**Supplementary Figures**



**Figure S1. Distribution of 10 000 permutation results for 115 genes in training set.**



**Figure S2. Identification of CRC subclasses using NMF consensus clustering. (A)** GO analysis of 115 metabolism-associated genes. **(B, C)** The heatmap of consensus matrix when k = 3 in training set **(B)** and testing set **(C)**. GO: gene ontology.



**Figure S3. Validation of the metabolism-related signature** **in testing set. (A)** Distribution of risk scores in CRC subclasses of testing set. **(B)** Survival analysis of the metabolism-related signature in CRC subclasses of testing set. \*\*\*\*P<0.0001.