GSE96583 input audit: two batches, two gene references, two annotation tables

A. Which file belongs with which annotation

GSE96583_RAW.tar
(76,195,840 B)

5 matrices
+ 5 barcode files

GEO suppl. dir
(official files)

batch2: 35,635 genes
2.1 ctrl 14,619 cells
2.2 stim 14,446 cells

batch2.genes
35,635 rows

batch2.total.tsne
29,065 x 7 cols
(+ row index)

batch1: 32,738 genes
A 3,639 / B 4,246 / C 6,145
= 14,030 cells

batch1.genes
32,738 rows

batch1.total.tsne
14,030 x 7 cols
(+ row index)

THIS STUDY USES: batch2 (8 donors, paired ctrl/stim)
batch1 also has its own annotation (batch A/B/C, 8 donors) - but its gene reference
is 32,738 rows, not 35,635. Two gene references must never share one annotation file.
Duplicate barcodes: batch2 = 313, batch1 = 93 (the repeats get an extra '1' suffix)

B. Cells per matrix
(batch1 total = 14,030; batch2 total = 29,065)

