

Fig. S1 Impact on cancer cell line survival of UMG lists before the DepMap filtering step compared to other methods' lists. Extension to Figure 4.

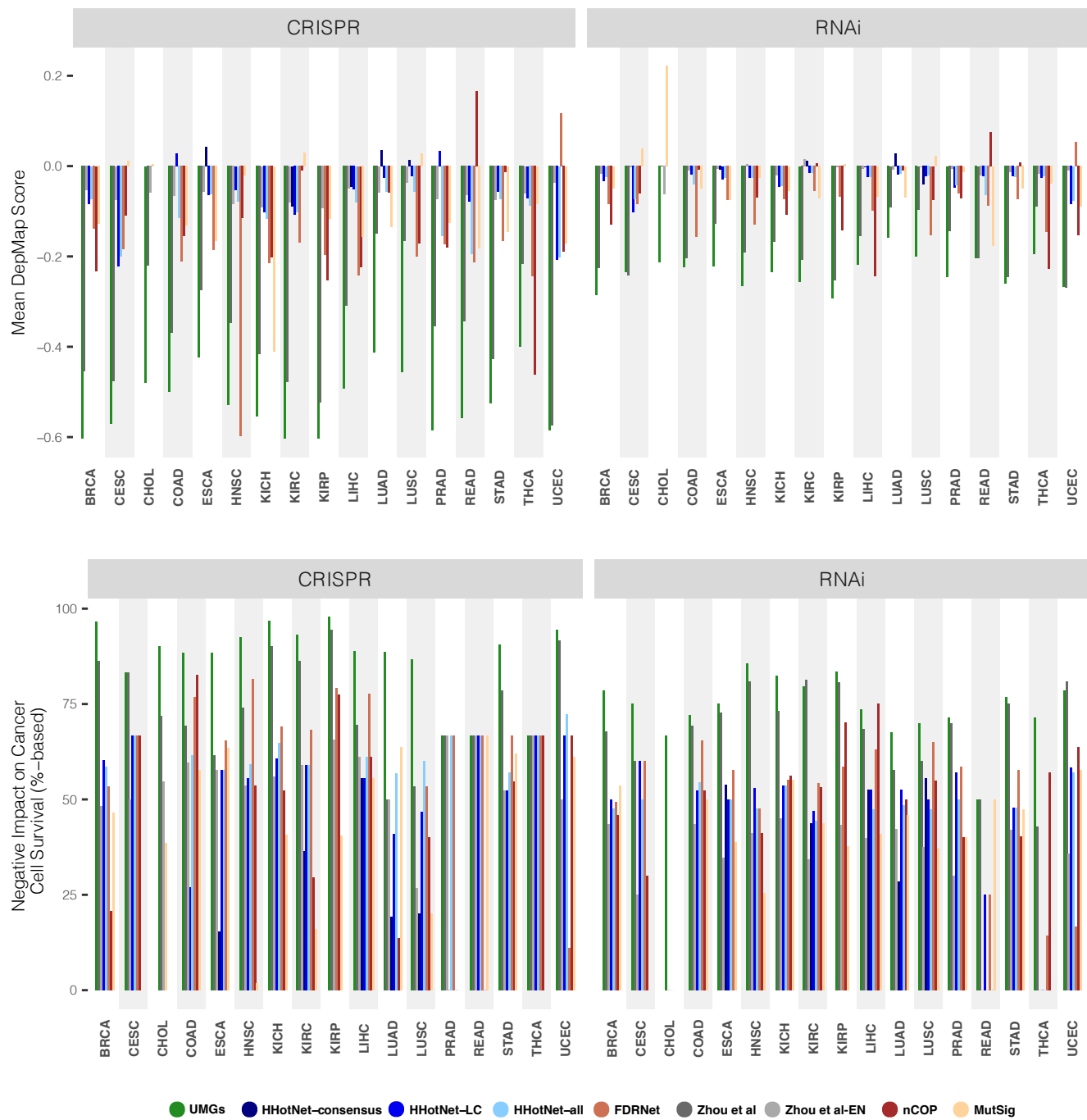


Fig. S2 Impact on cancer cell line survival of UMG lists compared to other methods' lists, all including known driver genes. Extension to Figure 4.

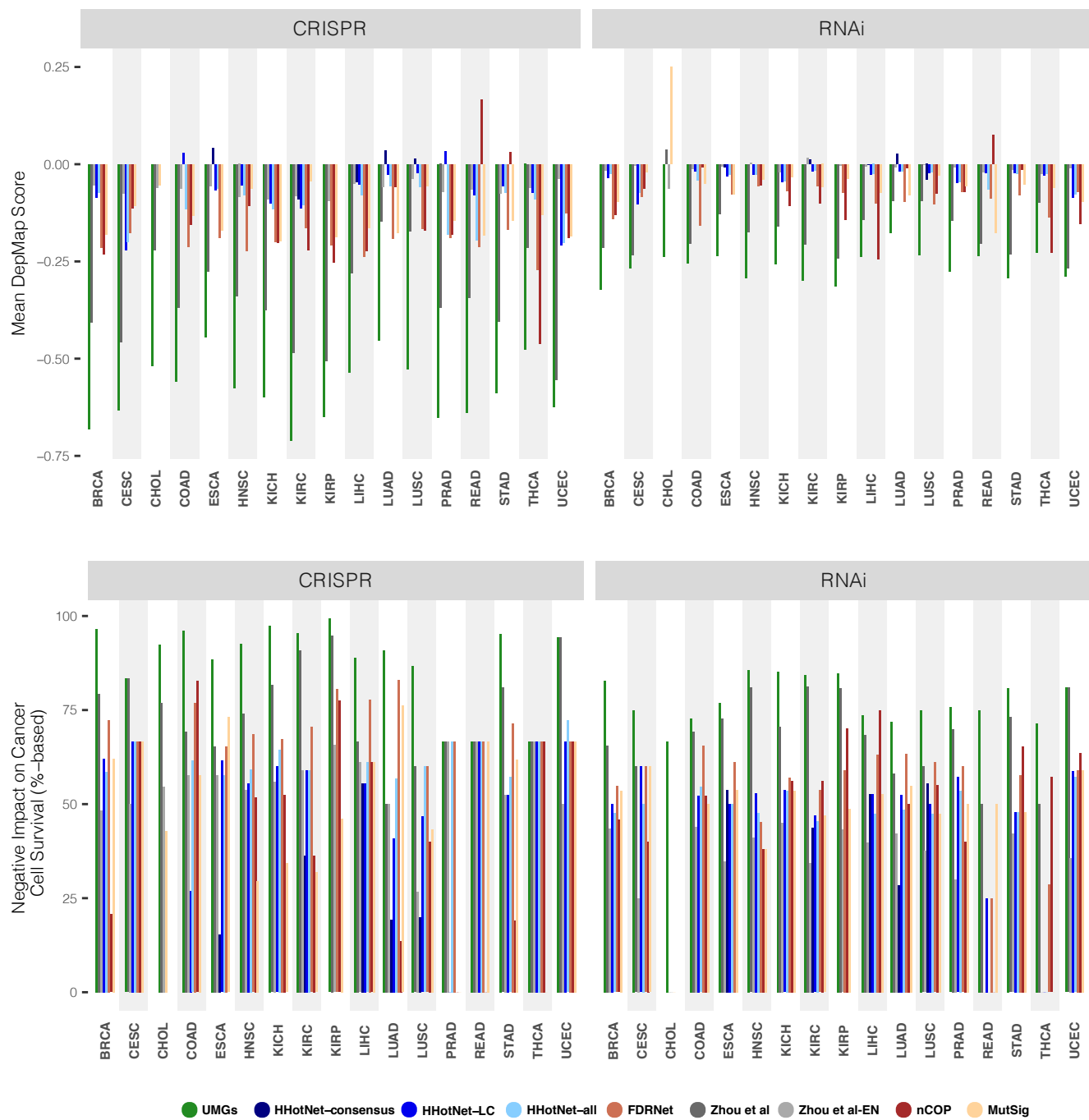


Fig. S3 Impact on cancer cell line survival of UMG lists before the DepMap filtering step compared to other methods' lists, all including known driver genes. Extension to Figure 4.

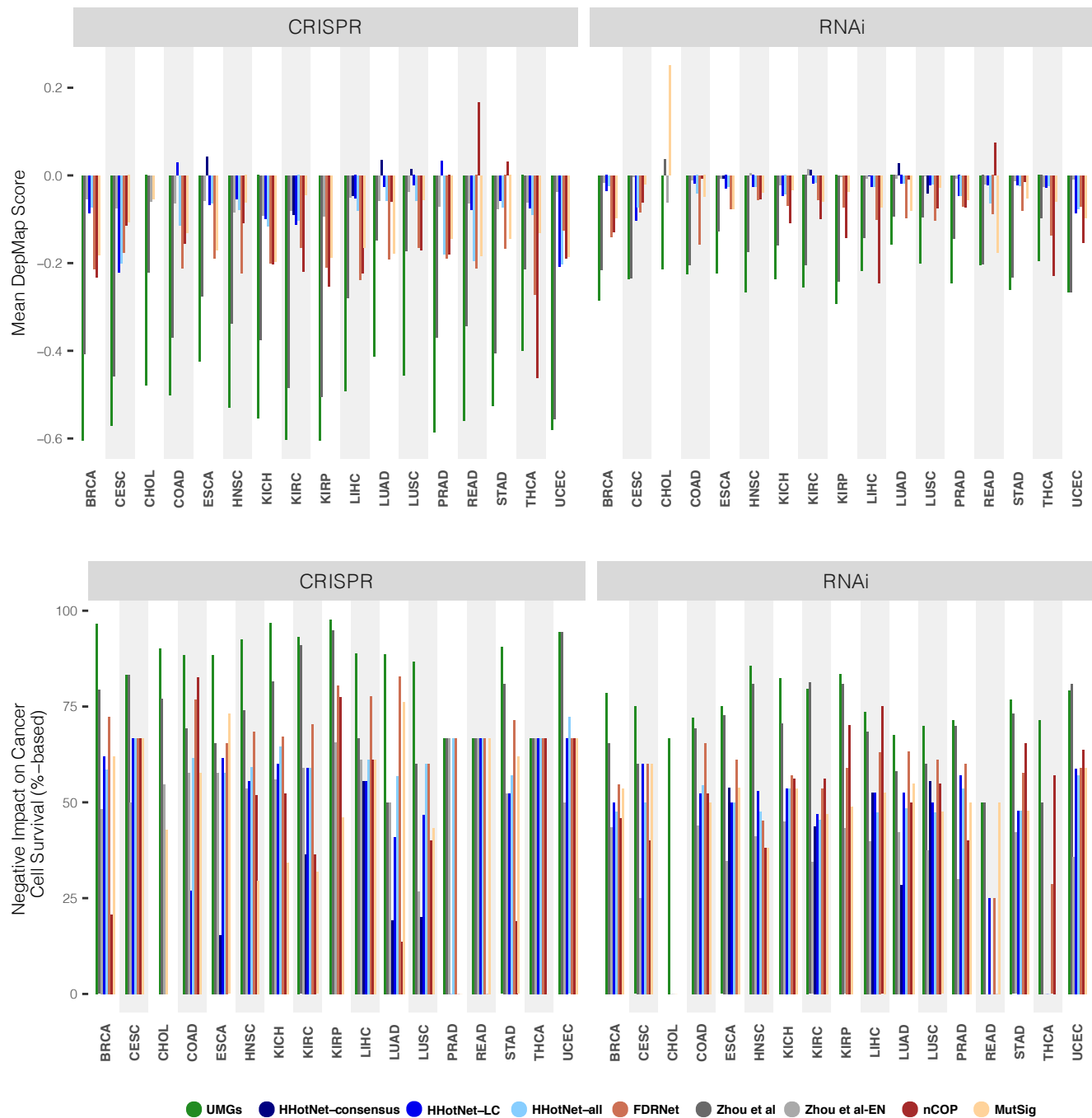


Fig. S4 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in CESC. Extension to Figure 5.

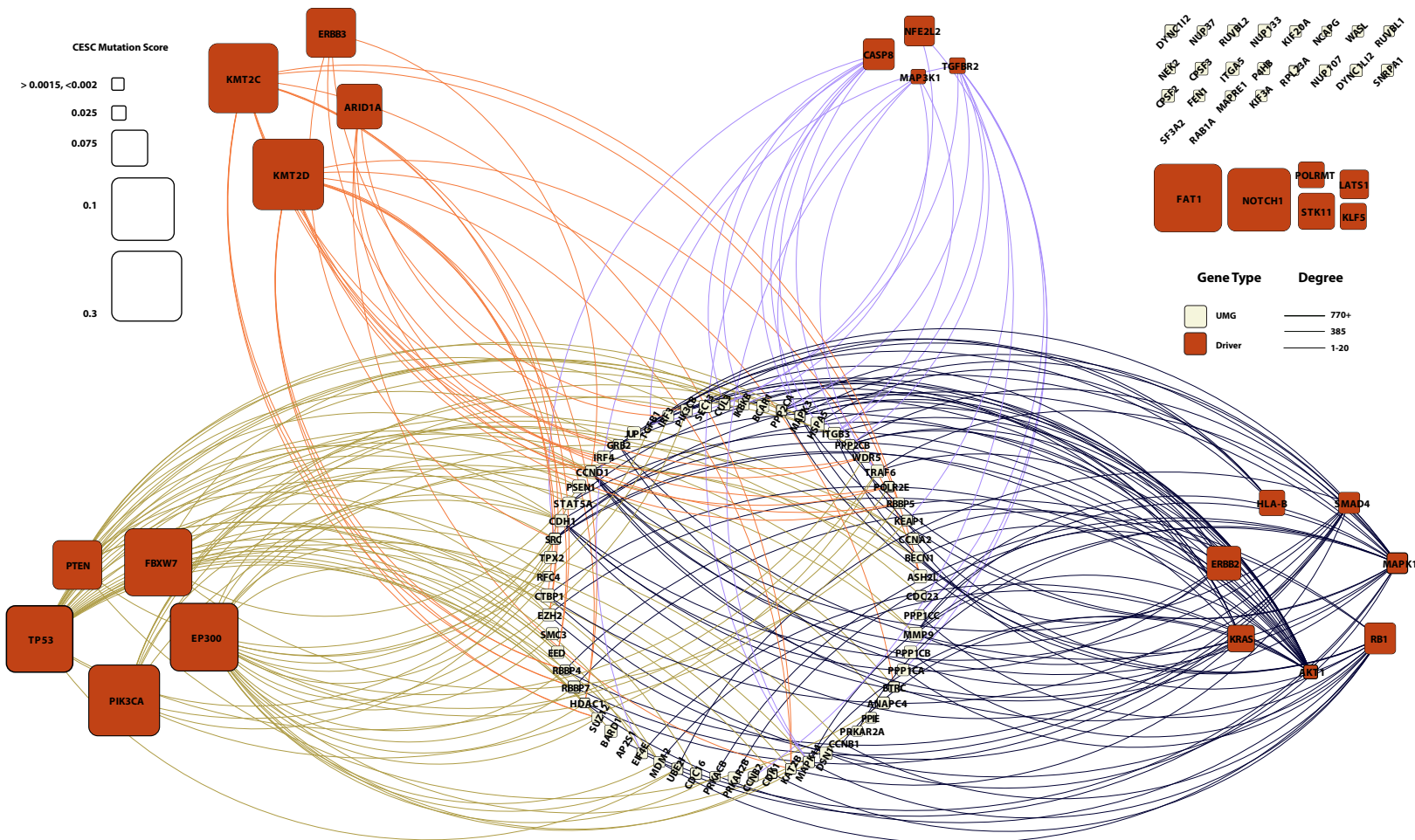
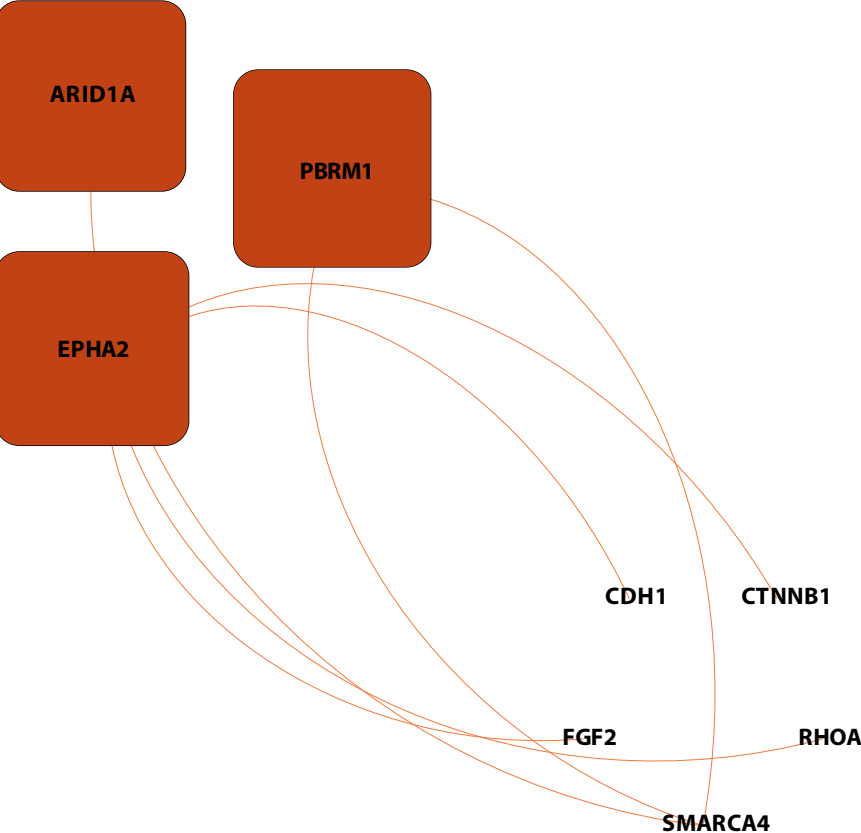
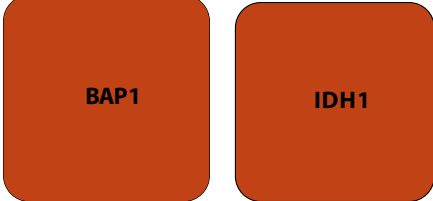


Fig. S5 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in CHOL. Extension to Figure 5.



- CREB1
- PRKAR2B
- ITGA1
- HDAC1
- TRAF2
- AKT1
- DYNC1H1
- PPP1CC
- PPP1CA
- RBBP5
- MAP3K7
- P5MC5
- EIF4E
- RFC4
- ITGB3
- P5MC5
- RUVBL1
- CCNB2
- TUBB4B
- CCNB1
- POLR2E
- PPP2CB
- WDR5
- TRAF6



Gene Type

No Frame UMG

Driver

Degree

150

50

CHOL Mutation Score

0.35

0.1

< 0.0015

No Frame

Fig. S7 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in ESCA. Extension to Figure 5.

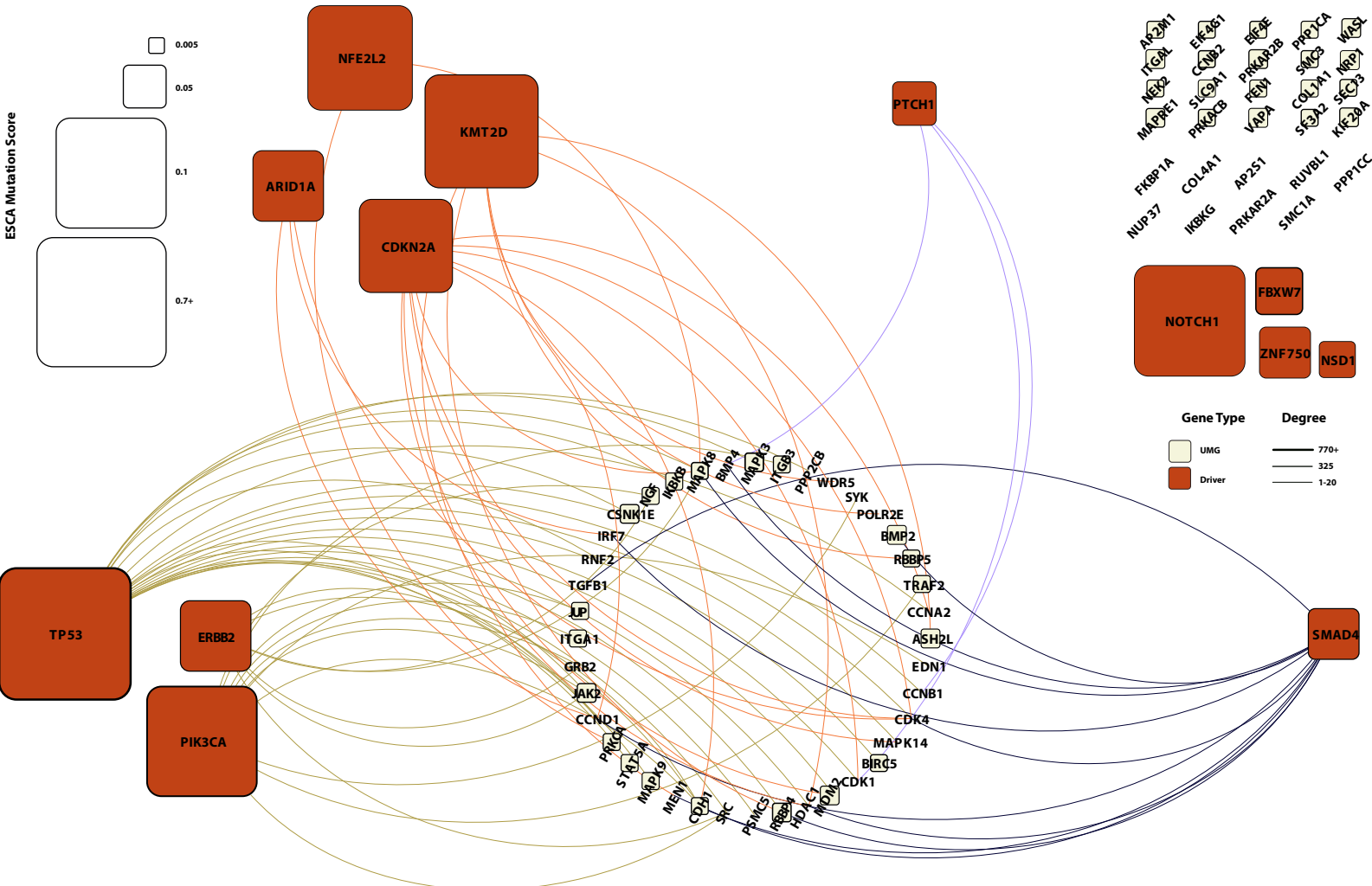


Fig. S9 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in KICH. Extension to Figure 5.

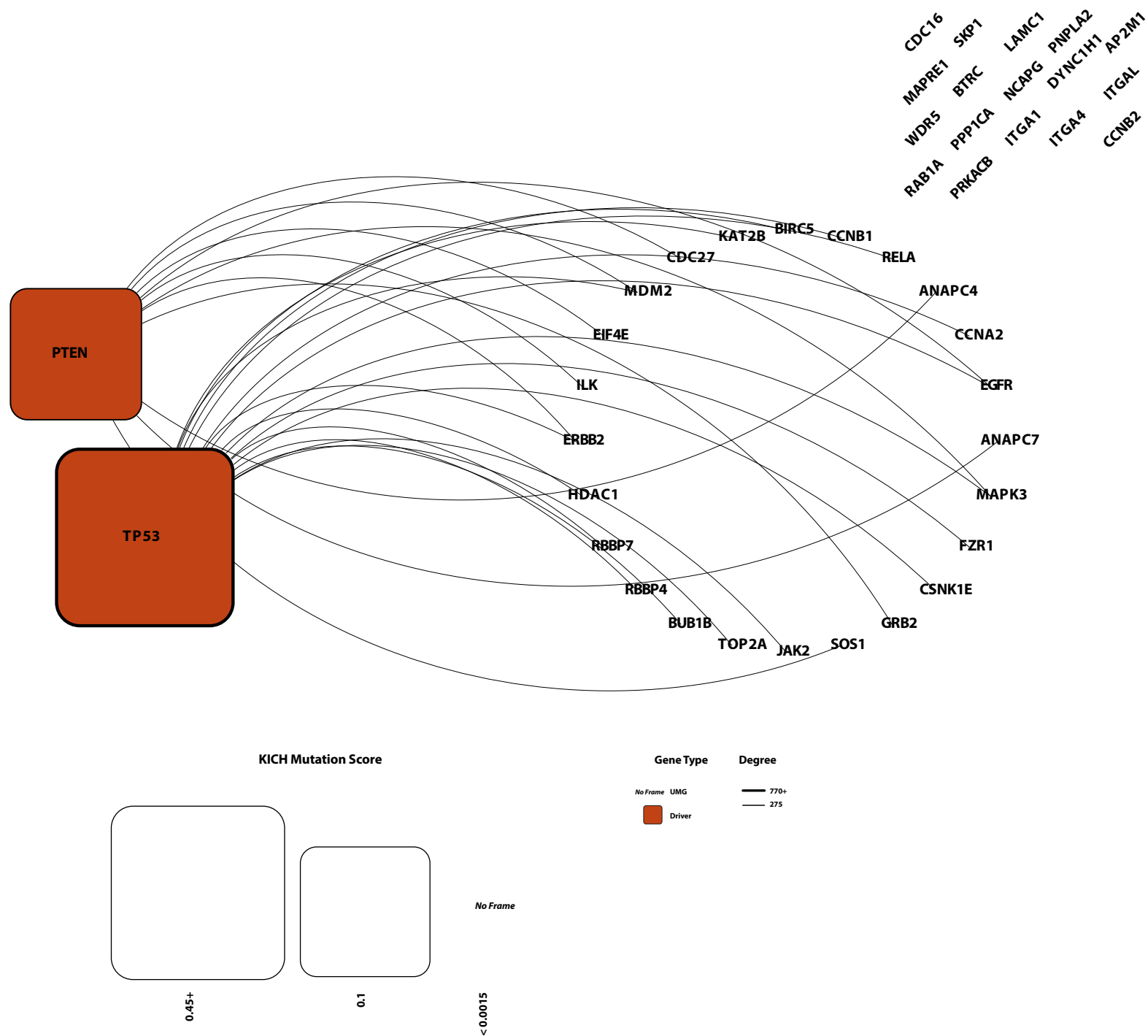


Fig. S10 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in KIRC. Extension to Figure 5.

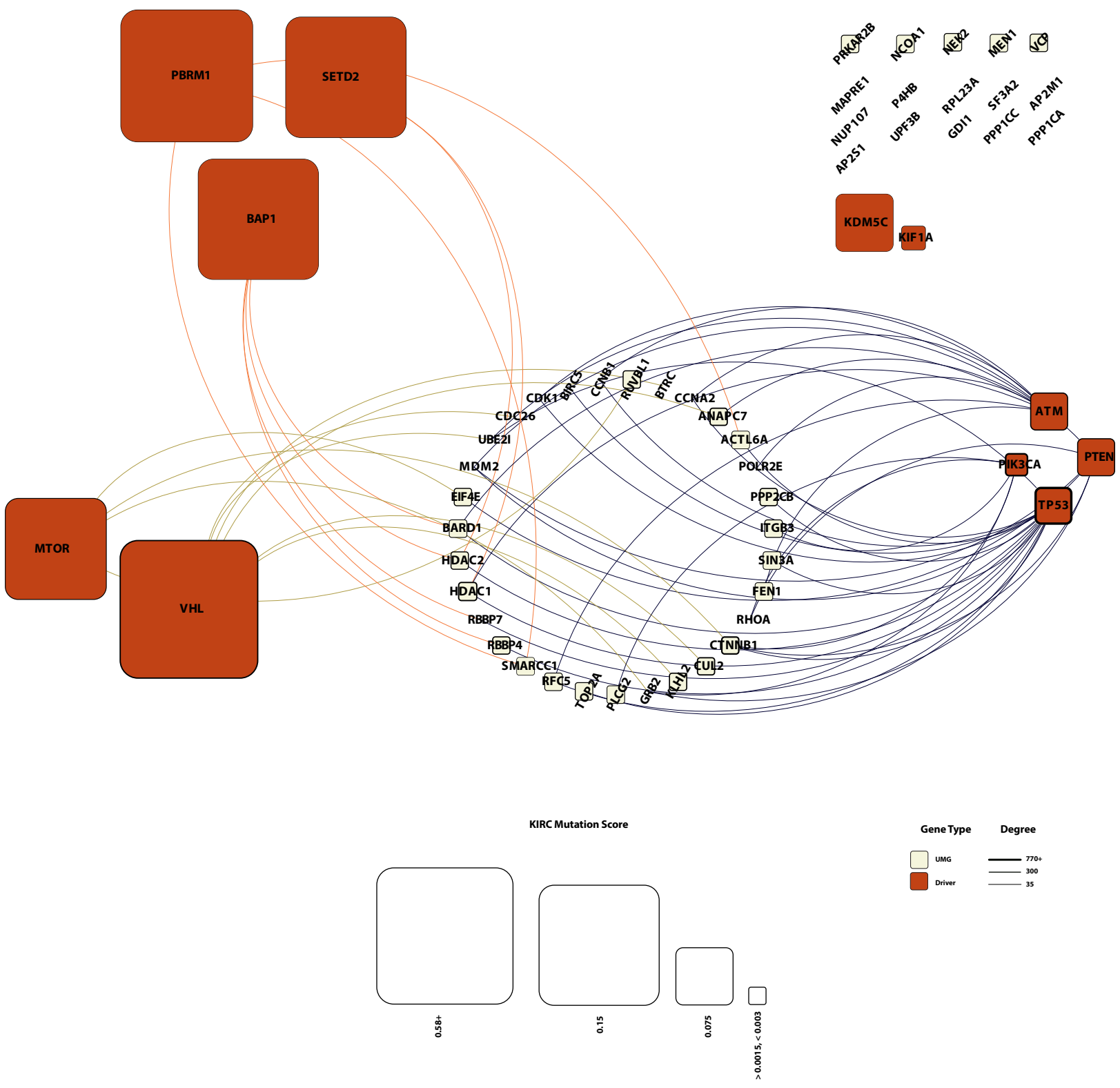


Fig. S11 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in KIRP. Extension to Figure 5.

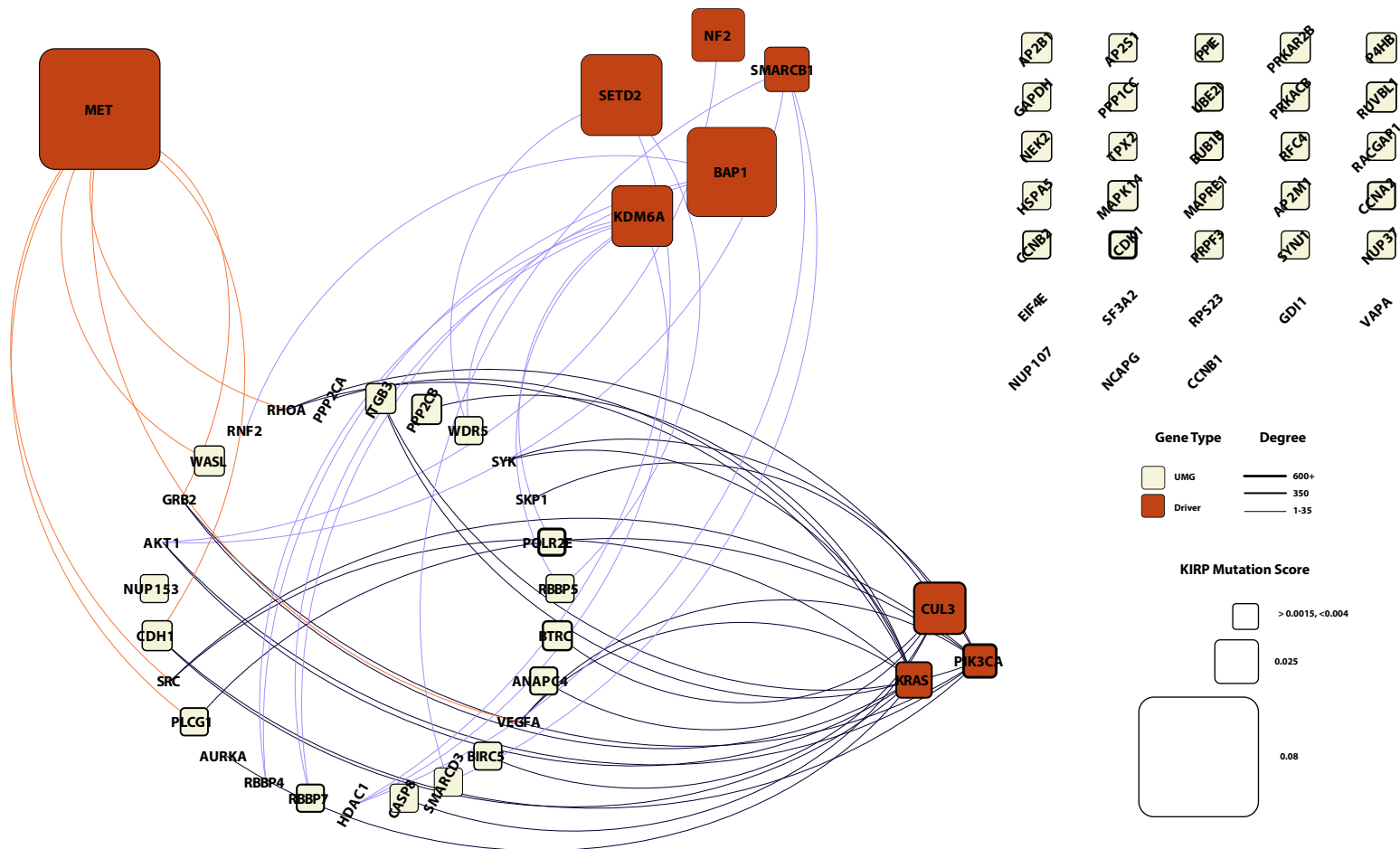


Fig. S12 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in LIHC. Extension to Figure 5.

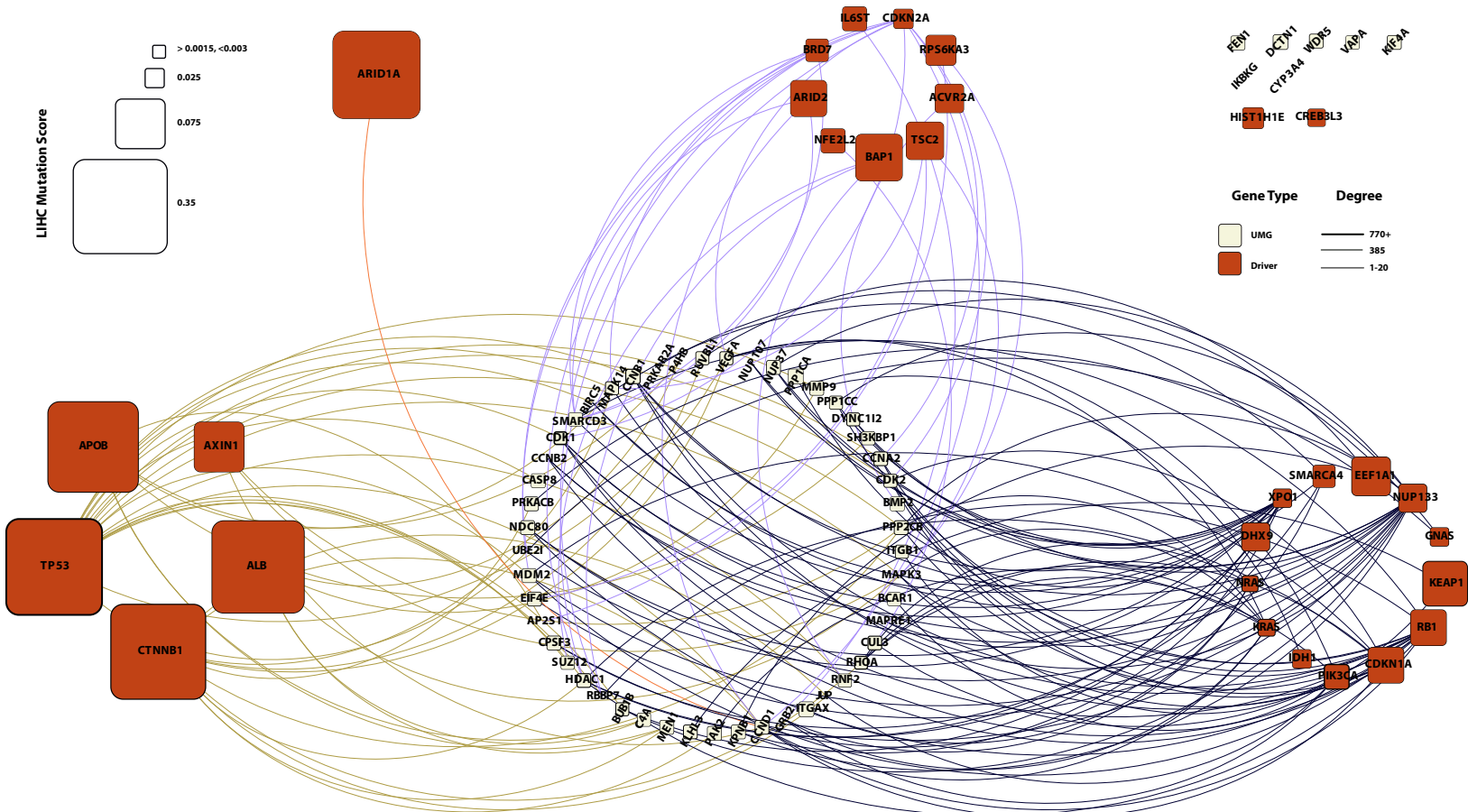


Fig. S16 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in READ. Extension to Figure 5.



Fig. S17 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in STAD. Extension to Figure 5.

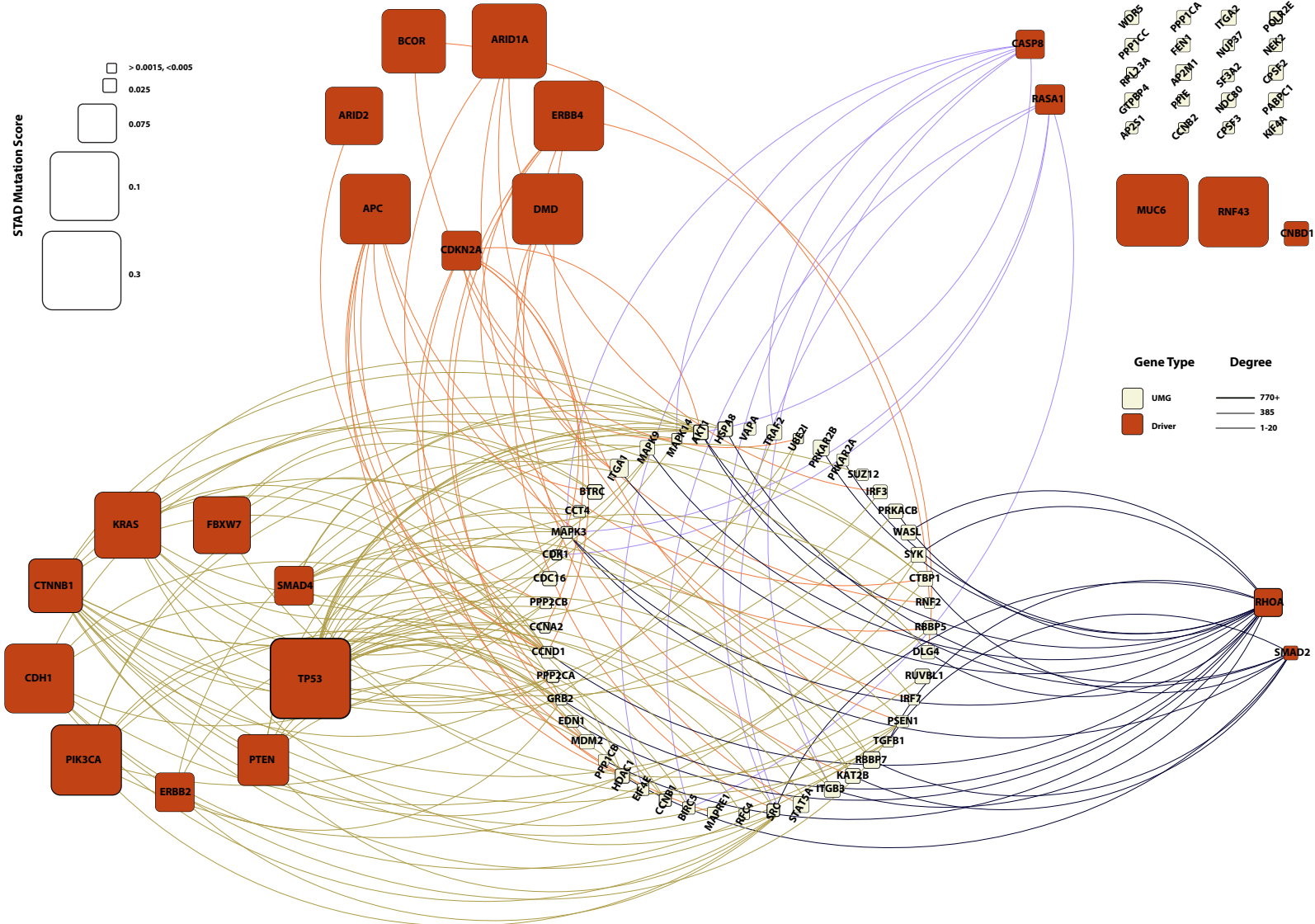


Fig. S18 PPI network analysis of the relationships between UMGs (white nodes) and known driver genes (red) in THCA. Extension to Figure 5.

