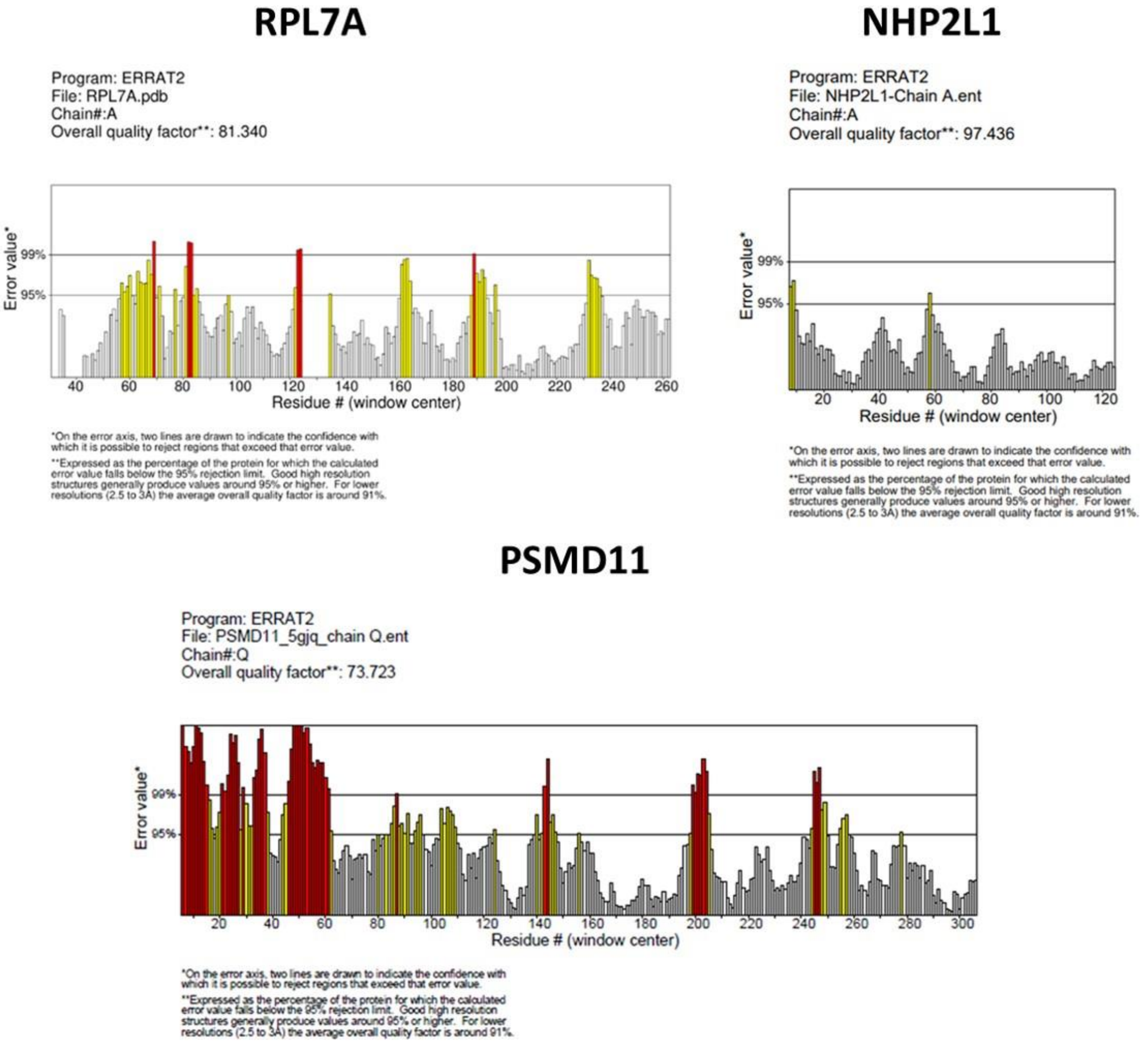


```
Program: ERRAT2
File: RPL7A.pdb
Chain#:A
Overall quality factor**: 81.340
```

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3A) the average overall quality factor is around 91%.

```
Program: ERRAT2
File: NHP2L1-Chain A.ent
Chain#:A
Overall quality factor**: 97.436
```

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3A) the average overall quality factor is around 91%.

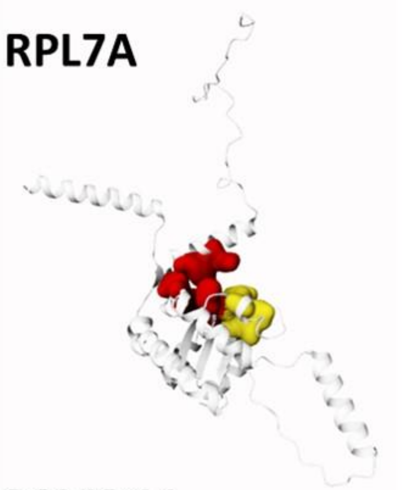
```
Program: ERRAT2
File: PSMD11_5gjq_chain Q.ent
Chain#:Q
Overall quality factor**: 73.723
```

*On the error axis, two lines are drawn to indicate the confidence with which it is possible to reject regions that exceed that error value.

**Expressed as the percentage of the protein for which the calculated error value falls below the 95% rejection limit. Good high resolution structures generally produce values around 95% or higher. For lower resolutions (2.5 to 3A) the average overall quality factor is around 91%.

Figure 1S. Validation of predicted models of protein by ERRAT server

RPL7A



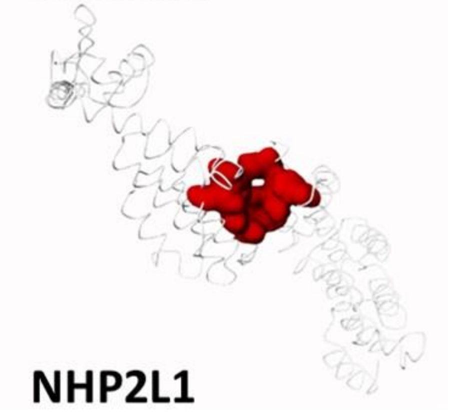
	Tools	Rank	Score	Probability	# of residues ↓	Avg conservation
^	👁 🔍	1	1.75	0.031	8	0.682

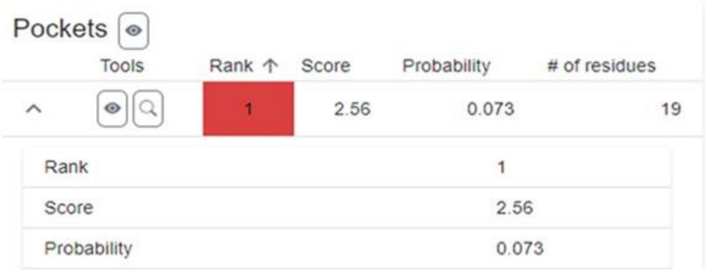
Rank	1
Score	1.75
Probability	0.031

Residues

Arg67, Tyr71, Val76, Ile80, Thr84, His159, Val161, Val164

PSMD11





Pockets 👁

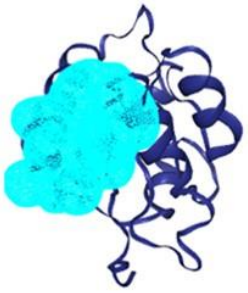
	Tools	Rank ↑	Score	Probability	# of residues
^	👁 🔍	1	2.56	0.073	19

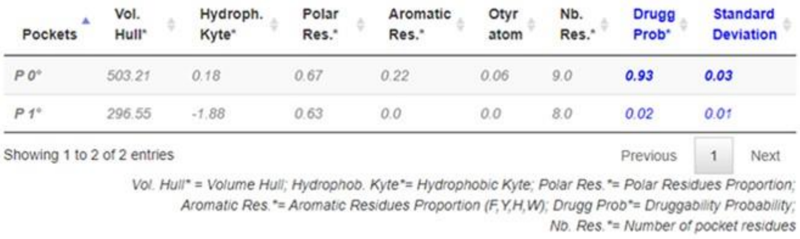
Rank	1
Score	2.56
Probability	0.073

Residues

Phe138, Leu171, Lys175, His178, Thr209, Met212, Gln213, Ile216, Tyr253, Ile318

NHP2L1





Pockets	Vol. Hull*	Hydroph. Kyte*	Polar Res.*	Aromatic Res.*	Otyr atom	Nb. Res.*	Drugg Prob*	Standard Deviation
P 0*	503.21	0.18	0.67	0.22	0.06	9.0	0.93	0.03
P 1*	296.55	-1.88	0.63	0.0	0.0	8.0	0.02	0.01

Showing 1 to 2 of 2 entries

Previous 1 Next

Vol. Hull = Volume Hull; Hydrophob. Kyte*= Hydrophobic Kyte; Polar Res.*= Polar Residues Proportion; Aromatic Res.*= Aromatic Residues Proportion (F,Y,H,W); Drugg Prob*= Druggability Probability; Nb. Res.*= Number of pocket residues*

Residues

Leu18, Thr19, Leu22, Val26, Cys73, Asp75, Pro79, Glu124

Figure 2S. Prediction of binding pocket of protein studied.

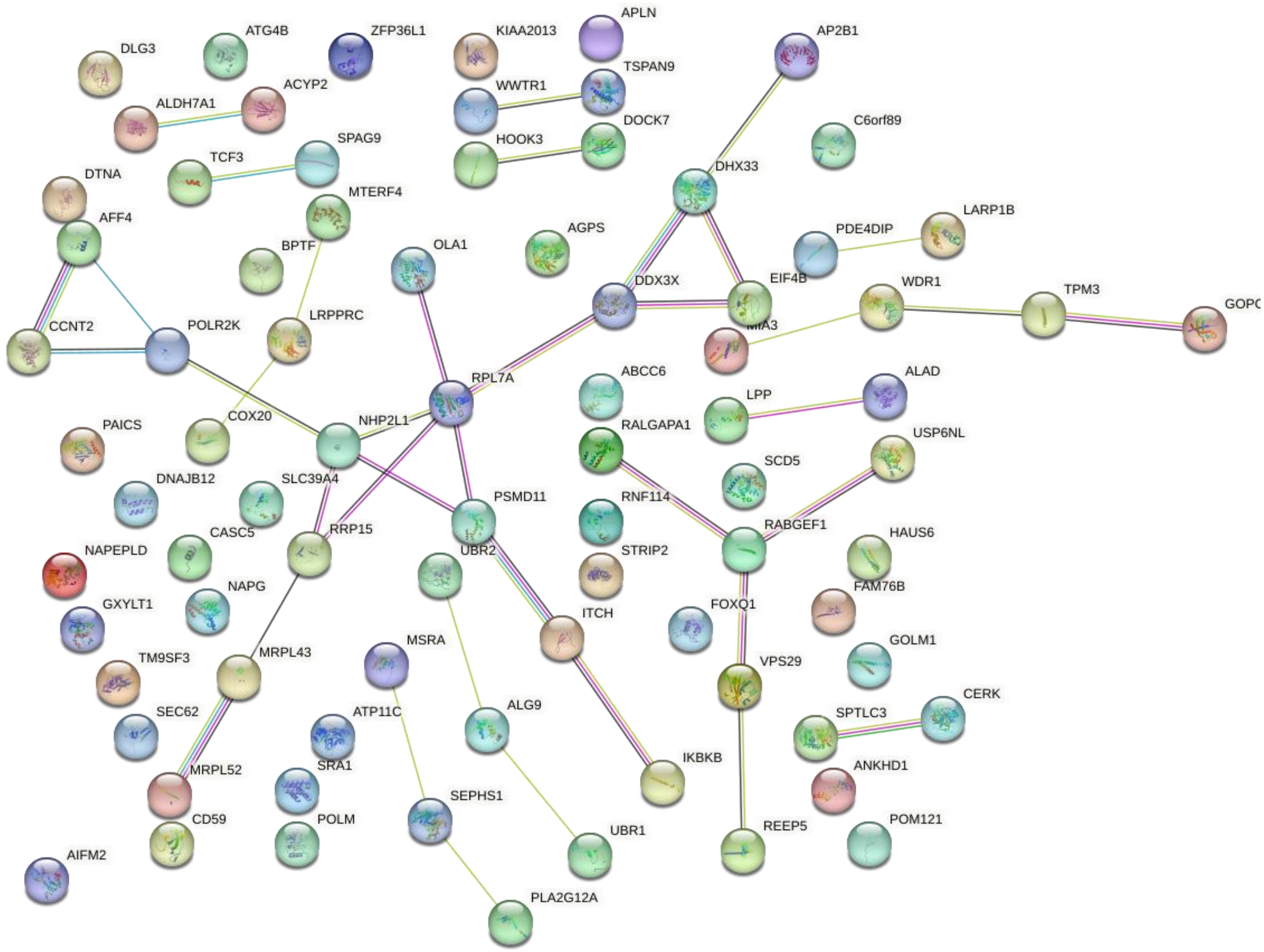


Figure 3S. Protein-protein interaction network. Identification of 81 nodes of GED network by STRING.

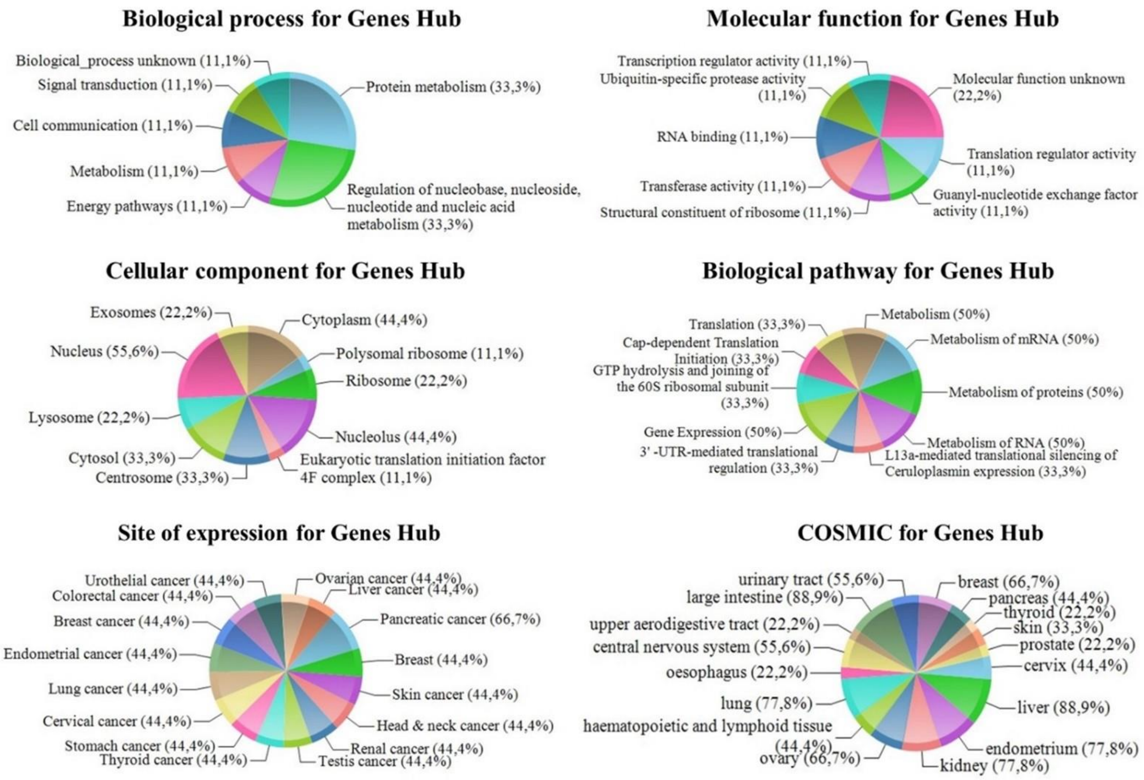


Figure 4S. Enrichment of Hub Genes. Identification of biological processes, molecular functions, cellular components, and biological pathways of the Hub genes. Identification of expression sites and Catalogue Of Somatic Mutations In Cancer (COSMIC) of Hub genes.

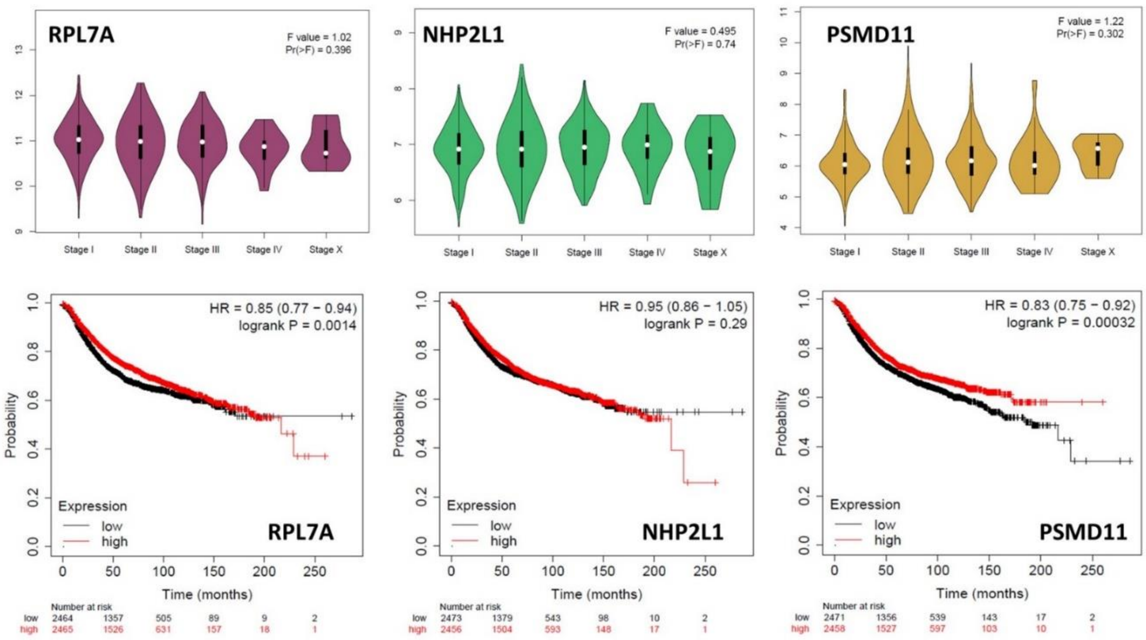


Figure 5S. Stage plot and Survival plot of Hub genes associated to TNBC. RPL7A, 60S ribosomal protein L7a; NHP, NHP2-like protein 1; PSMD11, 26S proteasome non-ATPase regulatory subunit 11.