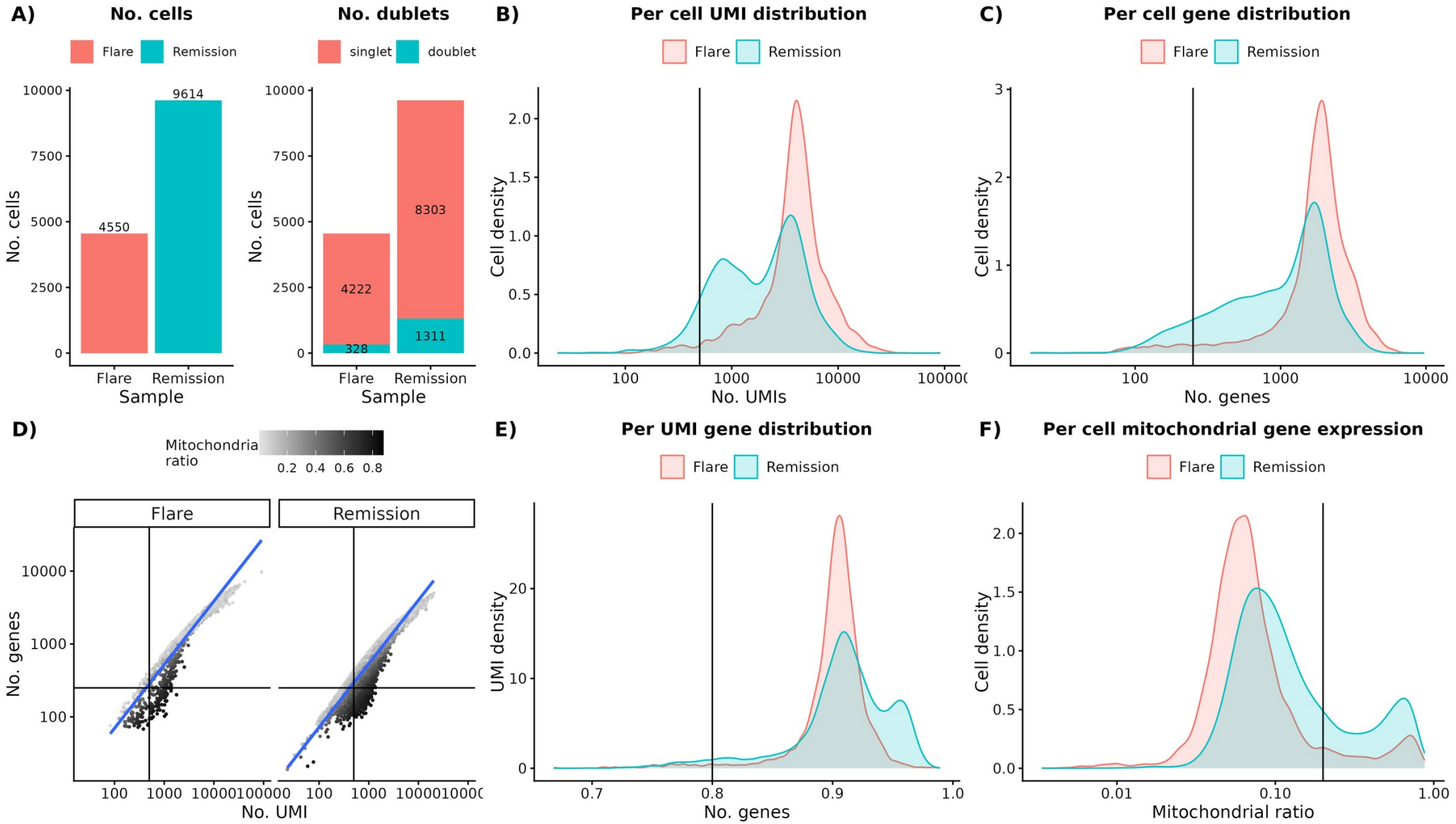
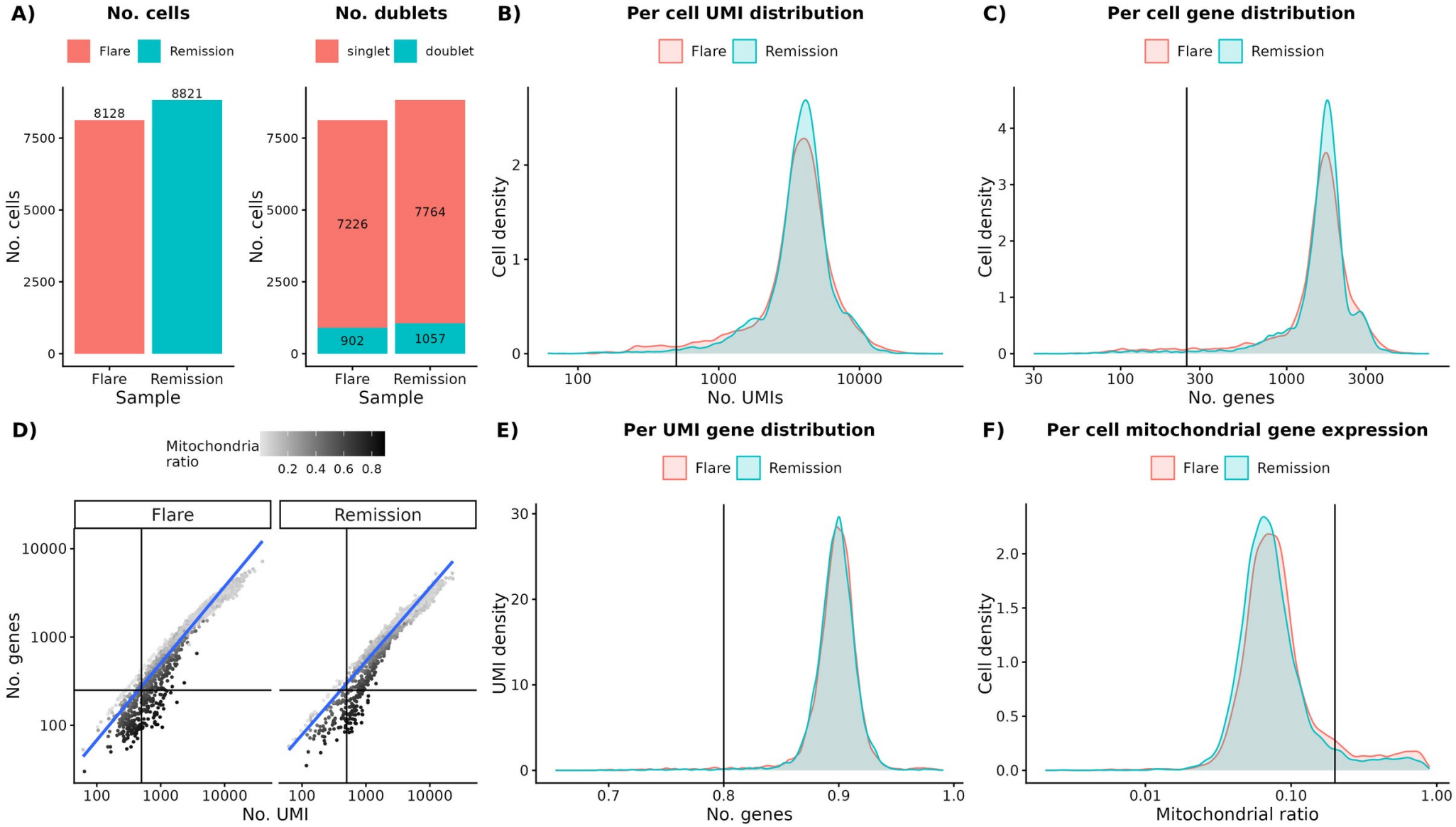
Supplementary Figure S1. Quality-control metrics for single-cell multiome libraries.

Patient P1. (A) Cell counts and doublet classification per condition. (B) Per-cell UMI distribution. (C) Per-cell gene distribution. (D) Genes versus UMIs coloured by mitochondrial ratio. (E) Per-UMI gene distribution. (F) Per-cell mitochondrial gene expression. Vertical and horizontal lines indicate filtering thresholds; red, flare; teal, remission.



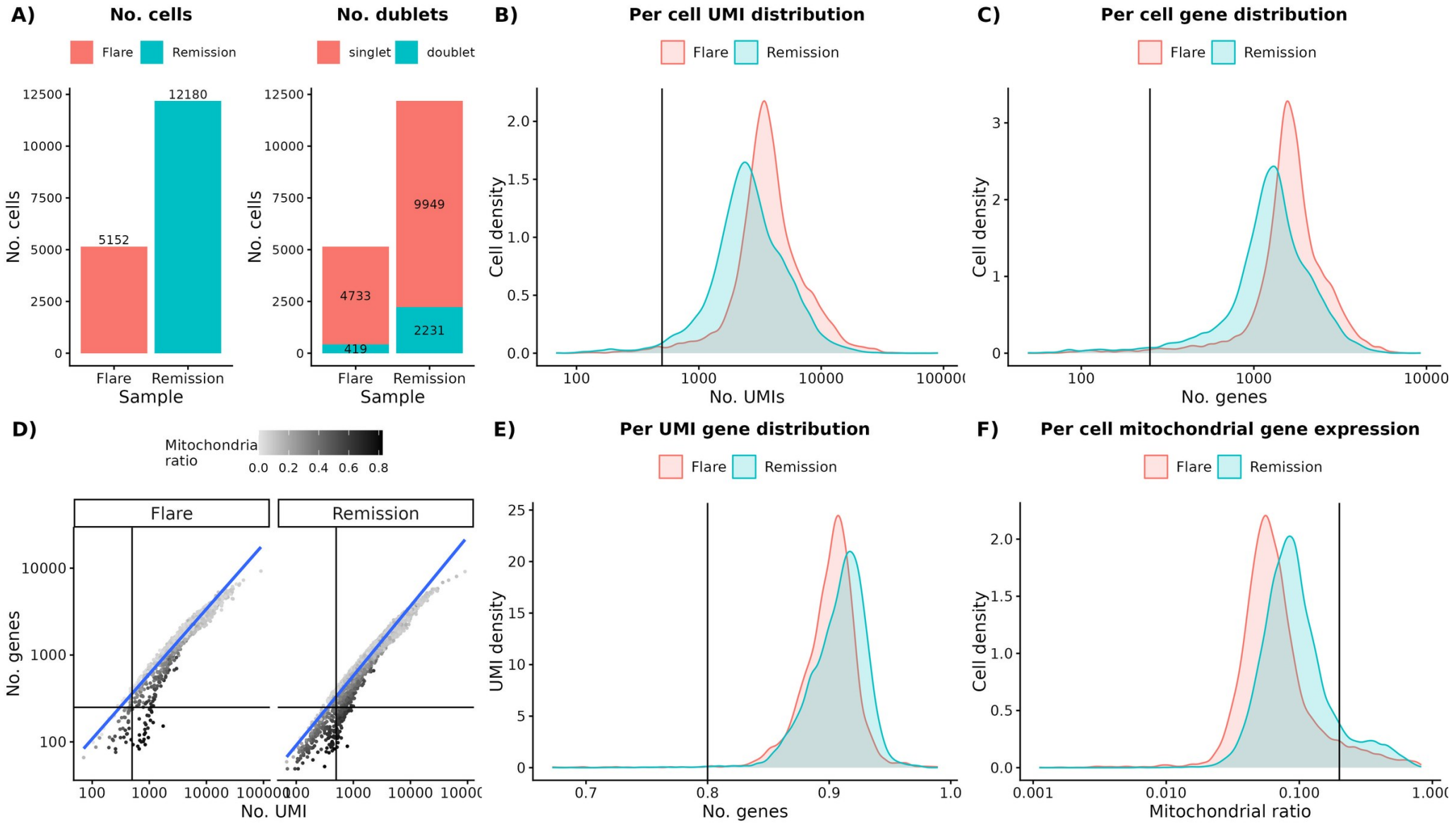
Supplementary Figure S1 (continued). Quality-control metrics — Patient P2.

Panels A–F as defined for Patient P1 on the first page of this figure.



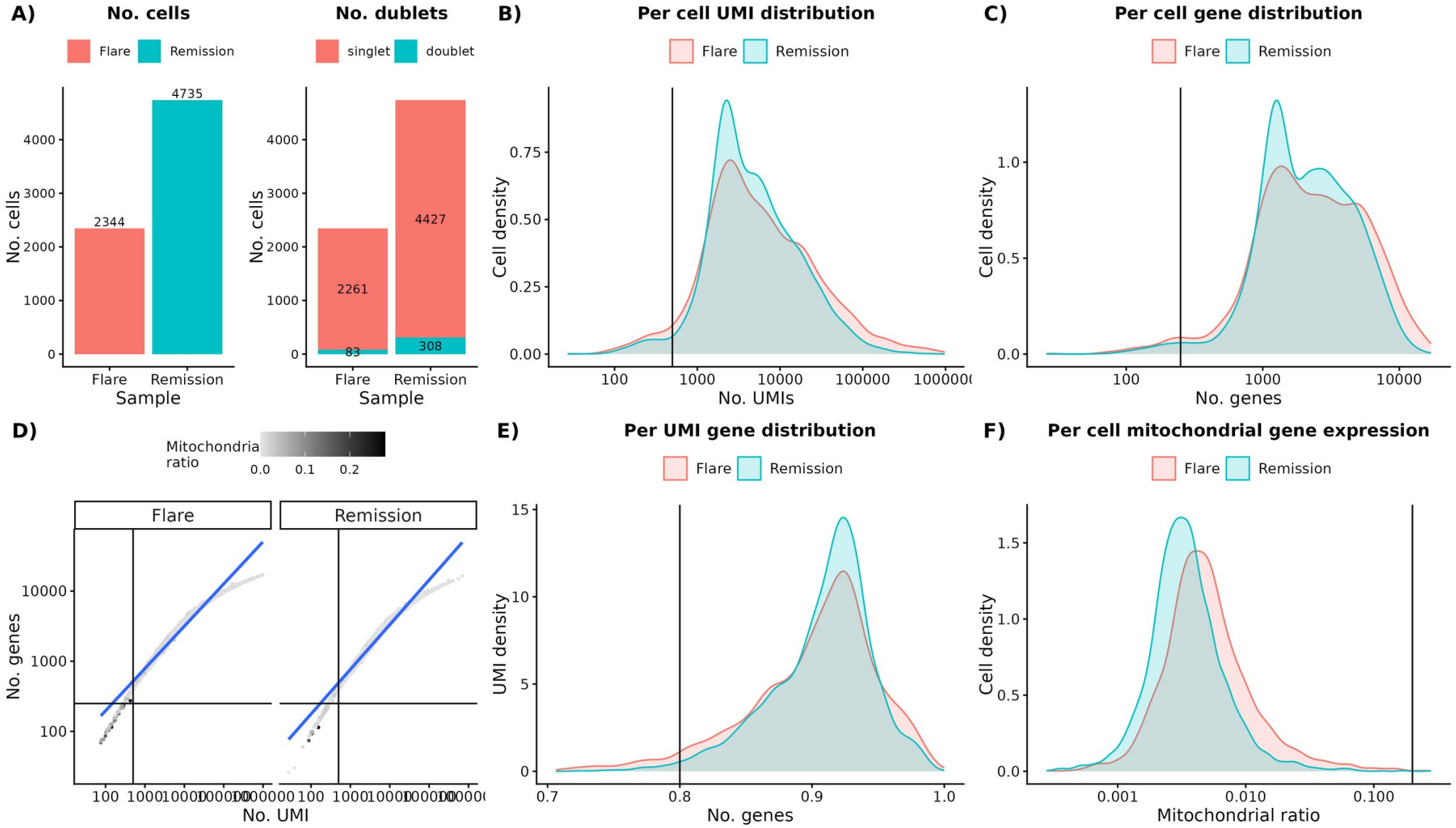
Supplementary Figure S1 (continued). Quality-control metrics — Patient P3.

Panels A–F as defined for Patient P1 on the first page of this figure.



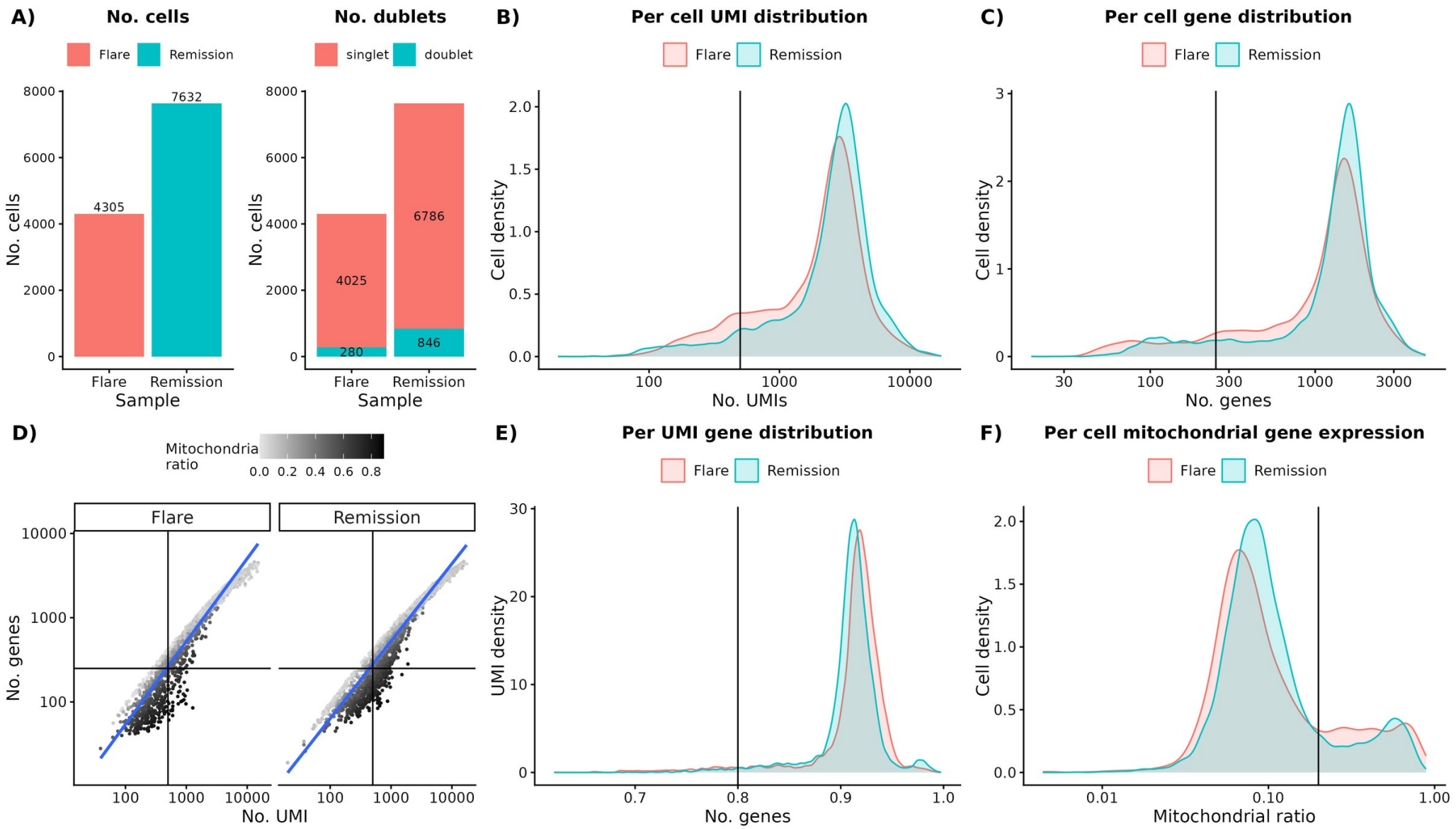
Supplementary Figure S1 (continued). Quality-control metrics — Patient P4.

Panels A–F as defined for Patient P1 on the first page of this figure.



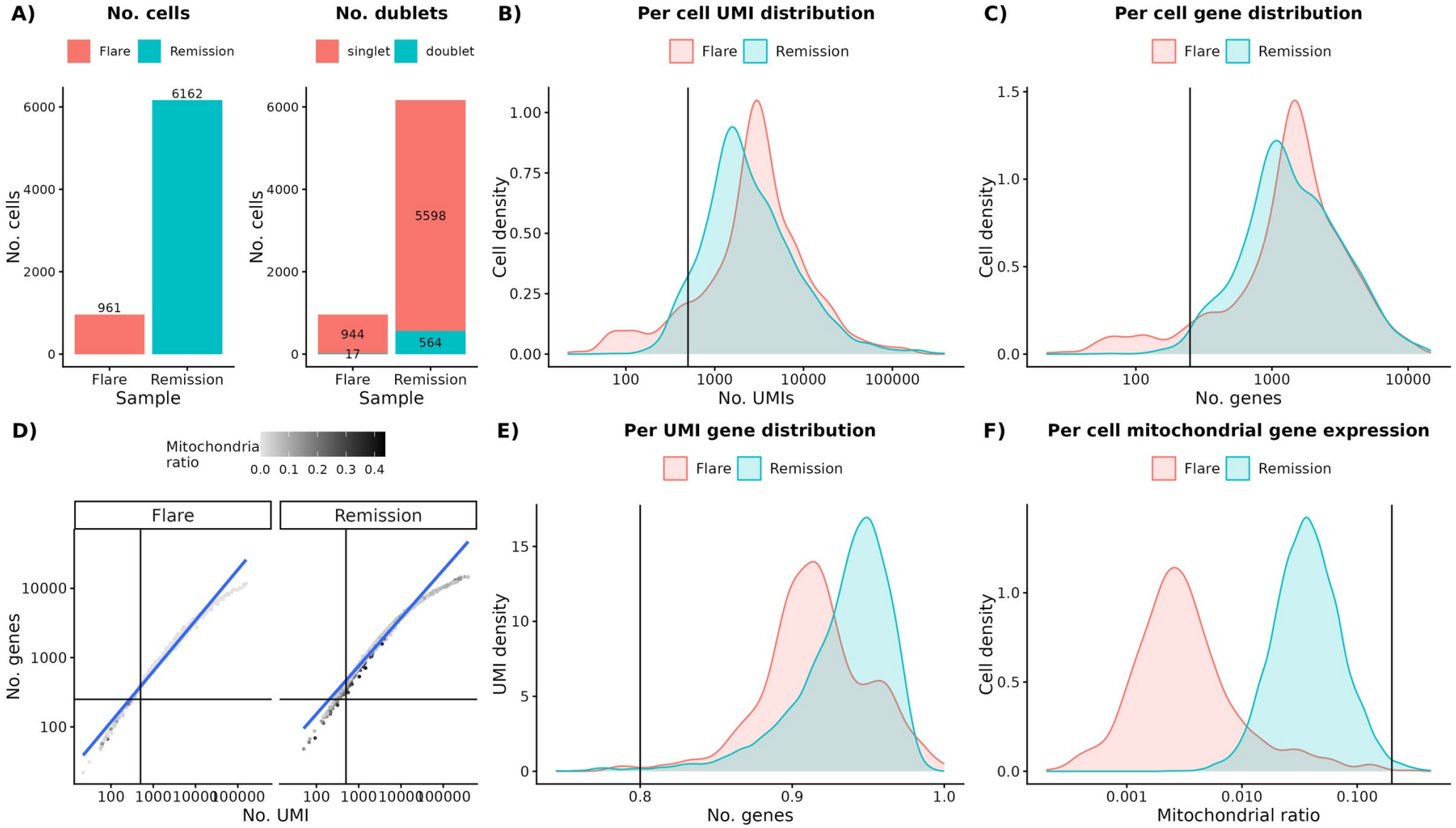
Supplementary Figure S1 (continued). Quality-control metrics — Patient P5.

Panels A–F as defined for Patient P1 on the first page of this figure.



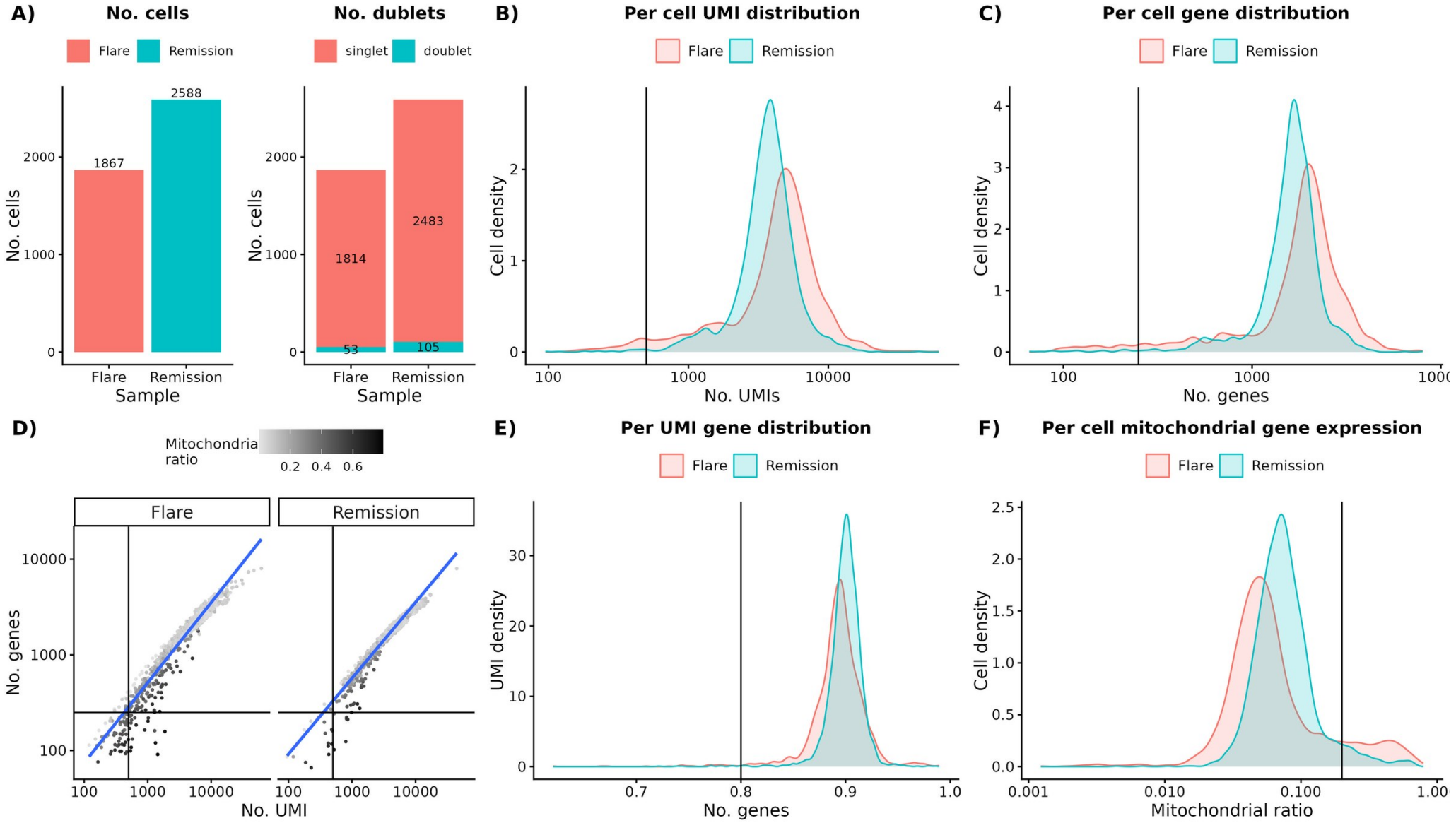
Supplementary Figure S1 (continued). Quality-control metrics — Patient P6.

Panels A–F as defined for Patient P1 on the first page of this figure.



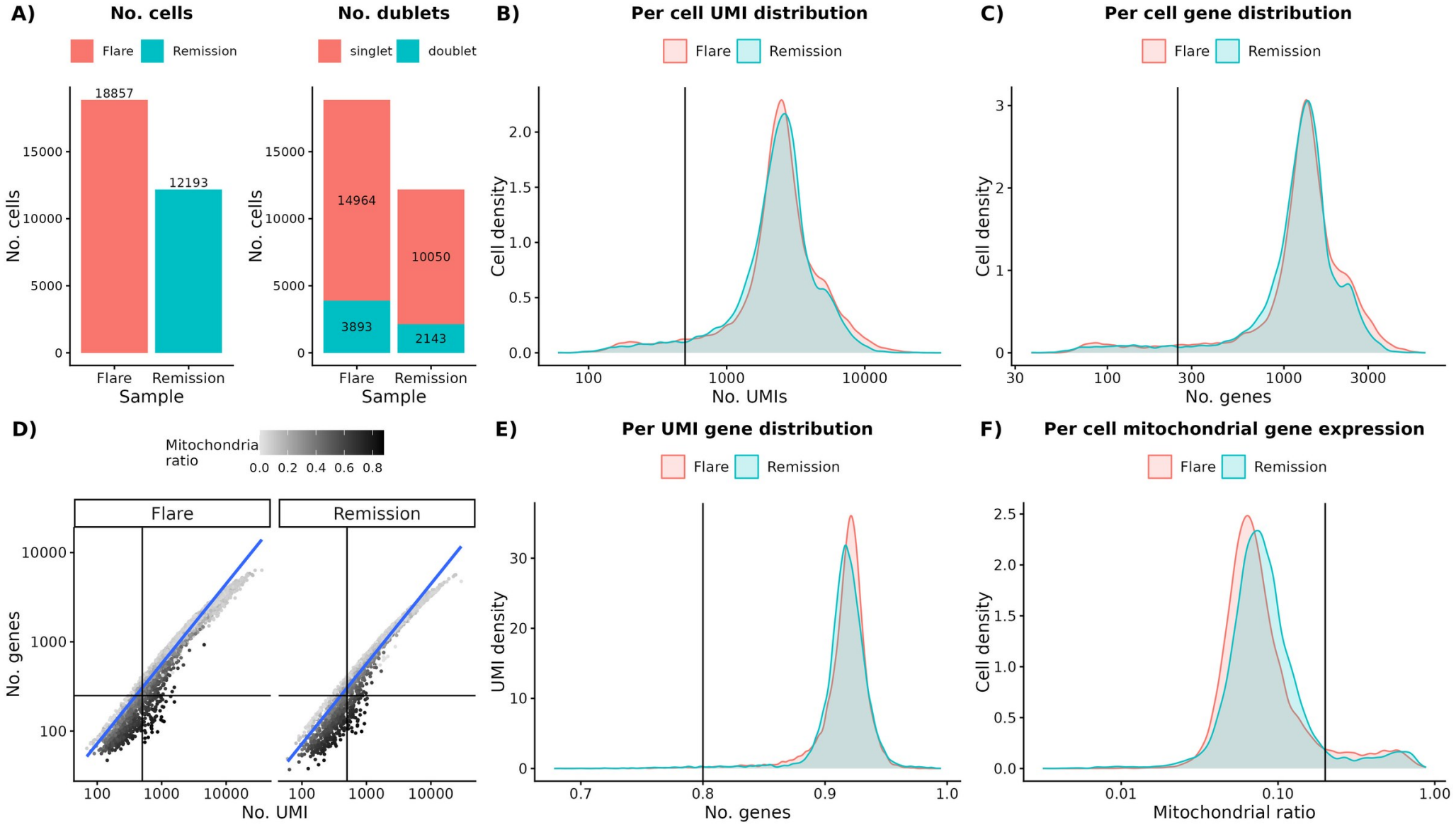
Supplementary Figure S1 (continued). Quality-control metrics — Patient P7.

Panels A–F as defined for Patient P1 on the first page of this figure.



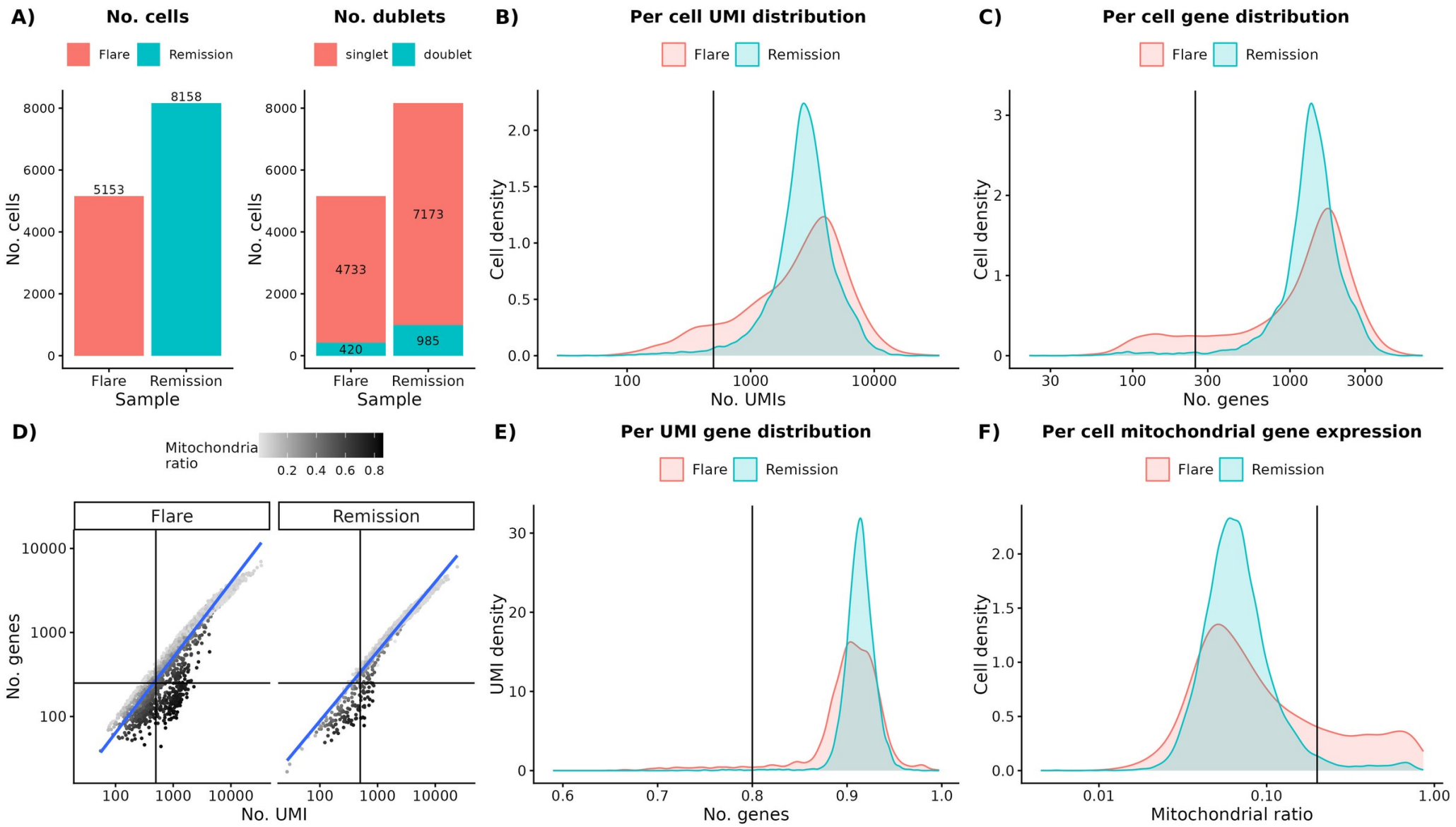
Supplementary Figure S1 (continued). Quality-control metrics — Patient P8.

Panels A–F as defined for Patient P1 on the first page of this figure.



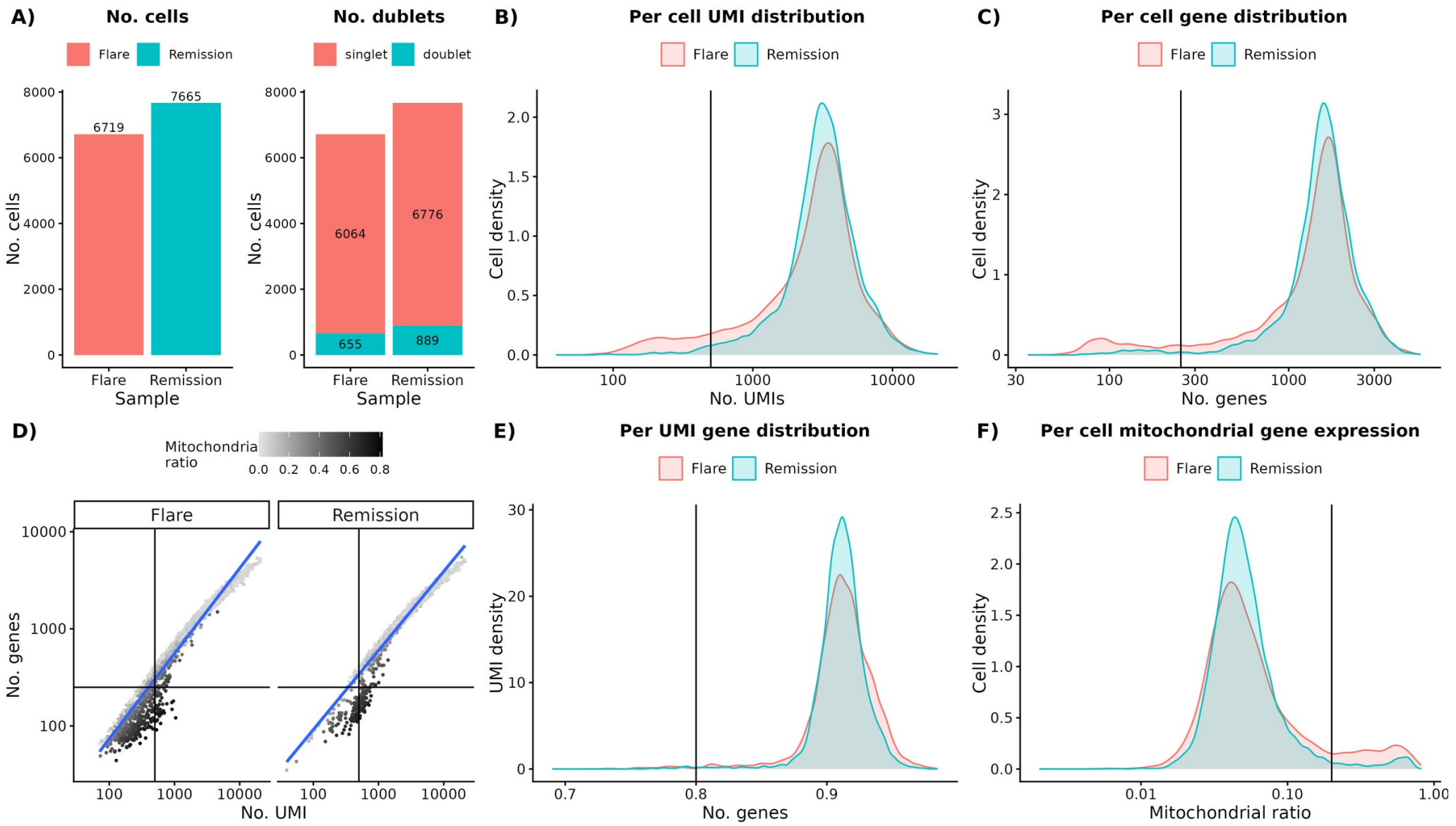
Supplementary Figure S1 (continued). Quality-control metrics — Patient P9.

Panels A–F as defined for Patient P1 on the first page of this figure.



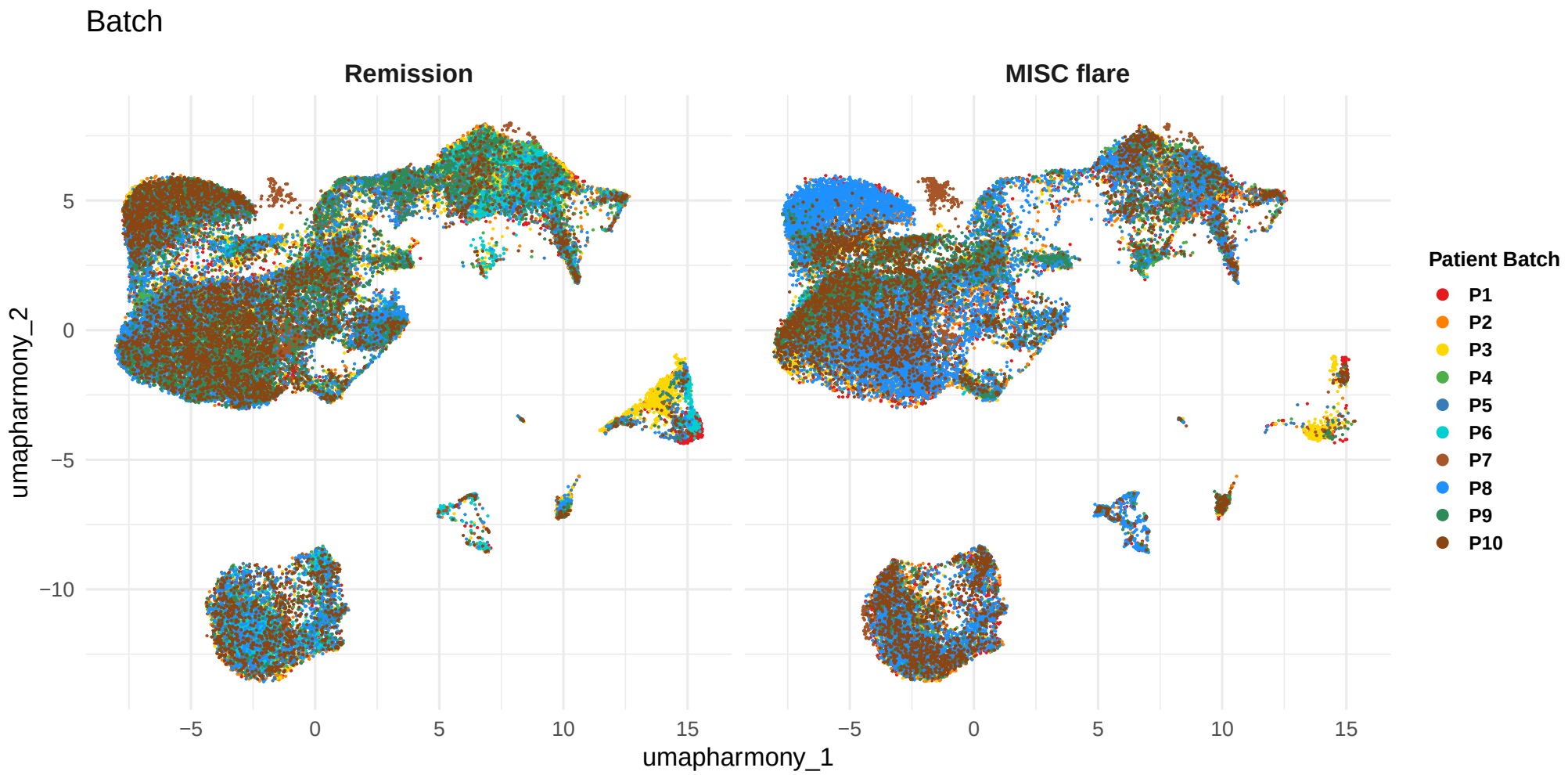
Supplementary Figure S1 (continued). Quality-control metrics — Patient P10.

Panels A–F as defined for Patient P1 on the first page of this figure.



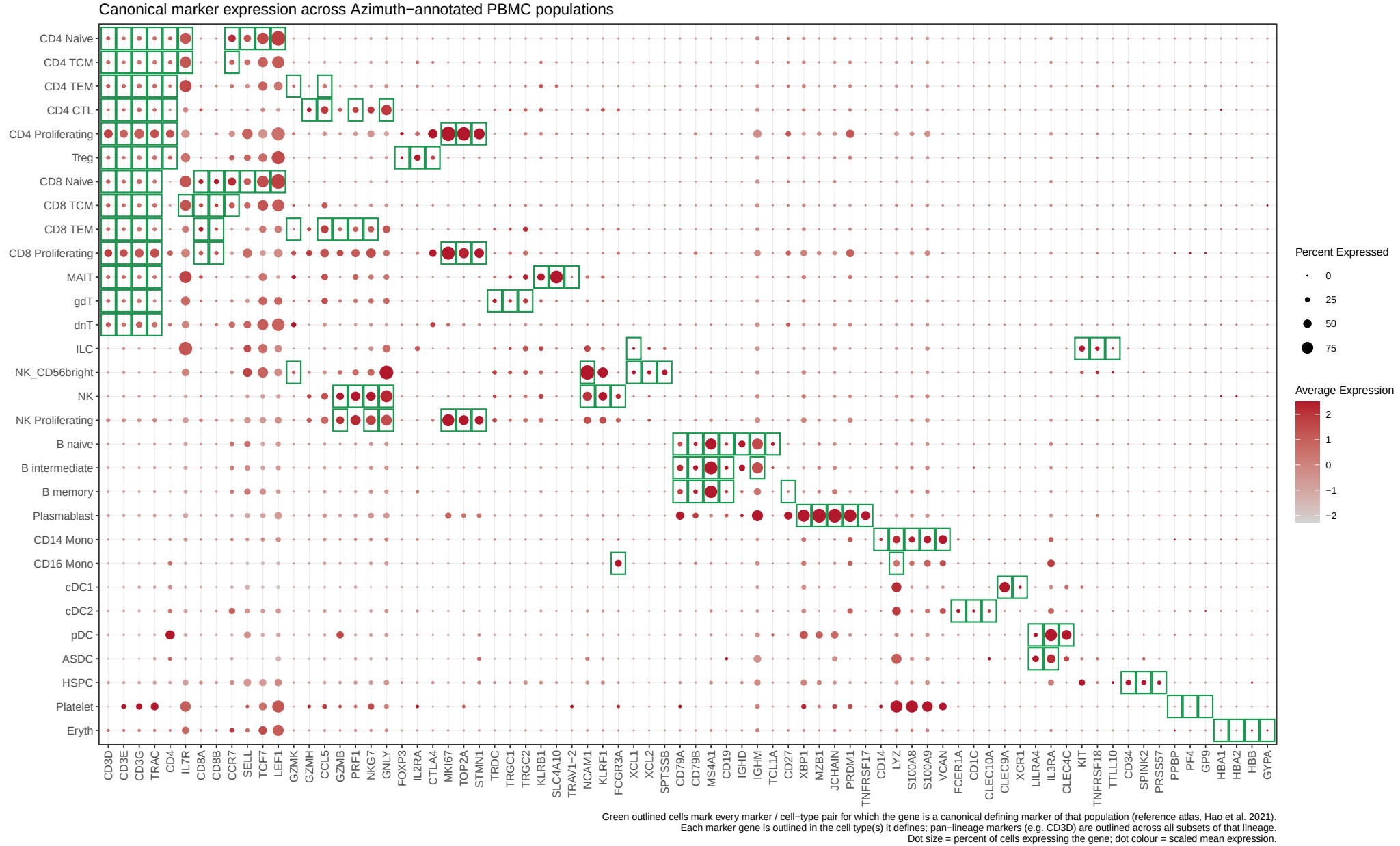
Supplementary Figure S2. UMAP visualisation of patient batch distribution after Harmony integration.

Joint UMAP of harmony-integrated nuclei, split by condition (remission, left; MIS-C flare, right) and coloured by patient (P1–P10). Even intermixing of patient colours across clusters indicates effective batch correction.



Supplementary Figure S3. Validation of Azimuth-based cell-type annotation using canonical markers.

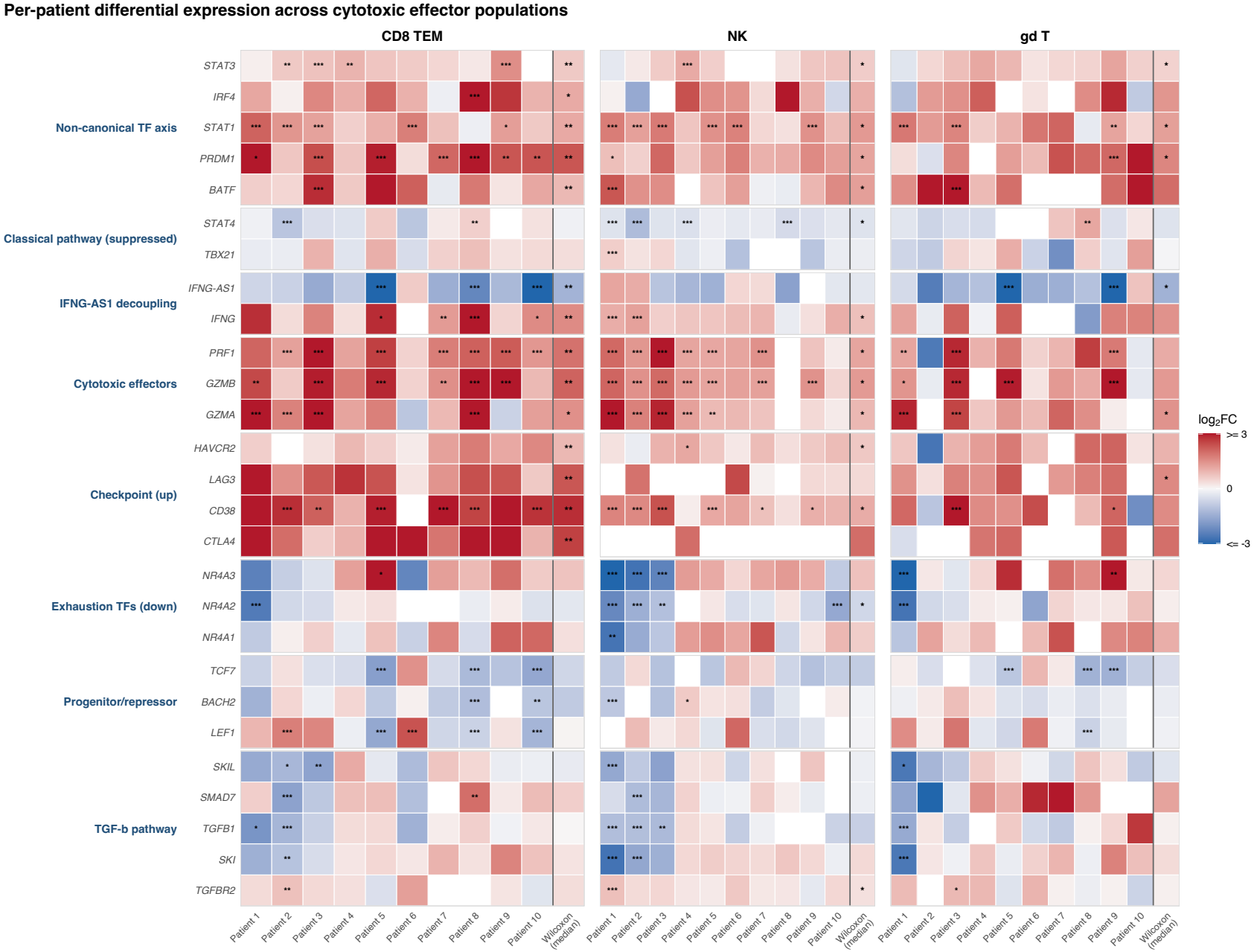
Dot plot of canonical marker expression across Azimuth-annotated PBMC populations. Green outlines mark each marker/cell-type pair for which the gene is a canonical defining marker in the reference atlas (Hao et al. 2021). Dot size, percent of cells expressing the gene; colour, scaled mean expression.



Green outlined cells mark every marker / cell−type pair for which the gene is a canonical defining marker of that population (reference atlas, Hao et al. 2021).
Each marker gene is outlined in the cell type(s) it defines; pan−lineage markers (e.g. CD3D) are outlined across all subsets of that lineage.
Dot size = percent of cells expressing the gene; dot colour = scaled mean expression.

Supplementary Figure S4. Per-patient differential expression across cytotoxic effector populations.

Heatmap of per-patient log■ fold-changes (flare versus remission) for manuscript-relevant genes grouped by functional category, shown for CD8■ TEM, NK, and γδ T cells. Right-hand column shows the paired Wilcoxon median across patients. Red, upregulated in flare; blue, downregulated. * adj.p < 0.05; ** adj.p < 0.01; *** adj.p < 0.001.



Supplementary Figure S5. Cross-cohort bulk RNA-seq validation of the non-canonical transcription-factor axis.

(A) Cross-cohort concordance of log■ fold-changes between the main (n=10) and external validation (n=9) bulk cohorts; points coloured by significance category. (B) Forest plot of log■ fold-changes for key genes grouped by functional category; circles, main cohort; squares, validation cohort; black borders indicate adj.p < 0.05. (C, D) Volcano plots for the main and validation cohorts with manuscript-curated genes labelled.