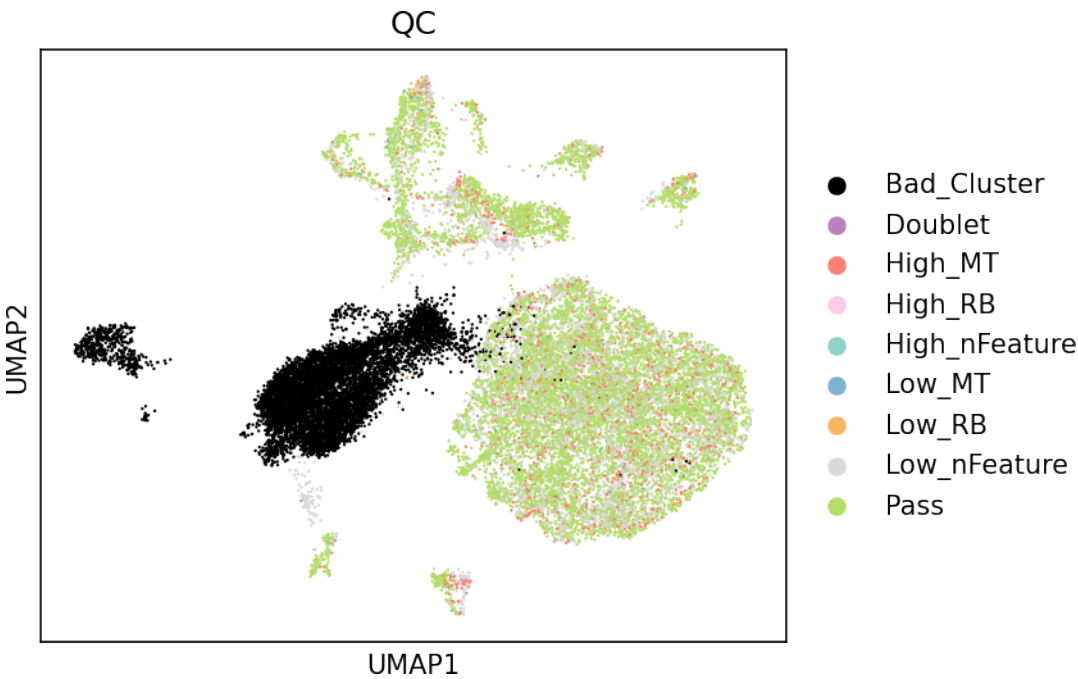
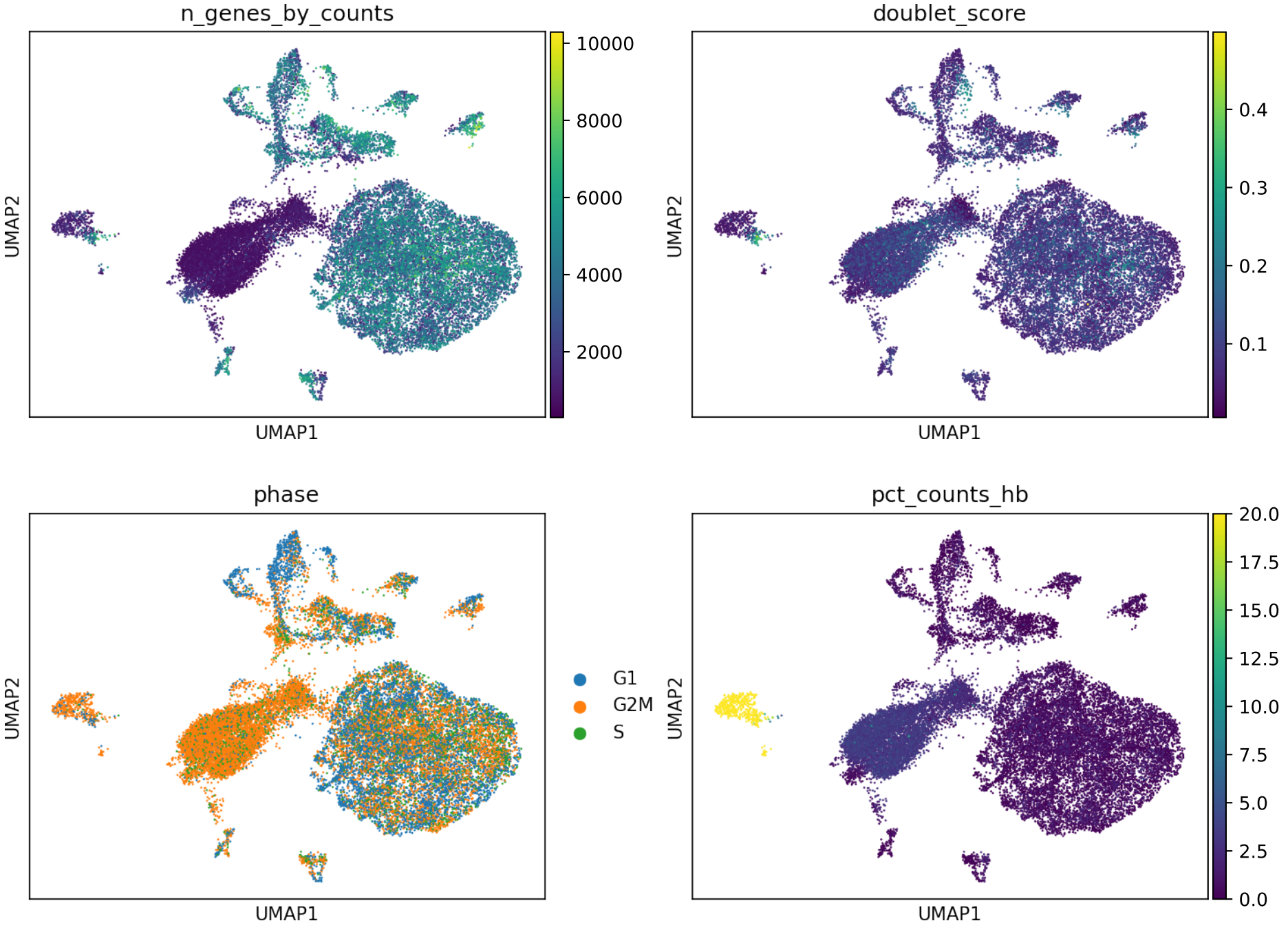
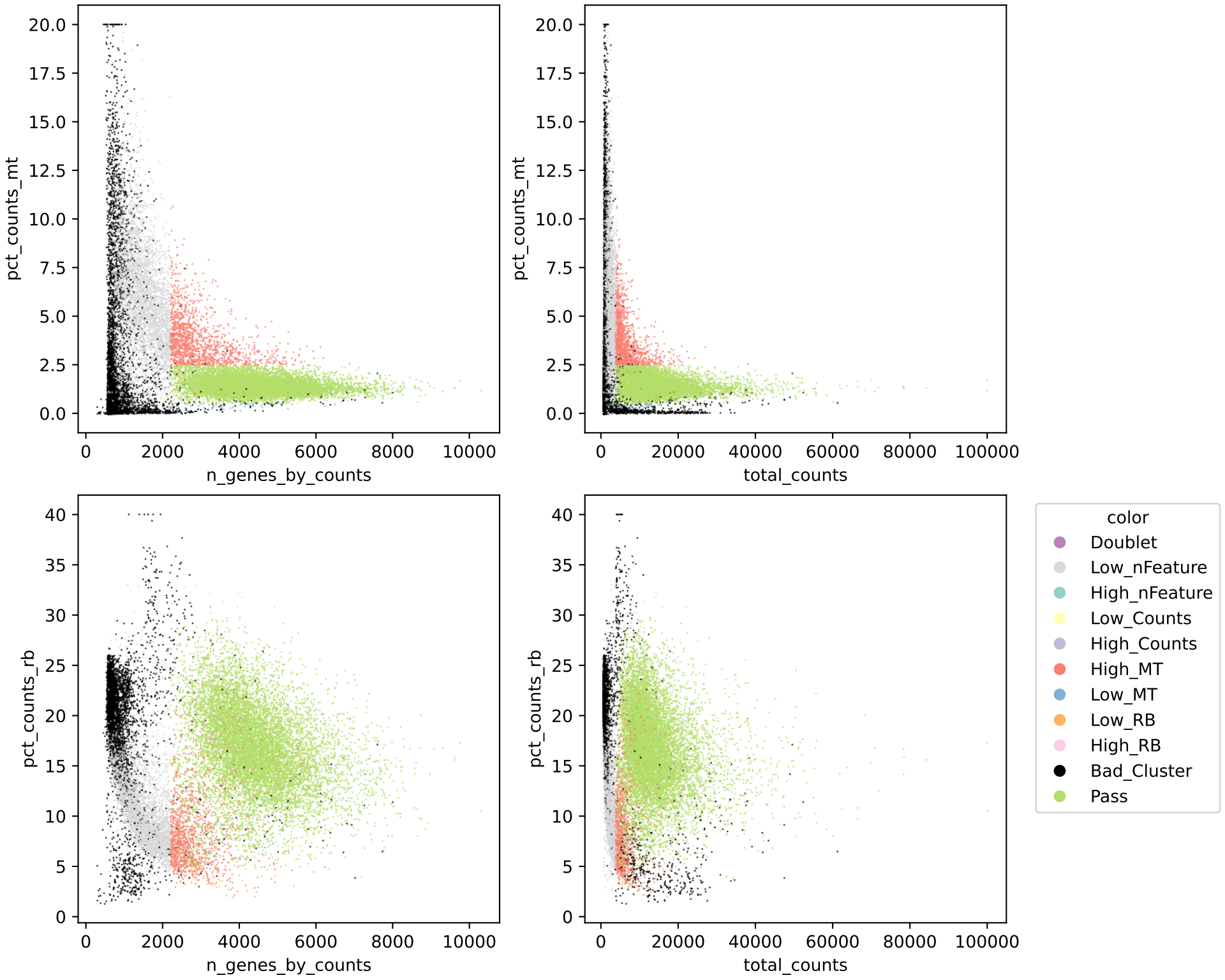

QC
UMAP2
UMAP1
Bad_Cluster
Doublet
High_MT
High_RB
High_nFeature
Low_MT
Low_RB
Low_nFeature
Pass


n_genes_by_counts
UMAP2
UMAP1
10000
8000
6000
4000
2000
doublet_score
UMAP2
UMAP1
0.4
0.3
0.2
0.1
phase
UMAP2
UMAP1
G1
G2M
S
pct_counts_hb
UMAP2
UMAP1
20.0
17.5
15.0
12.5
10.0
7.5
5.0
2.5
0.0


pct_counts_mt
n_genes_by_counts
pct_counts_mt
total_counts
pct_counts_rb
n_genes_by_counts
pct_counts_rb
total_counts
color
Doublet
Low_nFeature
High_nFeature
Low_Counts
High_Counts
High_MT
Low_MT
Low_RB
High_RB
Bad_Cluster
Pass