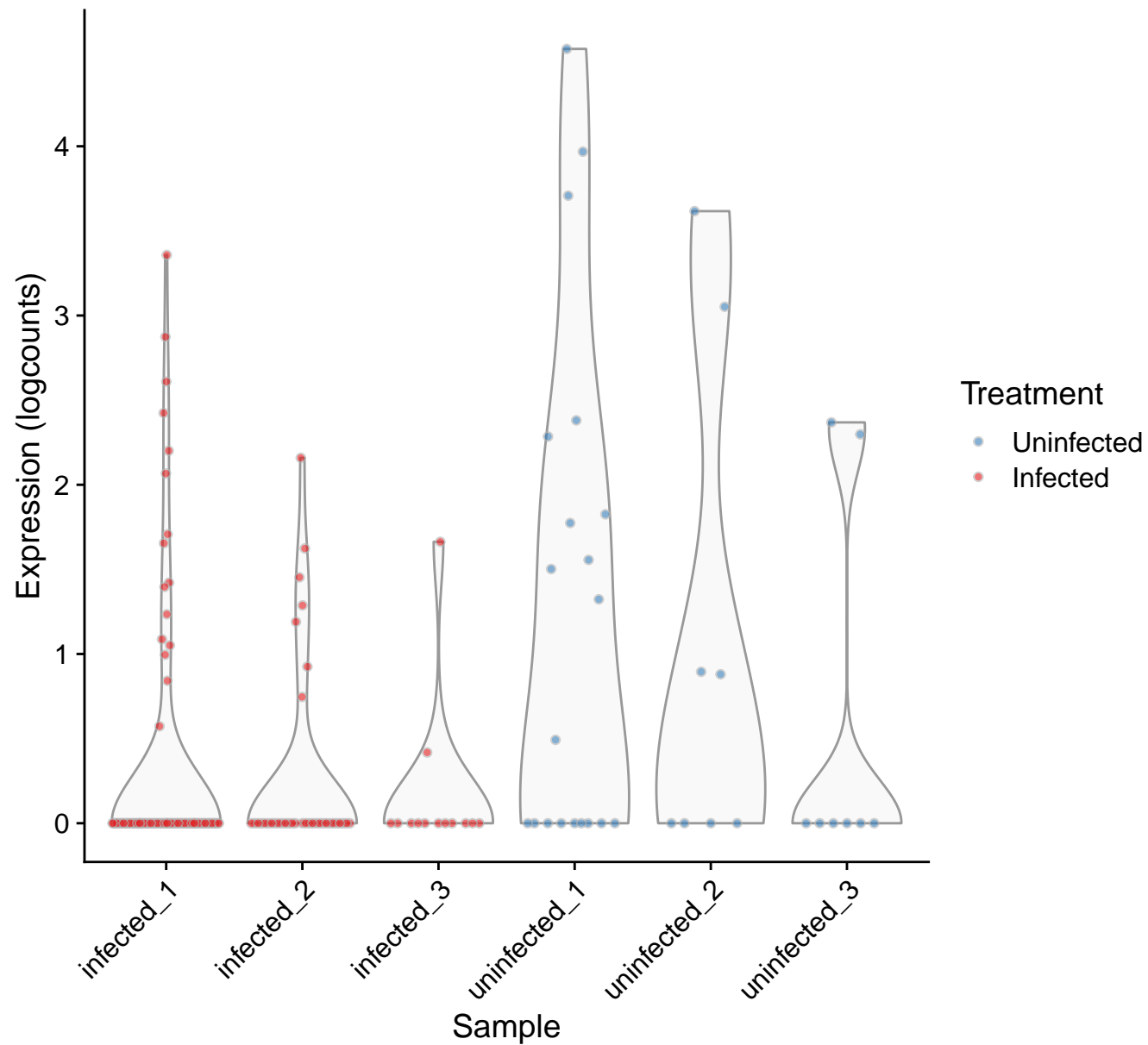


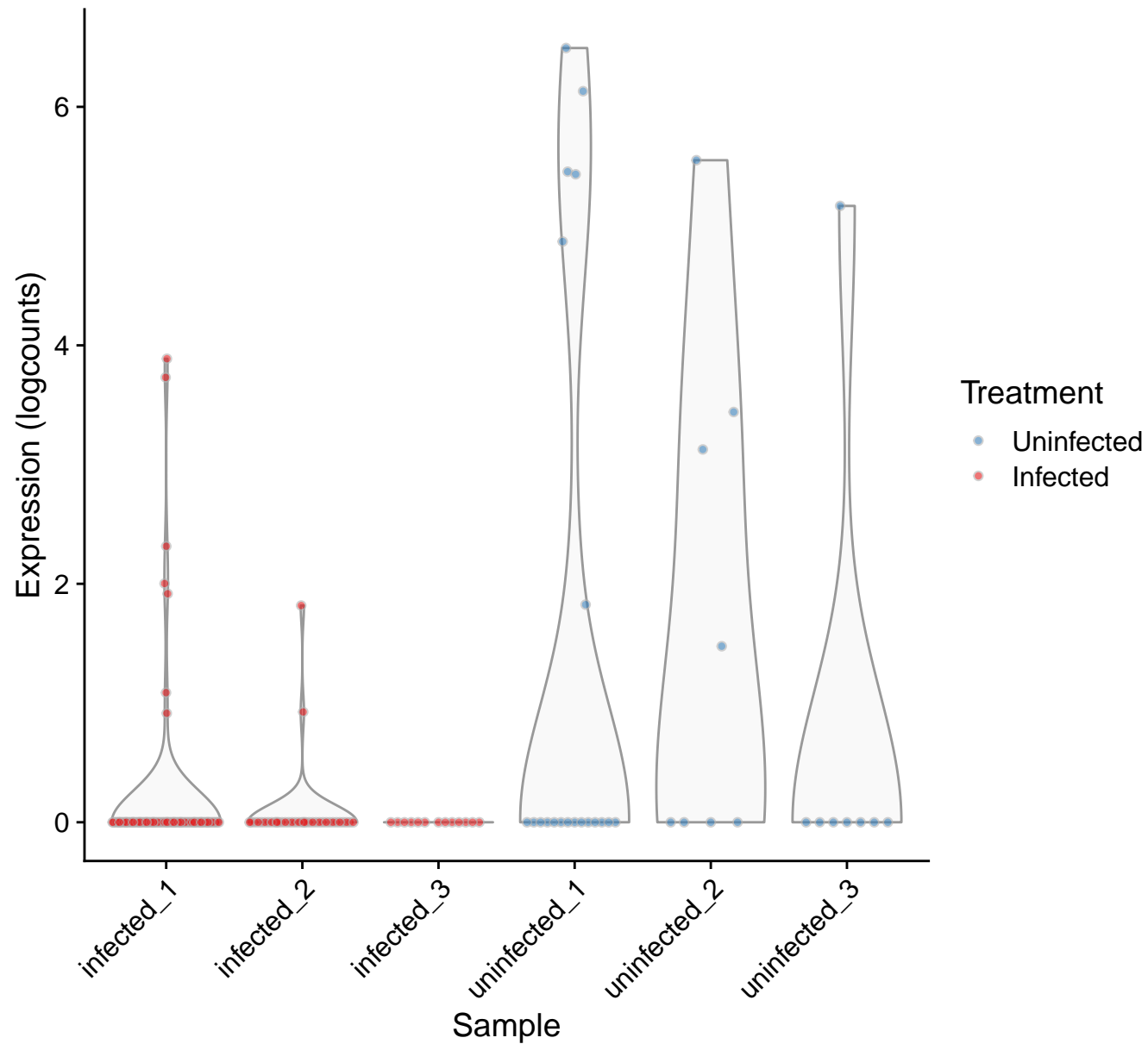
TIGIT (FDR = 1e-05)

cluster_9



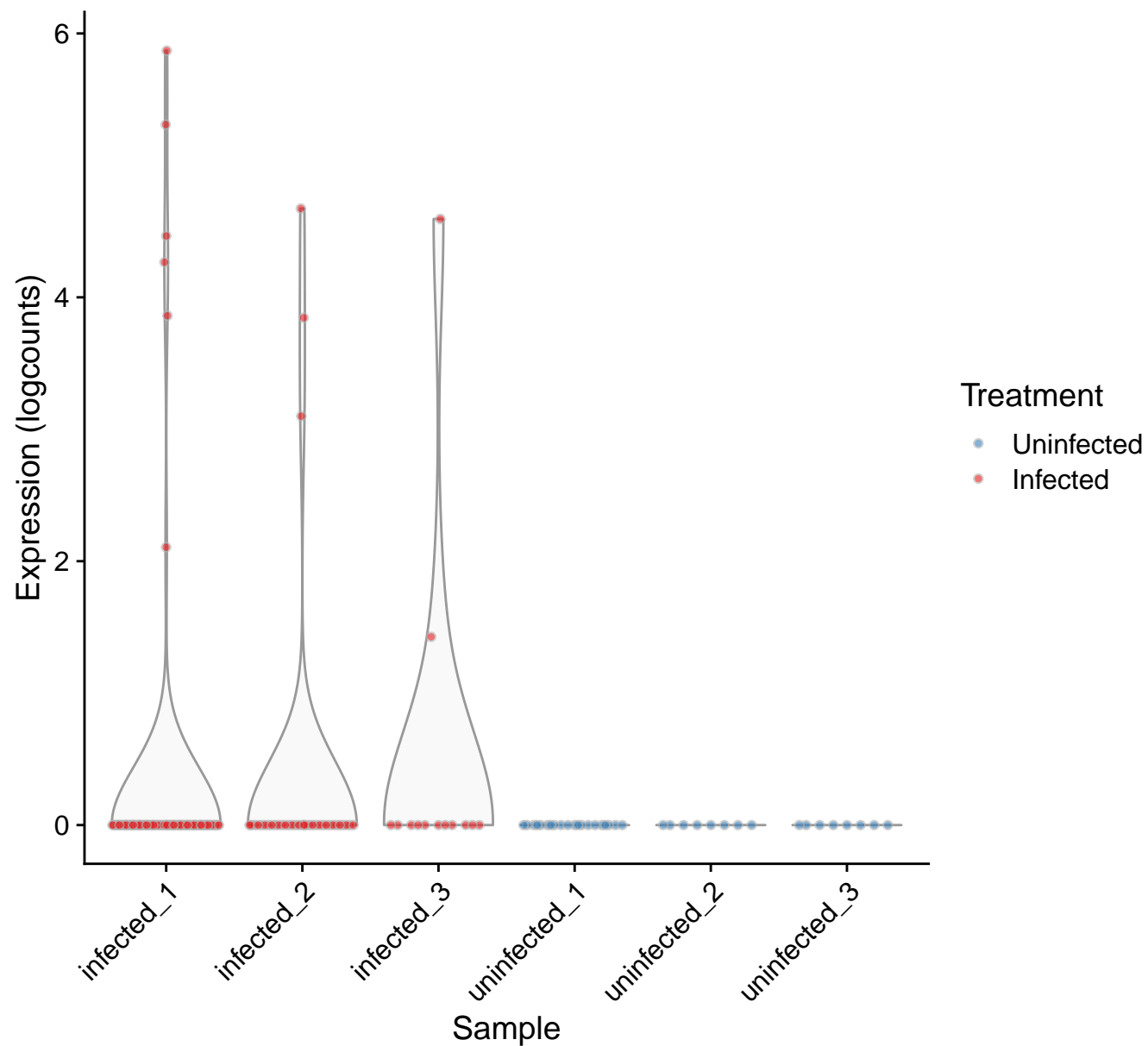
TRBV4-2 (FDR = 1e-05)

cluster_9



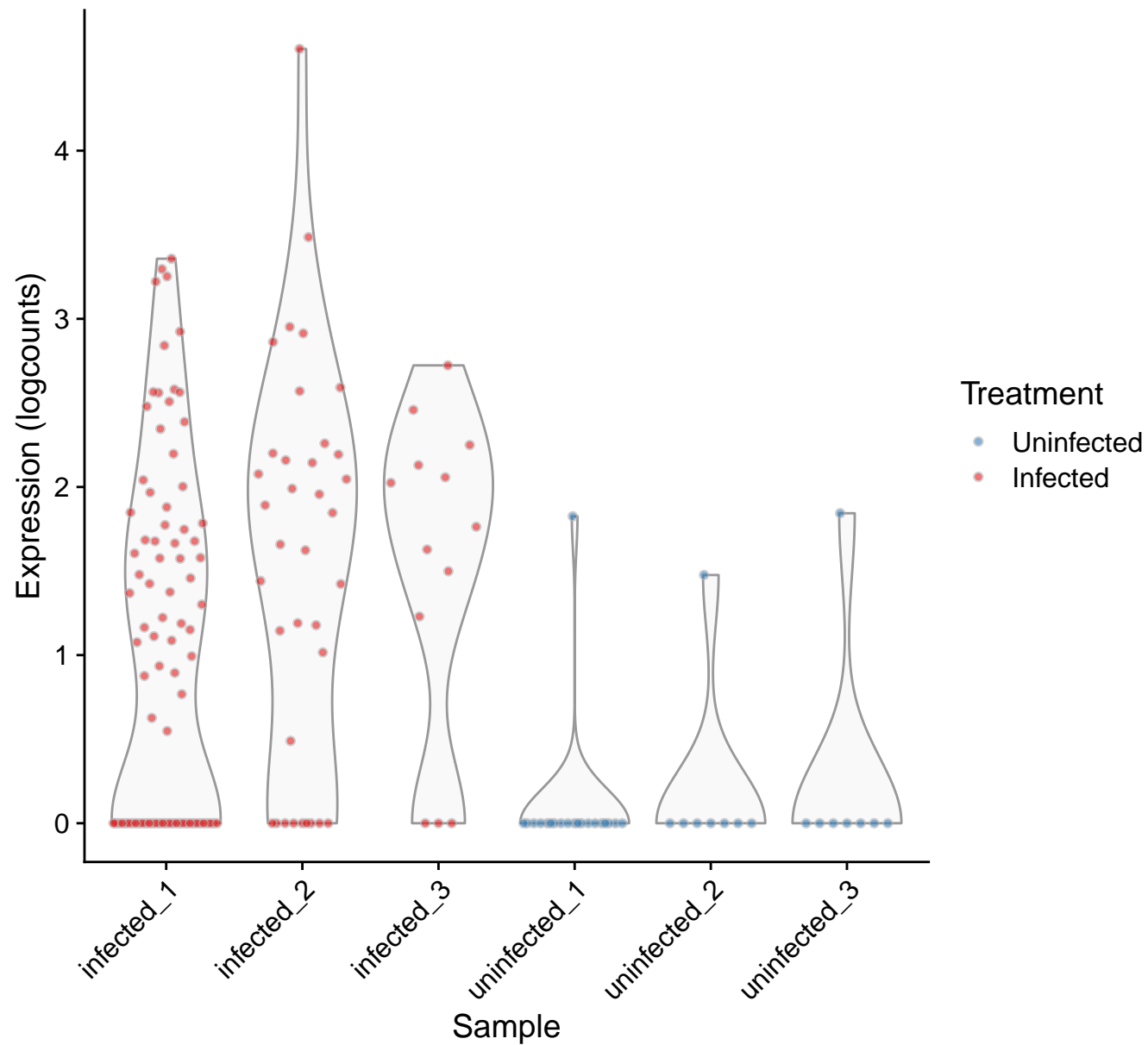
TRBV12-4 (FDR = 2e-05)

cluster_9



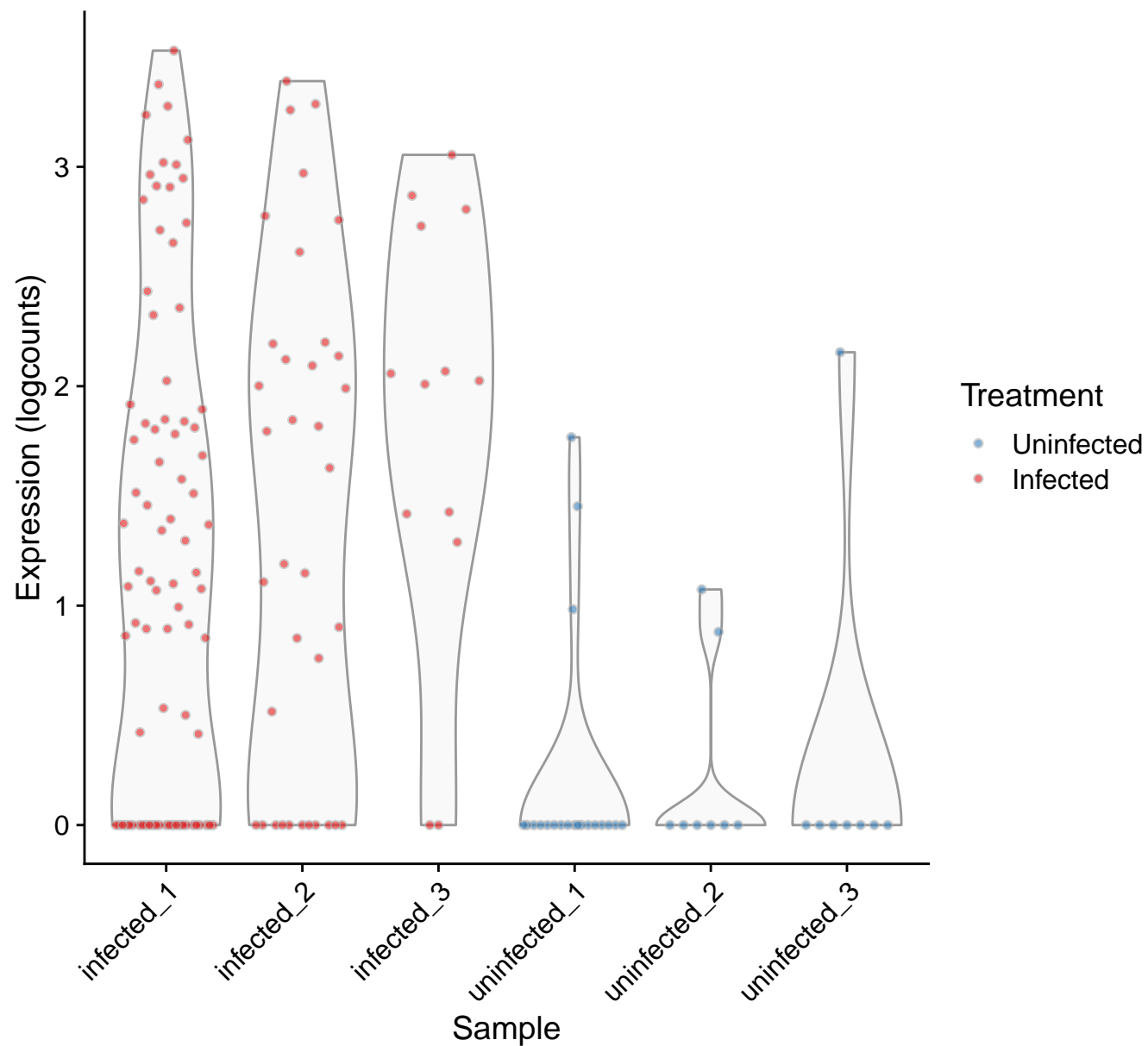
HLA-DRA (FDR = 1e-04)

cluster_9



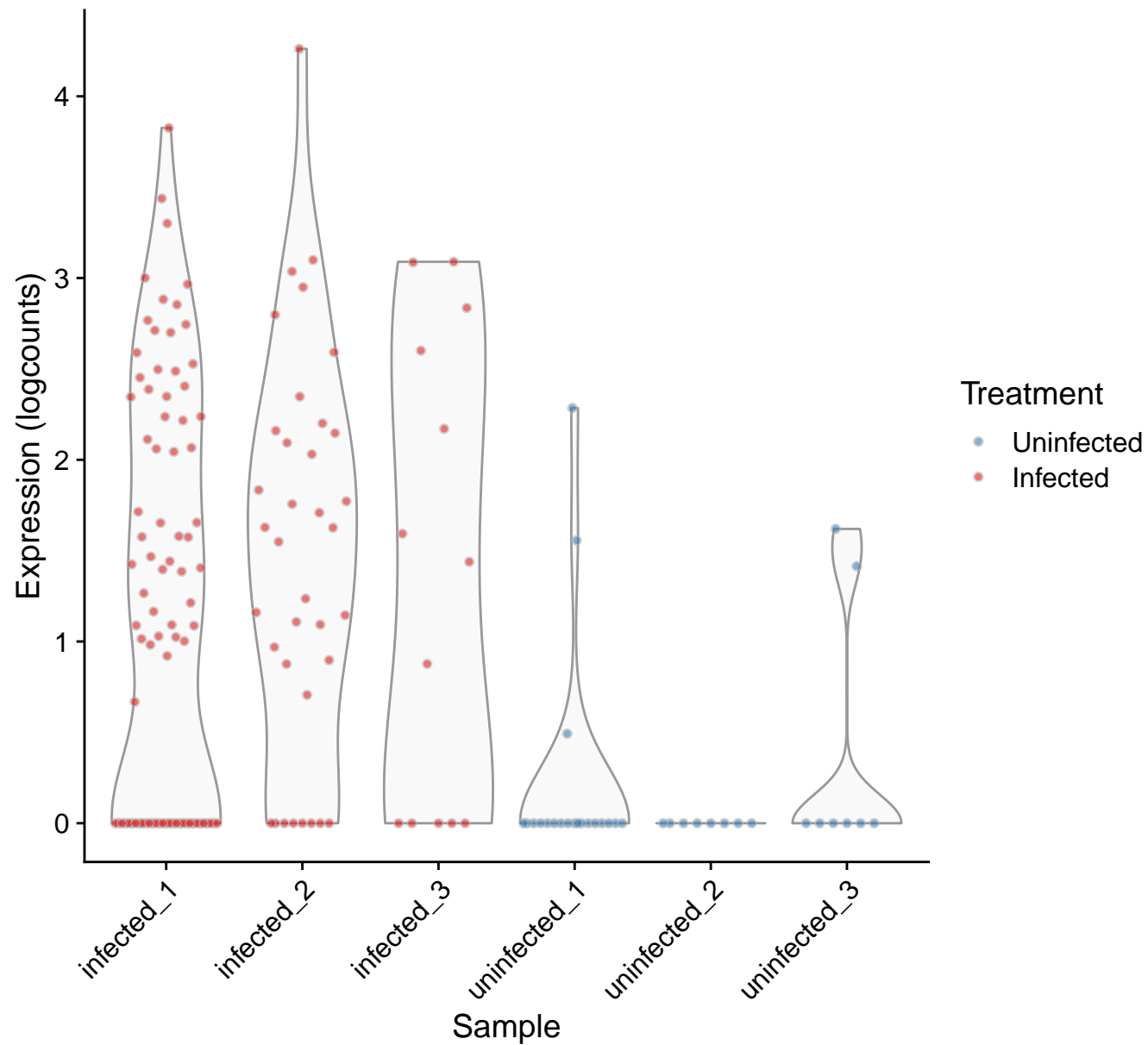
HLA-DRB5 (FDR = 4e-04)

cluster_9



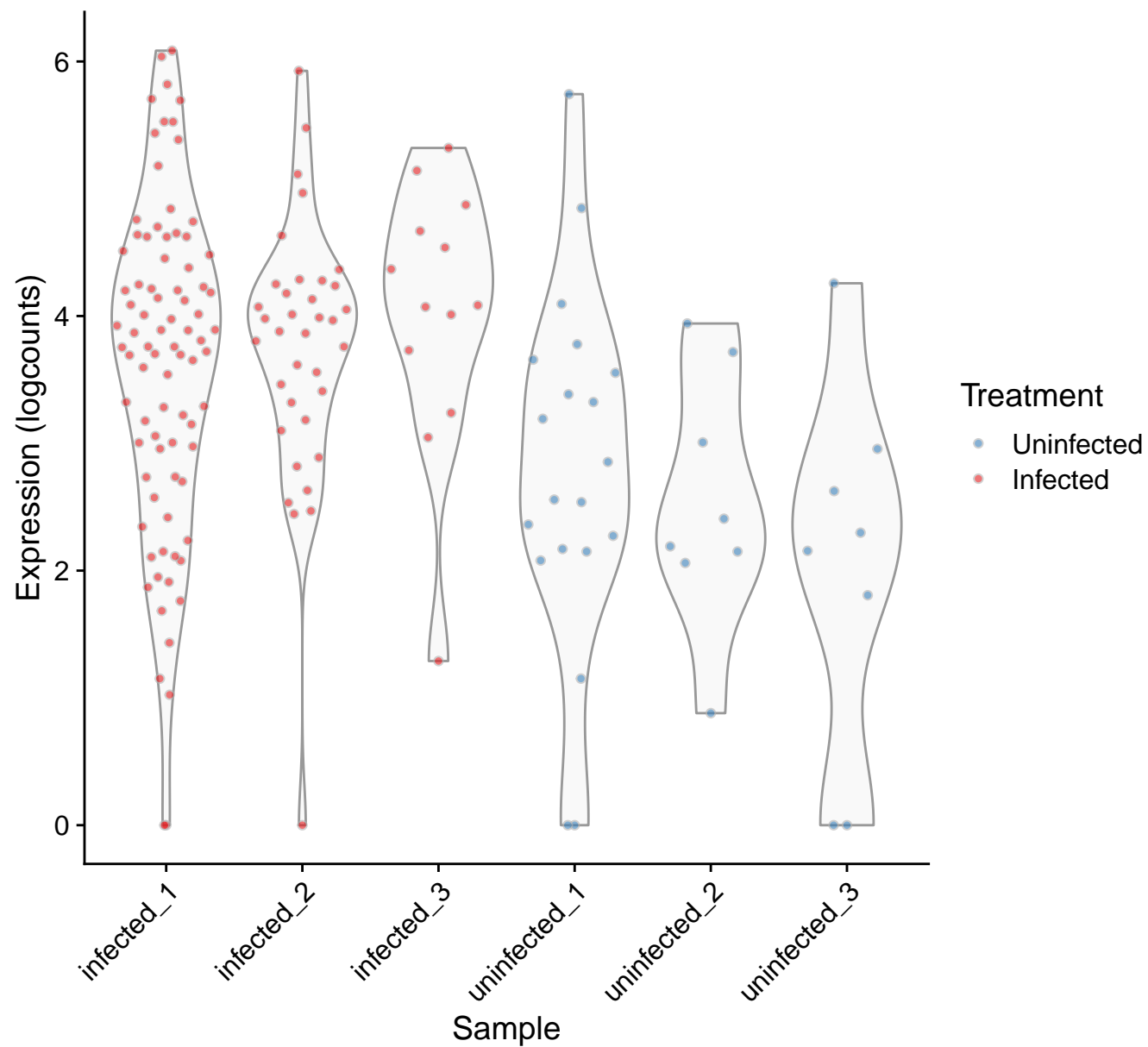
LINC01871 (FDR = 4e-04)

cluster_9



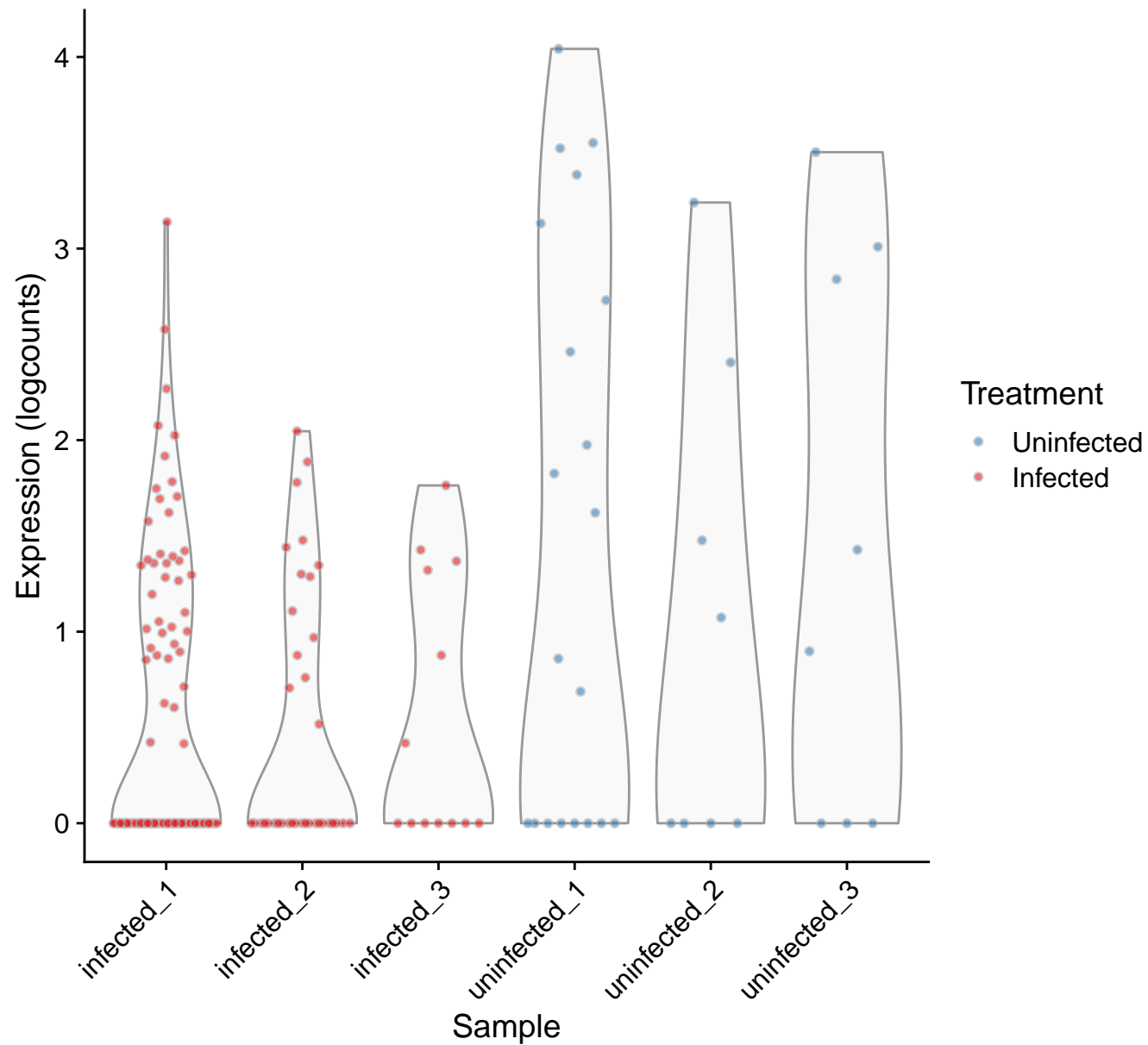
CD74 (FDR = 0.002)

cluster_9



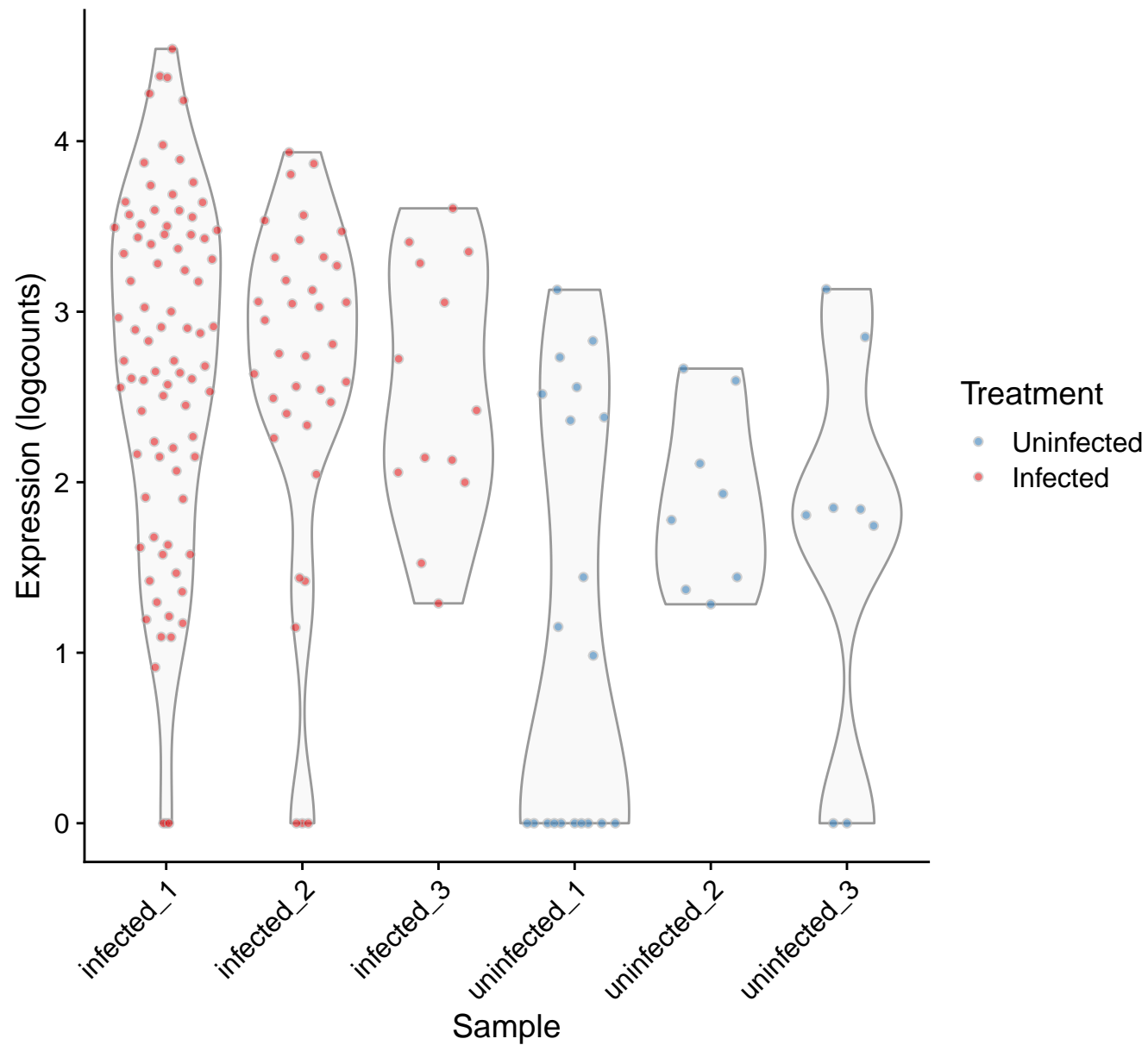
MX1 (FDR = 0.002)

cluster_9



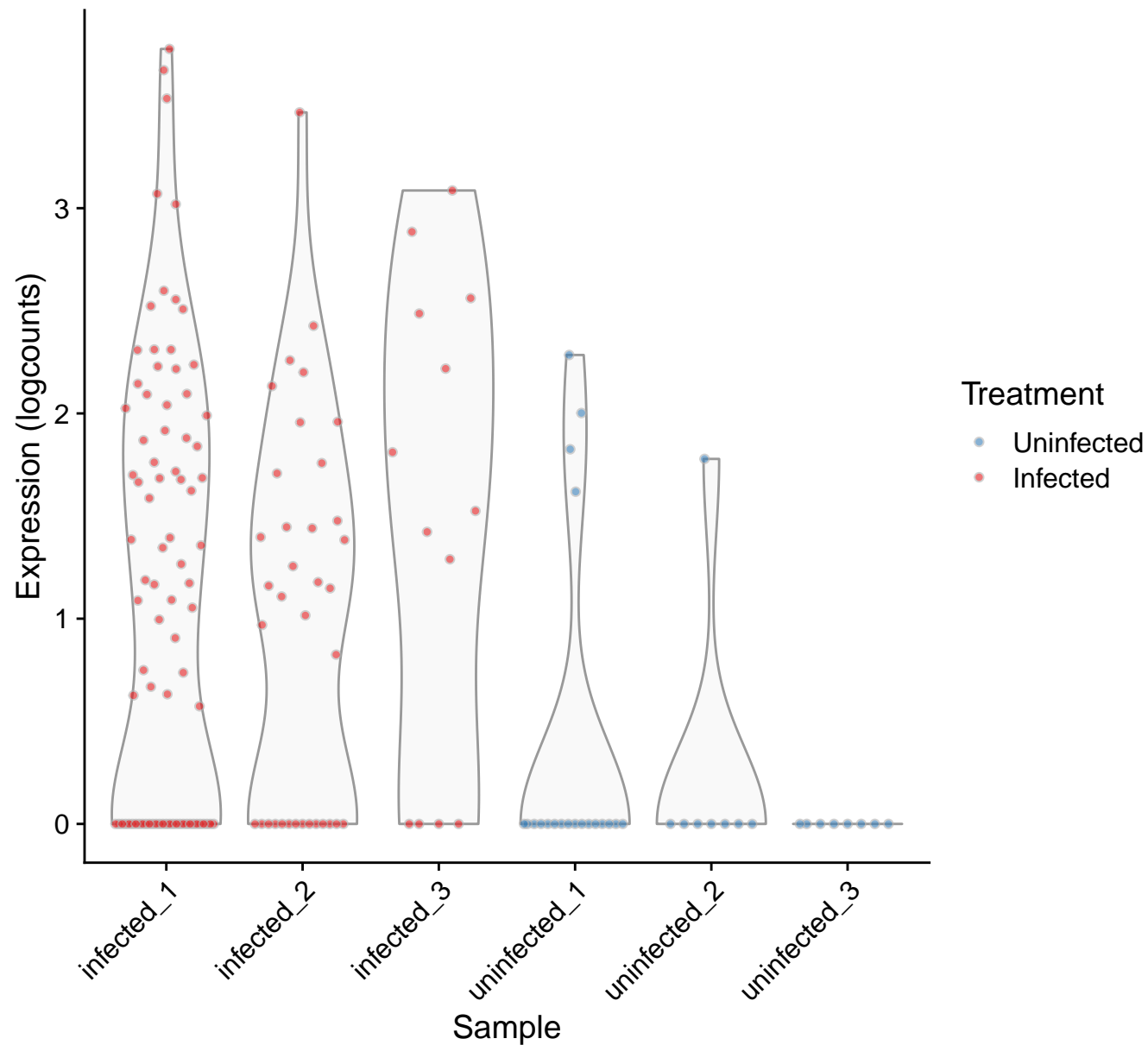
COTL1 (FDR = 0.003)

cluster_9



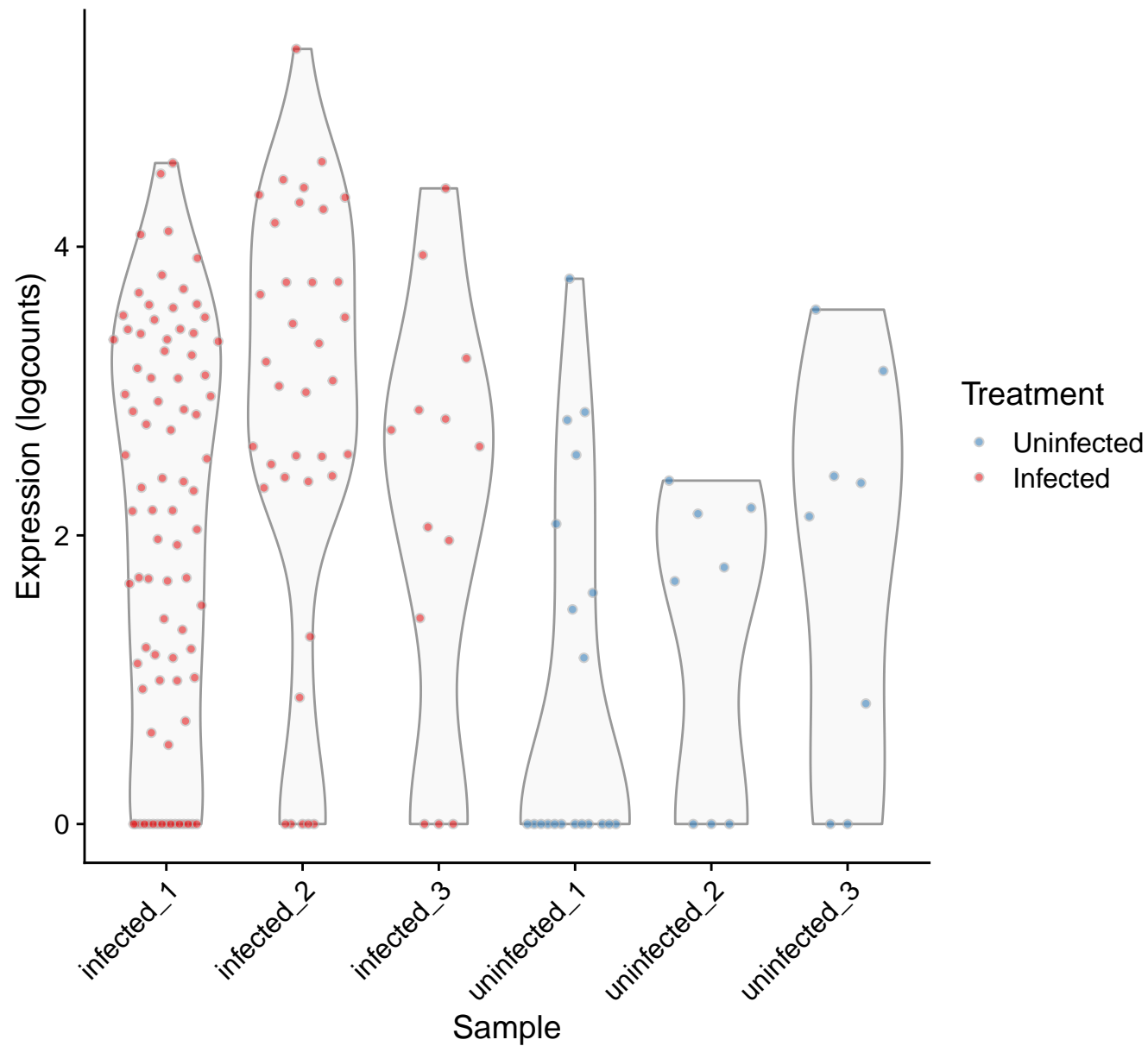
HLA-DRB1 (FDR = 0.004)

cluster_9



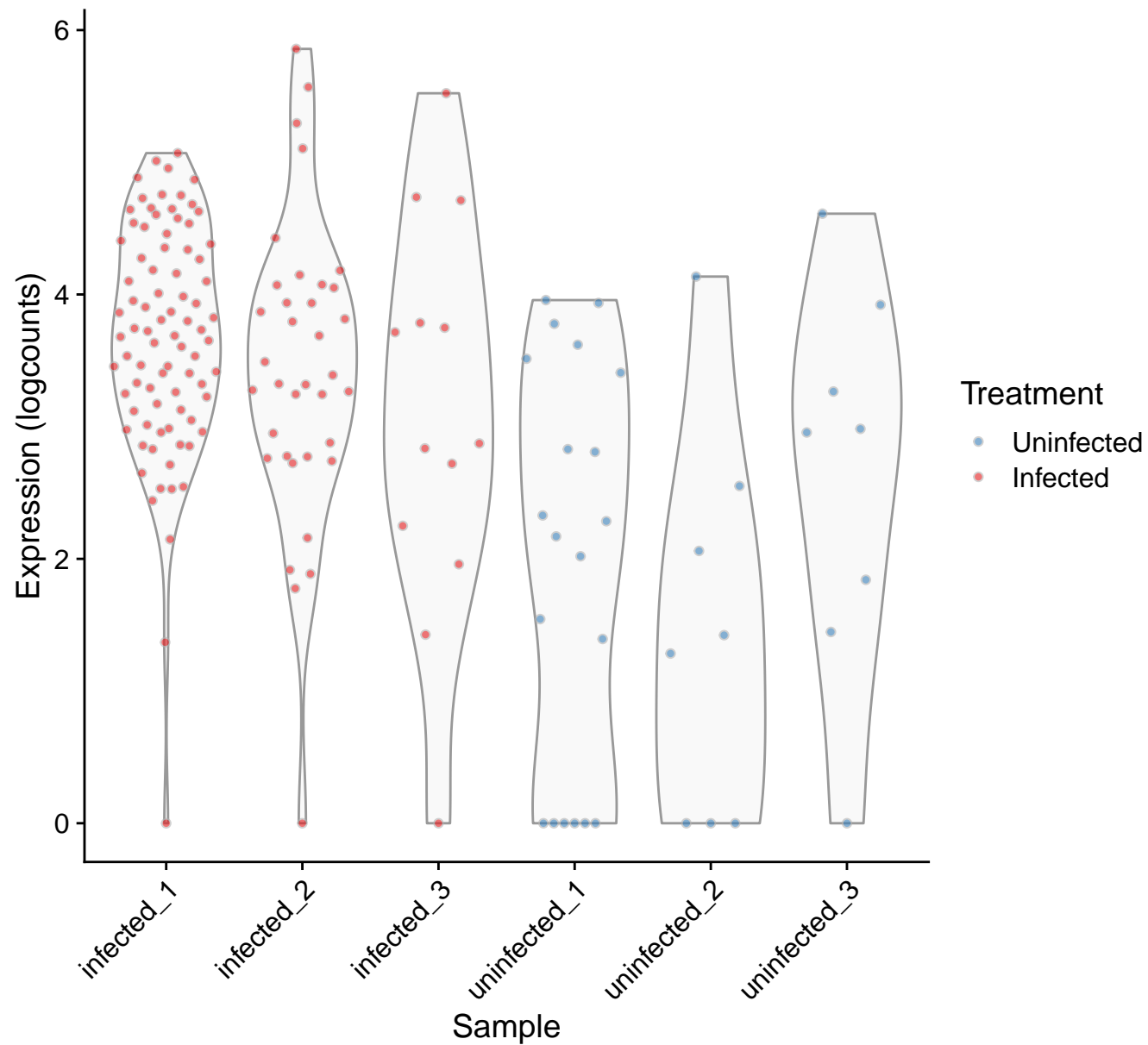
LGALS1 (FDR = 0.005)

cluster_9



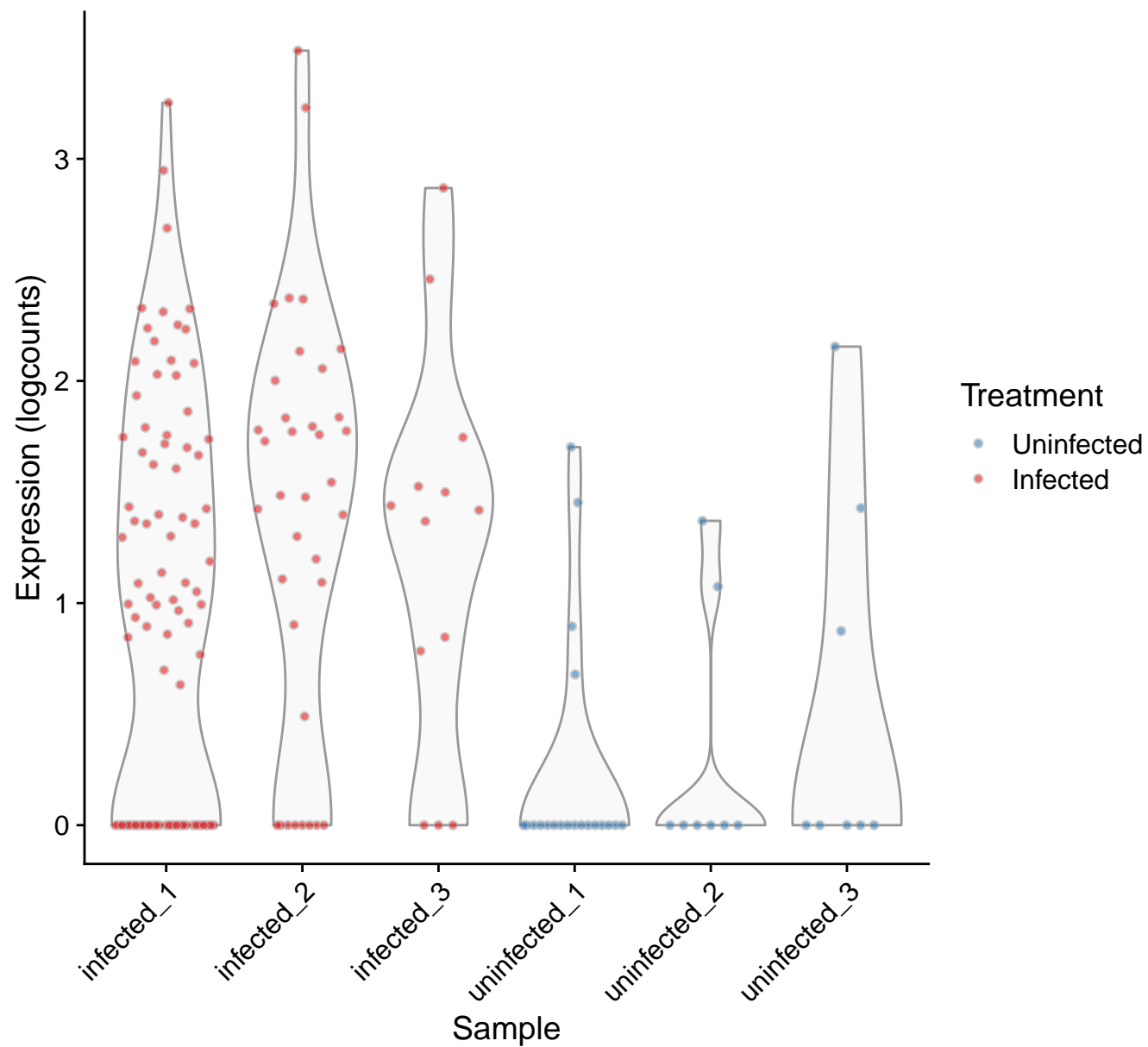
ITGB1 (FDR = 0.005)

cluster_9



HLA-DPA1 (FDR = 0.005)

cluster_9



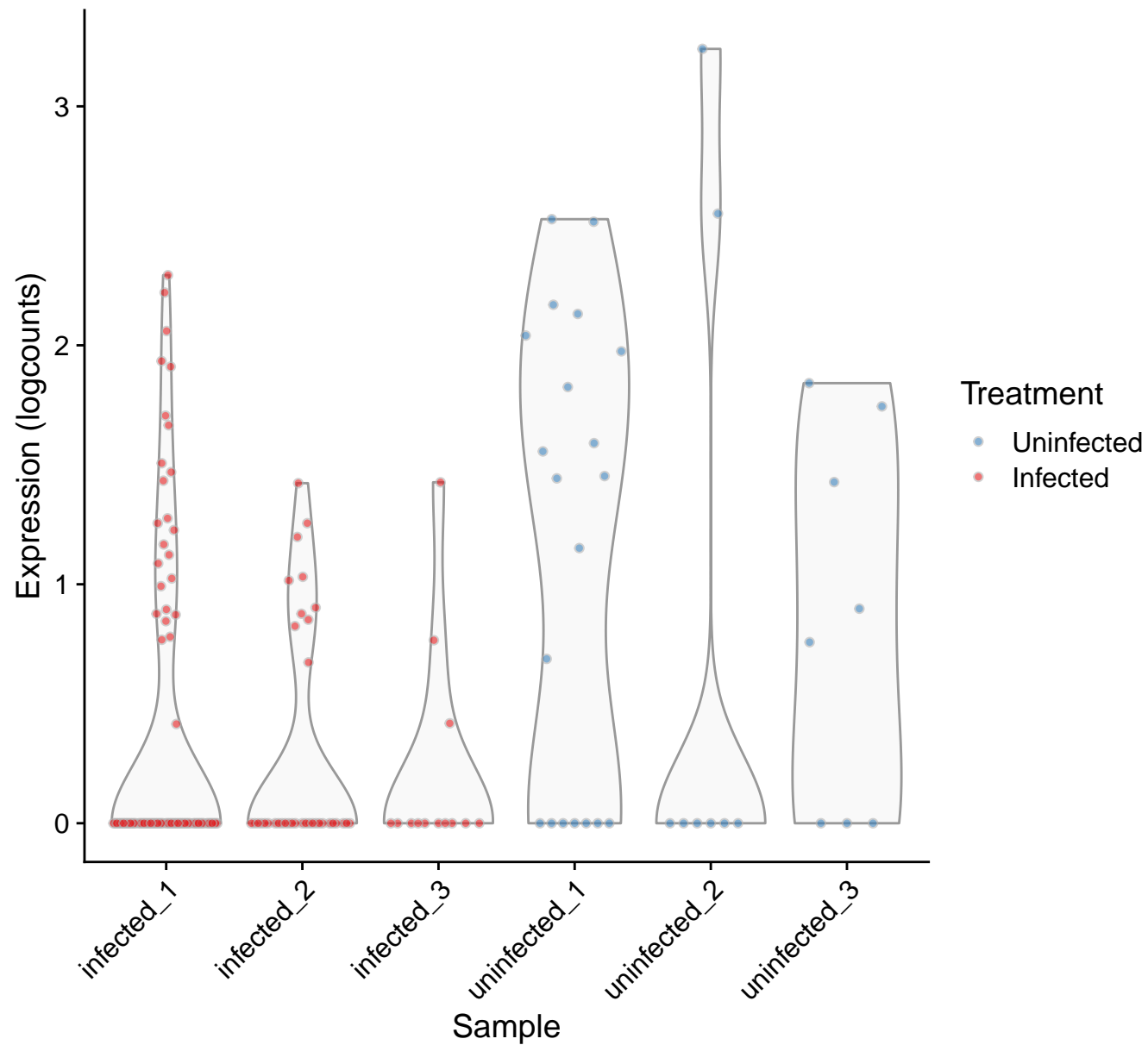
cluster_9

[illegible]

- Uninfected
- Infected

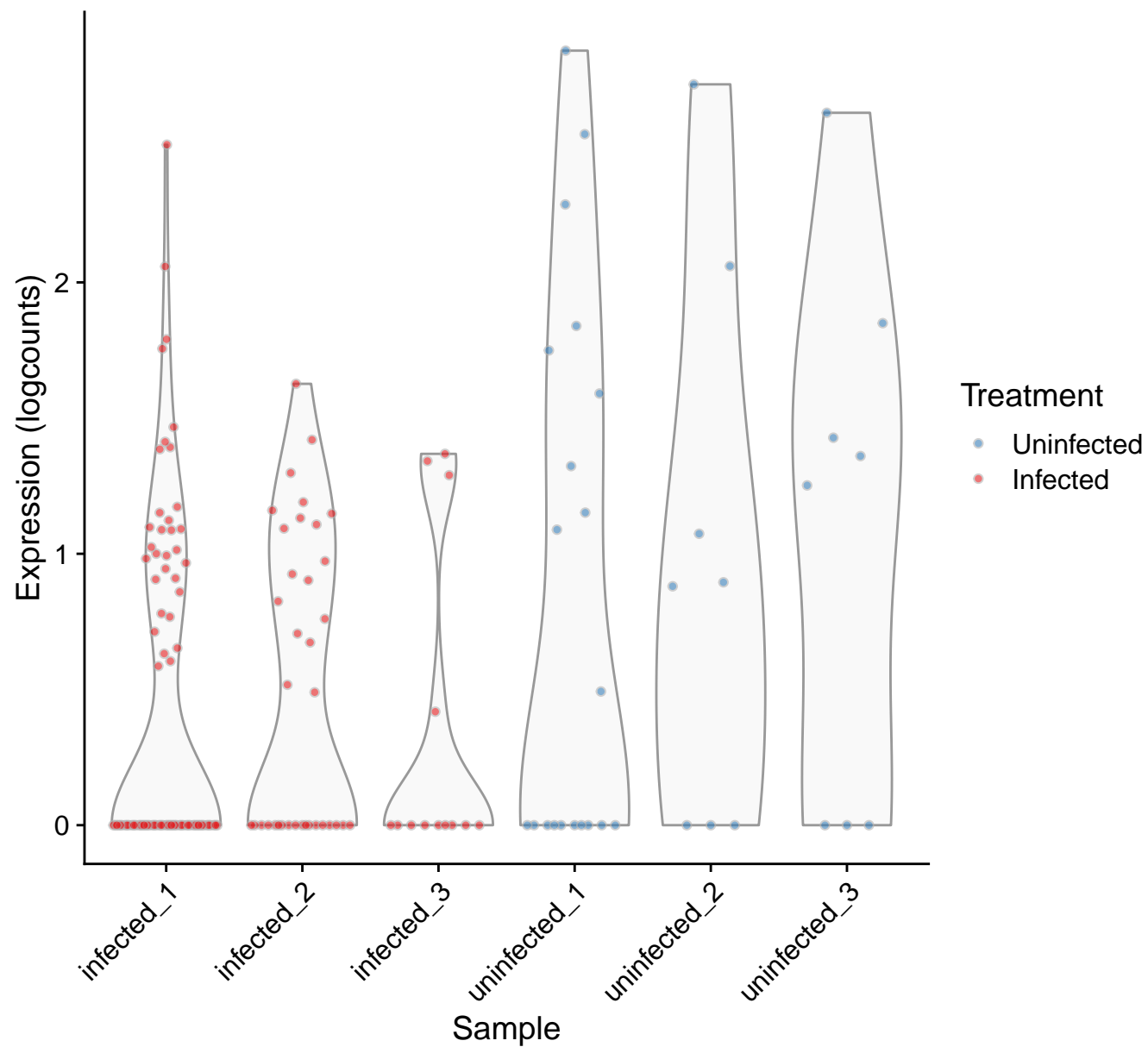
OAS1 (FDR = 0.02)

cluster_9



TRIM22 (FDR = 0.02)

cluster_9

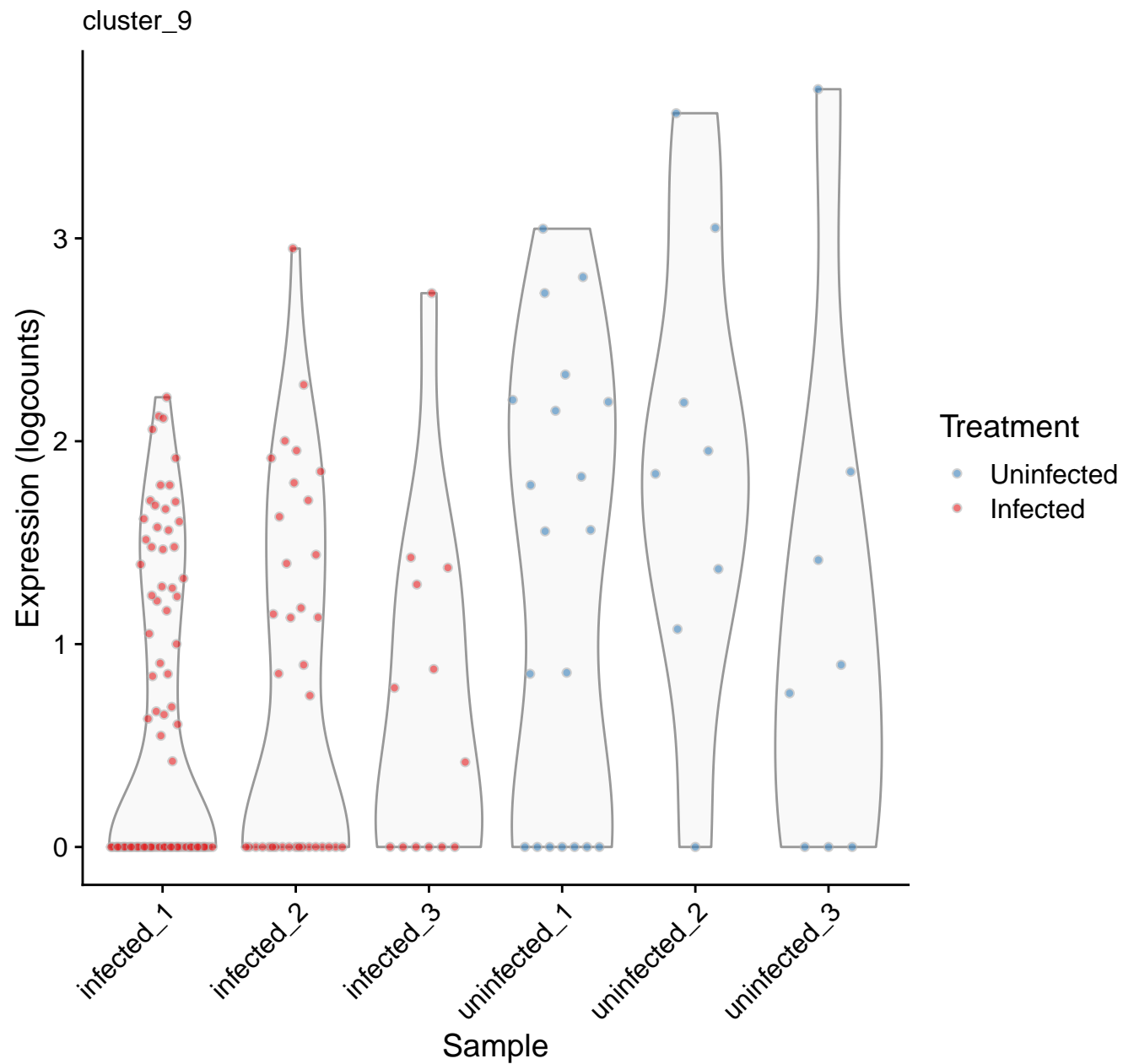


cluster_9

Violin plot showing the distribution of read counts for six samples: infected_1, infected_2, infected_3, uninfected_1, uninfected_2, and uninfected_3. The y-axis represents read counts on a log scale from 10^0 to 10^4 . The x-axis is labeled 'Sample'. Infected samples show a peak at high read counts (around $10^{3.5}$), while uninfected samples show a peak at low read counts (around $10^{0.5}$).

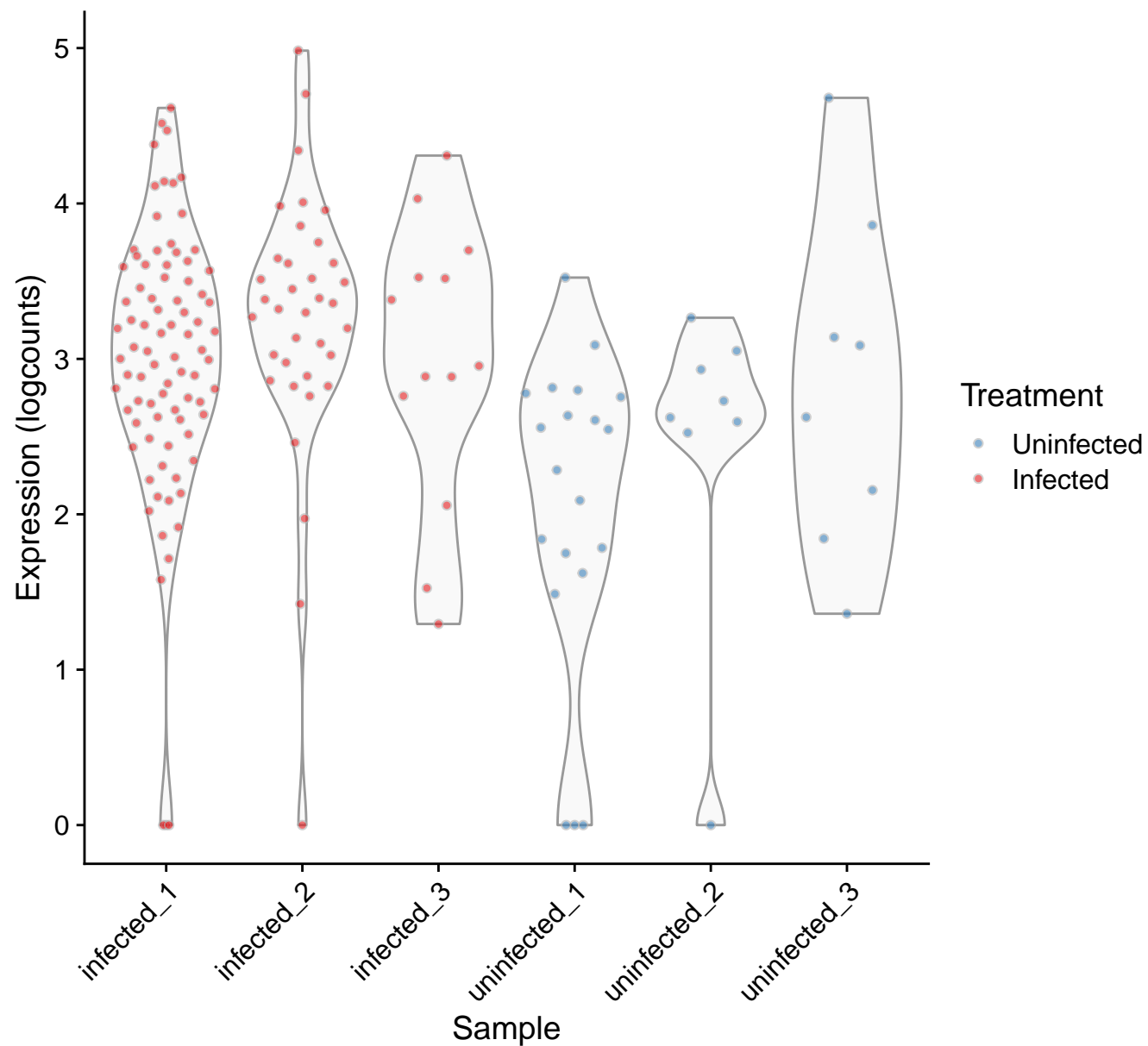
- Uninfected
- Infected

cluster_9



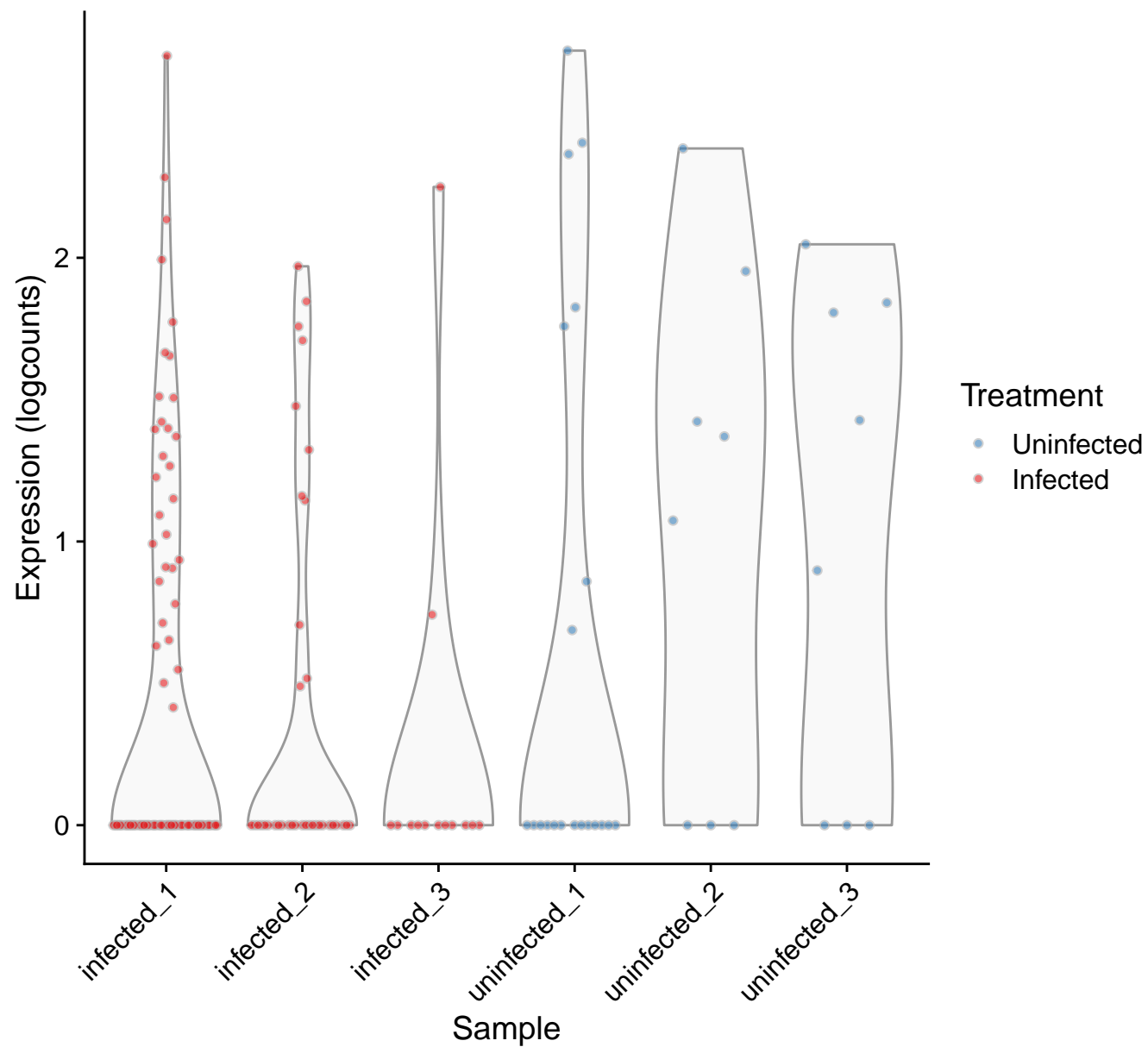
CD99 (FDR = 0.02)

cluster_9



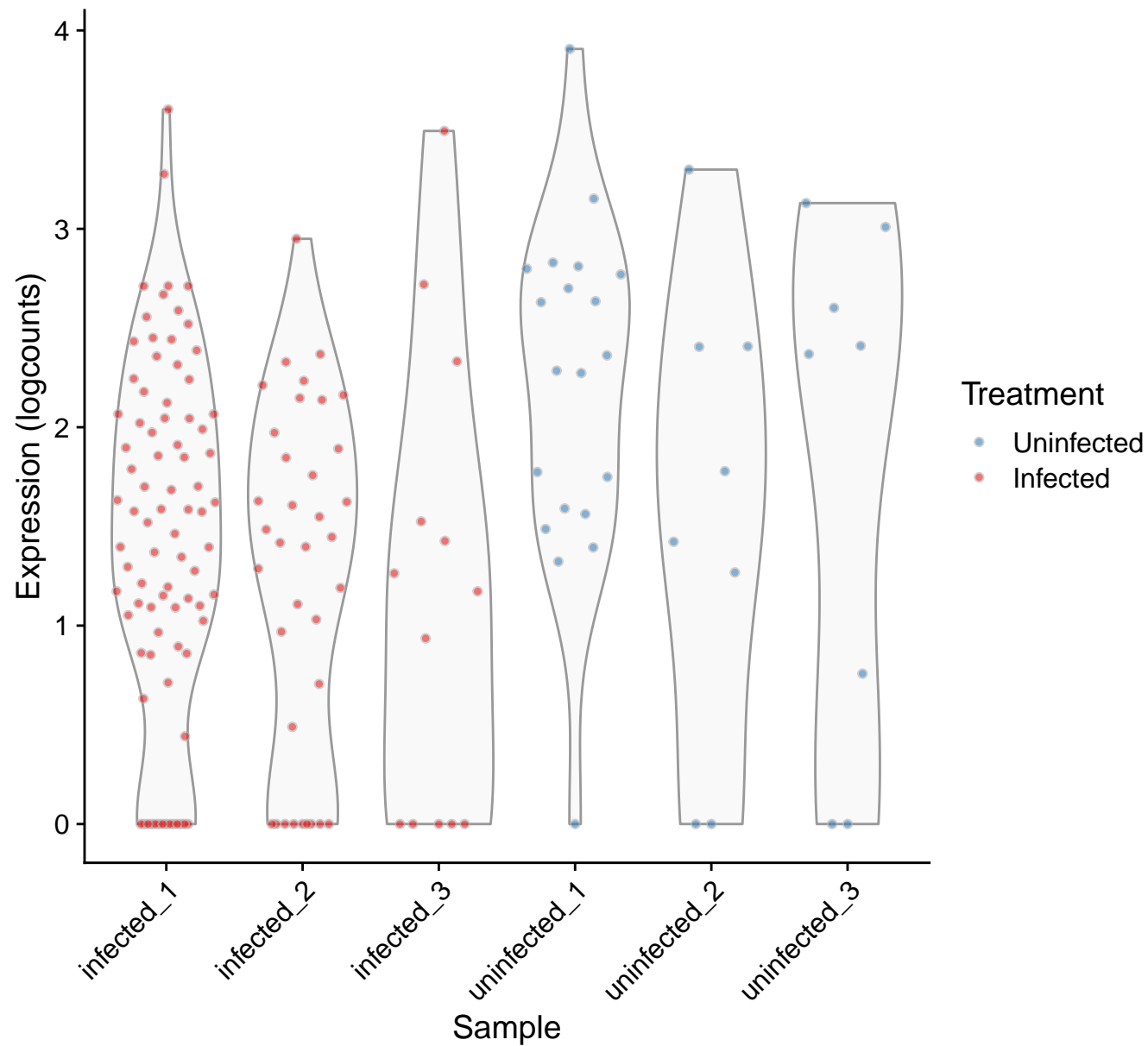
EIF2AK2 (FDR = 0.03)

cluster_9



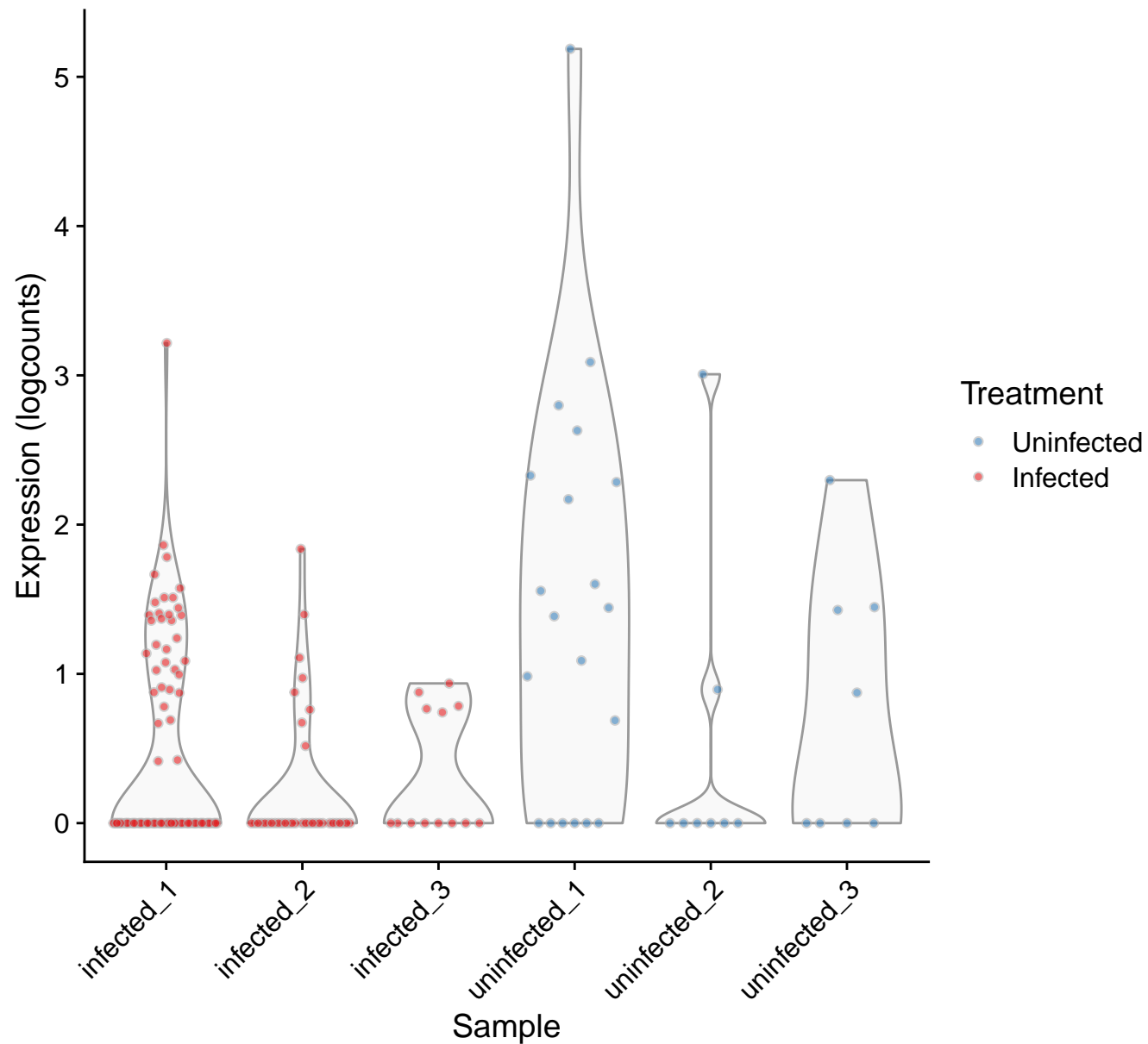
SAMHD1 (FDR = 0.04)

cluster_9



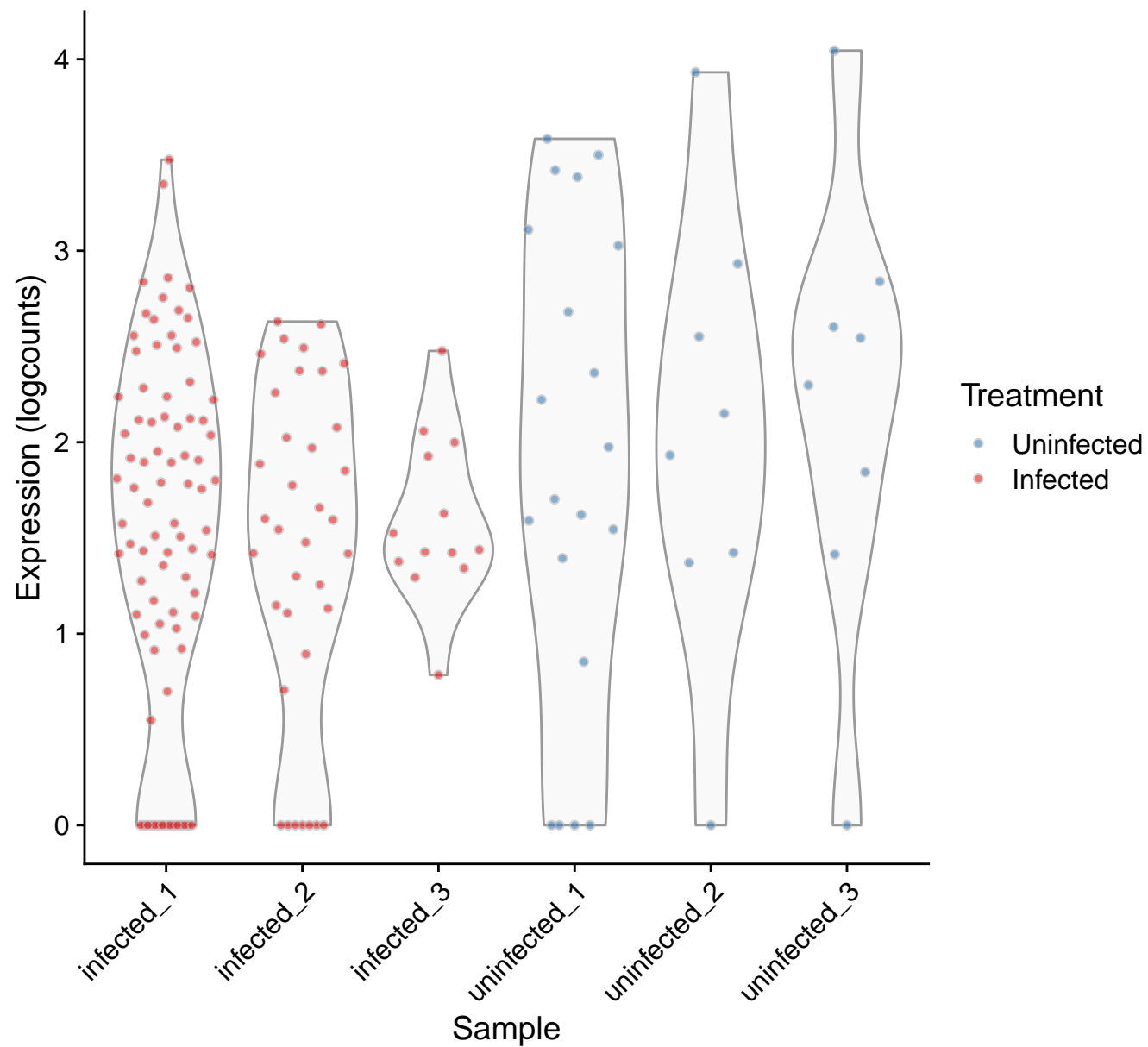
IFI6 (FDR = 0.04)

cluster_9



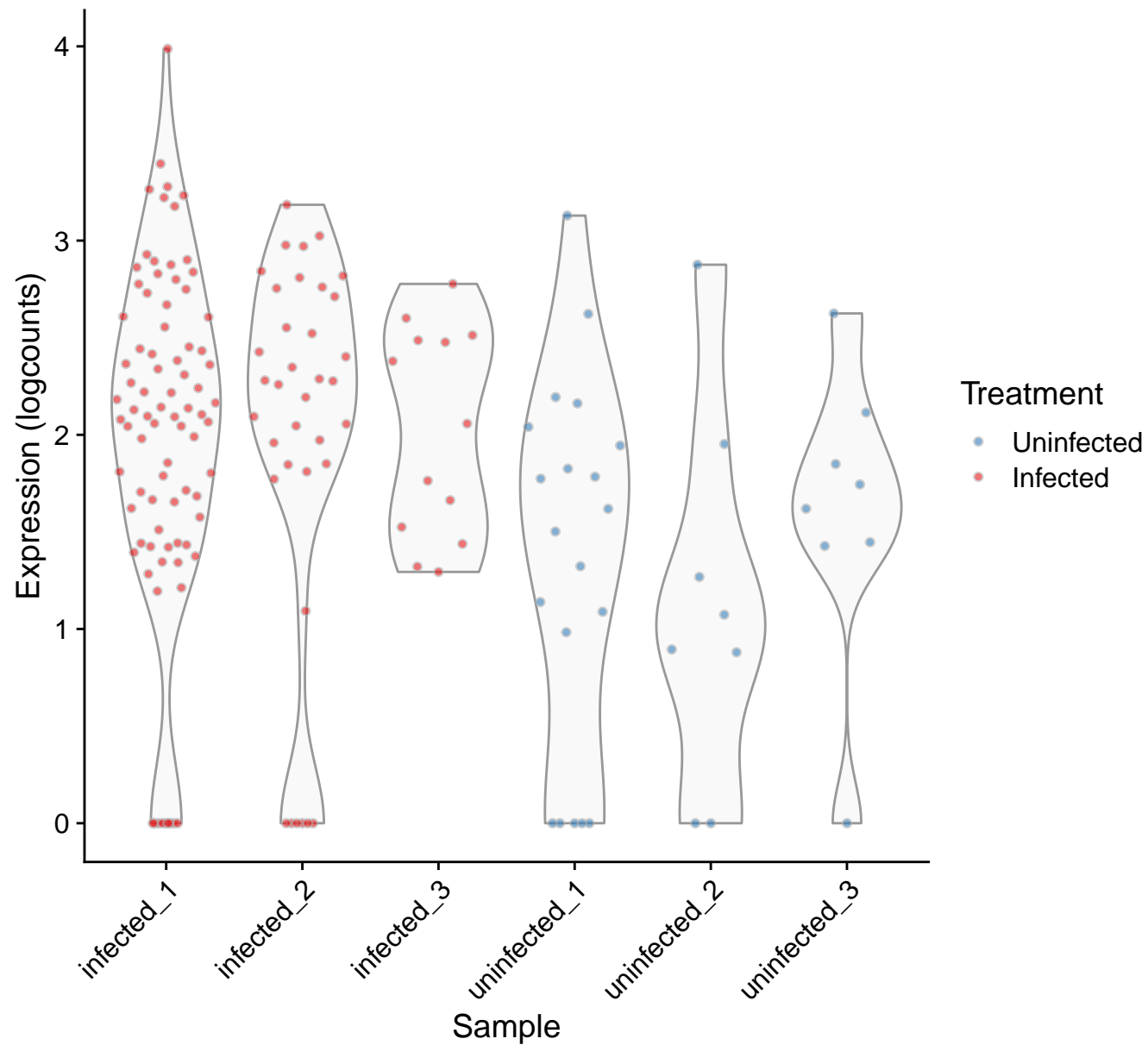
STK17B (FDR = 0.04)

cluster_9



CAPZB (FDR = 0.04)

cluster_9



cluster_9

Violin plot showing the distribution of the number of reads for six samples: infected_1, infected_2, infected_3, uninfected_1, uninfected_2, and uninfected_3. The y-axis represents the number of reads, ranging from 0 to 100. The x-axis is labeled 'Sample'. The infected samples (1, 2, 3) show a distribution skewed towards higher read counts, with infected_1 having the highest peak. The uninfected samples (1, 2, 3) show a distribution skewed towards lower read counts, with uninfected_3 having the highest peak. The plot uses red dots for infected samples and blue dots for uninfected samples.

- Uninfected
- Infected

IKZF3 (FDR = 0.04)

cluster_9

