

Figure S1. Consensus unsupervised clustering of 760 BLCA patients based on 18 m7G-related genes. **A** Consensus matrixes of 760 BLCA patients when k=3. **B** The correlation between consensus index and CDF when k=2-6. **C** The relative change under the CDF curve when k=2-6. **D** The tracking plot of 760 patients when k=2-6.

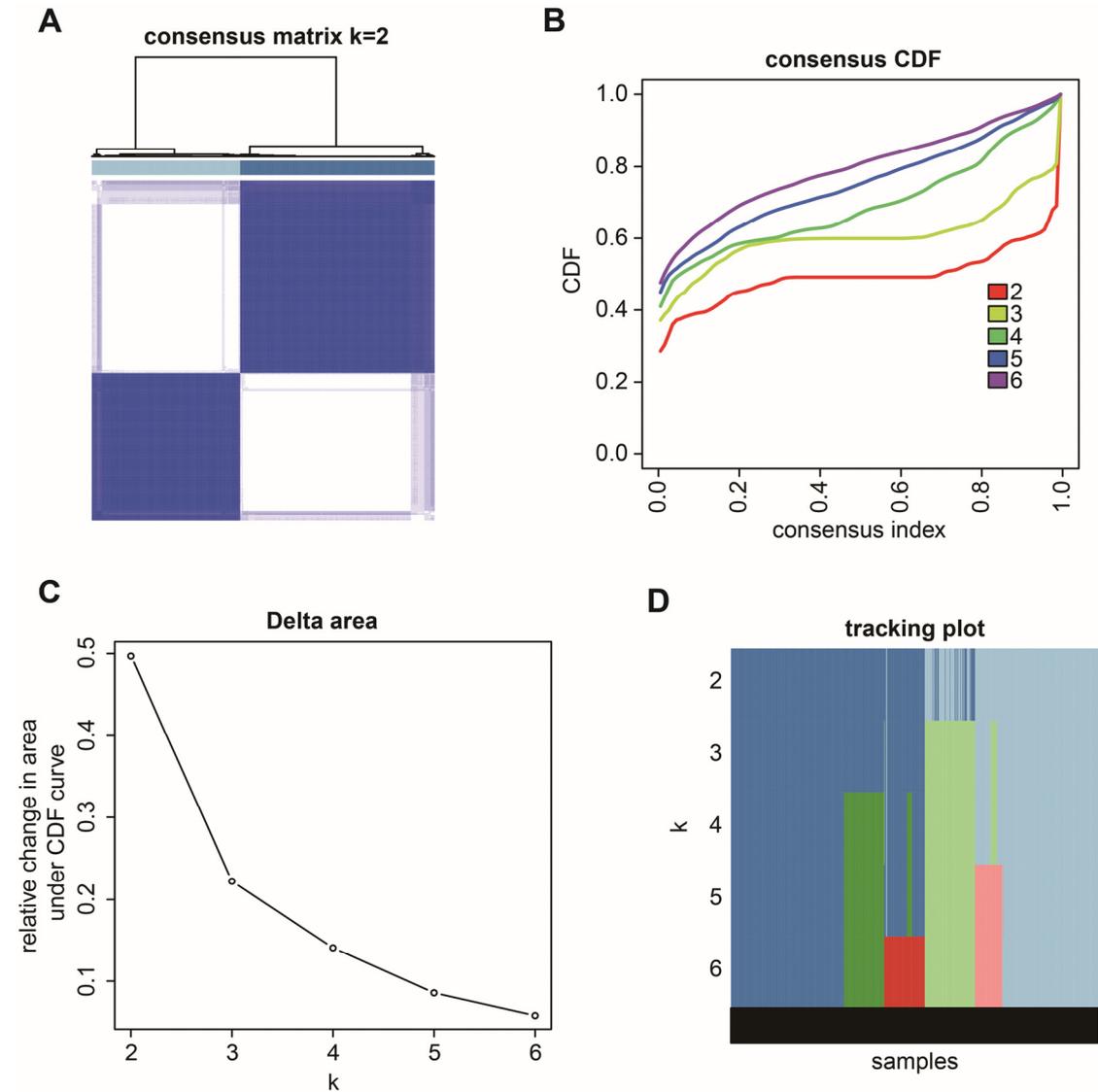


Figure S2. Consensus unsupervised clustering of 760 BLCA patients based on 1108 differentially expressed genes relevant to three m7G-related clusters. **A** Consensus matrixes of 760 BLCA patients when $k=2$. **B** The correlation between consensus index and CDF when $k=2-6$. **C** The relative change under the CDF curve when $k=2-6$. **D** The tracking plot of 760 patients when $k=2-6$.

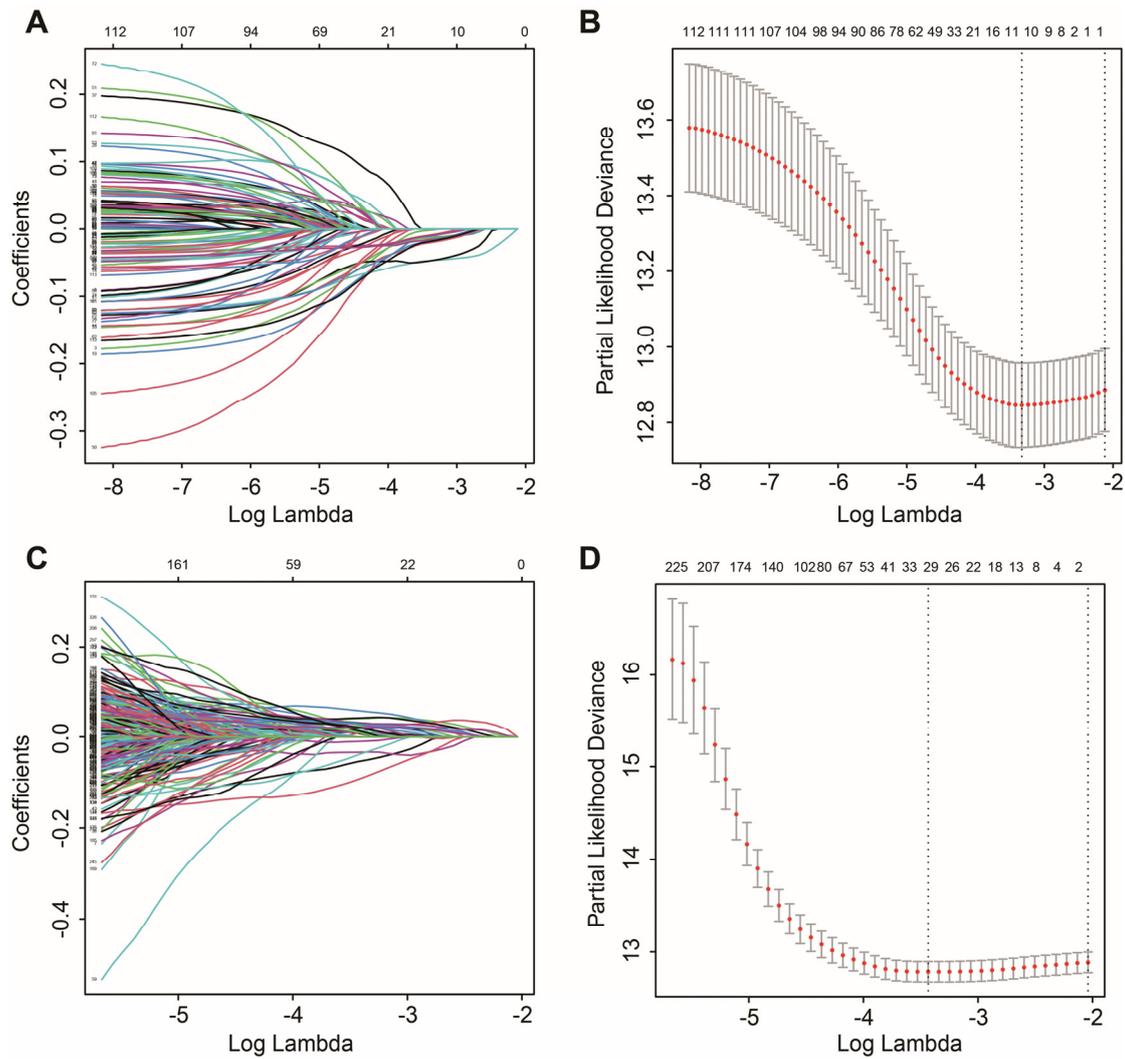


Figure S3. Selection of candidate genes via “LASSO” algorithm. **A** LASSO coefficient profiles of 114 prognostic genes in signature A. **B** Partial likelihood deviance of prognostic genes in signature A. **C** LASSO coefficient profiles of 340 prognostic genes in signature B. **D** Partial likelihood deviance of prognostic genes in signature B.