

Figure S1 (A-C) Consensus clustering matrix based on 20 m⁶A genes for k=3-5. **(D-E)** The consensus distribution and Delta area for k=2-5. **(F)** The PCA of the m⁶A clusters.

Figure S2 (A-C) The previral genes between the m⁶A clusters

Figure S3 (A-C) The stimular genes **(A)**, inhibitor genes **(B)** and MHC genes **(C)** between the m⁶A clusters. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

Figure S4 (A-C) Consensus clustering matrix based on 6771 DEGs for k=2-5. **(D)** The consensus distribution area for k=2-5. **(E)** The PCA of the Gene clusters. **(F)** The 20 m⁶A genes between the Gene clusters. *p<0.05, **p<0.01, ***p<0.001, ****p<0.0001.

Figure S5 (A-B) The HFD45 **(A)** and m⁶A score **(B)** between the Gene clusters. **(C-F)** The boxplot of m⁶A score in groups of different clinical characteristics including sex **(C)**, ICU **(D)**, mechanical ventilation **(E)** and diabetes **(F)**. **(G)** The correlation between m⁶A score and common pathways.

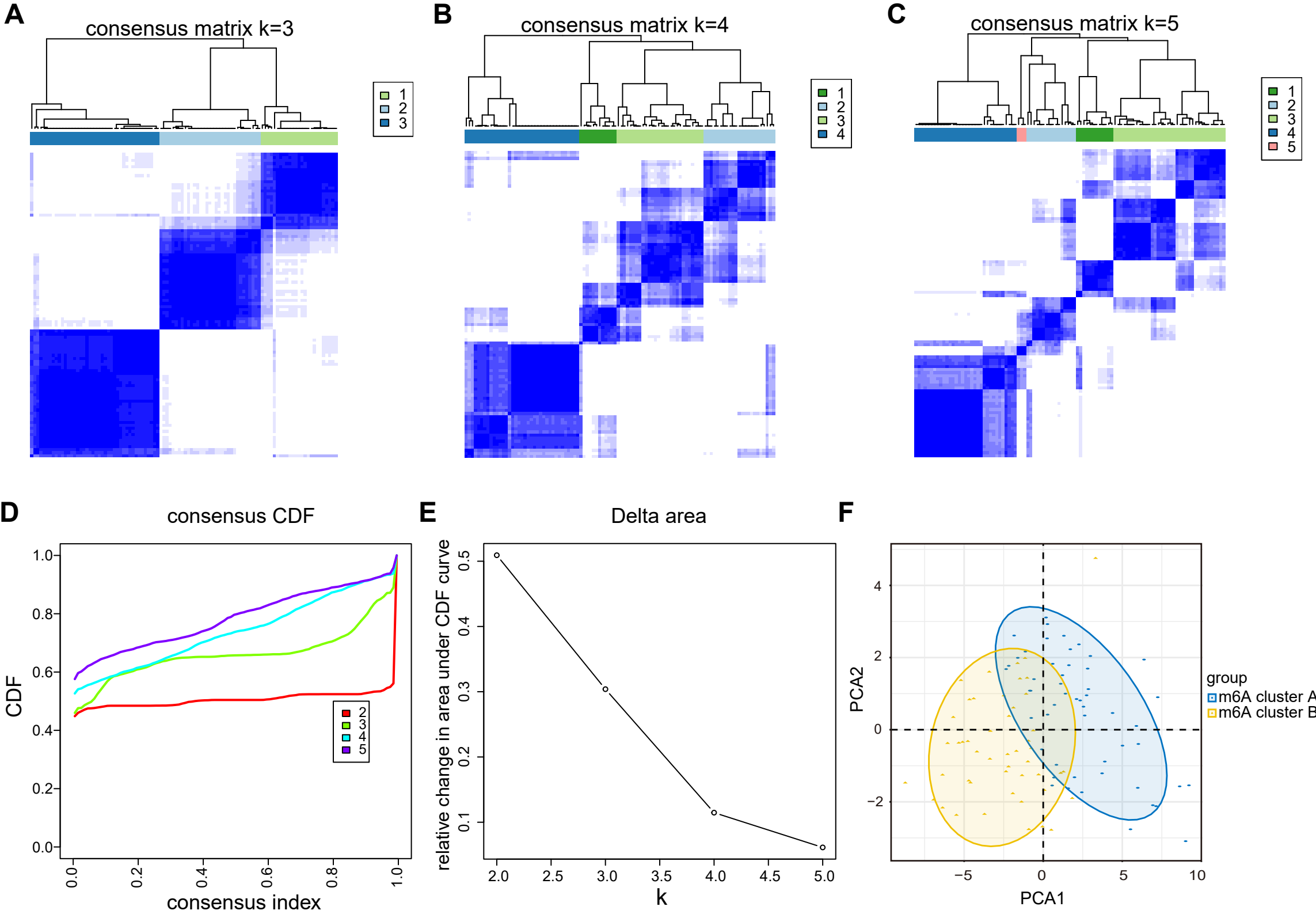


Figure S1

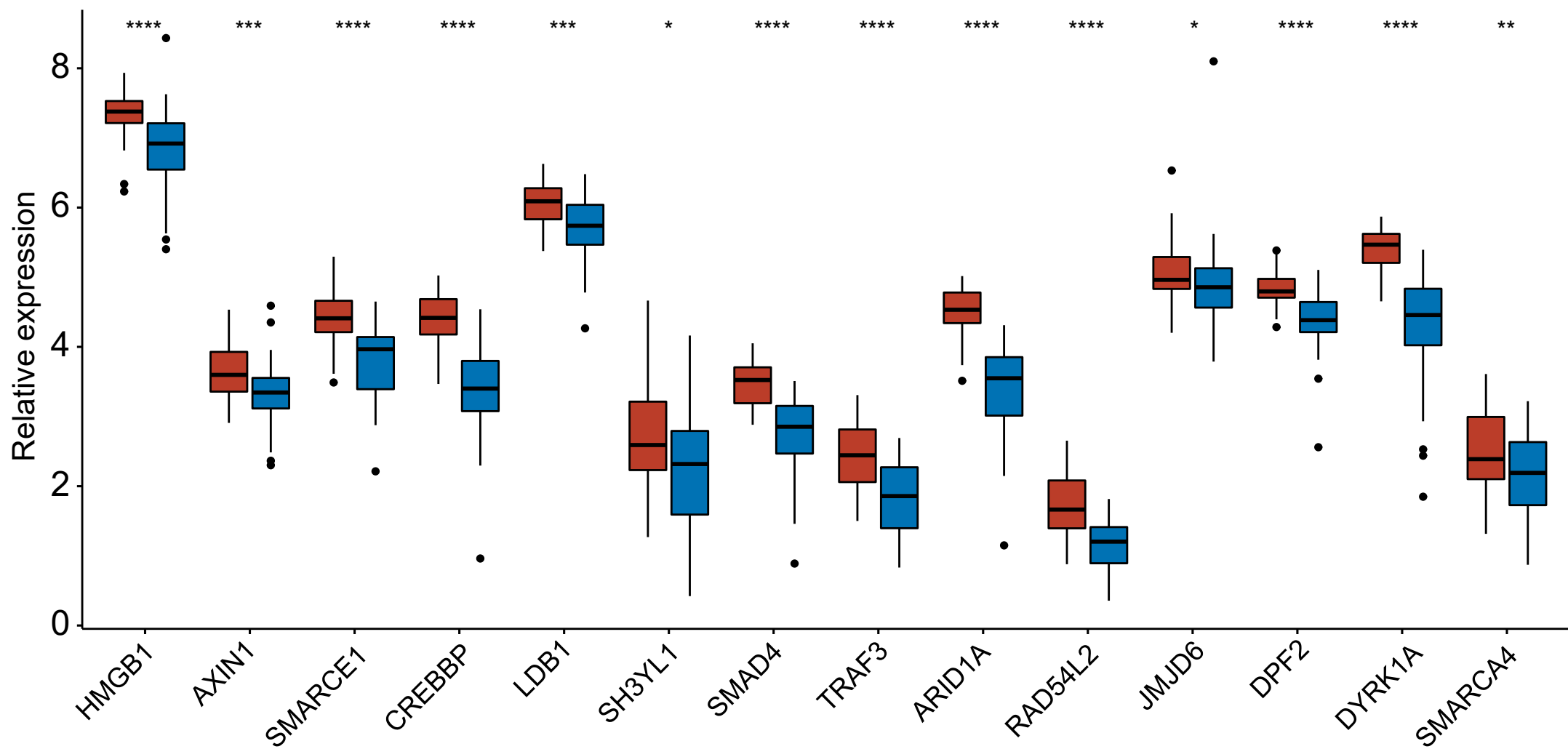
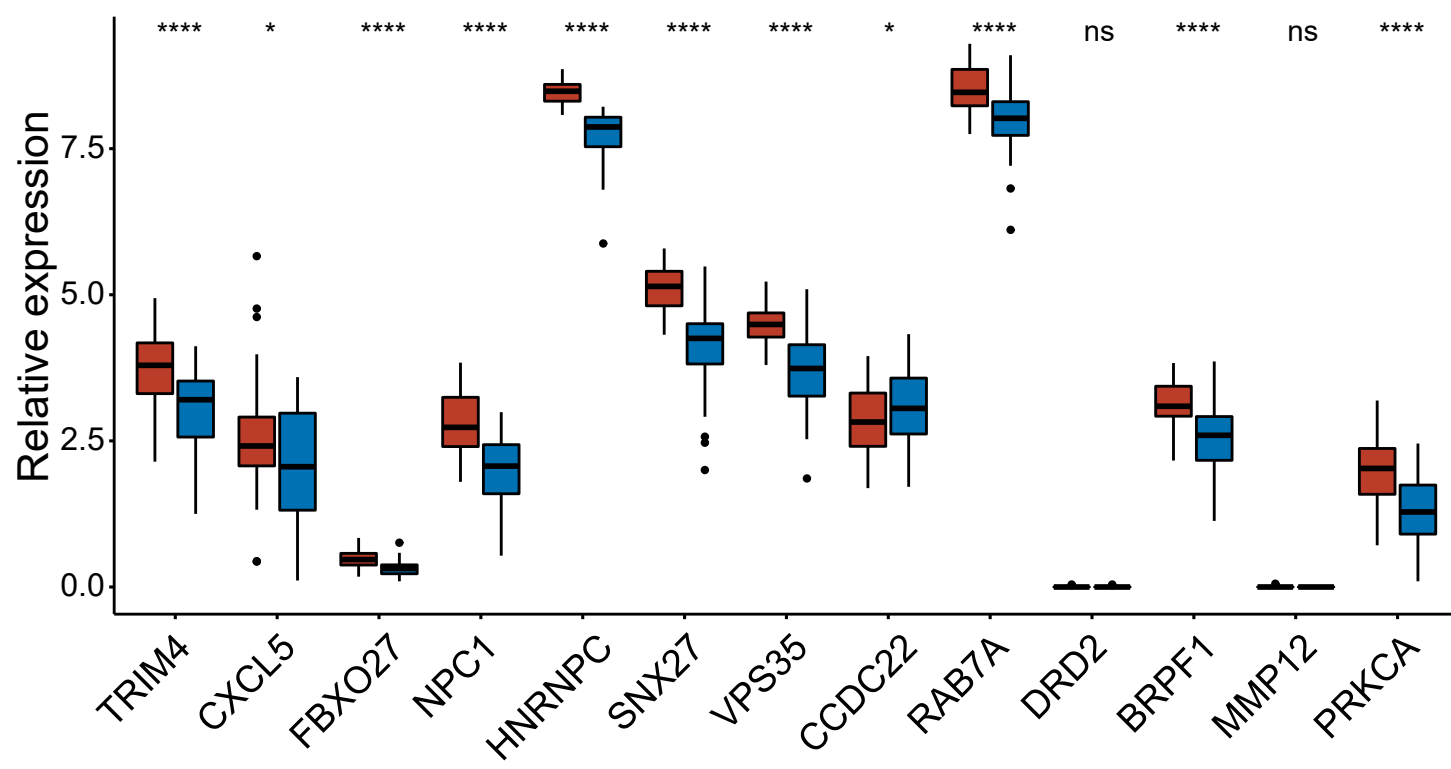
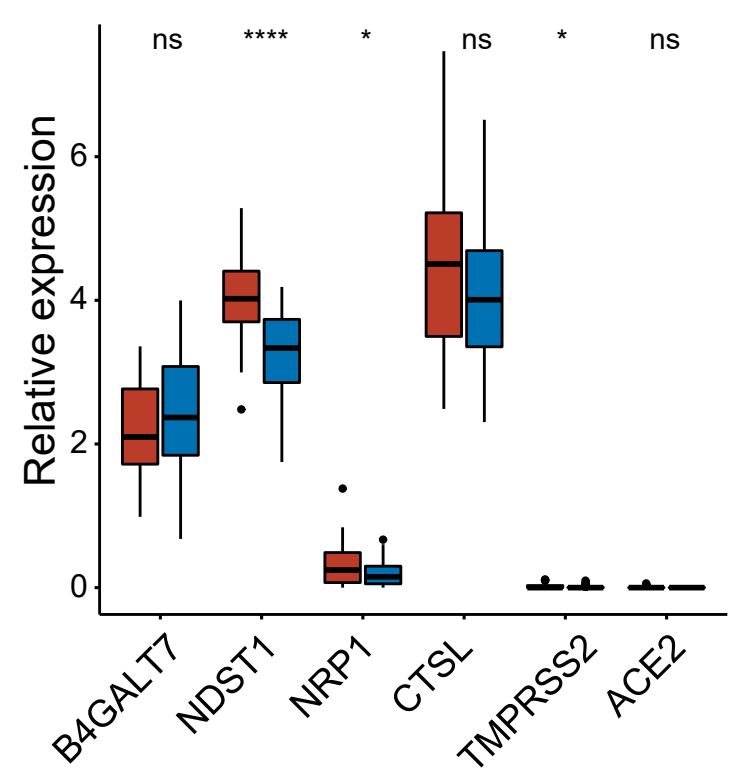
Agroup ■ m6A cluster A ■ m6A cluster B**B**group ■ m6A cluster A ■ m6A cluster B**C**group ■ m6A cluster A ■ m6A cluster B

Figure S2

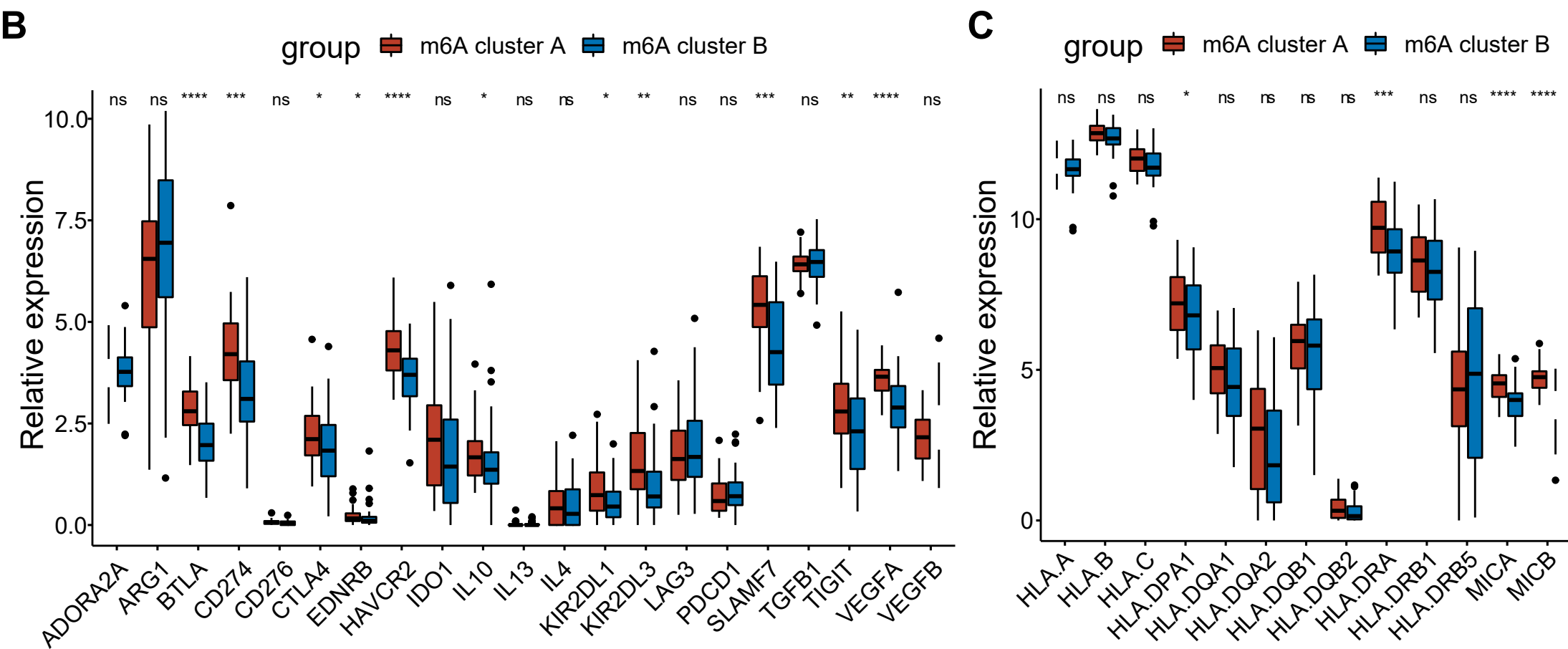
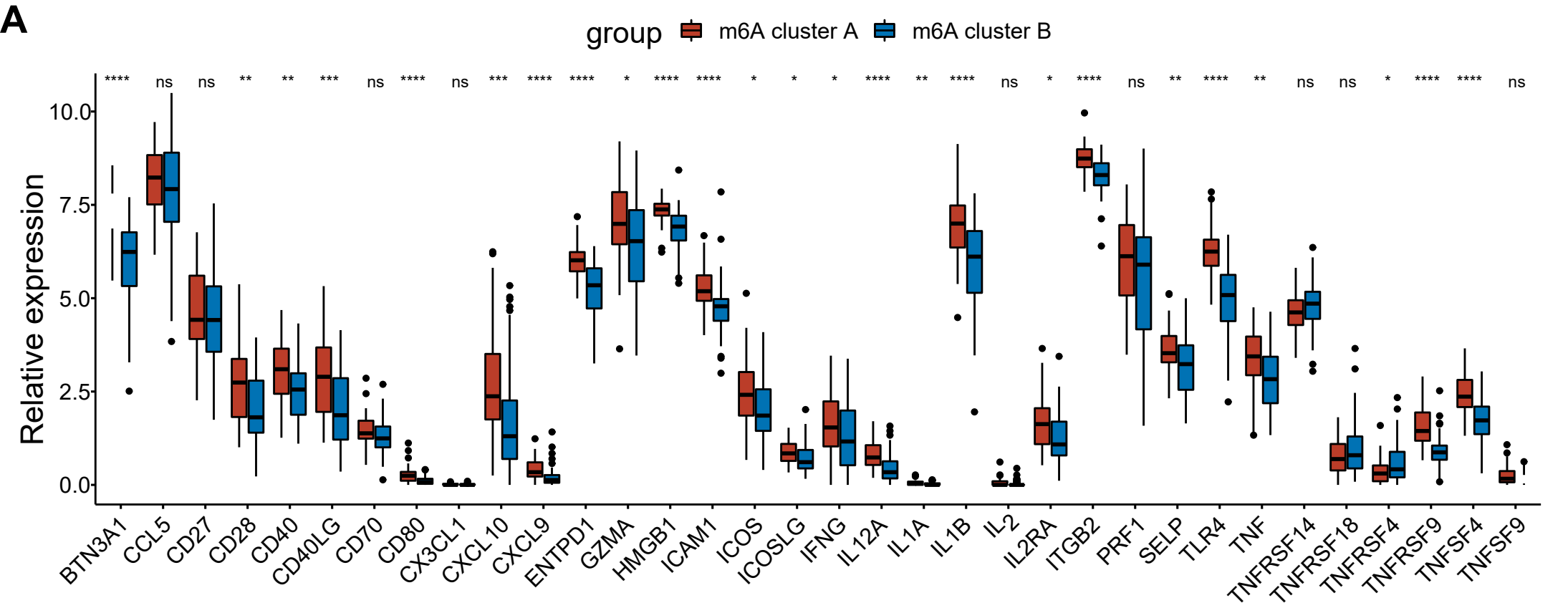


Figure S3

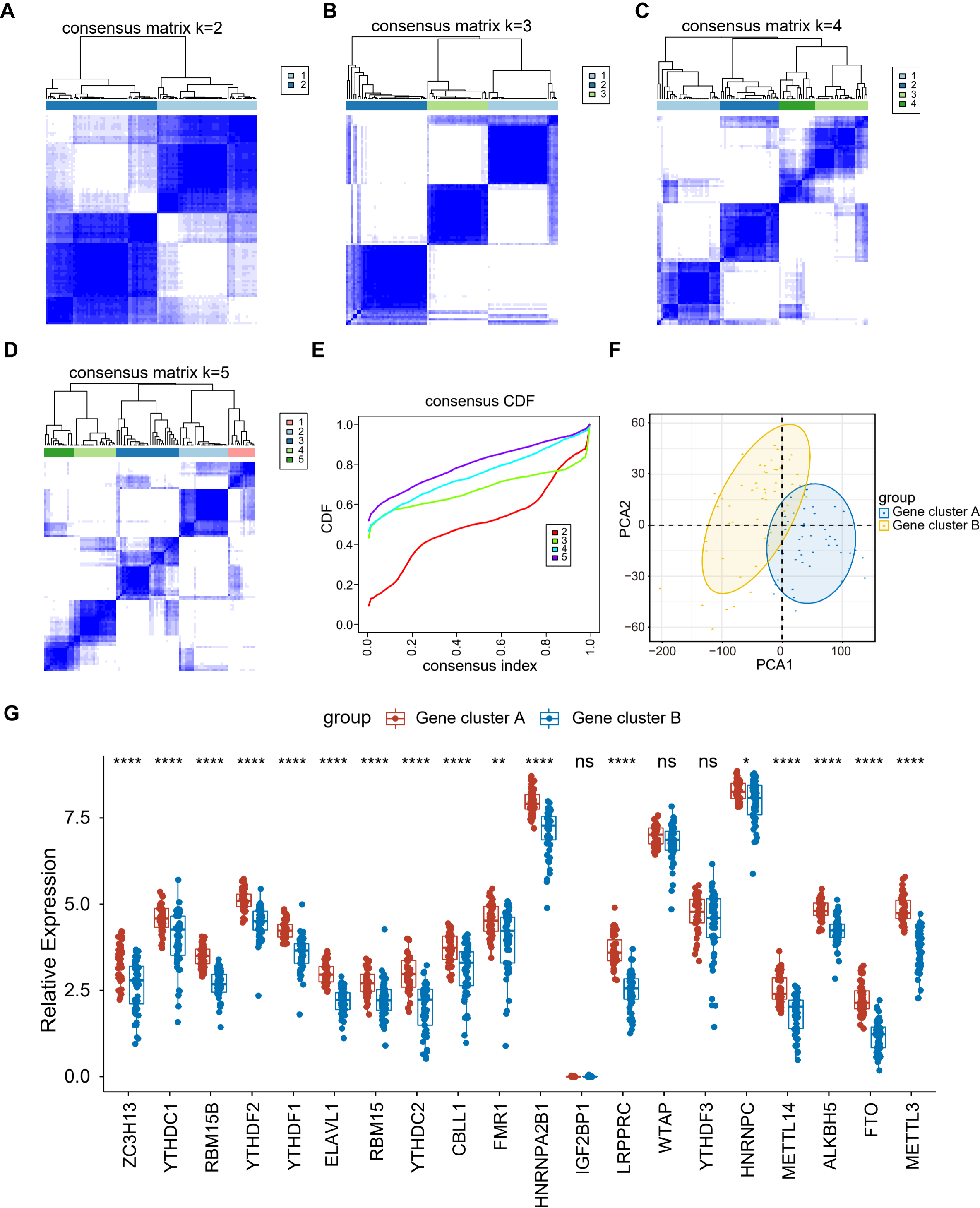


Figure S4

