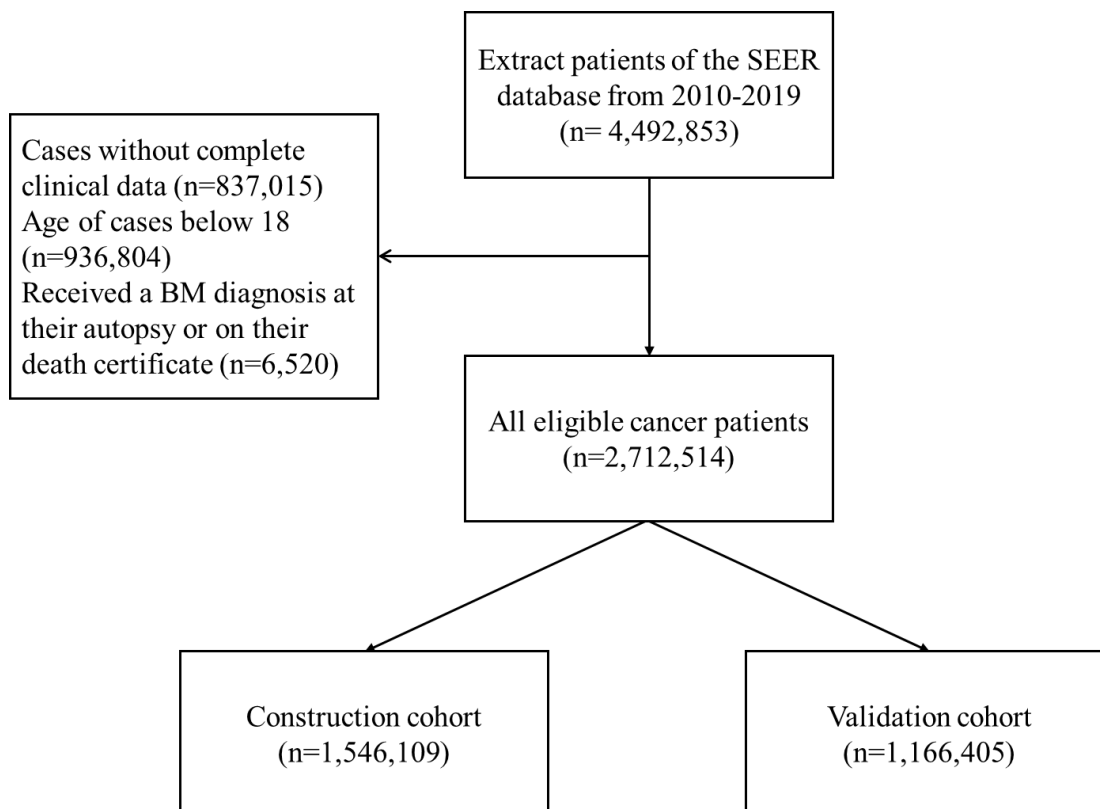


SUPPLEMENTARY FIGURES



Supplementary Figure 1. A flow chart of the patient selection for the construction and validation cohorts in cancer patients with bone metastasis (BM).

```
1 HCdata<- read.csv("C:\\data.csv", header=T, row.names = 1)
2 head(HCdata)
3 dim(HCdata)
4 hc<- hclust(dist(HCdata[,1:17],method = "euclidean"))
5 library(ggdendro)
6 library(cluster)
7 df <- dendro_data(hc, type="rectangle")
8 df1 <- df$segments
9 df2 <- df$labels
10 head(df1)
11 head(df2)
12 library(ggplot2)
13 ggplot()+
14   theme_void() +
15   coord_flip()+
16   geom_segment(data=df1, aes(x=x,y=y,xend=xend,yend=yend))+
17   geom_text(data=df2, aes(x=x,y=y-4,label=label,size=3,hjust=0, vjust=0.5))
```

Supplementary Figure 2. The hierarchical clustering code and visualization used in R.