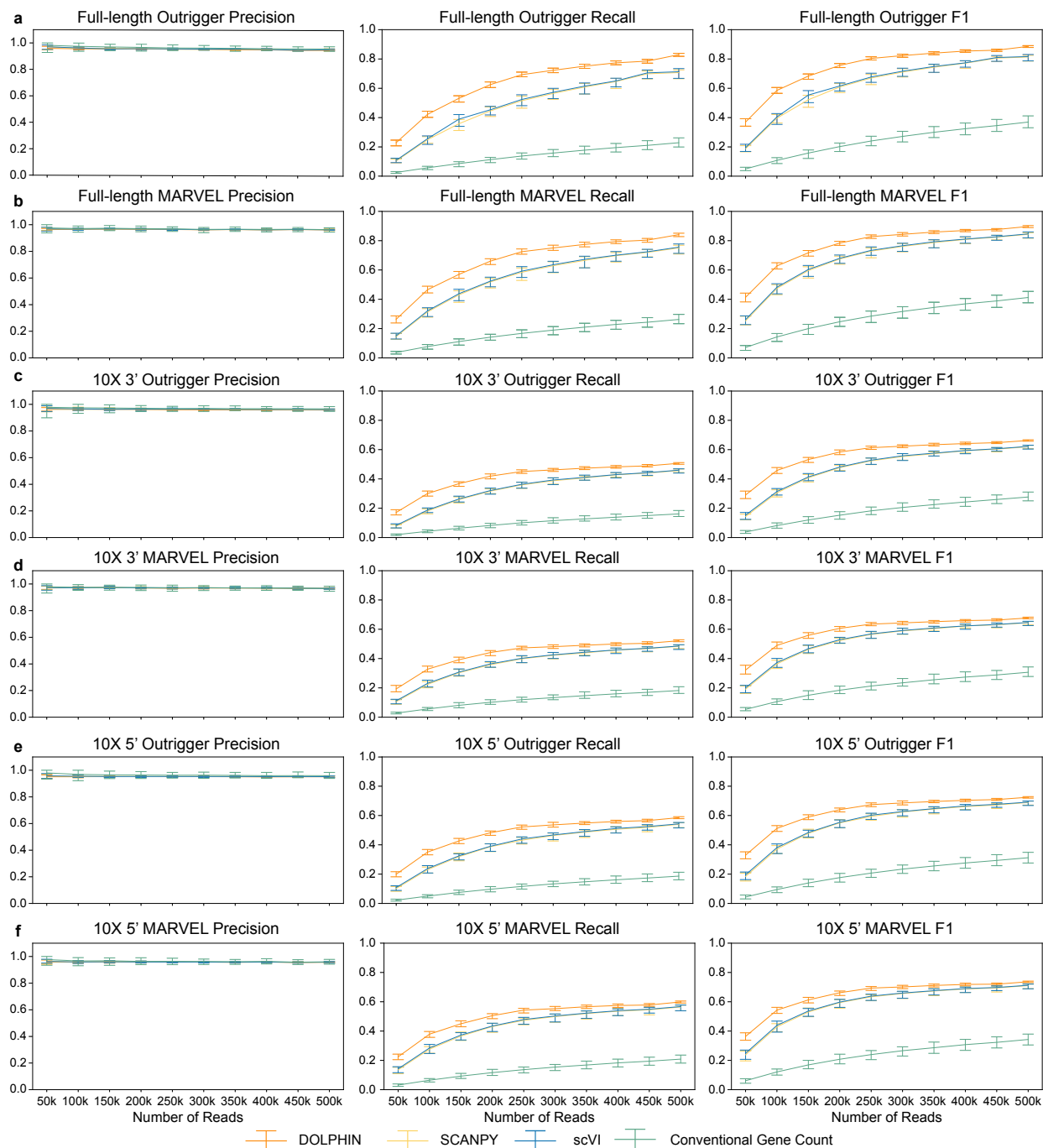


Fig. S35 Performance comparison of exon skipping detection under varying read depths and sequencing technologies in simulated datasets. a–f, Precision, recall, and F1 scores are plotted against increasing read depths (50k to 500k reads per cell) for full-length (a, b), 3'-biased (c,d), and 5'-biased (e,f) simulated single-cell RNA-seq data. Two AS detection tools Outtrigger (a, c, e) and MARVEL (b, d, f) are evaluated in combination with four aggregation strategies: DOLPHIN, no aggregation, SCANPY-based aggregation, and scVI-based aggregation. Source data are provided as a Source Data file.

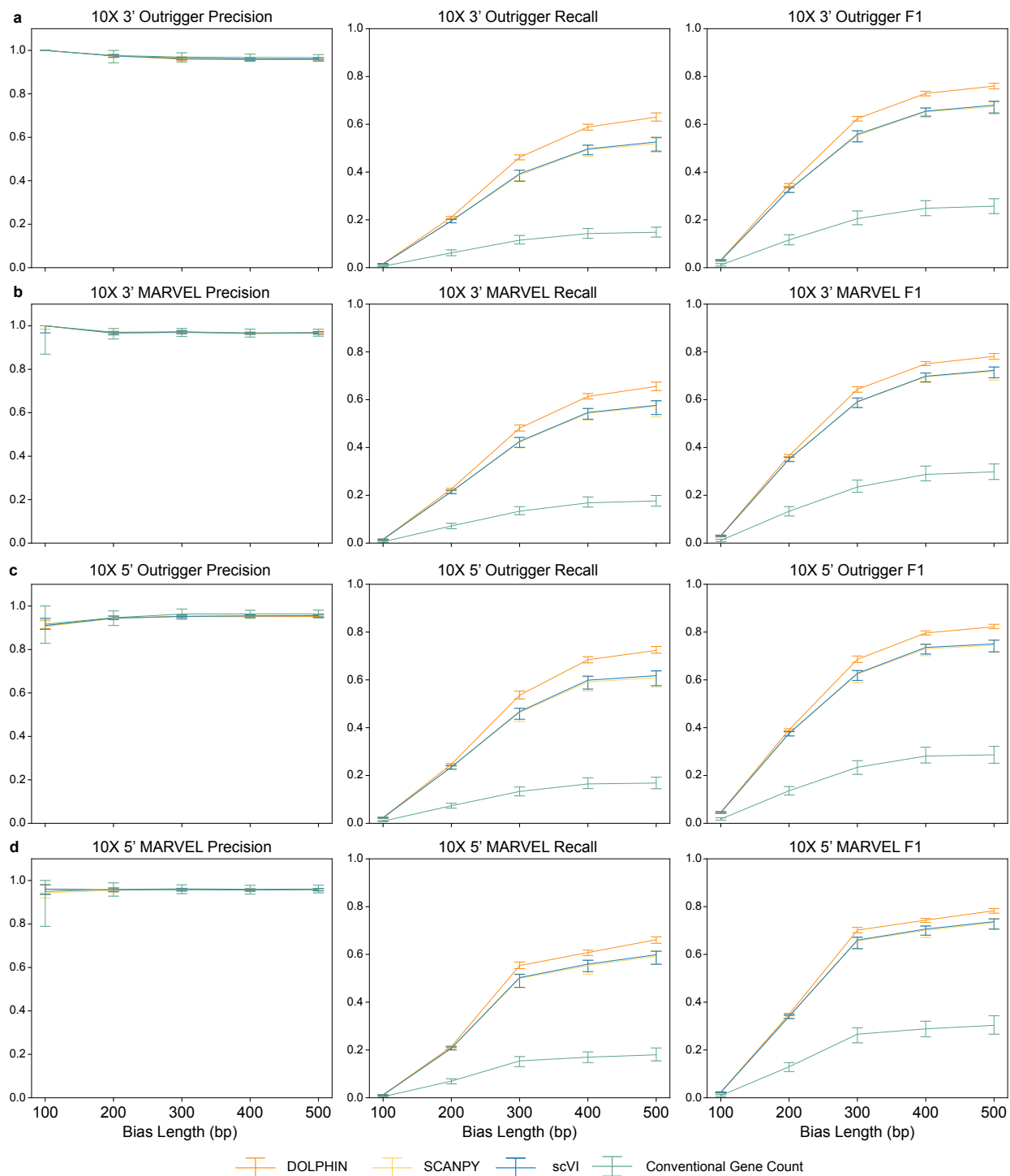


Fig. S36 Performance comparison of exon skipping detection under varying tag bias in simulated datasets. **a-d**, show precision, recall, and F1 scores plotted against increasing tag bias length (100 bp to 500 bp) for 3'-biased (**a**, **b**) and 5'-biased (**c**, **d**) simulated single-cell RNA-seq data. Two alternative splicing detection tools, Outtrigger (**a**, **c**) and MARVEL (**b**, **d**), were evaluated in combination with four aggregation strategies: no aggregation, SCANPY-based aggregation, scVI-based aggregation and DOLPHIN. Source data are provided as a Source Data file.

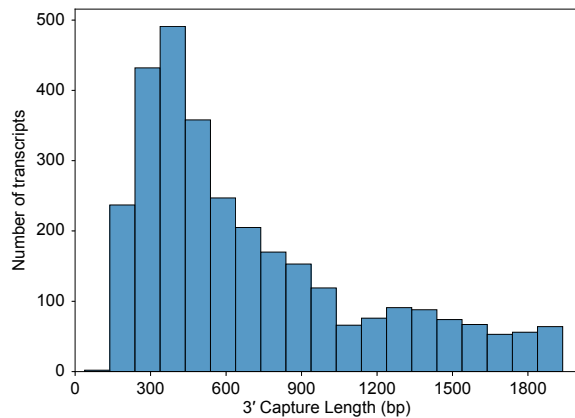


Fig. S37 Distribution of 3' capture lengths across transcripts in 10X colon dataset. The x-axis denotes the 3' capture length (in base pairs), and the y-axis indicates the number of transcripts with the corresponding maximum coverage length.

Supplementary Tables

Table S1. Top 5 Differential Alternative Splicing Events Identified by DOLPHIN in Full-Length PBMC

Event	Event Information
PTPRC: Event 1	isoform1=junction:1:198699705-198703297:+ isoform2=junction:1:198699705-198702386:+@exon:1:198702387-198702530:+@junction:1:198702531-198703297:+
PTPRC: Event 2	isoform1=junction:1:198692374-198699563:+ isoform2=junction:1:198692374-198696711:+@exon:1:198696712-198696909:+@junction:1:198696910-198699563:+
S100A4: Event 1	isoform1=junction:6:32642254-32642951:+ isoform2=junction:6:32642254-32642609:+@exon:6:32642610-32642784:+@junction:6:32642785-32642951:+
S100A4: Event 2	isoform1=junction:1:153544810-153545752:- isoform2=junction:1:153545519-153545752:-@exon:1:153545470-153545518:-@junction:1:153544810-153545469:-
PRCC: Event 1	isoform1=junction:1:153544810-153545752:- isoform2=junction:1:153545519-153545752:-@novel exon:1:153545480-153545518:-@junction:1:153544810-153545479:-
HLA-DQA1: Event 1	isoform1=junction:1:156787175-156791696:+ isoform2=junction:1:156787175-156791066:+@exon:1:156791067-156791162:+@junction:1:156791163-156791696:+
PLSCR1: Event 1	isoform1=junction:3:146517168-146525604:- isoform2=junction:3:146521706-146525604:-@exon:3:146521544-146521705:-@junction:3:146517168-146521543:-
XAF1: Event 1	isoform1=junction:17:6760602-6762154:+ isoform2=junction:17:6760602-6761885:+@exon:17:6761886-6762037:+@junction:17:6762038-6762154:+
ST6GAL1: Event 1	isoform1=junction:3:187051347-187072848:+ isoform2=junction:3:187051347-187064519:+@exon:3:187064520-187064616:+@junction:3:187064617-187072848:+
C17orf49: Event 1	isoform1=junction:17:7016686-7017256:+ isoform2=junction:17:7016686-7016949:+@exon:17:7016950-7017014:+@junction:17:7017015-7017256:+
TMEM176B: Event 1	isoform1=junction:7:150793601-150796365:- isoform2=junction:7:150794072-150796365:-@exon:7:150793961-150794071:-@junction:7:150793601-150793960:-
CPVL: Event 1	isoform1=junction:7:29096218-29120892:- isoform2=junction:7:29112823-29120892:-@exon:7:29112704-29112822:-@junction:7:29096218-29112703:-
CPVL: Event 2	isoform1=junction:7:29030760-29066022:- isoform2=junction:7:29064235-29066022:-@exon:7:29064061-29064234:-@junction:7:29030760-29064060:-
SLC11A1: Event 1	isoform1=junction:2:218383103-218385146:+ isoform2=junction:2:218383103-218384242:+@exon:2:218384243-218384365:+@junction:2:218384366-218385146:+
LYZ: Event 1	isoform1=junction:12:69350273-69353152:+ isoform2=junction:12:69350273-69352219:+@exon:12:69352220-69352298:+@junction:12:69352299-69353152:+
TRDC: Event 1	isoform1=junction:14:22463211-22464203:+ isoform2=junction:14:22463211-22463773:+@exon:14:22463774-22463839:+@junction:14:22463840-22464203:+
FCGR3A: Event 1	isoform1=junction:1:161543200-161548420:- isoform2=junction:1:161544959-161548420:-@exon:1:161544701-161544958:-@junction:1:161543200-161544700:-
IL2RB: Event 1	isoform1=junction:22:37139223-37143520:- isoform2=junction:22:37142513-37143520:-@exon:22:37142434-37142512:-@junction:22:37139223-37142433:-
GZMB: Event 1	isoform1=junction:14:24632119-24632914:- isoform2=junction:14:24632460-24632914:-@exon:14:24632324-24632459:-@junction:14:24632119-24632323:-
MATK: Event 1	isoform1=junction:19:3778423-3778991:- isoform2=junction:19:3778596-3778991:-@exon:19:3778509-3778595:-@junction:19:3778423-3778508:-
CCL5: Event 1	isoform1=junction:17:35872465-35880229:- isoform2=junction:17:35878640-35880229:-@exon:17:35878528-35878639:-@junction:17:35872465-35878527:-
NKG7: Event 1	isoform1=junction:19:51372075-51372378:- isoform2=junction:19:51372308-51372378:-@exon:19:51372161-51372307:-@junction:19:51372075-51372160:-
GZMA: Event 1	isoform1=junction:5:55102753-55107793:+ isoform2=junction:5:55102753-55105473:+@exon:5:55105474-55105618:+@junction:5:55105619-55107793:+
CTSW: Event 1	isoform1=junction:11:65882527-65882778:+ isoform2=junction:11:65882527-65882608:+@exon:11:65882609-65882689:+@junction:11:65882690-65882778:+
NKG7: Event 2	isoform1=junction:19:51371836-51372160:- isoform2=junction:19:51372075-51372160:-@exon:19:51371940-51372074:-@junction:19:51371836-51371939:-
PRDX1: Event 1	isoform1=junction:1:45515808-45518937:- isoform2=junction:1:45518829-45518937:-@novel exon:1:45518770-45518828:-@junction:1:45515808-45518769:-
SAT1: Event 1	isoform1=junction:X:23783884-23785327:+ isoform2=junction:X:23783884-23784293:+@exon:X:23784294-23784403:+@junction:X:23784404-23785327:+
LST1: Event 1	isoform1=junction:6:31587319-31588517:+ isoform2=junction:6:31587319-31587943:+@exon:6:31587944-31587966:+@junction:6:31587967-31588517:+
CARD16: Event 1	isoform1=junction:11:105044659-105045290:- isoform2=junction:11:105044932-105045290:-@novel exon:11:105044870-105044931:-@junction:11:105044659-105044869:-
LST1: Event 2	isoform1=junction:6:31587319-31588517:+ isoform2=junction:6:31587319-31587640:+@exon:6:31587641-31587733:+@junction:6:31587734-31588517:+
SERPINA1: Event 1	isoform1=junction:14:94383242-94390456:- isoform2=junction:14:94388664-94390456:-@exon:14:94388560-94388663:-@junction:14:94383242-94388559:-
LY86: Event 1	isoform1=junction:6:6649678-6654543:+ isoform2=junction:6:6649678-6652131:+@novel exon:6:6652132-6652152:+@junction:6:6652153-6654543:+
MS4A6A: Event 1	isoform1=junction:11:60175612-60178259:- isoform2=junction:11:60176000-60178259:-@novel exon:11:60175964-60175999:-@junction:11:60175612-60175963:-
CD8B: Event 1	isoform1=junction:2:86844959-86852996:- isoform2=junction:2:86846774-86852996:-@exon:2:86846684-86846773:-@junction:2:86844959-86846683:-
CD3D: Event 1	isoform1=junction:11:118339495-118340374:- isoform2=junction:11:118339907-118340374:-@exon:11:118339775-118339906:-@junction:11:118339495-118339774:-
CD3E: Event 1	isoform1=junction:11:118312171-118313706:+ isoform2=junction:11:118312171-118312617:+@exon:11:118312618-118312866:+@junction:11:118312867-118313706:+
CD3D: Event 2	isoform1=junction:11:118339907-118342552:- isoform2=junction:11:118340594-118342552:-@exon:11:118340375-118340593:-@junction:11:118339907-118340374:-
IL7R: Event 1	isoform1=junction:5:35860991-35871055:+ isoform2=junction:5:35860991-35867305:+@exon:5:35867306-35867463:+@junction:5:35867464-35871055:+

Table S2. Top 5 Differential Alternative Splicing Events Identified by DOLPHIN in 10X Colon

Event	Event Information
RPS9: Event 1	isoform1=junction:19:54206463-54207397:+ isoform2=junction:19:54206463-54206552:+@exon:19:54206553-54206724:+@junction:19:54206725-54207397:+
LMO7: Event 1	isoform1=junction:13:75804542-75817160:+ isoform2=junction:13:75804542-75809153:+@exon:13:75809154-75809183:+@junction:13:75809184-75817160:+
LMO7: Event 2	isoform1=junction:13:75804542-75817160:+ isoform2=junction:13:75804542-75805478:+@exon:13:75805479-75805760:+@junction:13:75805761-75817160:+
PSMB3: Event 1	isoform1=junction:17:38755991-38764118:+ isoform2=junction:17:38755991-38760430:+@exon:17:38760431-38760608:+@junction:17:38760609-38764118:+
CAMLG: Event 1	isoform1=junction:5:134741524-134750758:+ isoform2=junction:5:134741524-134743986:+@exon:5:134743987-134744052:+@junction:5:134744053-134750758:+
MRPL43: Event 1	isoform1=junction:10:100983818-100986748:- isoform2=junction:10:100984075-100986748:-@exon:10:100984034-100984074:-@junction:10:100983818-100984033:-
RPS13: Event 1	isoform1=junction:11:17074467-17075453:- isoform2=junction:11:17075164-17075453:-@exon:11:17075097-17075163:-@junction:11:17074467-17075096:-
RPL27A: Event 1	isoform1=junction:11:8684082-8685677:+ isoform2=junction:11:8684082-8684717:+@exon:11:8684718-8684892:+@junction:11:8684893-8685677:+
YAF2: Event 1	isoform1=junction:12:422161766-42237598:- isoform2=junction:12:42210620-42237598:-@exon:12:42210548-42210619:-@junction:12:42161766-42210547:-
OCIAD2: Event 1	isoform1=junction:4:48897858-48904483:- isoform2=junction:4:48899826-48904483:-@exon:4:48899829-48899925:-@junction:4:48897858-48899828:-
RPS24: Event 1	isoform1=junction:10:78037305-78040614:+ isoform2=junction:10:78037305-78040203:+@exon:10:78040204-78040225:+@junction:10:78040226-78040614:+
RPS18: Event 1	isoform1=junction:6:33276067-33276390:+ isoform2=junction:6:33276067-33276175:+@exon:6:33276176-33276267:+@junction:6:33276268-33276390:+
CYBA: Event 1	isoform1=junction:16:88646198-88646754:- isoform2=junction:16:88646604-88646754:-@exon:16:88646520-88646603:-@junction:16:88646198-88646519:-
EIF3M: Event 1	isoform1=junction:11:32601823-32602278:+ isoform2=junction:11:32601823-32602078:+@exon:11:32602079-32602114:+@junction:11:32602115-32602278:+
SSBP1: Event 1	isoform1=junction:7:141745585-141750310:+ isoform2=junction:7:141745585-141745896:+@novel exon:7:141745897-141745948:+@junction:7:141745949-141750310:+
ARPC2: Event 1	isoform1=junction:2:218239485-218249363:+ isoform2=junction:2:218239485-21824519:+@exon:2:218245420-218245546:+@junction:2:218245547-218249363:+
SLPI: Event 1	isoform1=junction:20:45252420-45253574:- isoform2=junction:20:45253152-45253574:-@exon:20:45253002-45253151:-@junction:20:45252420-45253001:-
FXD3: Event 1	isoform1=junction:19:35121246-35123270:+ isoform2=junction:19:35121246-35122764:+@exon:19:35122765-35122839:+@junction:19:35122840-35123270:+
CCL15: Event 1	isoform1=junction:17:35997861-35998865:- isoform2=junction:17:35998392-35998865:-@exon:17:35998280-35998391:-@junction:17:35997861-35998279:-
CAST: Event 1	isoform1=junction:5:96722699-96729152:+ isoform2=junction:5:96722699-96727488:+@exon:5:96727489-96727530:+@junction:5:96727531-96729152:+
MYL6: Event 1	isoform1=junction:12:56160321-56161386:+ isoform2=junction:12:56160321-56160625:+@exon:12:56160626-56160670:+@junction:12:56160671-56161386:+
RPS24: Event 2	isoform1=junction:10:78037305-78040203:+ isoform2=junction:10:78037305-78037438:+@exon:10:78037439-78037441:+@junction:10:78037442-78040203:+
RPS24: Event 3	isoform1=junction:10:78037305-78040614:+ isoform2=junction:10:78037305-78037438:+@exon:10:78037439-78040225:+@junction:10:78040226-78040614:+
EPB41L4A-AS1: Event1	isoform1=junction:5:112161296-112162150:+ isoform2=junction:5:112161296-112161702:+@exon:5:112161703-112161775:+@junction:5:112161776-112162150:+
RPS12: Event 1	isoform1=junction:6:132814783-132816460:+ isoform2=junction:6:132814783-132814971:+@exon:6:132814972-132815224:+@junction:6:132815225-132816460:+
MTCH2: Event 1	isoform1=junction:11:47618920-47625673:- isoform2=junction:11:47622777-47625673:-@exon:11:47622701-47622776:-@junction:11:47618920-47622700:-
TECR: Event 1	isoform1=junction:19:14565291-14565743:+ isoform2=junction:19:14565291-14565617:+@exon:19:14565618-14565663:+@junction:19:14565664-14565743:+
MRPL21: Event 1	isoform1=junction:11:68892994-68896514:- isoform2=junction:11:68893456-68896514:-@exon:11:68893403-68893455:-@junction:11:68892994-68893402:-
PSMA3: Event 1	isoform1=junction:14:58270486-58271850:+ isoform2=junction:14:58270486-58270933:+@exon:14:58270934-58270998:+@junction:14:58270999-58271850:+
DEK: Event 1	isoform1=junction:6:18258063-18263842:- isoform2=junction:6:18258406-18263842:-@exon:6:18258304-18258405:-@junction:6:18258063-18258303:-
HSPD1: Event 1	isoform1=junction:2:197489248-197493323:- isoform2=junction:2:197490297-197493323:-@exon:2:197490197-197490296:-@junction:2:197489248-197490196:-
MLEC: Event 1	isoform1=junction:12:120695001-120696315:+ isoform2=junction:12:120695001-120695094:+@exon:12:120695095-120695152:+@junction:12:120695153-120696315:+
UQC22: Event 1	isoform1=junction:6:33700514-33701345:- isoform2=junction:6:33700514-33701345:-@exon:6:33700444-33700513:-@junction:6:33697751-33700443:-

Table S3. Top 5 Differential Alternative Splicing Events in Single-Cell Analysis

Event	Event Information
Full-Lnephg PBMC	
ENSA: Event 1	isoform1=junction:1:150625809-150627466;- isoform2=junction:1:150626527-150627466;-@exon:1:150626479-150626526;-@junction:1:150625809-150626478;-
TP53TG1: Event 1	isoform1=junction:7:87341685-87345304;- isoform2=junction:7:87345234-87345304;-@exon:7:87345043-87345233;-@junction:7:87341685-87345042;-
ICAM2: Event 1	isoform1=junction:17:64006736-64020522;- isoform2=junction:17:64007823-64020522;-@exon:17:64007741-64007822;-@junction:17:64006736-64007740;-
MBD2: Event 1	isoform1=junction:18:54166167-54188873;- isoform2=junction:18:54187838-54188873;-@exon:18:54187714-54187837;-@junction:18:54166167-54187713;-
LILRA2: Event 1	isoform1=junction:19:54576110-54587200;+ isoform2=junction:19:54576110-54577464;+@exon:19:54577465-54577723;+@junction:19:54577724-54587200;+
AKAP9: Event 1	isoform1=junction:7:91980334-91992157;+@exon:7:91992158-91992211;+@junction:7:91992212-91992884;+ isoform2=junction:7:91980334-91980872;+@exon:7:91980873-91980958;+@junction:7:91980959-91992884;+
BIN1: Event 1	isoform1=junction:2:127051244-127059010;- isoform2=junction:2:127057602-127059010;-@exon:2:127057473-127057601;-@junction:2:127051244-127057472;-
PHB2: Event 1	isoform1=junction:12:6969578-6970195;- isoform2=junction:12:6970017-6970195;-@novel_exon:12:6969956-6970016;-@junction:12:6969578-6969955;-
RBM3: Event 1	isoform1=junction:20:34073867-34075873;+ isoform2=junction:20:34073867-34074117;+@novel_exon:20:34074118-34074117;+@junction:20:34074118-34075873;+
RALY: Event 1	isoform1=junction:20:35732136-35738967;- isoform2=junction:20:35735082-35738967;-@exon:20:35734186-35735081;-@junction:20:35732136-35734185;-
FCER1A: Event 1	isoform1=junction:1:159302875-159305987;+ isoform2=junction:1:159302875-159303927;+@exon:1:159303928-159304182;+@junction:1:159304183-159305987;+
CD79B: Event 1	isoform1=junction:17:63929889-63931334;- isoform2=junction:17:63930386-63931334;-@exon:17:63930074-63930385;-@junction:17:63929889-63930073;-
HLA-DMB: Event 1	isoform1=junction:6:32935378-32937171;- isoform2=junction:6:32935653-32937171;-@exon:6:32935536-32935652;-@junction:6:32935378-32935535;-
HLA-DQA1: Event 1	isoform1=junction:6:32642254-32642951;+ isoform2=junction:6:32642254-32642609;+@exon:6:32642610-32642784;+@junction:6:32642785-32642951;+
CD47: Event 1	isoform1=junction:3:108051971-10805566;- isoform2=junction:3:10805567-10805566;-@exon:3:108055620-10805566;-@junction:3:108051971-108055619;-
LYZ: Event 1	isoform1=junction:12:69350273-69353152;+ isoform2=junction:12:69350273-69352219;+@exon:12:69352220-69352298;+@junction:12:69352299-69353152;+
LYZ: Event 2	isoform1=junction:12:69348545-69352219;+ isoform2=junction:12:69348545-69350107;+@exon:12:69350108-69350272;+@junction:12:69350273-69352219;+
ALF1: Event 1	isoform1=junction:6:31615737-31616343;+ isoform2=junction:6:31615737-31616103;+@exon:6:31616104-31616145;+@junction:6:31616146-31616343;+
TYROBP: Event 1	isoform1=junction:19:35907581-35908167;- isoform2=junction:19:35907763-35908167;-@exon:19:35907730-35907762;-@junction:19:35907581-35907729;-
TYROBP: Event 2	isoform1=junction:19:35904635-35907445;- isoform2=junction:19:35907265-35907445;-@exon:19:35907218-35907264;-@junction:19:35904635-35907217;-
NGK7: Event 1	isoform1=junction:19:51372075-51372378;- isoform2=junction:19:51372308-51372378;-@exon:19:51372161-51372307;-@junction:19:51372075-51372160;-
GNLY: Event 1	isoform1=junction:2:85696057-85698563;+ isoform2=junction:2:85696057-85697505;+@exon:2:85697506-85697677;+@junction:2:85697678-85698563;+
CTSW: Event 1	isoform1=junction:11:65882527-65882778;- isoform2=junction:11:65882527-65882608;+@exon:11:65882609-65882689;+@junction:11:65882690-65882778;+
GZMB: Event 1	isoform1=junction:14:24632119-24632914;- isoform2=junction:14:24632460-24632914;-@exon:14:24632324-24632459;-@junction:14:24632119-24632323;-
CALM1: Event 1	isoform1=junction:14:90397234-90401258;+ isoform2=junction:14:90397234-90400064;+@exon:14:90400065-90400095;+@junction:14:90400096-90401258;+
IL32: Event 1	isoform1=junction:16:3067614-3068179;+ isoform2=junction:16:3067614-3067983;+@exon:16:3067984-3068010;+@junction:16:3068011-3068179;+
KLRB1: Event 1	isoform1=junction:12:9595422-9598498;- isoform2=junction:12:9598162-9598498;-@exon:12:9598046-9598161;-@junction:12:9595422-9598045;-
RACK1: Event 1	isoform1=junction:5:181238240-181239486;- isoform2=junction:5:181239178-181239486;-@exon:5:181239067-181239177;-@junction:5:181238240-181239066;-
RPLP0: Event 1	isoform1=junction:12:120197463-120198853;- isoform2=junction:12:120198740-120198853;-@exon:12:120198554-120198739;-@junction:12:120197463-120198553;-
HLA-DMA: Event 1	isoform1=junction:6:32950804-32952948;- isoform2=junction:6:32952462-32952948;-@exon:6:32952284-32952461;-@junction:6:32950804-32952283;-
CTSH: Event 1	isoform1=junction:15:78931507-78932371;- isoform2=junction:15:78932039-78932371;-@exon:15:78931869-78932038;-@junction:15:78931507-78931868;-
MAL: Event 1	isoform1=junction:2:95025886-95049580;+ isoform2=junction:2:95025886-95047958;+@exon:2:95047959-95048126;+@junction:2:95048127-95049580;+
HNRNP9: Event 1	isoform1=junction:1:23338609-23344210;- isoform2=junction:1:23341021-23344210;-@exon:1:23340852-23341020;-@junction:1:23338609-23340851;-
CD3E: Event 1	isoform1=junction:11:118312171-118313706;+ isoform2=junction:11:118312171-118312617;+@exon:11:118312618-118312866;+@junction:11:118312667-118313706;+
TRBC2: Event 1	isoform1=junction:7:142801428-142802104;+ isoform2=junction:7:142801428-142801943;+@exon:7:142801944-142801961;+@junction:7:142801962-142802104;+
GAS5: Event 1	isoform1=junction:1:173866207-173866990;- isoform2=junction:1:173866797-173866990;-@exon:1:173866528-173866796;-@junction:1:173866207-173866527;-
TRAC: Event 1	isoform1=junction:14:22549683-22551604;+ isoform2=junction:14:22549683-22550556;+@exon:14:22550557-22550664;+@junction:14:22550665-22551604;+
GAS5: Event 2	isoform1=junction:1:173864305-173865228;- isoform2=junction:1:173864705-173865228;-@exon:1:173864484-173864704;-@junction:1:173864305-173864483;-
10X Colon	
E1F3K: Event 1	isoform1=junction:19:38635119-38636888;+ isoform2=junction:19:38635119-38636200;+@novel_exon:19:38636201-38636251;+@junction:19:38636252-38636888;+
RPS10-NUD3: Event 1	isoform1=junction:6:34421808-34424668;-
RPS10: Event 1	isoform2=junction:6:34422283-34424668;-@novel_exon:6:34422237-34422282;-@junction:6:34421808-34422236;-
RPS24: Event 1	isoform1=junction:10:78037442-78040203;+ isoform2=junction:10:78037442-78037964;+@exon:10:78037965-78037982;+@junction:10:78037983-78040203;+
RPS10: Event 1	isoform1=junction:6:34417548-34418368;- isoform2=junction:6:34417898-34418368;-@exon:6:34417798-34417897;-@junction:6:34417548-34417797;-
RPS10: Event 2	isoform1=junction:6:34417548-34418368;- isoform2=junction:6:34417871-34418368;-@novel_exon:6:34417798-34417870;-@junction:6:34417548-34417797;-
FABP1: Event 1	isoform1=junction:2:88123105-88124493;- isoform2=junction:2:88123944-88124493;-@novel_exon:2:88123848-88123943;-@junction:2:88123105-88123847;-
E1F3M: Event 1	isoform1=junction:11:32601823-32602278;+ isoform2=junction:11:32601823-32602078;+@exon:11:32602079-32602114;+@junction:11:32602115-32602278;+
SPINK1: Event 1	isoform1=junction:5:147824707-147829598;- isoform2=junction:5:147828129-147829598;-@exon:5:147828022-147828128;-@junction:5:147824707-147828021;-
RPL24: Event 1	isoform1=junction:3:101681216-101682770;- isoform2=junction:3:101682493-101682770;-@exon:3:101682429-101682492;-@junction:3:101681216-101682428;-
CRIP1: Event 1	isoform1=junction:14:105488261-105488470;+ isoform2=junction:14:105488261-105488330;+@exon:14:105488331-105488388;+@junction:14:105488389-105488470;+
FABP1: Event 2	isoform1=junction:2:88123105-88126175;- isoform2=junction:2:88124587-88126175;-@exon:2:88124494-88124586;-@junction:2:88123105-88124493;-
MT1E: Event 1	isoform1=junction:16:56625880-56626879;+ isoform2=junction:16:56625880-56626465;+@exon:16:56626466-56626531;+@junction:16:56626532-56626879;+
FXYD3: Event 1	isoform1=junction:19:35122840-35123270;+ isoform2=junction:19:35122840-35122917;+@exon:19:35122918-35122954;+@junction:19:35122955-35123270;+
MT1G: Event 1	isoform1=junction:16:56666971-56667965;- isoform2=junction:16:56667378-56667965;-@exon:16:56667312-56667377;-@junction:16:56666971-56667311;-
MEIS1: Event 1	isoform1=junction:2:66435869-66437736;- isoform2=junction:2:66435869-66436895;+@novel_exon:2:66436896-66436943;+@junction:2:66436944-66437736;+
MPZL1: Event 1	isoform1=junction:1:167773369-1677787819;+ isoform2=junction:1:167773369-167776063;+@exon:1:167776064-167776166;+@junction:1:167776167-1677787819;+
PHIP: Event 1	isoform1=junction:6:78983118-78988208;- isoform2=junction:6:78985429-78988208;-@exon:6:78985352-78985428;-@junction:6:78983118-78985351;-
ACOT9: Event 1	isoform1=junction:X:23707945-23721880;- isoform2=junction:X:23713209-23721880;-@exon:X:23713135-23713208;-@junction:X:23707945-23713134;-
PNISR: Event 1	isoform1=junction:6:99402711-99404602;- isoform2=junction:6:99403883-99404602;-@exon:6:99403829-99403882;-@junction:6:99402711-99403828;-
SSBP1: Event 1	isoform1=junction:7:141743990-141750310;+ isoform2=junction:7:141743990-141745495;+@exon:7:141745496-141745584;+@junction:7:141745585-141750310;+
SNHG8: Event 1	isoform1=junction:8:66922115-66922813;- isoform2=junction:8:66922393-66922613;-@exon:8:66922324-66922392;-@junction:8:66922115-66922323;-
PSMB3: Event 1	isoform1=junction:17:38760609-38764118;+ isoform2=junction:17:38760609-38762410;+@exon:17:38762411-38762505;+@junction:17:38762506-38764118;+
ATP5PO: Event 1	isoform1=junction:21:33903640-33907340;- isoform2=junction:21:33904022-33907340;-@exon:21:33903935-33904021;-@junction:21:33903640-33903934;-
PDCD5: Event 1	isoform1=junction:19:32585908-32587252;+ isoform2=junction:19:32585908-32586857;+@exon:19:32586858-32586929;+@junction:19:32586930-32587252;+
MYL6: Event 1	isoform1=junction:12:56160321-56161386;+ isoform2=junction:12:56160321-56160625;+@exon:12:56160626-56160670;+@junction:12:56160671-56161386;+
PSMA4: Event 1	isoform1=junction:15:78545765-78548789;+ isoform2=junction:15:78545765-78546574;+@exon:15:78546575-78546698;+@junction:15:78546699-78548789;+
SEC11C: Event 1	isoform1=junction:18:59155808-59158631;+ isoform2=junction:18:59155808-59157607;+@exon:18:59157608-59157665;+@junction:18:59157666-59158631;+
GAS5: Event 1	isoform1=junction:1:173864507-173865228;- isoform2=junction:1:173864705-173865228;-@exon:1:173864675-173864704;-@junction:1:173864507-173864674;-
GAS5: Event 2	isoform1=junction:1:173864305-173865228;- isoform2=junction:1:173864705-173865228;-@exon:1:173864484-173864704;-@junction:1:173864305-173864483;-
RPS24: Event 2	isoform1=junction:10:78037305-78040614;+ isoform2=junction:10:78037305-78037438;+@exon:10:78037439-78040225;+@junction:10:78040226-78040614;+
RPS24: Event 3	isoform1=junction:10:78037305-78040203;+ isoform2=junction:10:78037305-78037438;+@exon:10:78037439-78037441;+@junction:10:78037442-78040203;+