

The cancers datasets from TCGA contained RNA-Seq data and included both tumor and tumor-adjacent samples. The tumor samples were divided into different stages according to corresponding clinical information of TCGA.

(<https://portal.gdc.cancer.gov/projects/TCGA-COAD>)

The tumor and tumor-adjacent samples can be respectively processed as a microarray. They have the same row size, but column size is different. The row represents gene expression level of samples. The column represents different cancer stages.

The recommended settings are shown in the figure below:

The 1st time point / stage :	<input type="text" value="1"/>	—	<input type="text" value="69"/>
The 2nd time point / stage :	<input type="text" value="70"/>	—	<input type="text" value="94"/>
The 3th time point / stage :	<input type="text" value="95"/>	—	<input type="text" value="126"/>
The 4th time point / stage :	<input type="text" value="127"/>	—	<input type="text" value="155"/>

<http://www.rpcomputationalbiology.cn/example4> Click to view details!