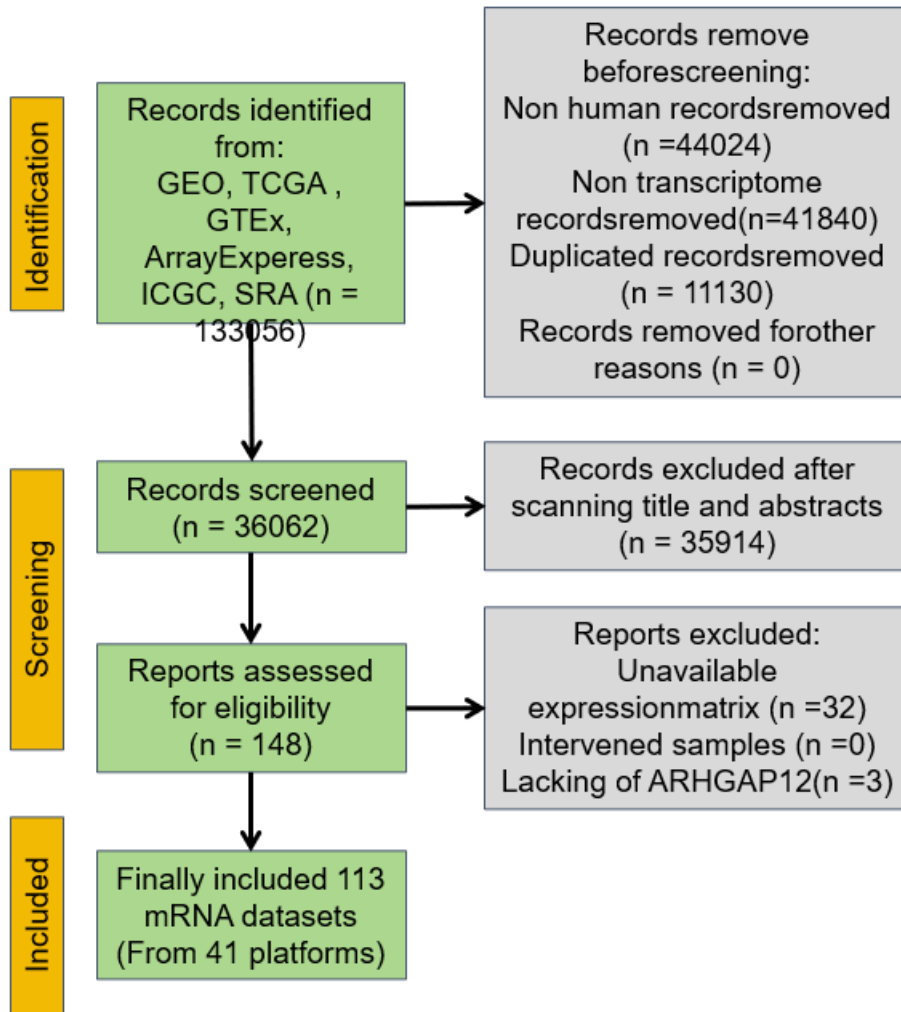
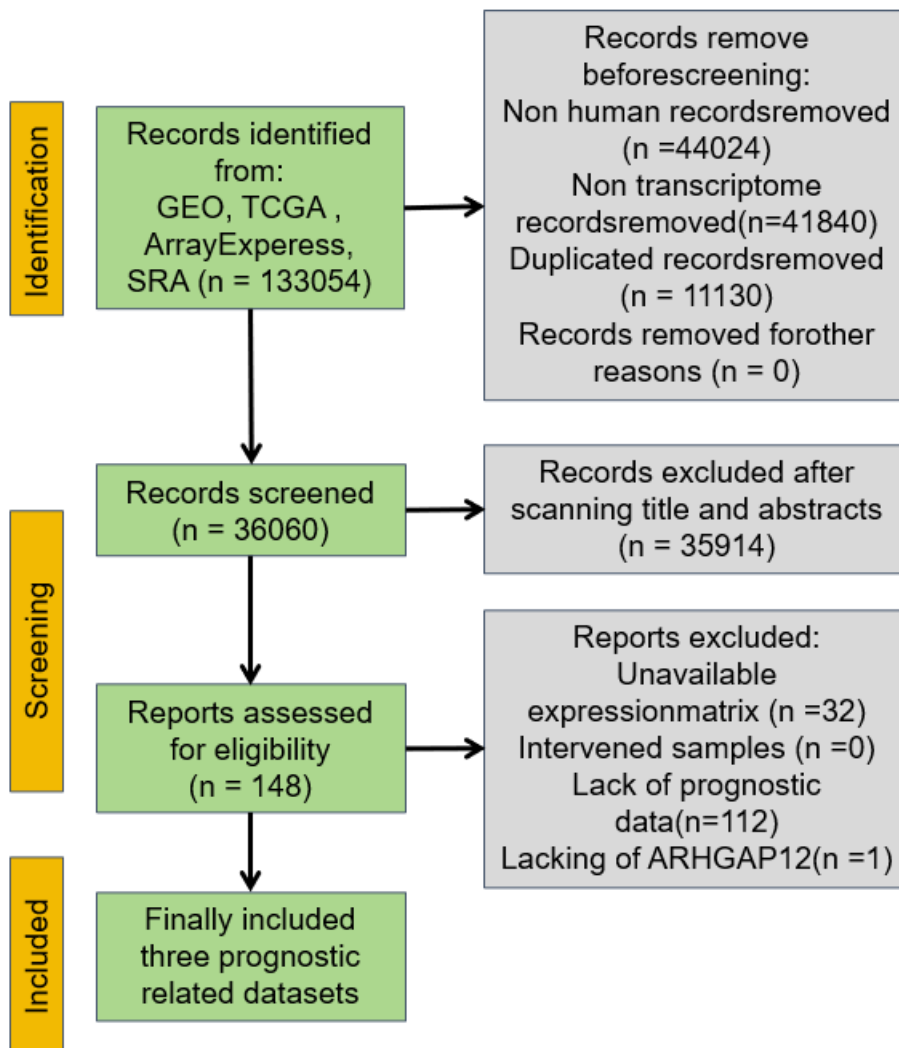


Identification of studies in HCC mRNA via databases and registers

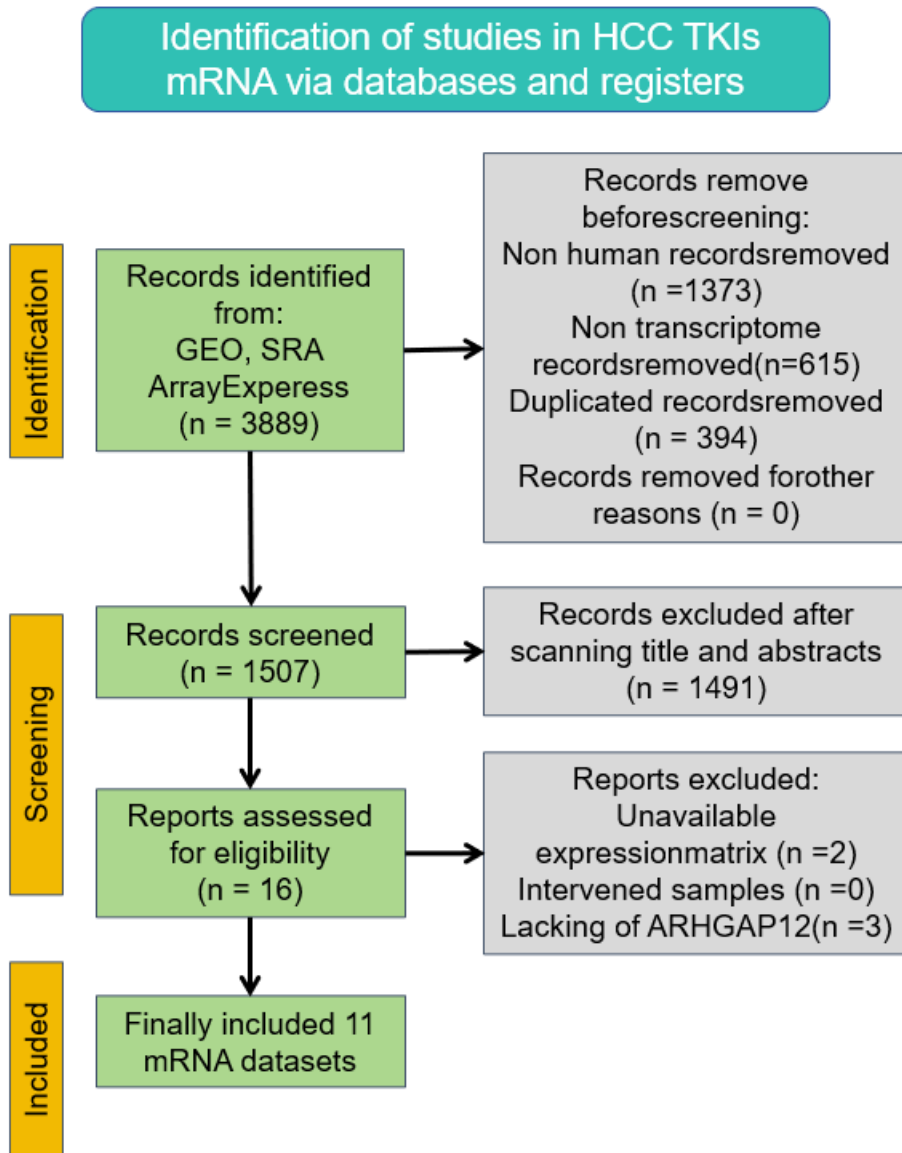


Supplementary Figure 1 Flow of HCC related datasets screening in this study.

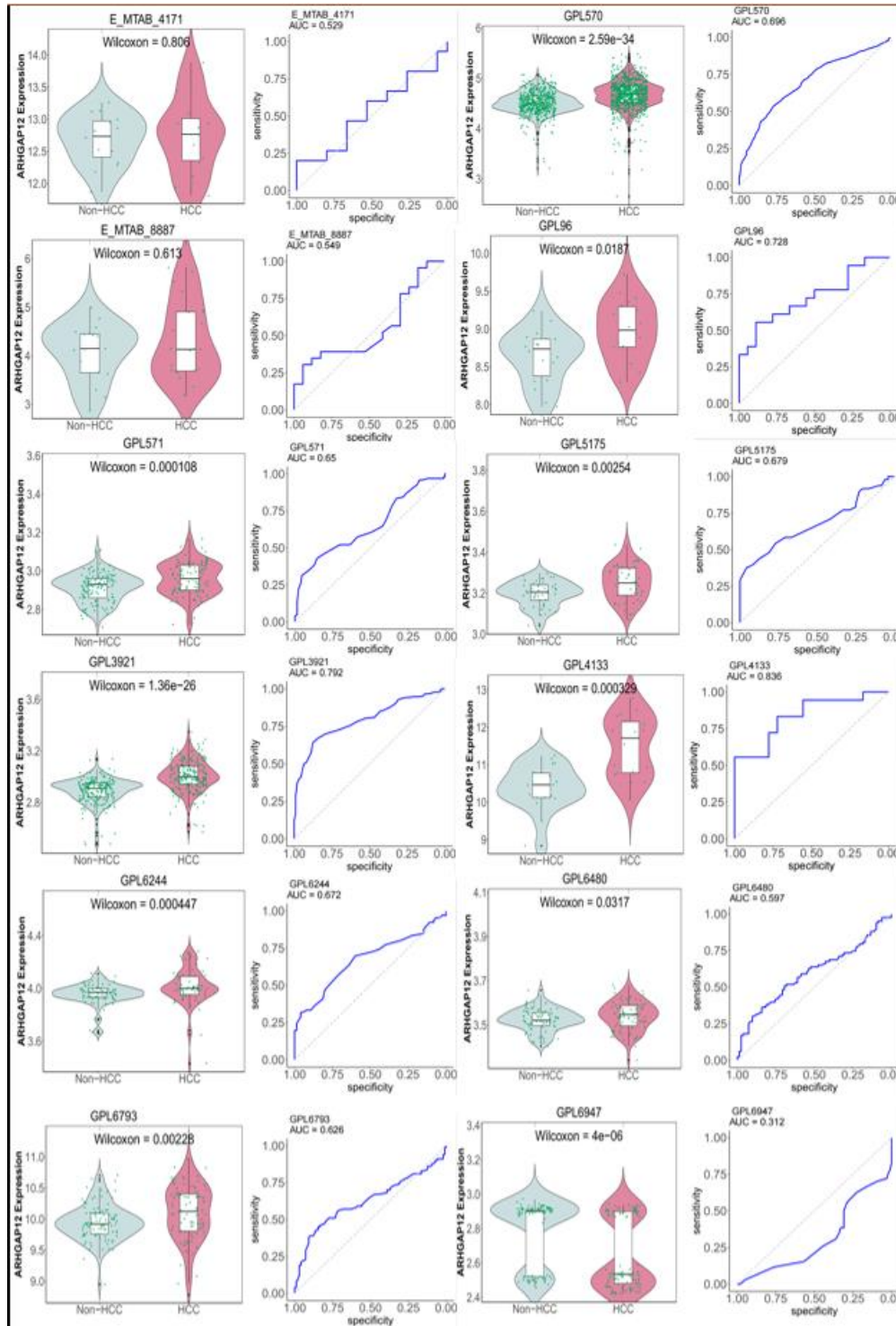
Identification of HCC prognostic level studies via database and registration



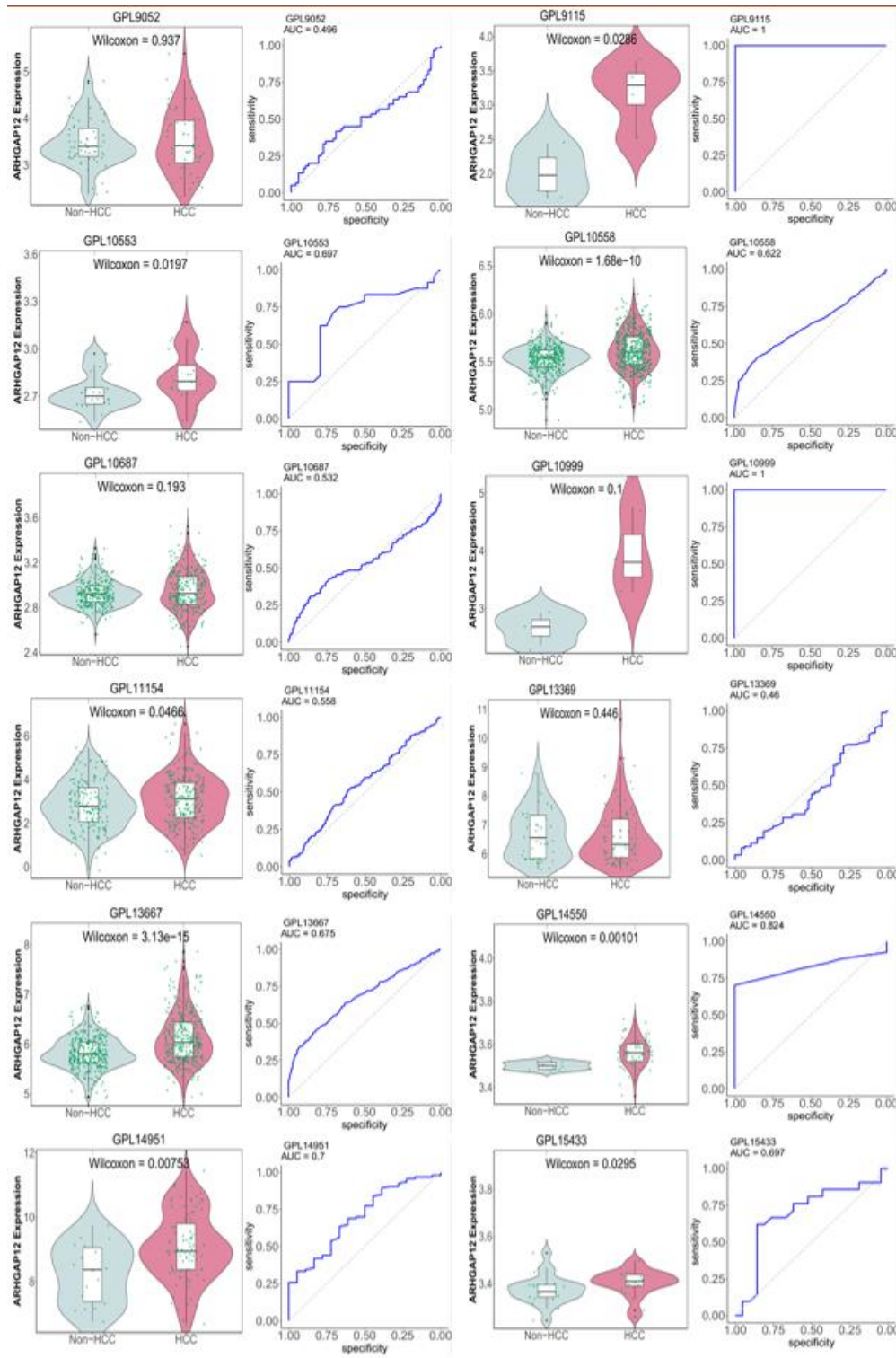
Supplementary Figure 2 Flow of HCC TKIs related datasets screening in this study.



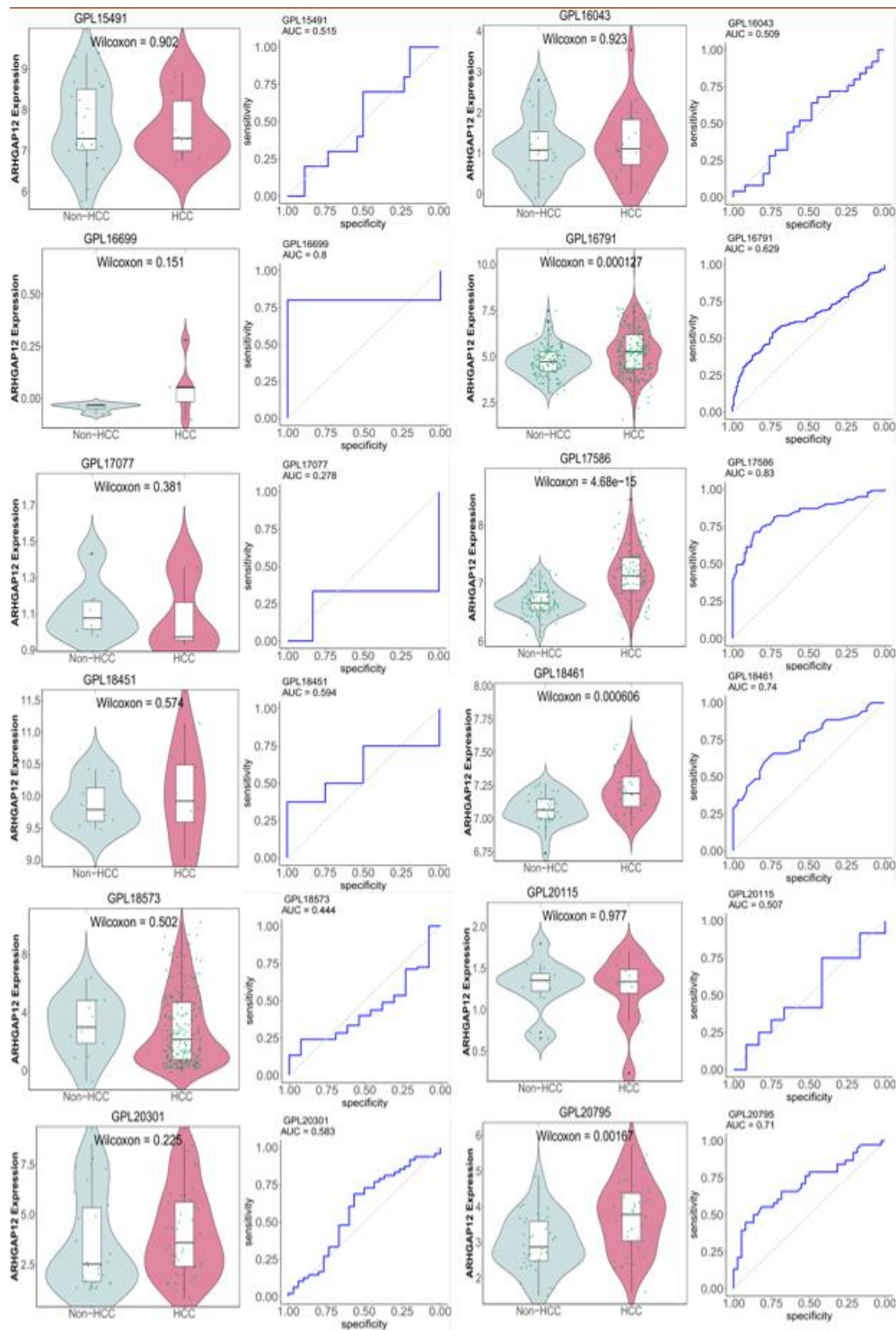
Supplementary Figure 3 Flow of HCC prognostic level related datasets screening in this study.



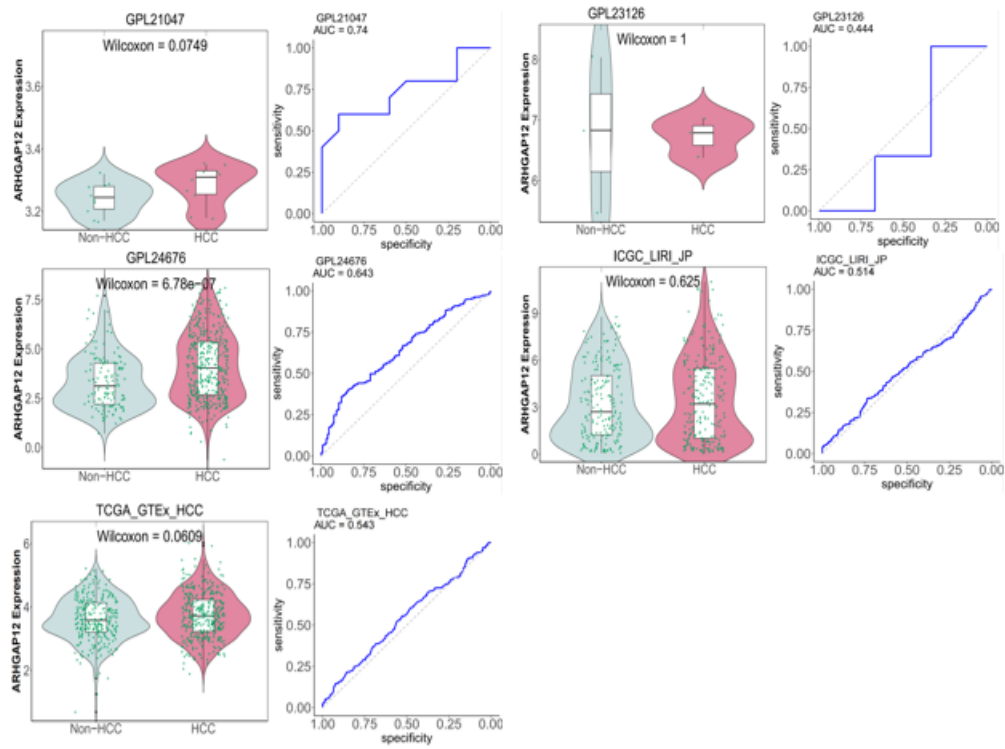
Supplementary Figure 4 Violin plots showing the differences in expression of ARHGAP12 between HCC cases (pink) and non-HCC cases (blue) in selected datasets.



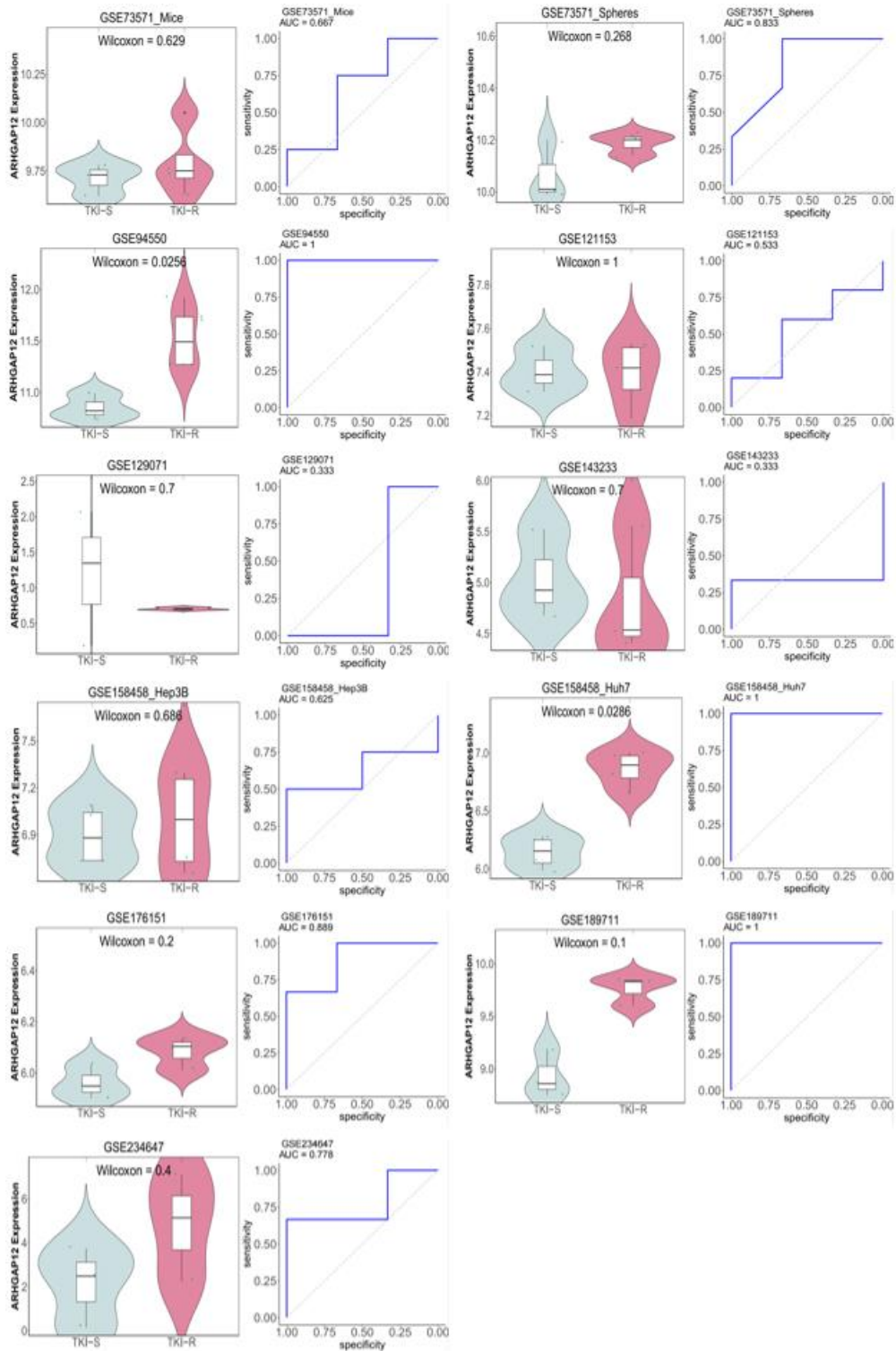
Supplementary Figure 5. Violin plots showing the differences in expression of ARHGAP12 between HCC cases (pink) and non-HCC cases (blue) in selected datasets.



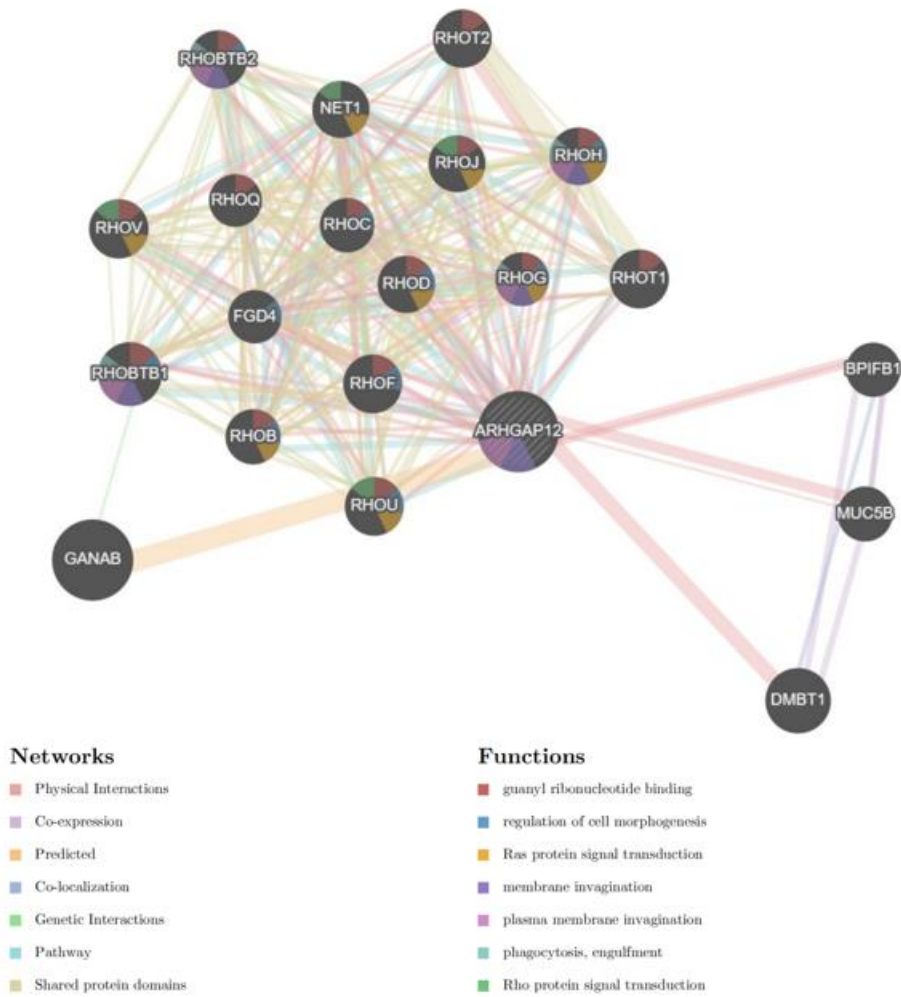
Supplementary Figure 6. Violin plots showing the differences in expression of ARHGAP12 between HCC cases (pink) and non-HCC cases (blue) in selected datasets.



Supplementary Figure 7. Violin plots showing the differences in expression of ARHGAP12 between HCC cases (pink) and non-HCC cases (blue) in selected datasets.



Supplementary Figure 8. Violin plot displays the distribution of ARHGAP12 mRNA expression levels in various HCC datasets with TKI resistance.



Supplementary Figure 9. The protein-protein interaction network and functional pathways based on ARHGAP12.