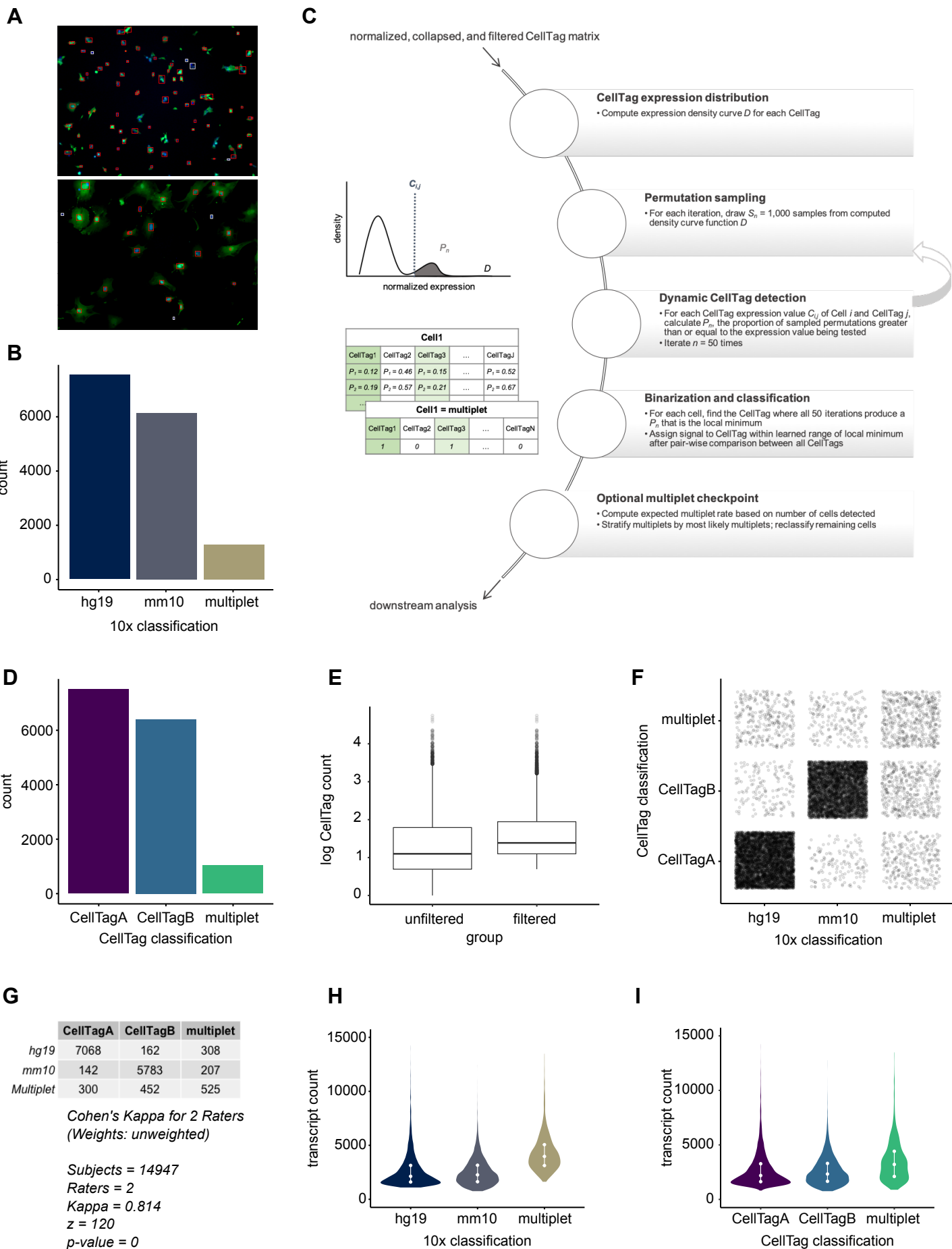


**Fig. S1** CellTag does not interfere with normal cell physiology or reprogramming. **A**, Schematic of B-cell to macrophage reprogramming and CellTagging. **B**, A median of 6 CellTag transcripts are detected per cell in CellTagged transcriptomes (CellTags were detected in all cells of this sample), while none are detected in control transcriptomes. **C**, CellTagged and control macrophages transcriptomes are interspersed with no independent clustering; both cluster separately from B cells. **D**, CellTagged and control macrophages transcriptomes share indistinguishable cluster composition, both distinct from B cell transcriptomes. **D**, CellTagged and control macrophages transcriptomes have similar macrophage marker expression and downregulate B cell marker expression. **E**, Genome-wide gene expression between CellTagged and control transcriptomes are strongly correlated with an  $R^2$  of 0.98.



**Fig. S2** CellTag classification compared with 10x-based classification the 2-tag species mixing experiment. **A**, Visualization and quantification of GFP expression in DAPI-stained HEK293Ts (top, 95%) and MEFs (bottom, 88%) transduced with CellTag virus for 24-48 hours. Red box, DAPI<sup>+</sup> GFP<sup>+</sup>; white box, DAPI<sup>+</sup> GFP<sup>-</sup>. **B**, 10x-based classification; excluding non-determined cells. **C**, Schematic workflow of the dynamic binarization and classification framework. **D**, CellTag classification; excluding non-determined cells. **E**, Log-normalized CellTag count before and after filtering for non-determined cells. **F**, Visual comparison of CellTag and 10x-based classification. **G**, Table comparing CellTag and 10x-based classification, benchmarked using Cohen's kappa as a measure of agreement. Unweighted Cohen's Kappa = 0.814. **H&I**, Total transcript count in different groups as classified by 10x- or CellTag-based classification. Dotted bars, first, median, and third quartiles.