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SUPPLEMENTARY INFORMATION

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Comprehensive Analysis of The Expression and Prognostic Value for SNRP Members in Hepatocellular Carcinoma

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Supplementary Description

In supplementary materials, we split patients by auto select best cutoff for OS, PFS, and RFS in Figure S1, S4, S7, and the prognostic value of PFS and RFS were showed in Figure S2, S5, the subgroup analyses shown in Figure S3, S6. Interaction network of SNRPs at the gene and protein levels in HCC patients in Figure S8.

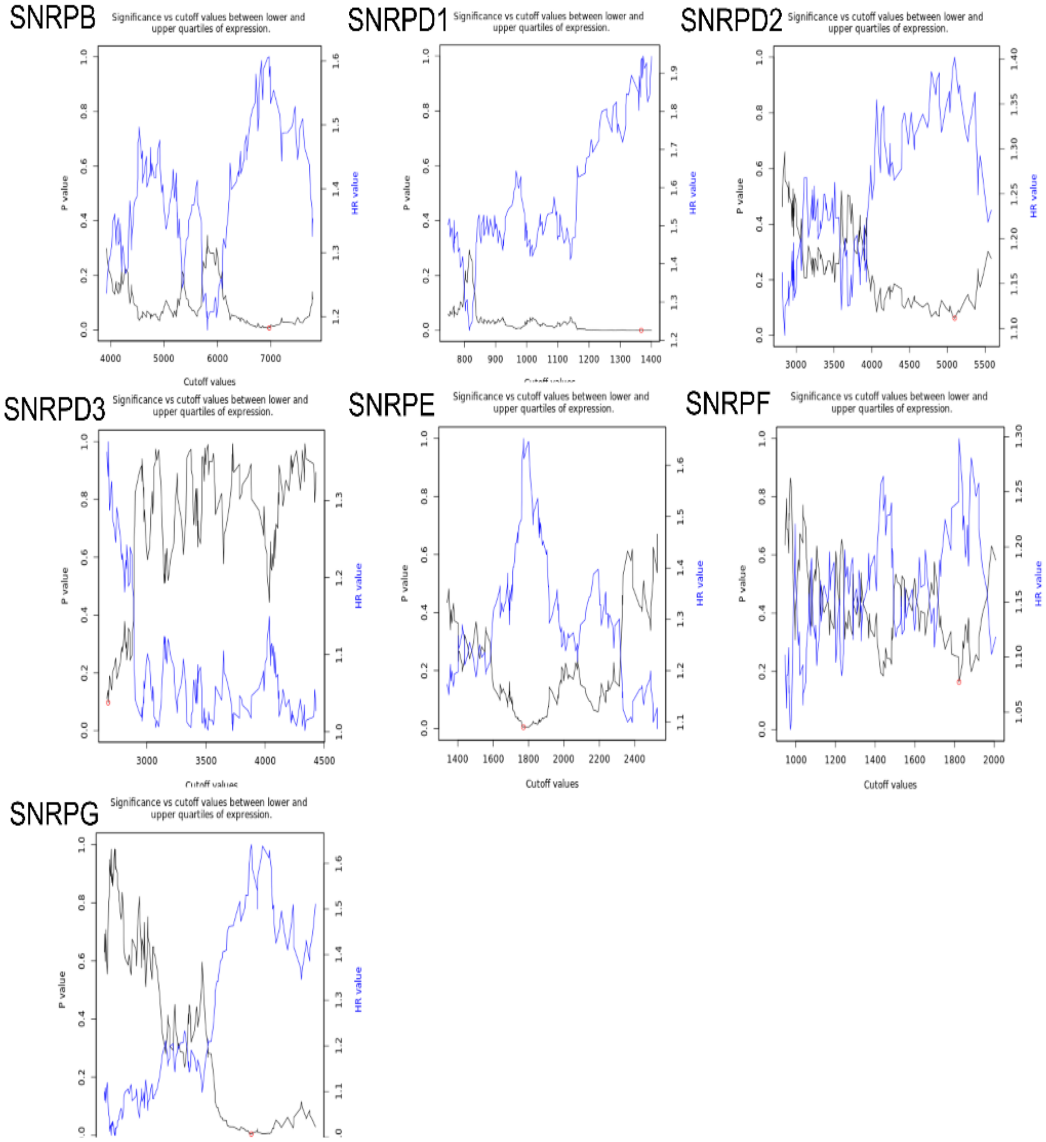

Figure S1: We split patients by auto select best cutoff [20] in each member by KM plotter and the corresponding cutoff can be seen based on Figure 4. (Can be checked in original manuscript)

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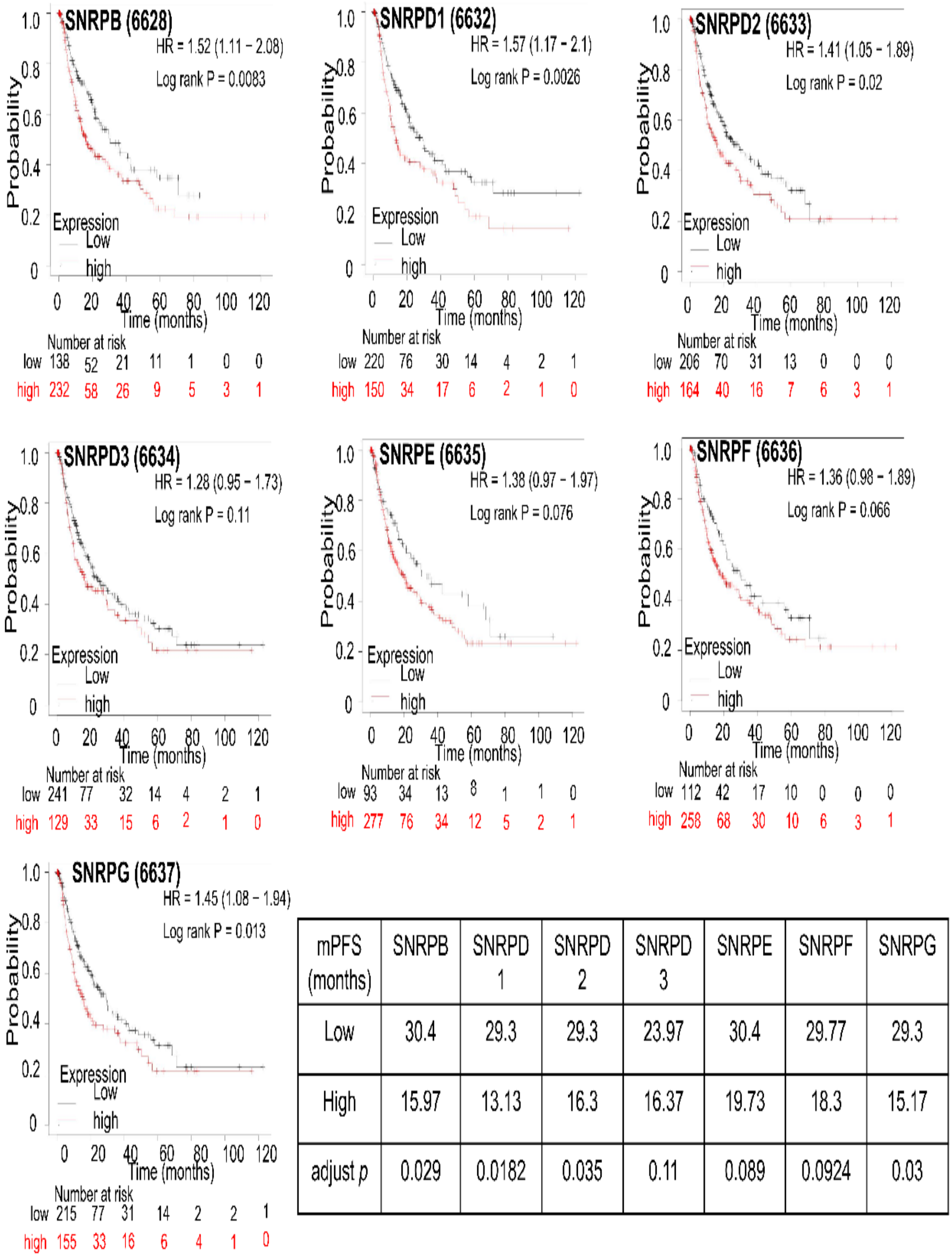

mPFS (months)	SNRPB	SNRPD 1	SNRPD 2	SNRPD 3	SNRPE	SNRPF	SNRPG
Low	30.4	29.3	29.3	23.97	30.4	29.77	29.3
High	15.97	13.13	16.3	16.37	19.73	18.3	15.17
adjust *p*	0.029	0.0182	0.035	0.11	0.089	0.0924	0.03

Figure S2: Prognostic value of mRNA expression of relative SNRPs in HCC patients (Kaplan–Meier plotter). The PFS survival curves were plotted using the Kaplan–Meier plotter database at p-value of <0.05.

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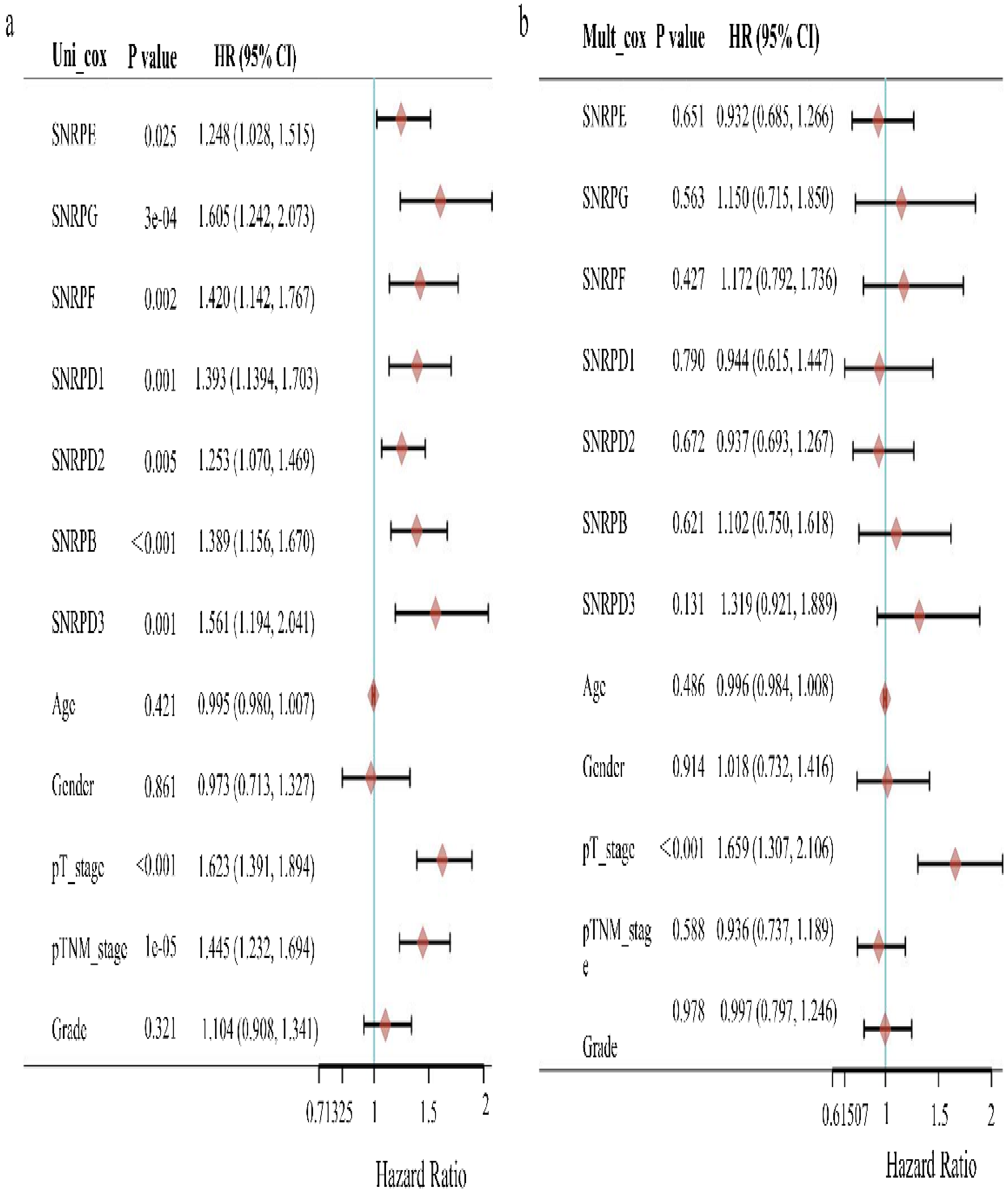

Figure S3: The subgroup analyses for PFS in each member by KM plotter in R version 3.6.1 (http://www.r-pro gect.org/).

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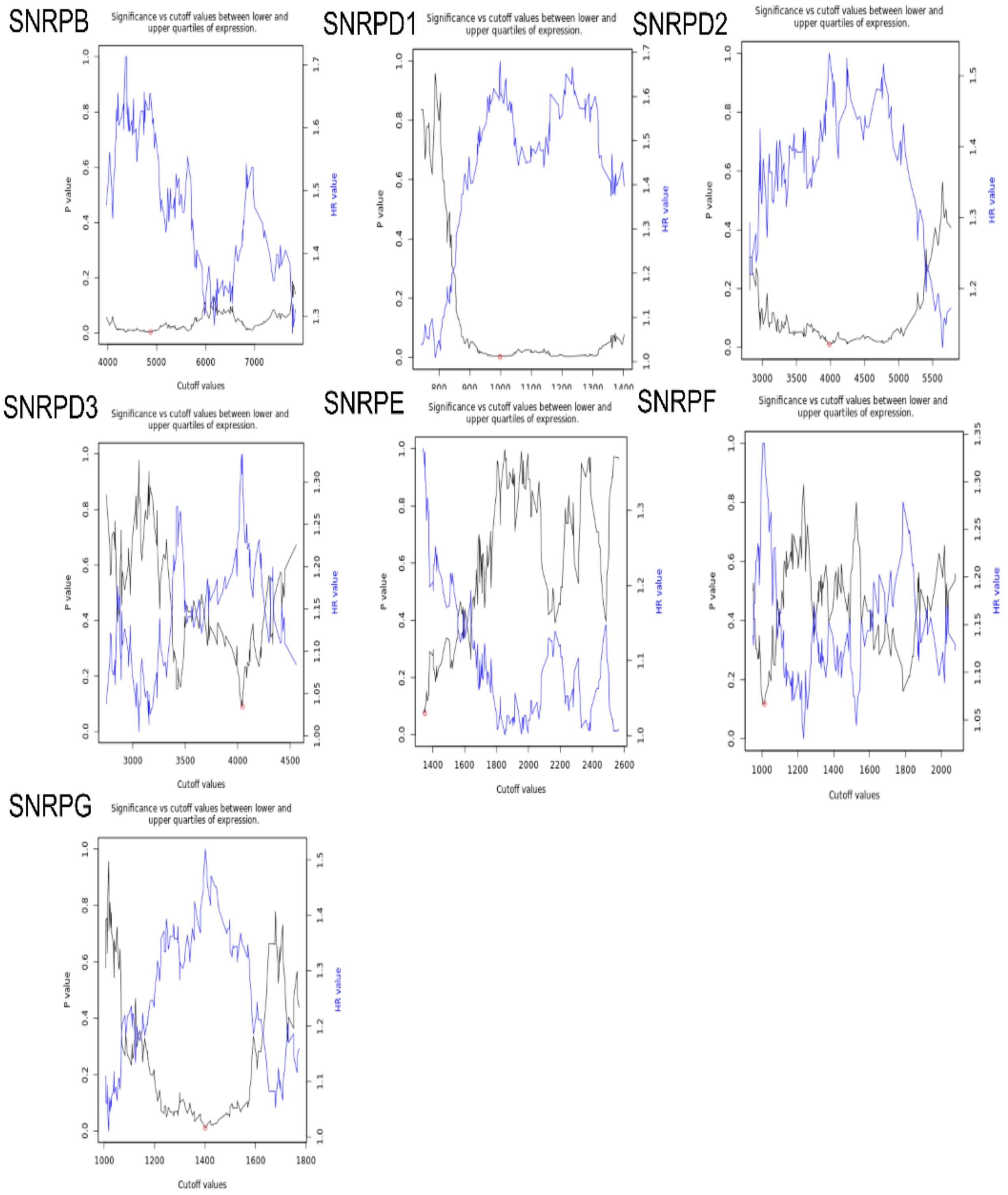

Figure S4: We split patients by auto select best cutoff [20] in each member by KM plotter and the corresponding cutoff can be seen based on Figure S2. (Refer above)

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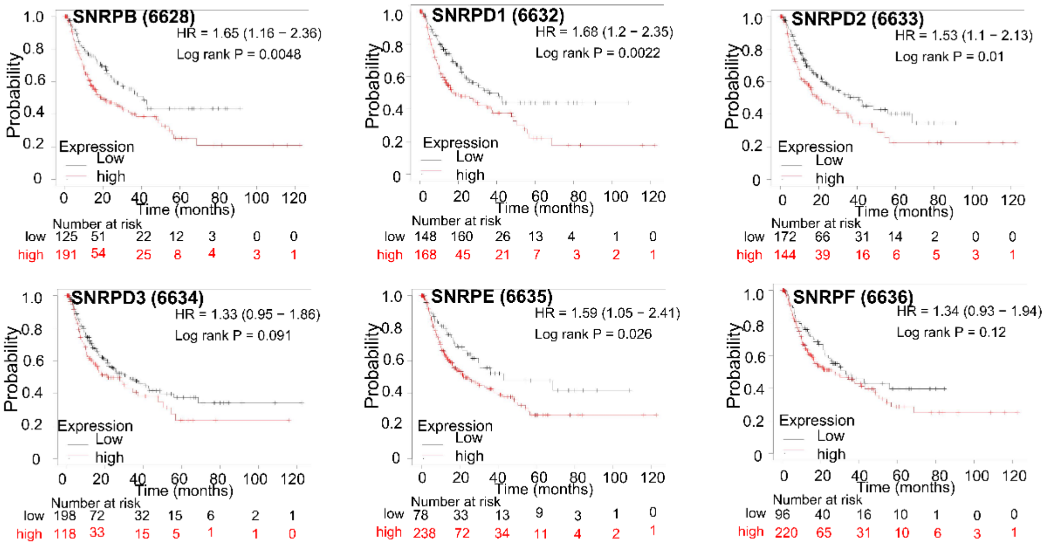

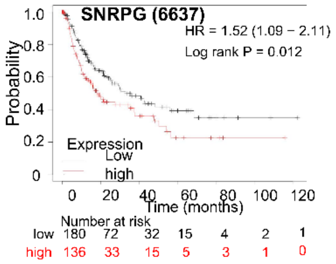

mRFS (months)	SNRPB	SNRPD 1	SNRPD 2	SNRPD 3	SNRPE	SNRPF	SNRPG
Low	40.97	36.1	40.97	33	42.87	33	33
High	19.73	16.7	19.73	21.23	21.93	27.6	18.3
adjust *p*	0.0168	0.0154	0.023	0.106	0.0364	0.12	0.021

Figure S5: Prognostic value of mRNA expression of relative SNRPs in HCC patients (Kaplan–Meier plotter). The RFS survival curves were plotted using the Kaplan–Meier plotter database at p-value of <0.05.

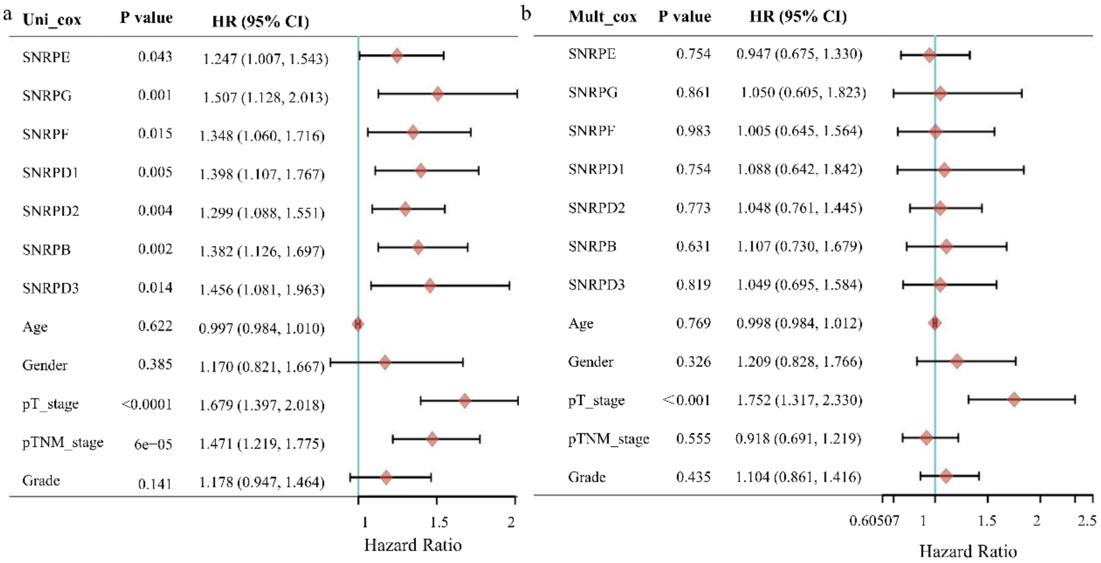

Figure S6: The subgroup analyses for RFS in each member by KM plotter in R version 3.6.1 (http://www.r-progect.org/).

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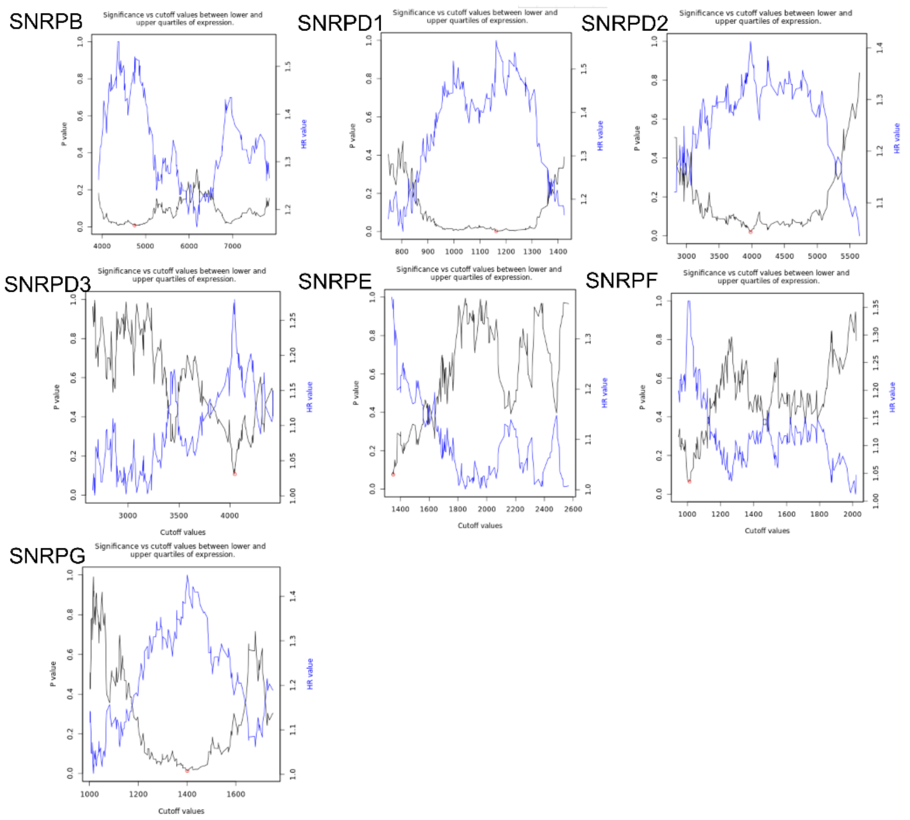

Figure S7: We split patients by auto select best cutoff [20] in each member by KM plotter and the corresponding cutoff can be seen based on Figure S5. (Refer above)

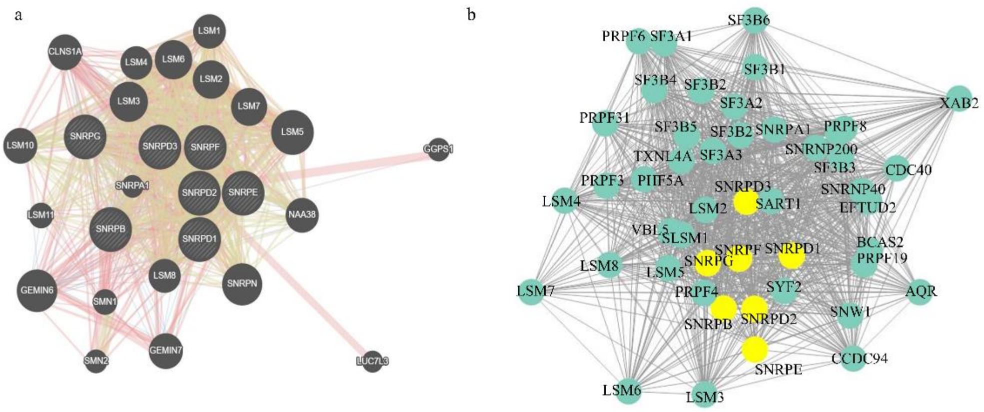

Figure S8: Interaction network of SNRPs at the gene and protein levels in HCC patients. (a) Gene–gene interaction network among SRNPs in the Gene MANIA dataset. (b) Protein–protein interaction network among SNRPs in the STRING dataset linking to Cytoscape.

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