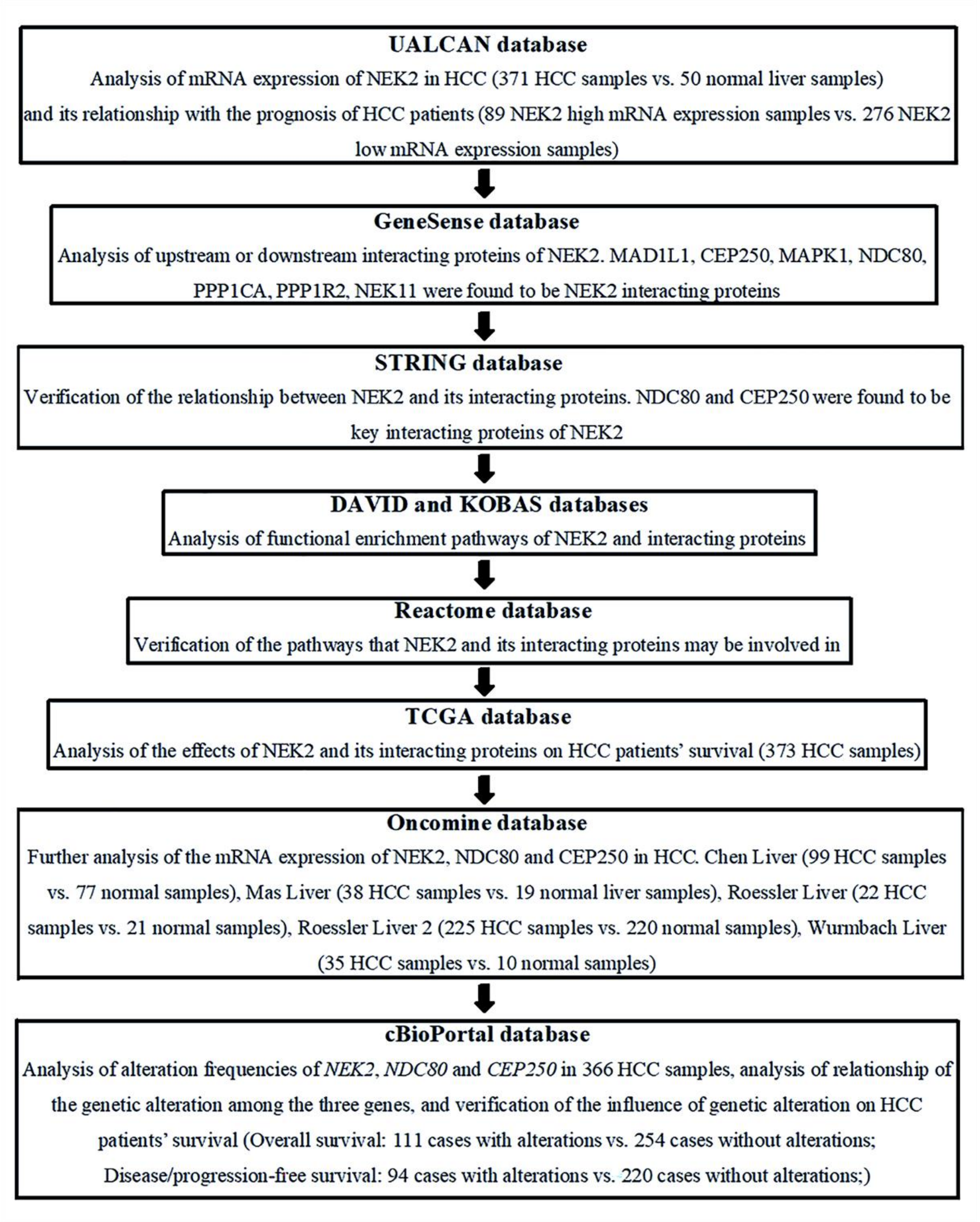

UALCAN database

Analysis of mRNA expression of NEK2 in HCC (371 HCC samples vs. 50 normal liver samples) and its relationship with the prognosis of HCC patients (89 NEK2 high mRNA expression samples vs. 276 NEK2 low mRNA expression samples)

GeneSense database

Analysis of upstream or downstream interacting proteins of NEK2. MAD1L1, CEP250, MAPK1, NDC80, PPP1CA, PPP1R2, NEK11 were found to be NEK2 interacting proteins

STRING database

Verification of the relationship between NEK2 and its interacting proteins. NDC80 and CEP250 were found to be key interacting proteins of NEK2

DAVID and KOBAS databases

Analysis of functional enrichment pathways of NEK2 and interacting proteins

Reactome database

Verification of the pathways that NEK2 and its interacting proteins may be involved in

TCGA database

Analysis of the effects of NEK2 and its interacting proteins on HCC patients' survival (373 HCC samples)

Oncomine database

Further analysis of the mRNA expression of NEK2, NDC80 and CEP250 in HCC. Chen Liver (99 HCC samples vs. 77 normal samples), Mas Liver (38 HCC samples vs. 19 normal liver samples), Roessler Liver (22 HCC samples vs. 21 normal samples), Roessler Liver 2 (225 HCC samples vs. 220 normal samples), Wurmbach Liver (35 HCC samples vs. 10 normal samples)

cBioPortal database

Analysis of alteration frequencies of *NEK2*, *NDC80* and *CEP250* in 366 HCC samples, analysis of relationship of the genetic alteration among the three genes, and verification of the influence of genetic alteration on HCC patients' survival (Overall survival: 111 cases with alterations vs. 254 cases without alterations; Disease/progression-free survival: 94 cases with alterations vs. 220 cases without alterations;)

Figure S1. Flow chart of the study and the sample numbers for each data mining part.