A

BRAF-like RAI-treated patients (*n* = 137)

B

C ATA risk stratification

P = 0.575
q = 0.738

- Low (orange)
- Intermediate (green)
- High (purple)
- N/A (black)

Cluster 1 (1 rec)
Cluster 2 (8 rec)
Cluster 3 (0 rec)
Cluster 4 (12 rec)

D Disease staging

P = 0.105
q = 0.440

- I (light blue)
- II (orange)
- III (pink)
- IVA/ IVC (purple)
- N/A (black)

Cluster 1 (1 rec)
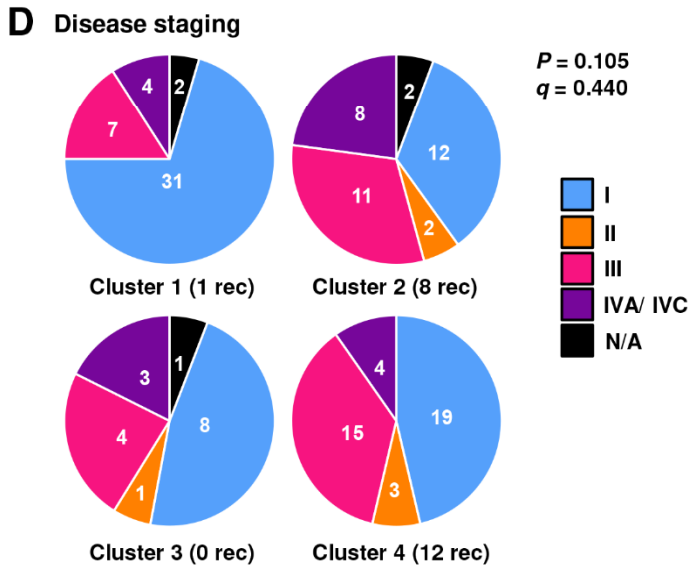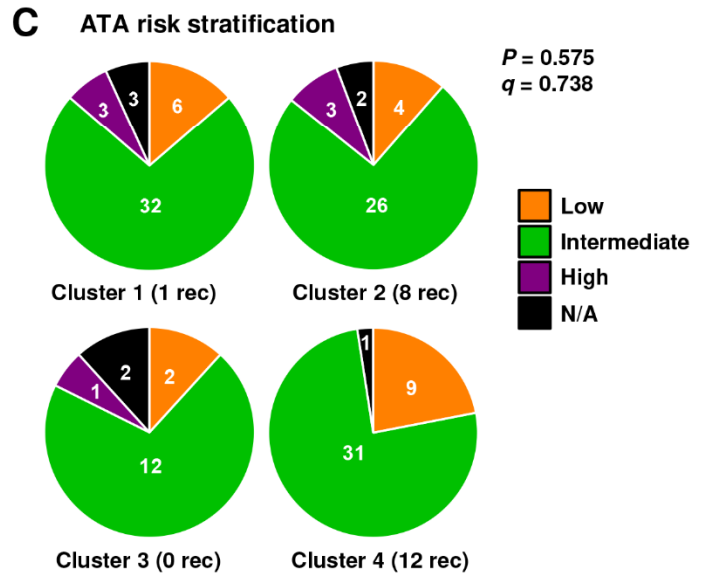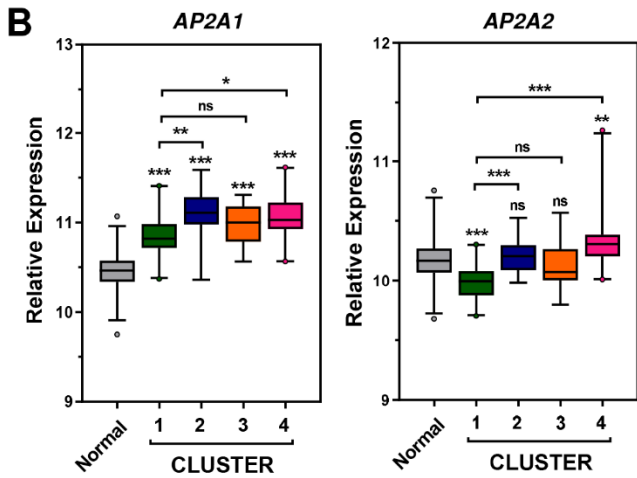Cluster 2 (8 rec)
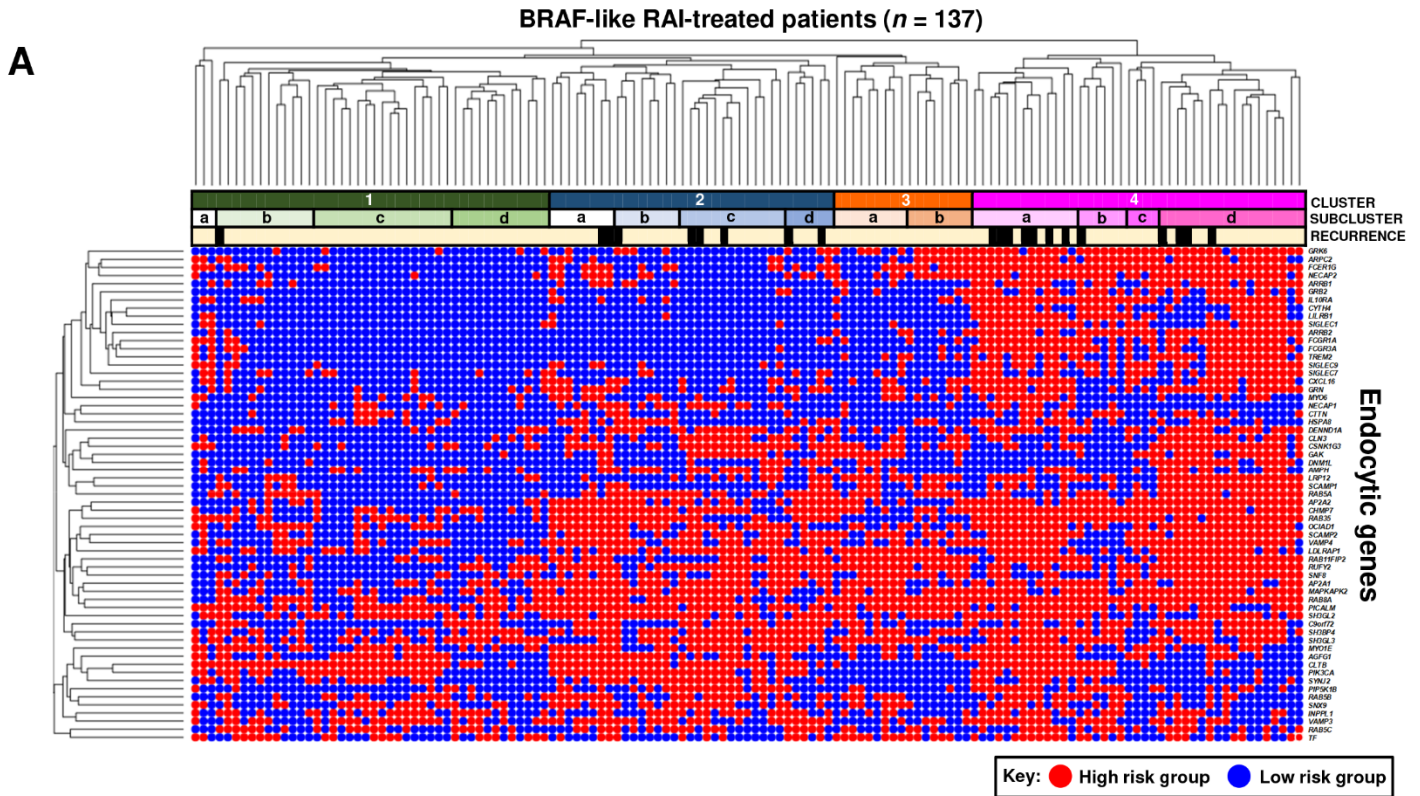Cluster 3 (0 rec)
Cluster 4 (12 rec)

Figure S8. Greater endocytic gene dysregulation and higher AP2α expression in recurrent PTC. **A,** Hierarchical cluster analysis of the BRAF-like, RAI-treated THCA cohort ($n = 137$) based on endocytic genes ($n = 61$) stratified into high and low risk expression groups. ROC analysis was used to determine optimal expression cut-off values for stratifying patients into high and low risk groups. Patients were divided into 4 major clusters (1 to 4) and 14 subclusters (1a to 4d). Patients with recurrent disease are indicated (black squares). **B,** Box and whisker plots showing expression ($\log_2$) of *AP2A1* (*left*) and *AP2A2* (*right*) in the BRAF-like, RAI-treated THCA cohort stratified into patient clusters 1 to 4 vs normal. Data presented as mean ± S.E.M., one-way ANOVA followed by Kruskal-Wallis test (ns, not significant; *$P <$ 0.05; **$P <$ 0.01; ***$P <$ 0.001). **C,** Pie charts showing the ATA risk stratification characteristics of BRAF-like, RAI-treated patients subdivided into 4 clusters. Rec- number of recurrences. **D,** Same as **C** but showing disease staging characteristics as indicated. P-values derived using Chi-Squared test and adjusted using the Benjamini-Hochberg FDR correction procedure.