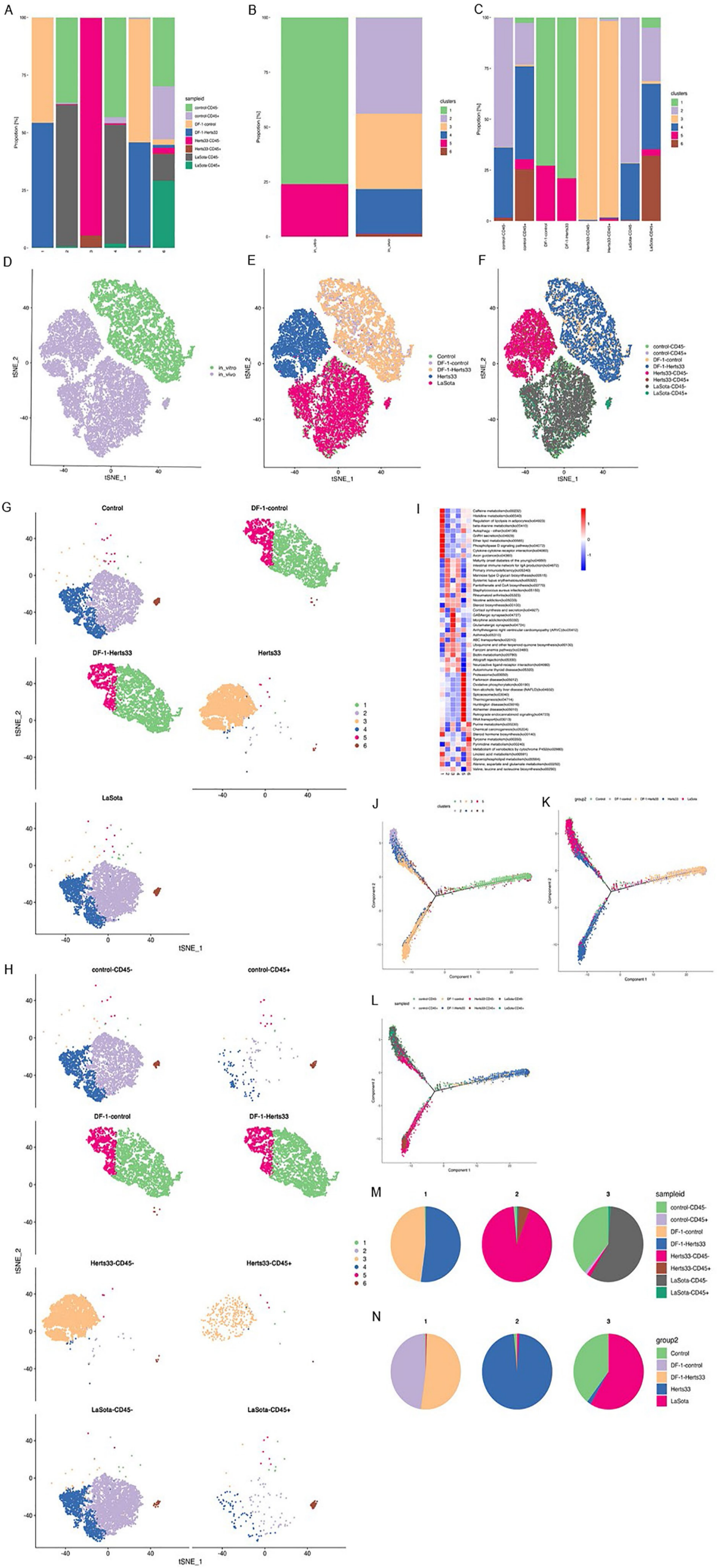
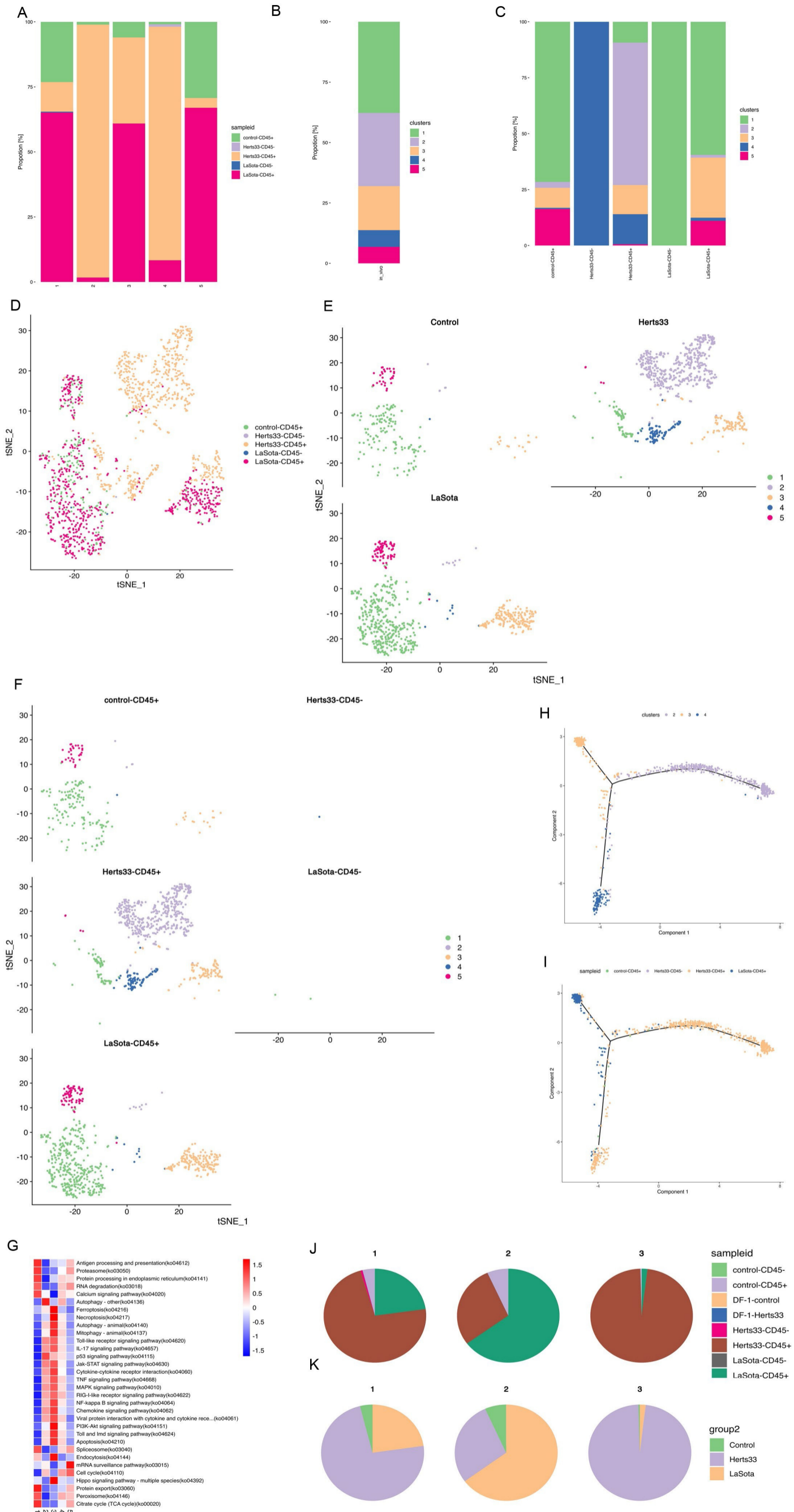


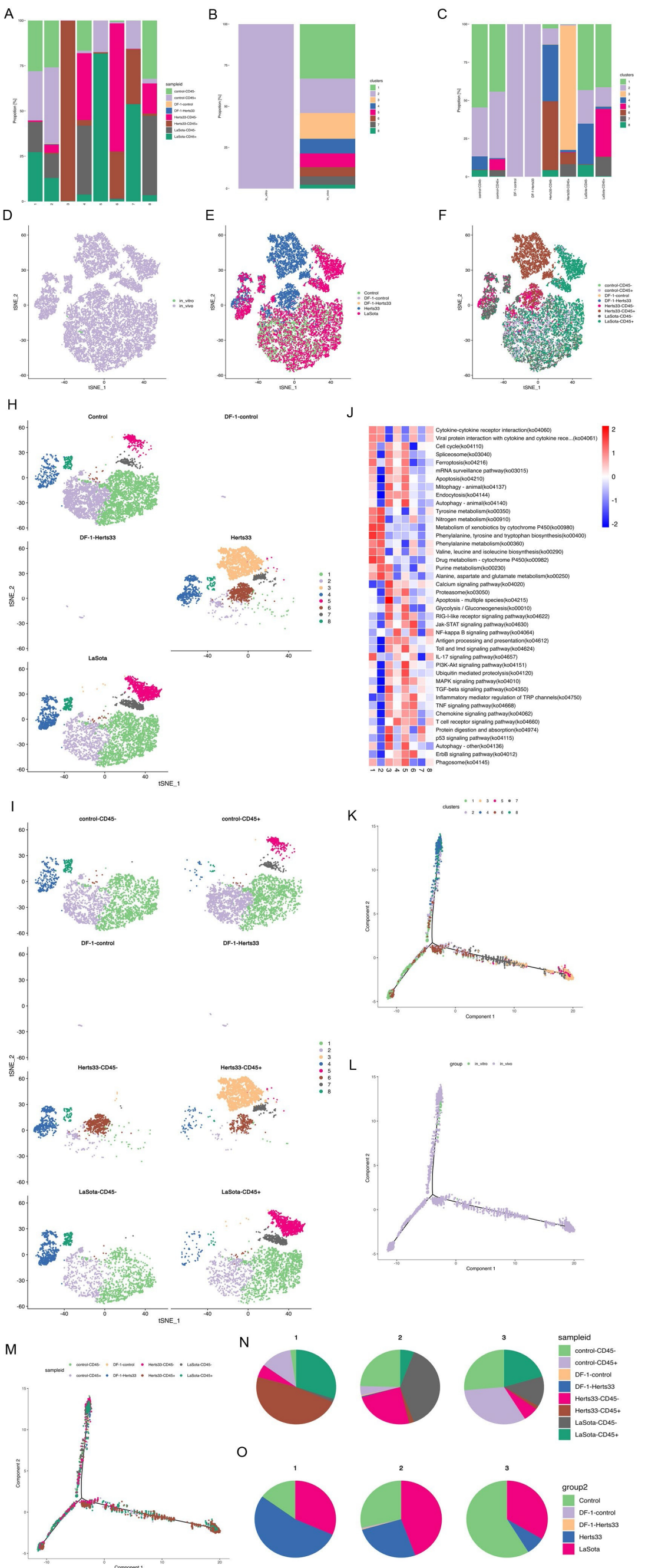
Supplementary Figure1



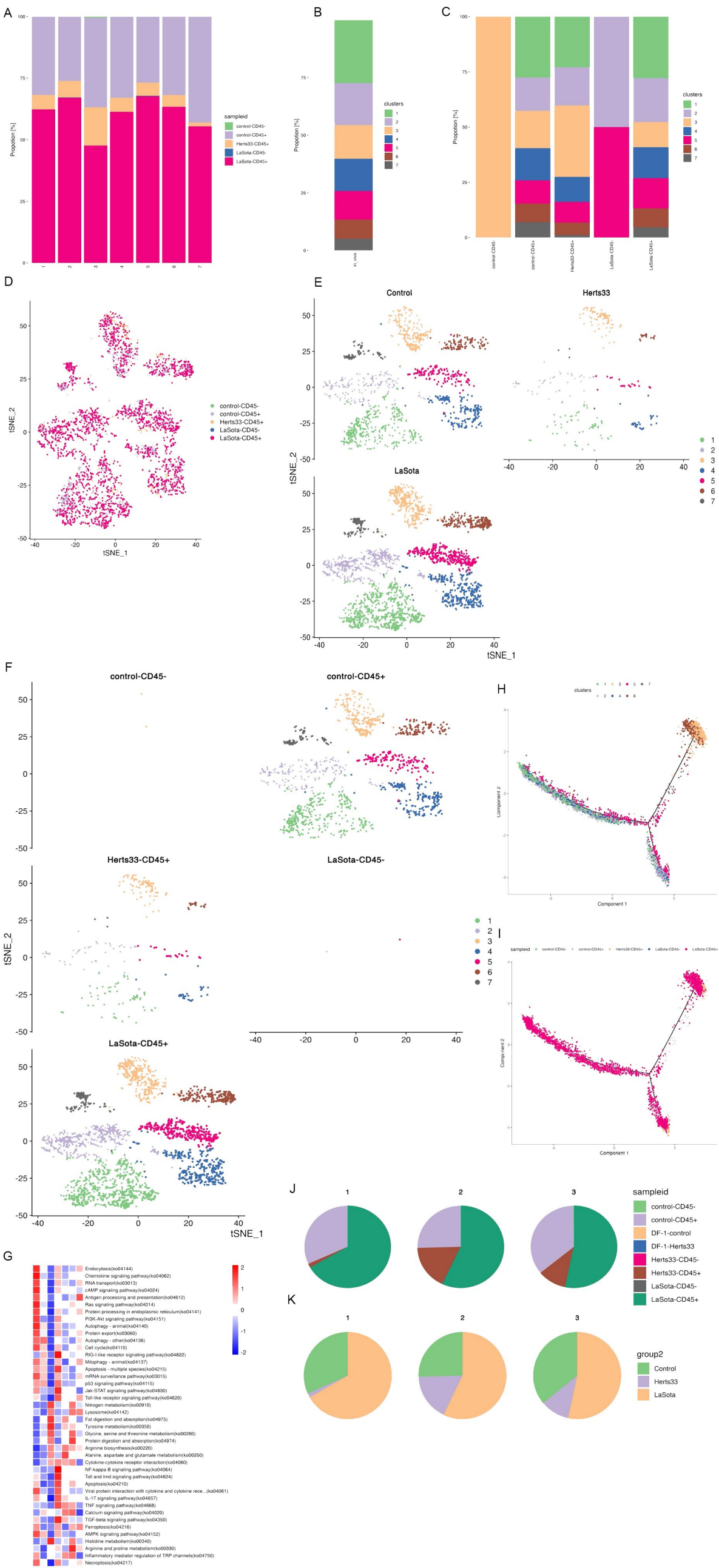
Supplementary Figure2



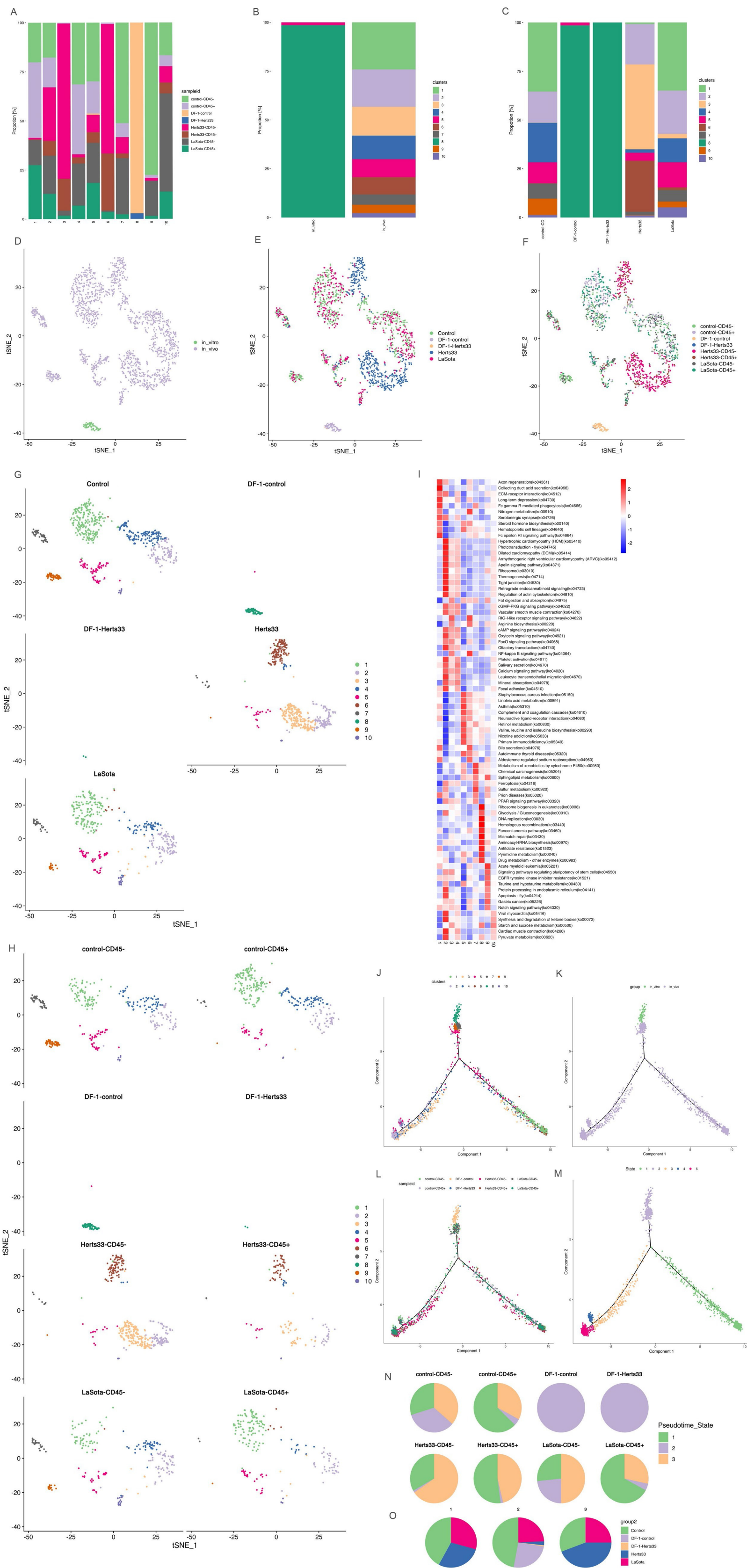
Supplementary Figure3



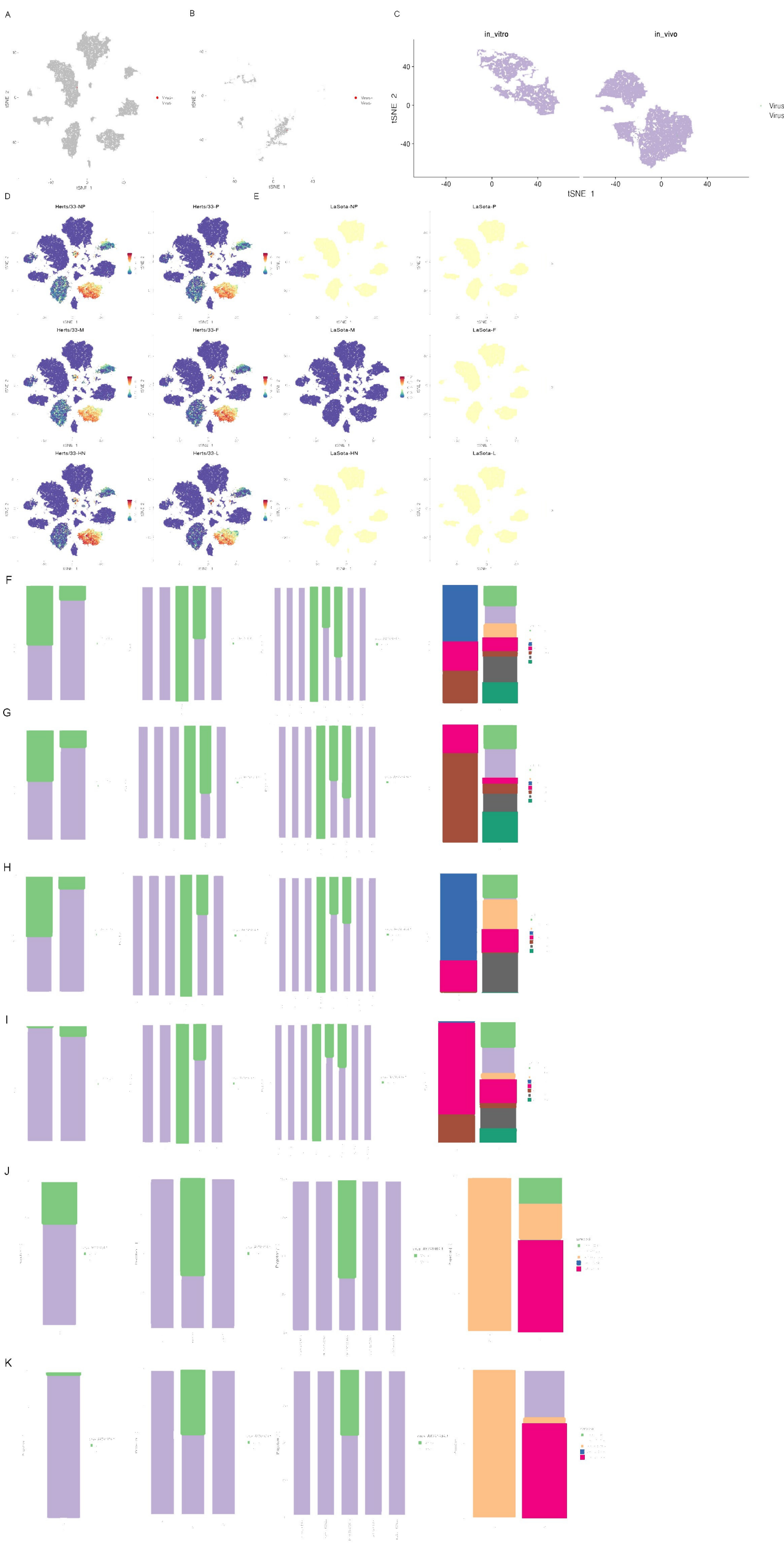
Supplementary Figure4



Supplementary Figure5

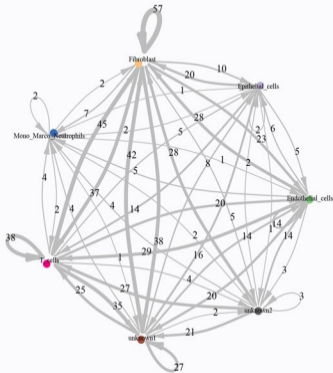


Supplementary Figure6

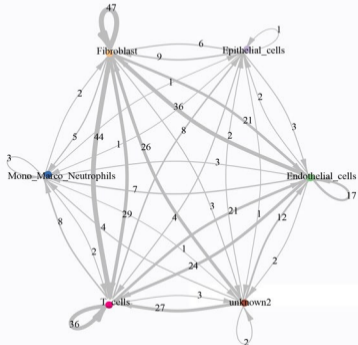


Supplementary Figure7

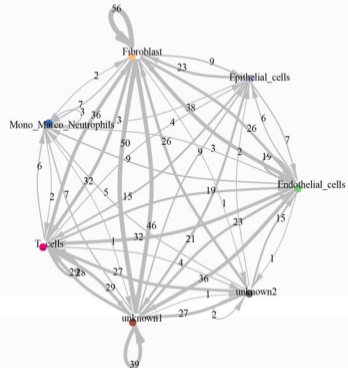
Control



Herts/33



LaSota



Supplementary Figure8

1 Supplementary Figure 1. Global single-cell transcriptional landscape in the chicken
2 lung and DF-1 cell line. A. Barplots showing the proportion of each cluster in each
3 cell type. B. Barplots showing the proportion of each cell type both *in vitro* and *in*
4 *vivo*. C. Barplots showing the proportion of each sample in each cell type. D. Barplots
5 showing the proportion of each cell type in each sample. t-SNE plot of the sample
6 both *in vitro* and *in vivo*. F. t-SNE plot of the sample in control, Herts/33, LaSota,
7 DF-1-control, and DF-1-Herts/33. G. t-SNE plot of the sample in
8 control-CD45⁺/CD45⁻, Herts/33-CD45⁺/CD45⁻, LaSota-CD45⁺/CD45⁻, DF-1-control,
9 and DF-1-Herts/33. H. t-SNE plot of the sample in control-CD45⁺/CD45⁻,
10 Herts/33-CD45⁺/CD45⁻, LaSota-CD45⁺/CD45⁻, DF-1-control, and DF-1-Herts/33. I.
11 t-SNE plot of the sample in control, Herts/33, LaSota, DF-1-control, and
12 DF-1-Herts/33. J. t-SNE plot of each cell type in each cluster.

13

14 Supplementary Figure 2. Single-cell profiling of fibroblast cells. A. Barplots showing
15 the proportion of each sample in each cluster. B. Barplots showing the proportion of
16 each cell type both *in vitro* and *in vivo*. C. Barplots showing the proportion of each
17 cluster in each sample. D. t-SNE plot of the sample both *in vitro* and *in vivo*. E. t-SNE
18 plot of the sample in control, Herts/33, LaSota, DF-1-control, and DF-1-Herts/33. F.
19 t-SNE plot of the sample in control-CD45⁺/CD45⁻, Herts/33-CD45⁺/CD45⁻,
20 LaSota-CD45⁺/CD45⁻, DF-1-control, and DF-1-Herts/33. G. t-SNE plot of each cell
21 cluster in control, Herts/33, LaSota, DF-1-control, and DF-1-Herts/33. H. t-SNE plot
22 of each cell cluster in control-CD45⁺/CD45⁻, Herts/33-CD45⁺/CD45⁻,

23 LaSota-CD45⁺/CD45⁻, DF-1-control, and DF-1-Herts/33. I. Differences in pathway
24 activities scored per cell by GSVA between epithelial cells isolated from different
25 epithelial clusters, with enriched KO terms; $P < 0.05$. J–L. Pseudotime trajectory plot
26 representing the features of each cluster (J) and in each sample (K and L) in the three
27 identified states. M and N. Pie charts showing the proportion of cells in each sample
28 in the three identified states.

29

30 Supplementary Figure 3. Single-cell profiling of myeloid cells. A. Barplots showing
31 the proportion of each sample in each cluster. B. Barplots showing the proportion of
32 each cell type *in vivo*. C. Barplots showing the proportion of each cluster in each
33 sample. D. t-SNE plot of the sample in control, Herts/33, LaSota, DF-1-control, and
34 DF-1-Herts/33. E. t-SNE plot of each cell cluster in the control, Herts/33, and LaSota
35 groups. H. t-SNE plot of each cell cluster in control-CD45⁺, Herts/33-CD45⁺/CD45⁻,
36 and LaSota-CD45⁺/CD45⁻. G. Differences in pathway activities scored per cell by
37 GSVA between myeloid cells isolated from different epithelial clusters, with enriched
38 KO terms; $P < 0.05$. H and I. Pseudotime trajectory plot representing the features of
39 clusters 2, 3, and 4 (H) and in each sample (I) in the three identified states. J and K.
40 Pie charts showing the proportion of cells in each sample in the three identified states.

41

42 Supplementary Figure 4. Single-cell profiling of endothelial cells. A. Barplots
43 showing the proportion of each sample in each cluster. B. Barplots showing the
44 proportion of each cell type both *in vitro* and *in vivo*. C. Barplots showing the

45 proportion of each cluster in each sample. D. t-SNE plot of the sample both *in vitro*
46 and *in vivo*. E. t-SNE plot of the sample in control, Herts/33, LaSota, DF-1-control,
47 and DF-1-Herts/33. F. t-SNE plot of the sample in control-CD45⁺/CD45⁻,
48 Herts/33-CD45⁺/CD45⁻, LaSota-CD45⁺/CD45⁻, DF-1-control, and DF-1-Herts/33. G.
49 t-SNE plot of each cell cluster in control, Herts/33, LaSota, DF-1-control, and
50 DF-1-Herts/33. H. t-SNE plot of each cell cluster in control-CD45⁺/CD45⁻,
51 Herts/33-CD45⁺/CD45⁻, LaSota-CD45⁺/CD45⁻, DF-1-control, and DF-1-Herts/33. I.
52 Differences in pathway activities scored per cell by GSVA between endothelial cells
53 isolated from different epithelial clusters, with enriched KO terms; $P < 0.05$. J–L.
54 Pseudotime trajectory plot representing the features of each cluster *in vivo* (J), *in vitro*
55 (K), and in each sample (L) in the three identified states. M and N. Pie charts showing
56 the proportion of cells in each sample in the three identified states.
57
58 Supplementary Figure 5. Single-cell profiling of epithelial cells. A. Barplots showing
59 the proportion of each sample in each cluster. B. Barplots showing the proportion of
60 each cell type *in vivo*. C. Barplots showing the proportion of each cluster in each
61 sample. D. t-SNE plot of the sample in control-CD45⁻/control-CD45⁺,
62 Herts/33-CD45⁺, and LaSota-CD45⁺/CD45⁻. E. t-SNE plot of each cell cluster in the
63 control, Herts/33, and LaSota groups. F. t-SNE plot of each cell cluster in
64 control-CD45⁻/control-CD45⁺, Herts/33-CD45⁺, and LaSota-CD45⁺/CD45⁻. G.
65 Differences in pathway activities scored per cell by GSVA between myeloid cells
66 isolated from different epithelial clusters, with enriched KO terms; $P < 0.05$. H and I.

67 Pseudotime trajectory plot representing the features of each cluster (H) and each
68 sample (I) in the three identified states. K. Pie charts showing the proportion of cells
69 in each sample in the three identified states.

70

71 Supplementary Figure 6. Single-cell profiling of T cells. A. Barplots showing the
72 proportion of each sample in each cluster. B. Barplots showing the proportion of each
73 cell type both *in vitro* and *in vivo*. C. Barplots showing the proportion of each cluster
74 in each sample. D. t-SNE plot of the sample both *in vitro* and *in vivo*. E. t-SNE plot of
75 the sample in control, Herts/33, LaSota, DF-1-control, and DF-1-Herts/33. F. t-SNE
76 plot of the sample in control-CD45⁺/CD45⁻, Herts/33-CD45⁺/CD45⁻,
77 LaSota-CD45⁺/CD45⁻, DF-1-control, and DF-1-Herts/33. G. t-SNE plot of each cell
78 cluster in control, Herts/33, LaSota, DF-1-control, and DF-1-Herts/33. H. t-SNE plot
79 of each cell cluster in control-CD45⁺/CD45⁻, Herts/33-CD45⁺/CD45⁻,
80 LaSota-CD45⁺/CD45⁻, DF-1-control, and DF-1-Herts/33. I. Differences in pathway
81 activities scored per cell by GSVA between T cells isolated from different T cell
82 clusters, with enriched KO terms; $P < 0.05$. J–M. Pseudotime trajectory plot
83 representing the features of each cluster *in vivo* (J), *in vitro* (K), and in each sample (L)
84 in the three identified states. The five states were considered as three because states 3,
85 4, and 5 were on the same branch (M). N and O. Pie charts showing the proportion of
86 cells in each sample in the three identified states.

87

88 Supplementary Figure 7. A. Only two cells with LaSota RNA were detected (UMI > 0)
89 from total cells *in vivo*. B. Cells with LaSota RNA detected (UMI > 0) from fibroblast
90 cells *in vivo*. C. Cells with LaSota RNA detected (UMI > 0) from cells *in vivo*. D.
91 t-SNE plot of the virus genes of Herts/33 in each cluster. E. t-SNE plot of the virus
92 genes of LaSota in each cluster. F–K. Proportion of virus⁺ and virus⁻ cells in different
93 samples, and the composition of different samples in virus⁺ and virus⁻ cells.

94

95 Supplementary Figure 8. Cell–cell communication. Predicted number of interactions
96 among mono-macro-neutrophil, T, fibroblast, endothelial, epithelial, unknown1, and
97 unknown2 cells based on CellPhoneDB in the control, Herts/33, and LaSota groups.

98

99

100 Supplementary Table 1. Gene quantitative quality control overview of the sequencing
101 library, alignment of scRNA-seq, and marker genes used for cell type identification.

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