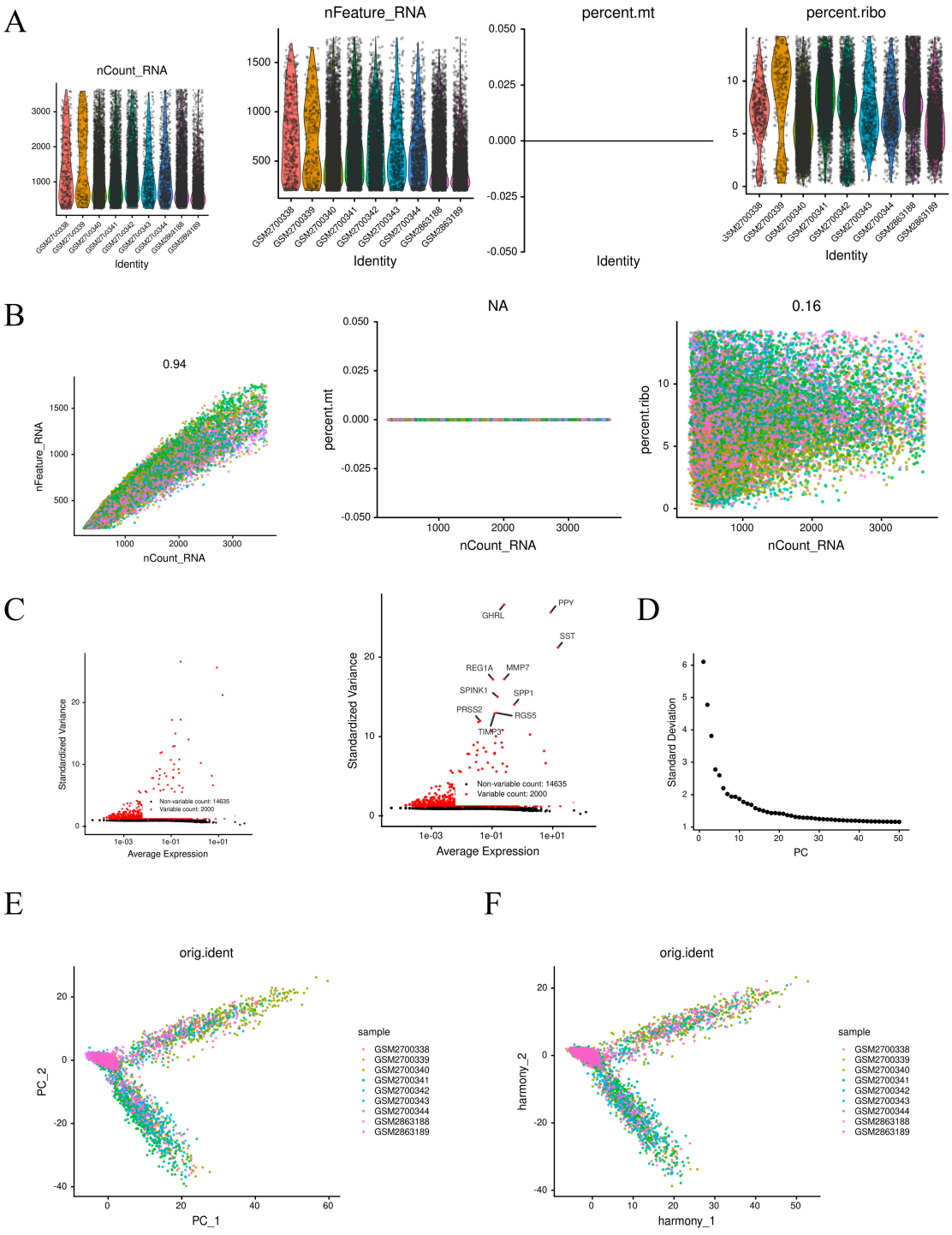


Figure S1. Single-cell data preprocessing.(A) Single-cell quality control results, showing the distribution of sequencing depth (nCount_RNA), gene number (nFeature_RNA), mitochondrial content (percent.mt), and ribosomal content (percent.ribo) of each sample.(B) Left panel: The relationship between sequencing depth and gene number of each cell; Middle panel: The relationship between mitochondrial content and sequencing depth; Right panel: The relationship between ribosomal content and sequencing depth. The scatter plots show the correlations between these QC metrics (correlation coefficients are indicated at the top), each point represents a single cell.(C) Identification of significantly variable genes among cells, shown by a feature variance plot

(the right panel highlights the top 2,000 variable genes and specific marker genes).(D) Variance ranking plot of each principal component (PC).(E-F) PCA visualization and Harmony-corrected embedding; dots represent cells, and colors represent different samples.

Table S1. Identification information of the four candidate overlapping metabolites.

Metabolite Name	m/z	Retention Time (min)	Annotation Level	Match Score	HMDB ID	KEGG ID
Cytidine	244.0928	0.612	B(i)	35.8	HMDB0000089;HMDB0248553;PW_C000061	C00475
L-Glutamine	145.0611	0.523	B(i)	85.8	HMDB0000641;PW_C000500	C00064
Thymidine	287.0887	1.748	B(ii)	61.7	HMDB0000273	C00214
Guanosine	282.0848	1.748	B(i)	98.5	HMDB0000133;PW_C000087	C00387