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Supplemental information

SkewC: Identifying cells with skewed gene body coverage in single-cell RNA sequencing data

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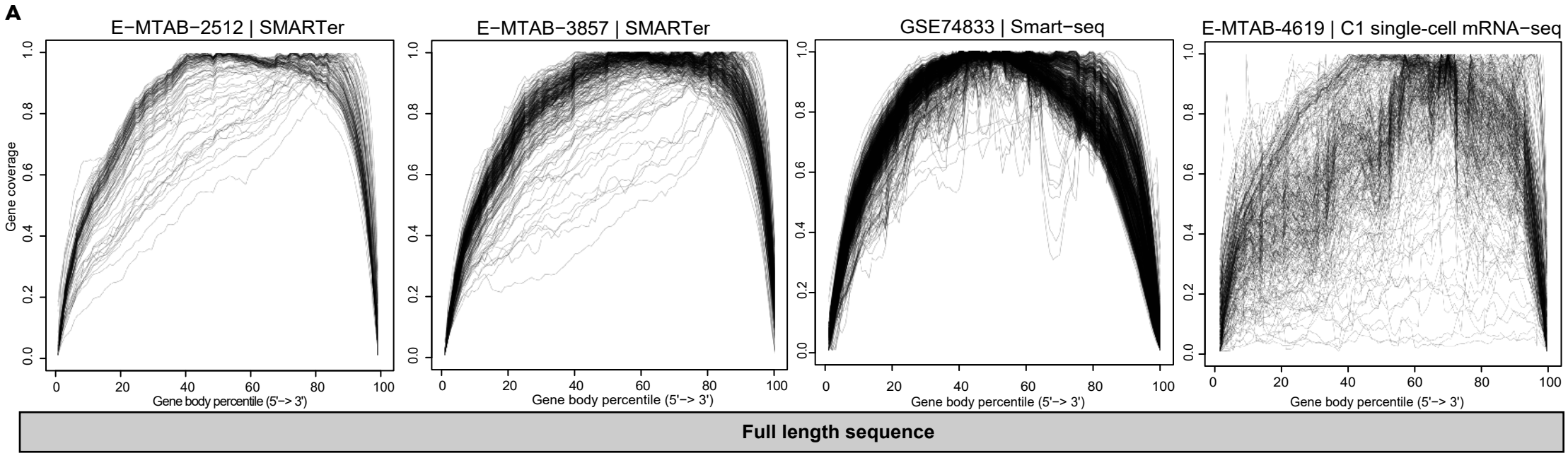
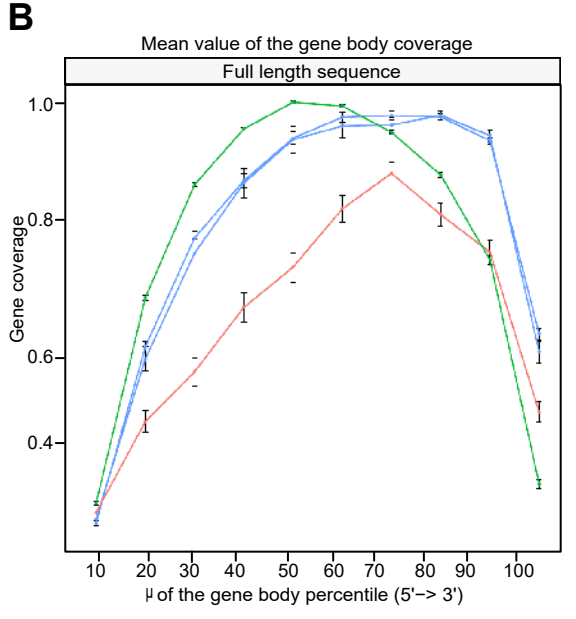
Figure S1. Gene coverage skewness and variation in expression among single-cell RNA-Seq protocols using mouse CD4 T cells, related to Figure 1.





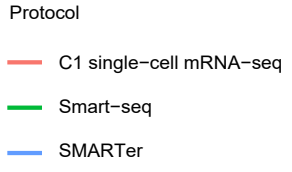
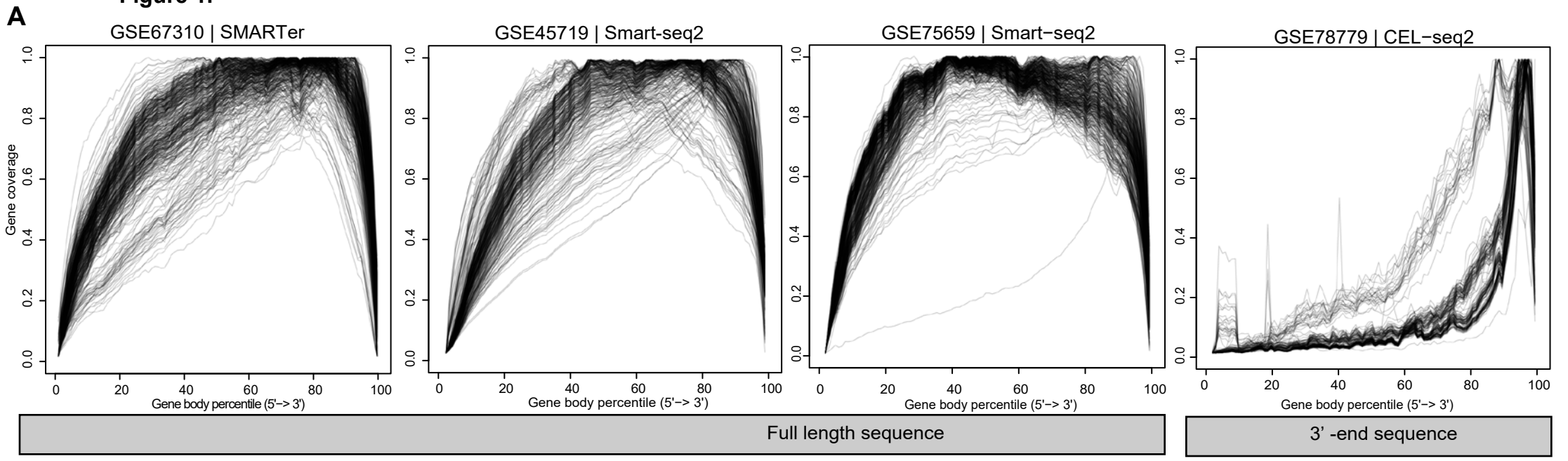
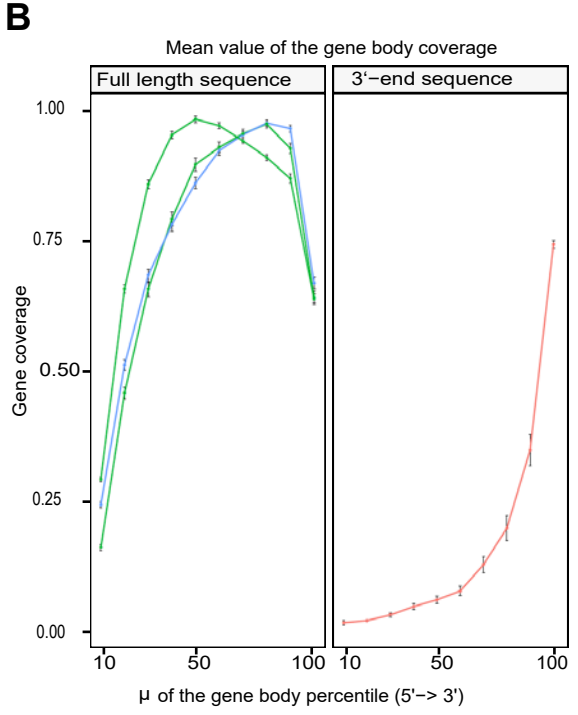


Figure S1: Four datasets from mouse CD4 T cells. (**a**) Distribution of the mapped reads (tags) across the genes. Each panel shows gene body coverage percentile per dataset. The x-axis represents the gene body from 5′ to 3′ end scaled from 0-100, and the y-axis gene coverage (0-1). Each line represents a single cell. (**b**) Mean value of the gene body coverage.

Figure S2. Gene coverage skewness and variation in expression among single-cell RNA-Seq protocols using mouse fibroblast cells, related to Figure 1.





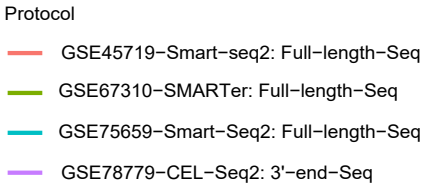
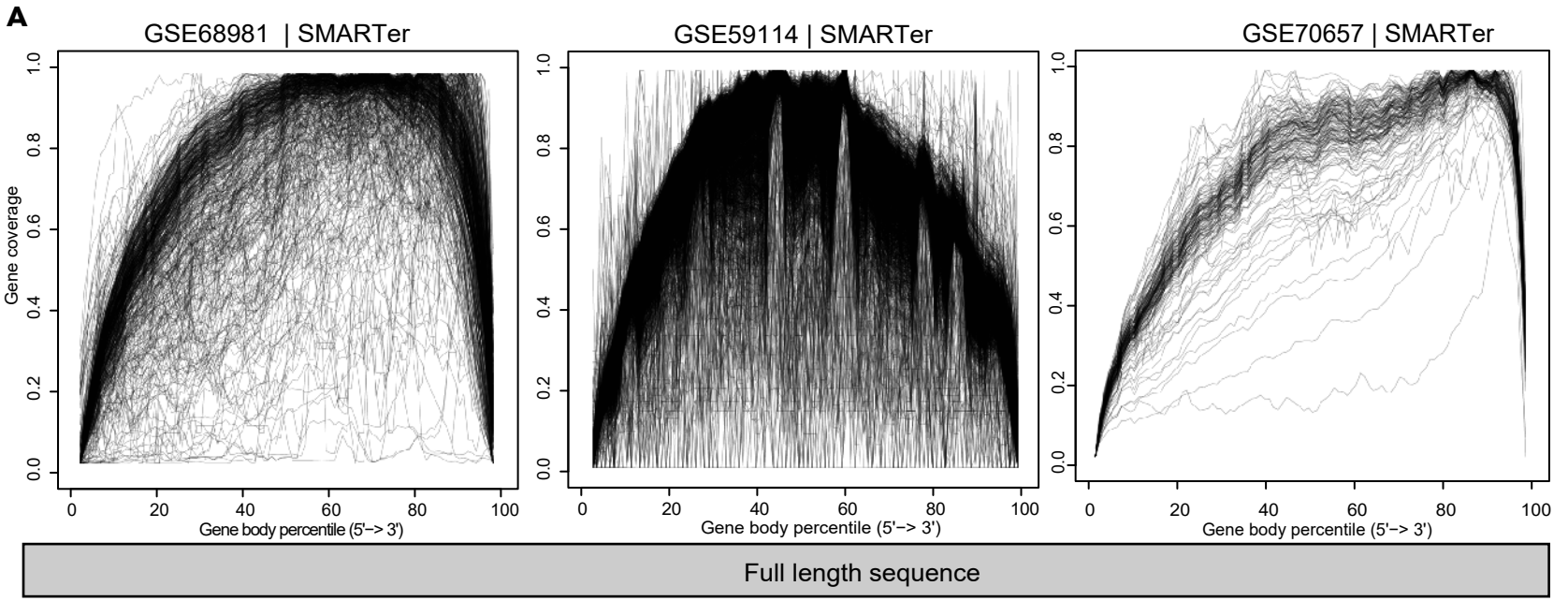


Figure S2 Four datasets from mouse fibroblast. (**a**) Distribution of the mapped reads (tags) across the genes. Each panel shows gene body coverage percentile per dataset. The x-axis represents the gene body from 5′ to 3′ end scaled from 0-100, and the y-axis gene coverage (0-1). Each line represents a single cell. (**b**) Mean value of the gene body coverage.

Figure S3. Gene coverage skewness and variation in expression among single-cell RNA-Seq protocols using mouse hematopoietic stem cells (HSCs), related to Figure 1.



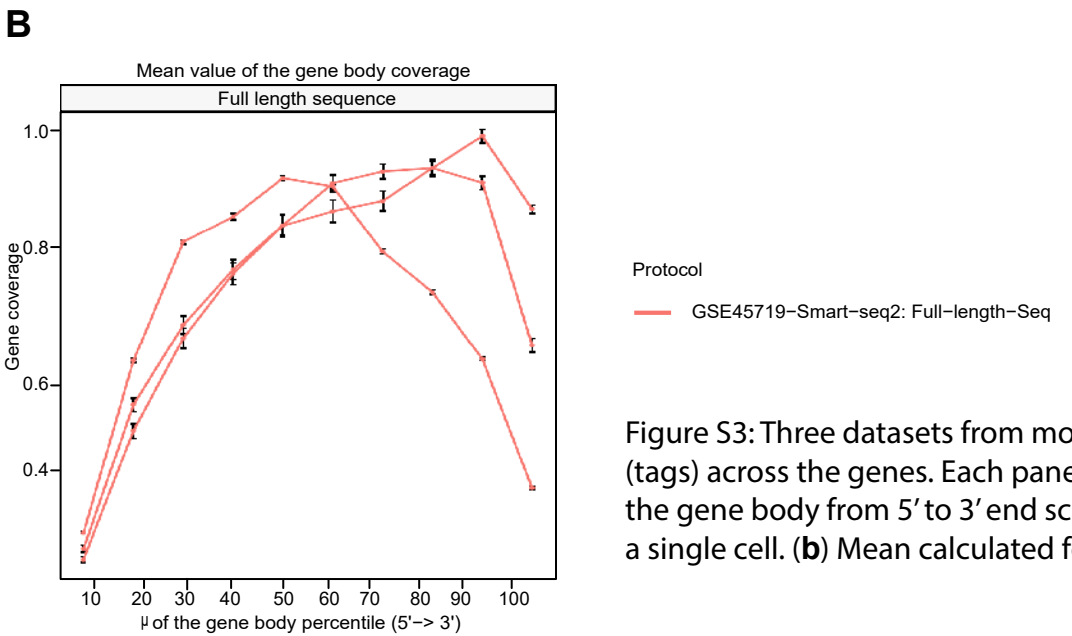
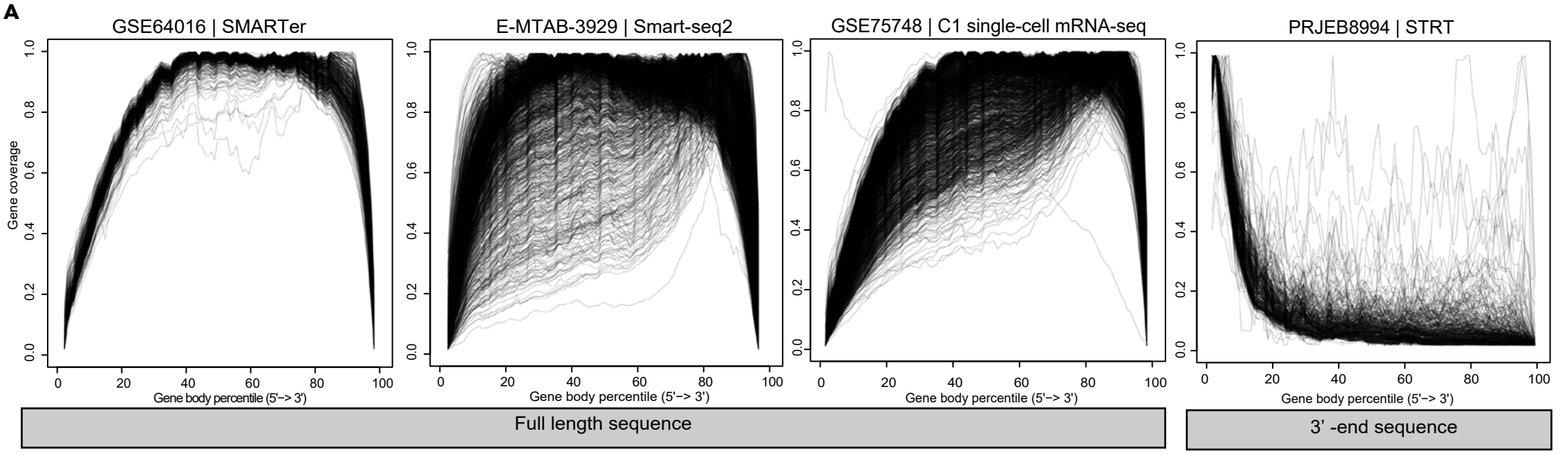


Figure S3: Three datasets from mouse hematopoietic stem cells (HSCs). (**a**) Distribution of the mapped reads (tags) across the genes. Each panel shows gene body coverage percentile per dataset. The x-axis represents the gene body from 5′ to 3′ end scaled from 0-100, and the y-axis gene coverage (0-1). Each line represents a single cell. (**b**) Mean calculated for bin size = 10.

Figure S4. Gene coverage skewness and variation in expression among single-cell RNA-Seq protocols using human embryonic stem cells (hESCs), related to Figure 1.



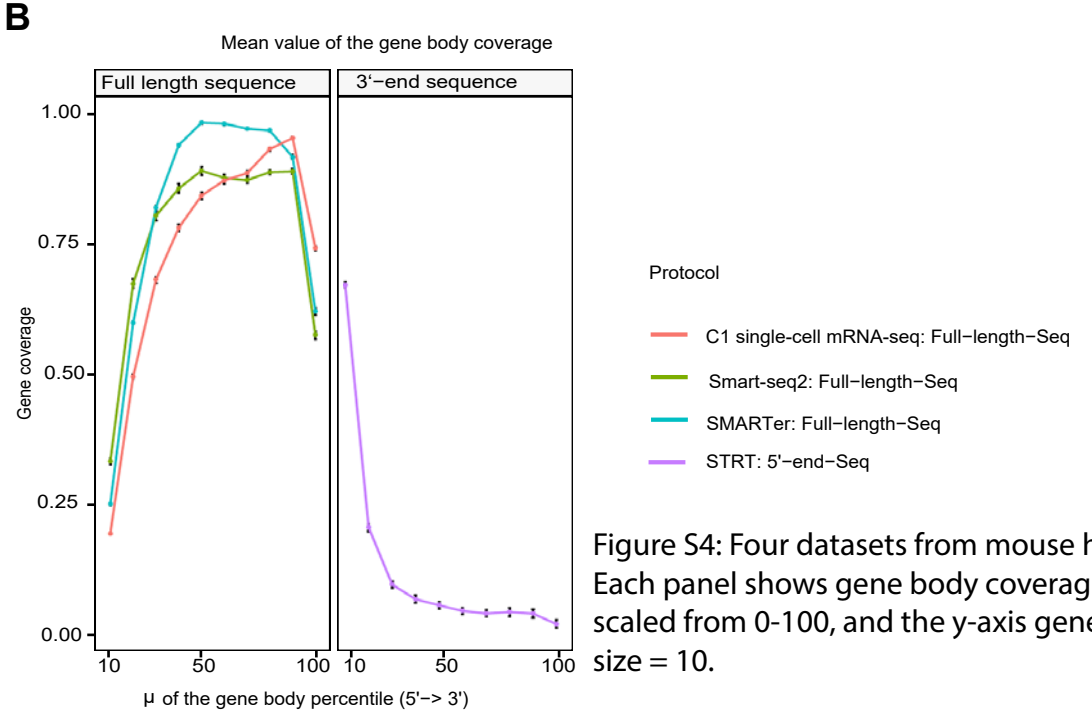


Figure S4: Four datasets from mouse human embryo cells. (**a**) Distribution of the mapped reads (tags) across the genes. Each panel shows gene body coverage percentile per dataset. The x-axis represents the gene body from 5′ to 3′ end scaled from 0-100, and the y-axis gene coverage (0-1). Each line represents a single cell. (**b**) Mean calculated for bin size = 10.

Figure S5. Gene coverage skewness and variation in expression among sc-RNA-Seq protocols using mouse adipocyte and mouse PBMC cells, related to Figure 1.

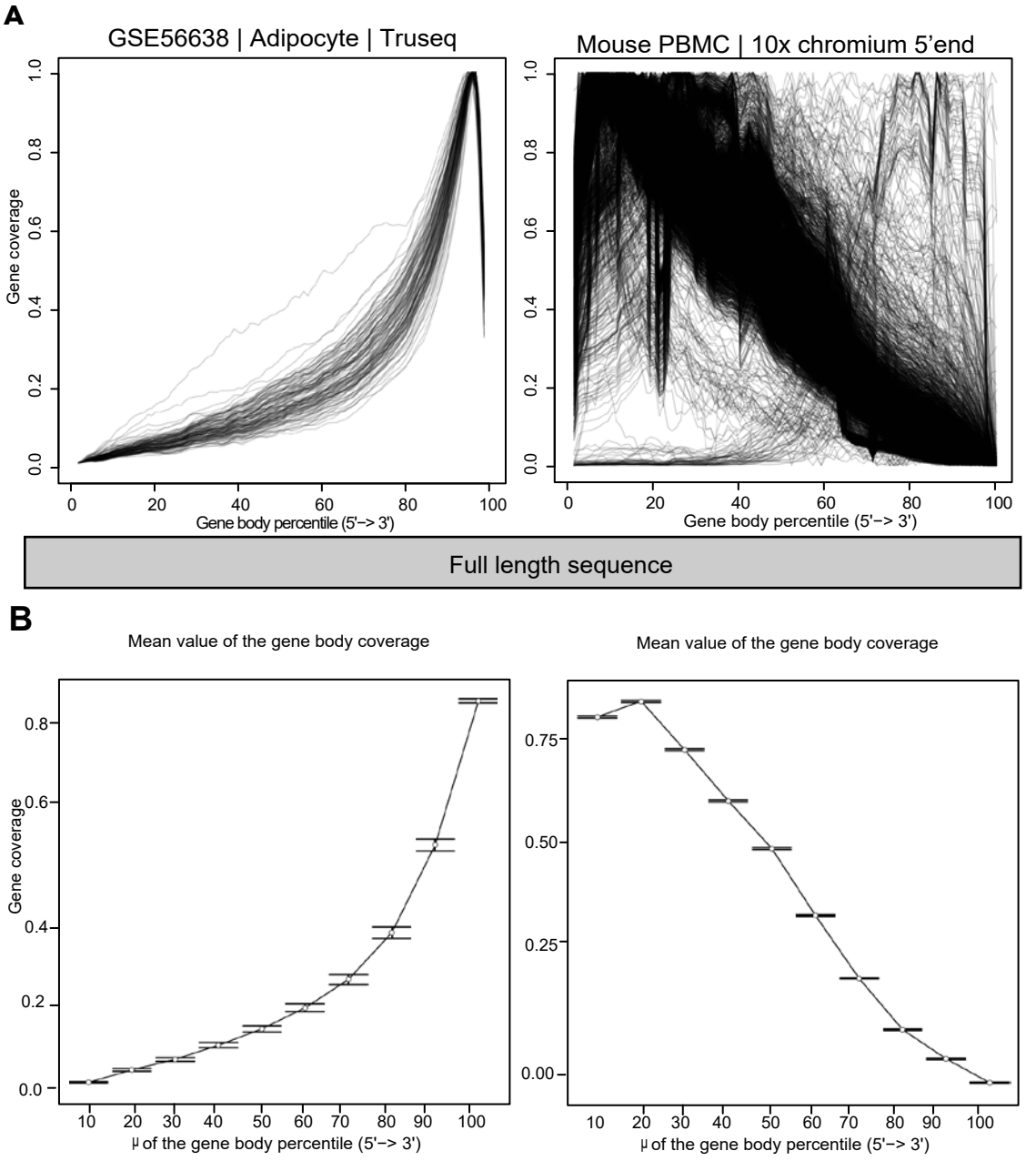


Figure S5: Two mouse dataset, the GSE56638 from Adipocyte tissue generated by Truseq and PBMC generated by 10x chromium 5′ end. (**a**) Distribution of the mapped reads (tags) across the genes. Each panel shows gene body coverage percentile per dataset. The x-axis represents the gene body from 5′ to 3′ end scaled from 0-100, and the y-axis gene coverage (0-1). Each line represents a single cell. (**b**) Mean calculated for bin size = 10.

Figure S6. Gene coverage skewness and variation in expression among single-cell RNA-Seq protocols using different human cell types, related to Figure 1.

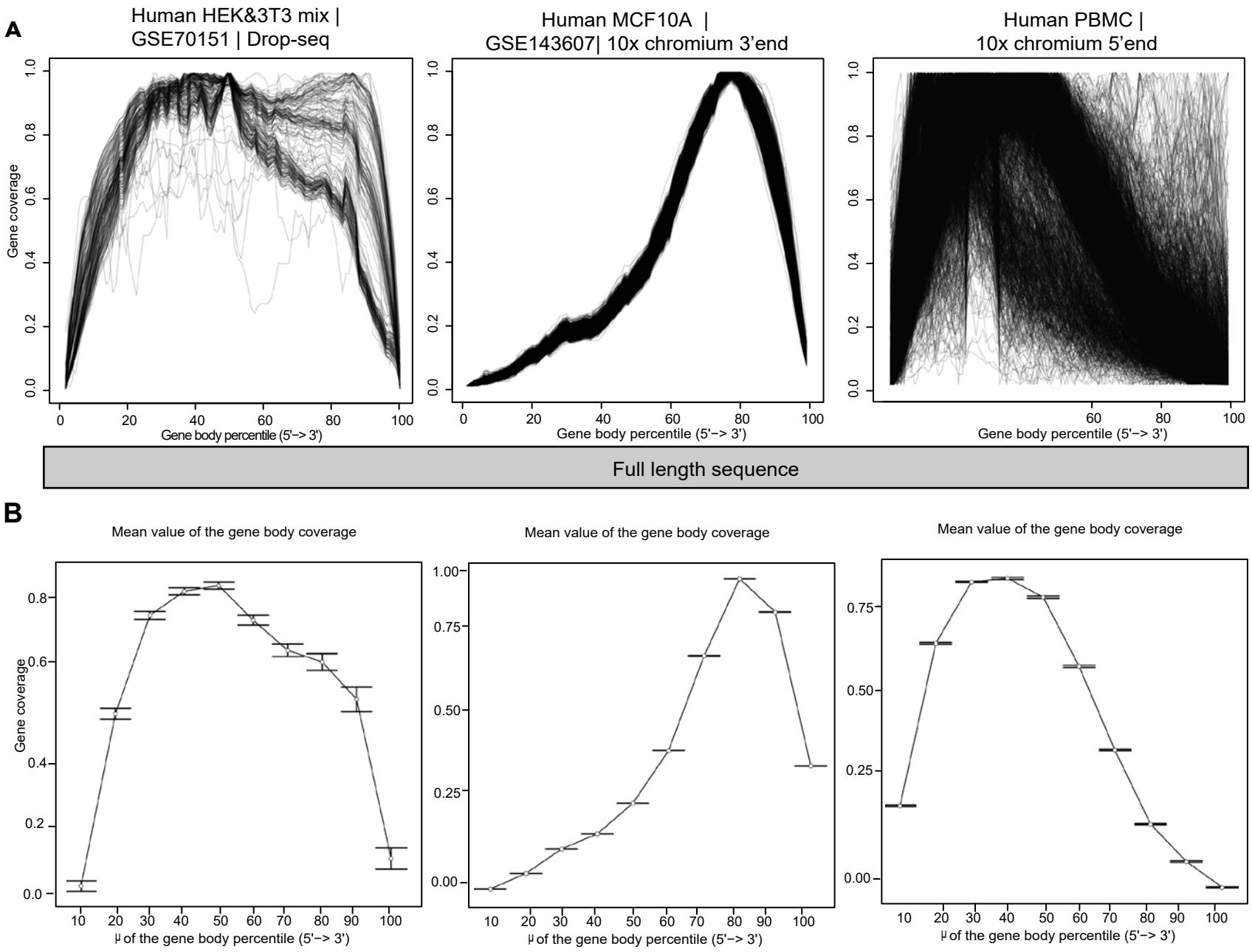


Figure S6: Three human dataset, the GSE70151 from HEK&3T3 cell line generated by Drop-seq, GSE143607 Human MCF10A cell line generated by 10x chromium 3′ end and PBMC generated by 10x chromium 5′ end. (**a**) Distribution of the mapped reads (tags) across the genes. Each panel shows gene body coverage percentile per dataset. The x-axis represents the gene body from 5′ to 3′ end scaled from 0-100, and the y-axis gene coverage (0-1). Each line represents a single cell. (**b**) Mean calculated for bin size = 10.

Figure S7. Gene coverage skewness among single-cell RNA-Seq protocols using different mESCs, related to Figure 1.

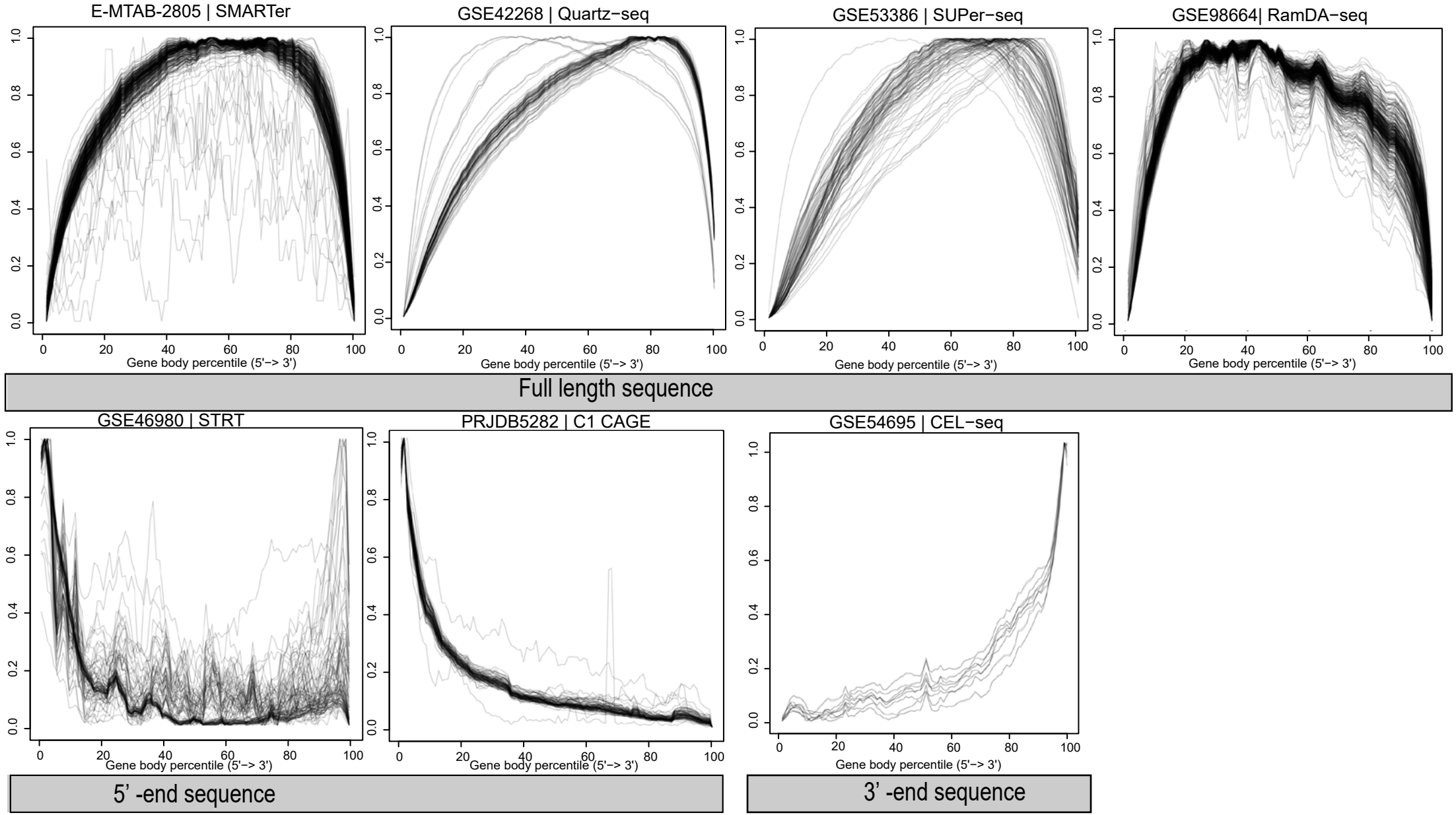


Figure S7: Seven mESCs dataset, top panel dataset generated by fill length sequence protocols (SMARTer, Quartz-seq, SUPer-seq, and RamDA-seq. Bottom panel dataset generated by STRT, C1 CAGE and CEL-seq.

Figure S8. Gene body coverage of typical and skewed cells as obtained by SkewC using Auto Alpha, related to Figure 5.

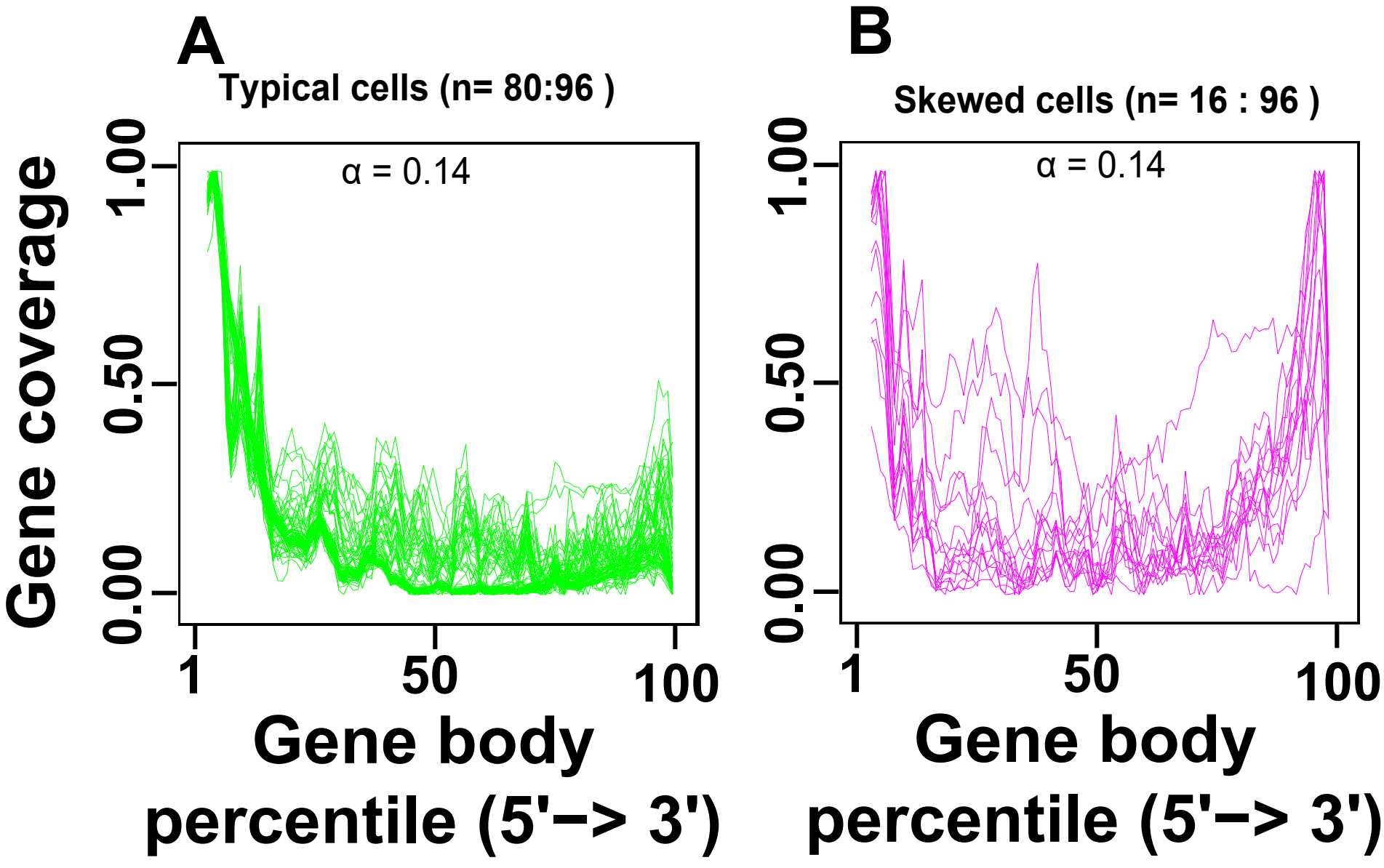


Figure S8: The dataset GSE46980 generated by STRT protocol. Panel (**a**) typical cells and panel (**b**) skewed cells.

Figure S9. Heatmap of the top100 genes between typical and skewed cells, related to Figure 5.

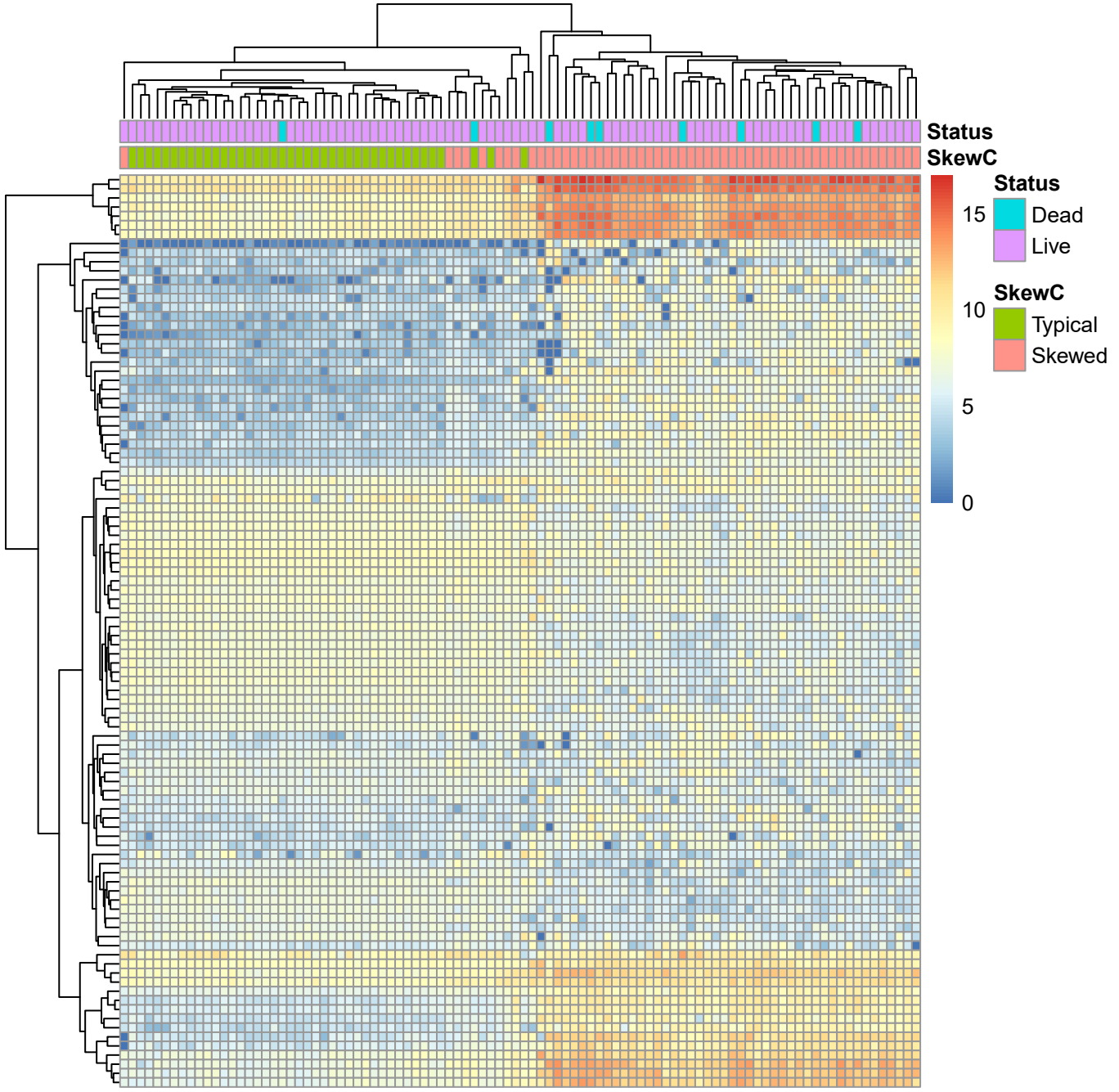


Figure S9: Heatmap of the top100 expressed genes between typical and skewed cells. from GSE46980.