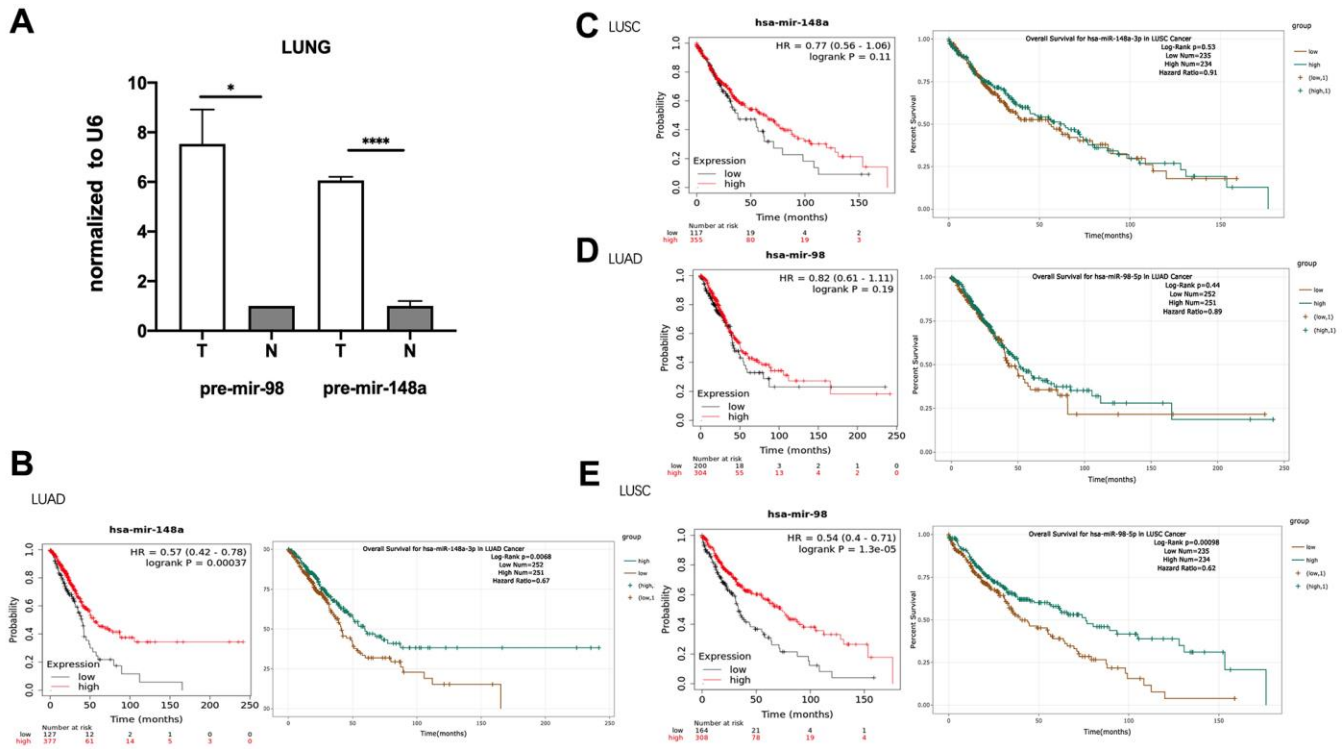
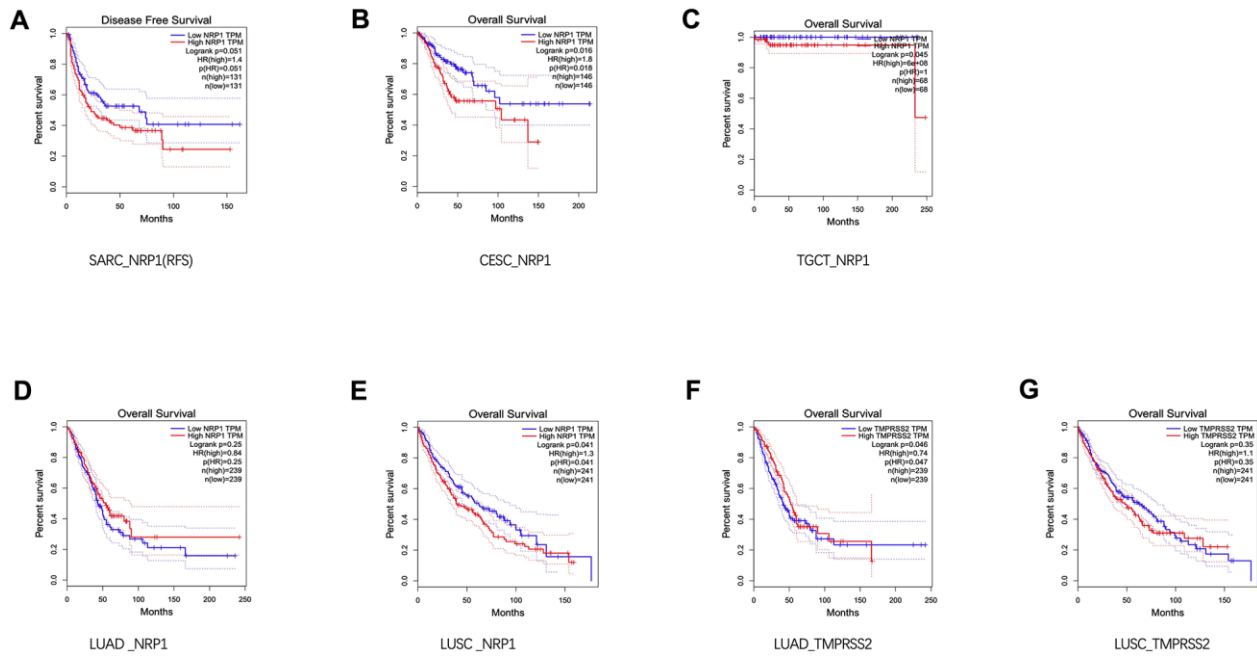


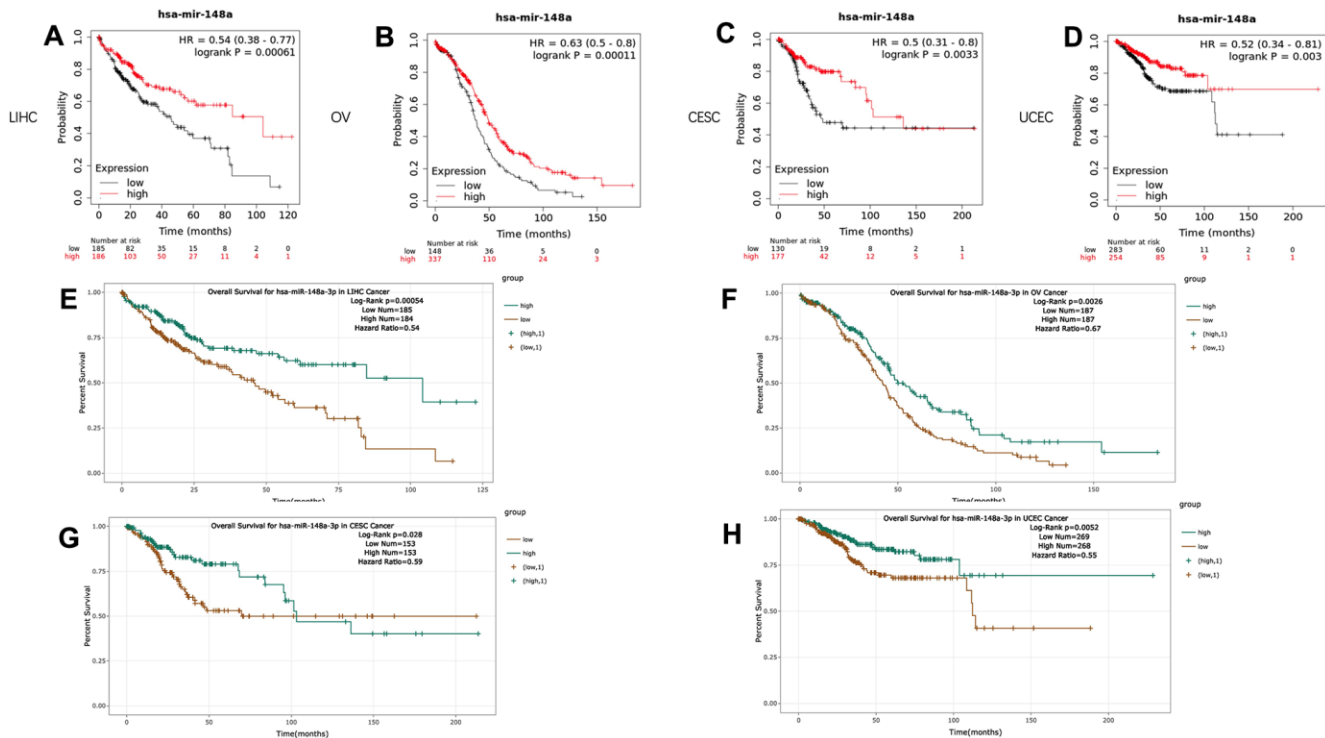
SUPPLEMENTARY FIGURES



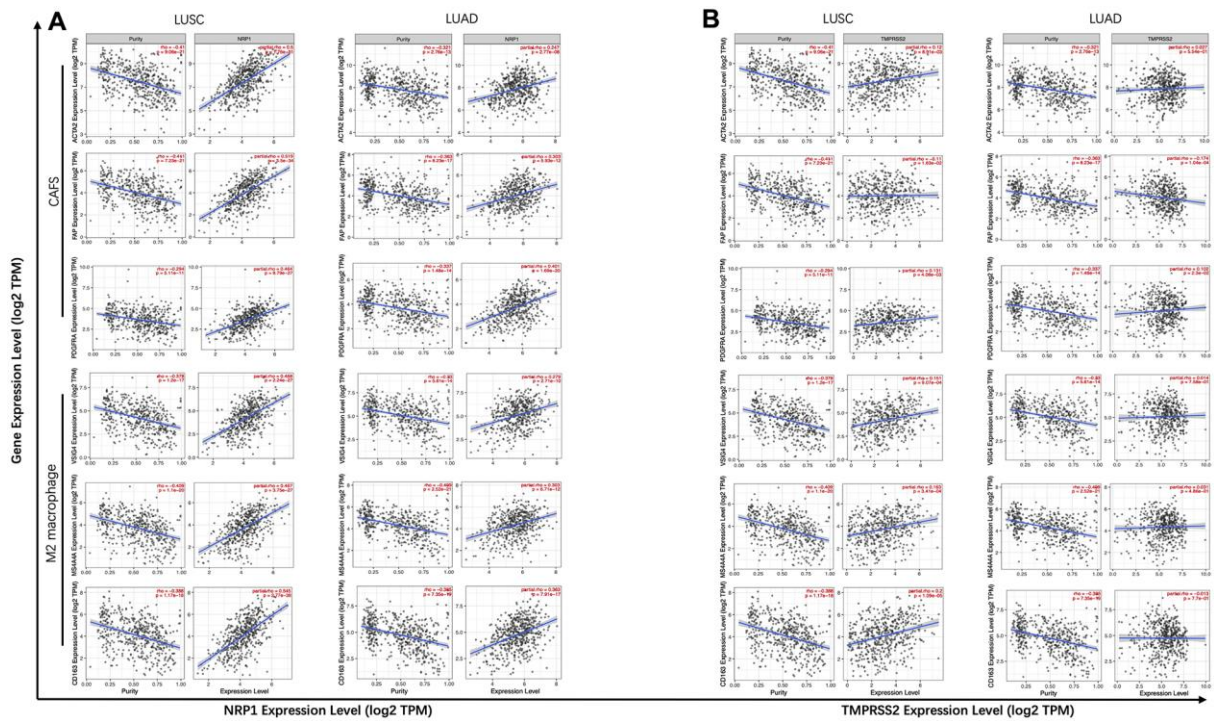
Supplementary Figure 1. Survival analysis of lung cancer patients with differential microRNA expression level. (A) qPCR analysis of pre-miR-98 and pre-miR-148a in LUAD tissues and paired normal tissues. n=3, * P<0.05, **** P<0.0001. (B, C) Survival curve of LUSC and LUAD patients with differential level of miR-148a expression. (D, E) Survival curve of LUSC and LUAD patients with differential level of miR-98 expression.



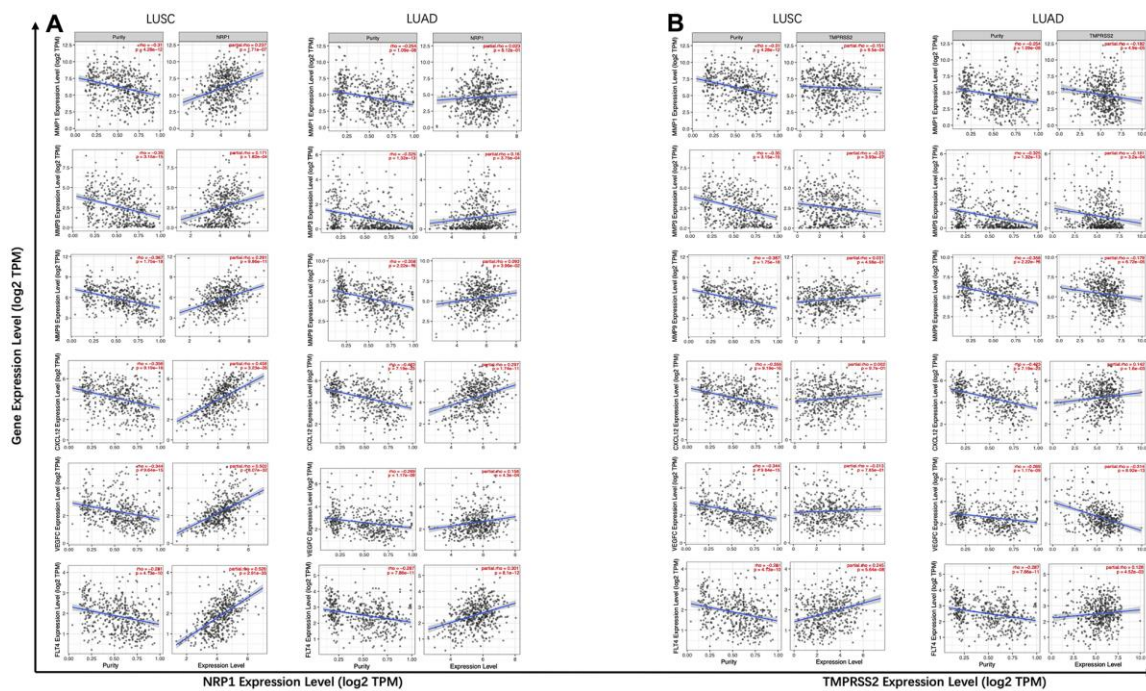
Supplementary Figure 2. Survival analysis of cancer patients with differential NRP1 or TMPRSS2 level. Survival curve of SARC (A), CESC (B), TGCT (C), LUAD (D) and LUSC (E) patients with different level of NRP1. Survival curve of LUAD (F), LUSC (G) patients with different level of TMPRSS2. Analysis was done by GEPIA database.



Supplementary Figure 3. Survival analysis of cancer patients with different miR-148a level. Survival curve of LIHC (A, E), OV (B, F), CESC (C, G) and UCEC (D, H) patients with differential level of miR-148a expression. Analysis was done with Kaplan-Meier Plotter and ENCORI.



Supplementary Figure 4. Correlation analysis between NRP1(TMPRSS2) and pro-tumorigenic factors. (A) Correlation analysis between NRP1 and markers for CAFs and M2 macrophage in LUSC (n=501) and LUAD(n=515). **(B)** Correlation analysis between TMPRSS2 and markers for CAFs and M2 macrophage in LUSC (n=501) and LUAD(n=515). Purity adjusted for all the panels.



Supplementary Figure 5. Correlation analysis between NRP1(TMPRSS2) and pro-tumorigenic factors (purity adjusted). (A) Correlation analysis between NRP1 and MMP1, MMP3, MMP9, VEGFC, FLT4 and CXCL12 in LUSC (n=501) and LUAD(n=515). **(B)** Correlation analysis between TMPRSS2 and MMP1, MMP3, MMP9, VEGFC, FLT4 and CXCL12 in LUSC (n=501) and LUAD(n=515). Purity adjusted for all the panels.