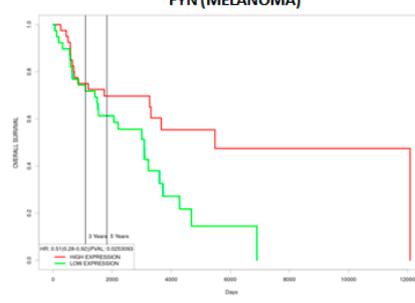
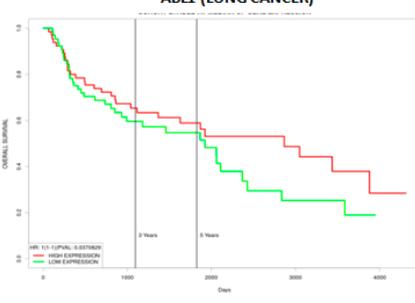
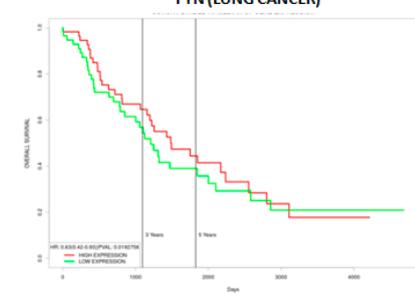
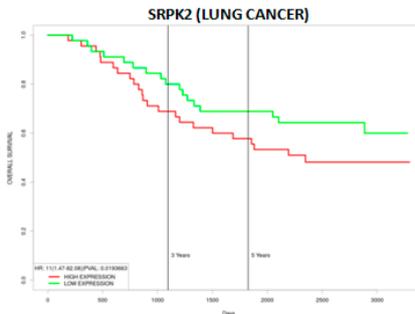
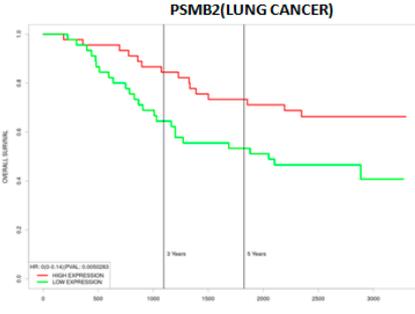
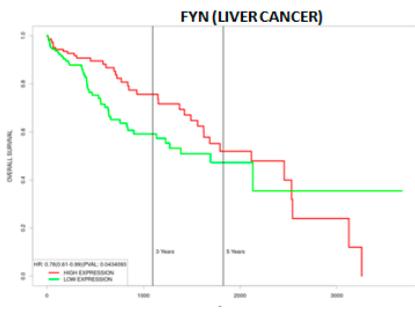
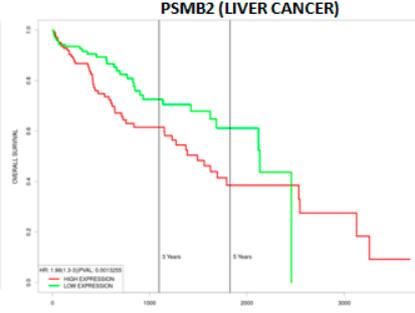
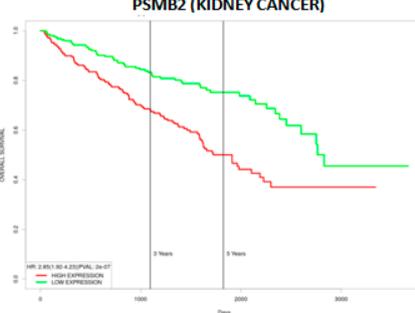
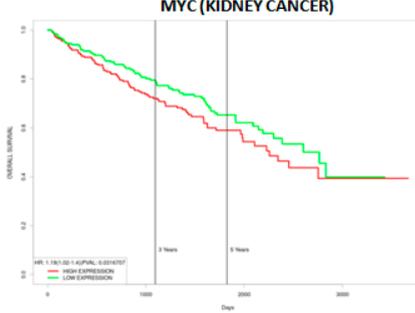
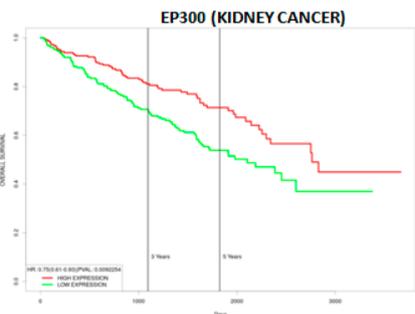
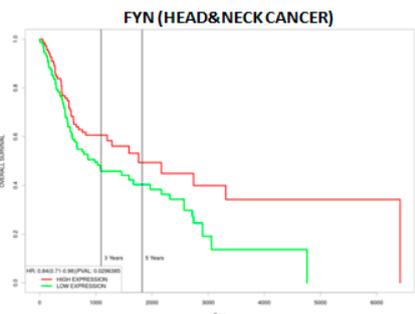
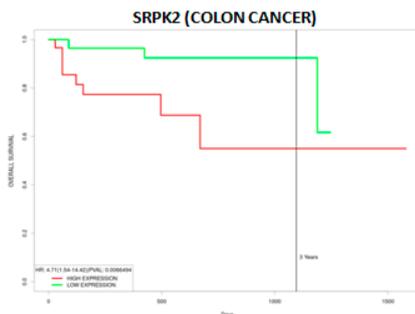
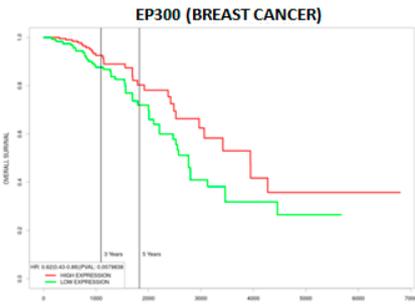
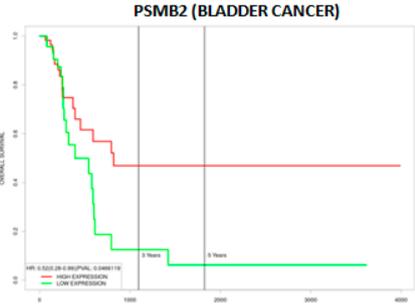
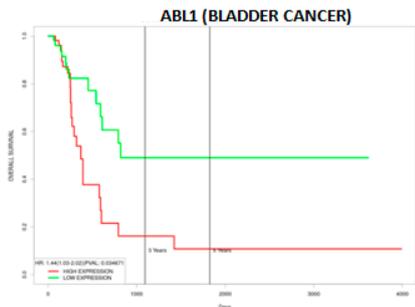


Figure S1. Evaluation of topological properties of network. (A) node degree distribution, (B) average clustering coefficient, (C) stress centrality, (D) closeness centrality and (E) betweenness centrality measure.



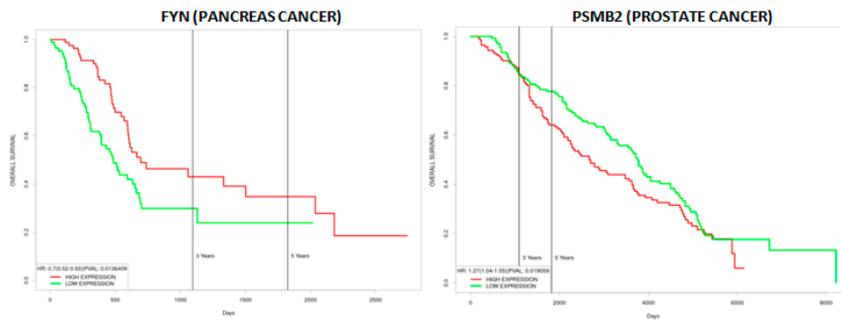


Figure S2. Kaplan-Mayer curves showing the overall survival (expressed in percentage) in solid cancer patients, using PROGgeneV2 online tool, in the case of high and low expression of HUB nodes reported by red and green curves, respectively.

Table S1. List of primer sequences

| Gene | Sequence 5'→3' |
|-------------|--|
| ABL1 | TGGAGATAACACTCTAAGCATAACTAAACCT (31) GATGTAGTTGCTTGGGACCCA (21) |
| DIO1 | AGCTTACTCTGGCTTTGCCGA (21) TATTACCCGTCTTCTCGCCA (21) |
| DIO2 | CTTACTCTGGCTTTGCCGAGA (21) CAGGATGTTCCGCTTGACTCT (21) |
| DIO3 | GGTAGTTTCCCCCGCTTGTTT (21) TTAGGTGCTGCTTTGAGGCC (21) |
| EP300 | TCCTTTCATACCGAACC (18) GGACAATACGCTCTGATACA (20) |
| FYN | ATGGAAACACAAAAGTAGCCATAAA (25) TCTGTGAGTAAGATTCCAAAAGACC (25) |
| GPX1 | TTATGACCGACCCCAAGCTCA (21) ATGTCAATGGTCTGGAAGCGG (21) |
| GPX2 | GGAGAATGAACCCAAGCGAA (20) CAGGTTTGTACAGCCAGTGAT (22) |
| GPX3 | TCTCATCCCATGTCCACCATG (21) TGCATCCATTTGTGCCAGG (19) |
| GPX4 | AGAGATCAAAGAGTTCGCCGC (21) TCTTCATCCACTTCCACAGCG (21) |
| GPX6 | CAGAAACCCACCTCACATGA (21) TGCCATGACCTGAATGCACT (20) |
| MSRB1 | AGCGGCTGTTGCTCCATAACT (21) ATTCAGCATCACCCACCCTC (21) |
| MYC | TGAATTAGAATCTCGGGAGTGC (22) GAGTGAGACCCCATCTCAGAA (21) |
| PSMB2 | AGAGGGCAGTGGAACCTCCTT (20) AGGTTGGCAGATTCAGGATG (20) |
| SELENOF | ATCGGAGGCATGCAGAGAGTT (21) TCTGCAATCAGGATCCAGCTG (21) |
| SELENOH | GGTGGTGAAGAGTTGAAGAA (21) AGGGACACAAAGCTCAGCAT (20) |
| SELENOI | AAAGGCCAGGTTCCAGAA (19) CAATCCTGCTGCAGTCCAAGT (21) |
| SELENOK | AATCAATCATCTGCGTGGCC (20) TGGTCAGCCTTCCACTTCTTG (21) |
| SELENOM | TCACGCAGGACATTCCATTCT (21) CCTGCACTAGCGCATTGATCT (21) |
| SELENON | AGGCAGATGCTCATTGTTCCC (21) |

| | |
|----------------|---|
| | CCCCAAATCCAGATGCAGACT (21) |
| SELENOO | CGGTTGTGTTGCGTGTAGCTT (21) TGCACTCGAATGTCGTTCCCTC (21) |
| SELENOP | TAGGAGCTGATGCTGCCATTG (21) ATGTTCTCCTCTGCCCGAAGT (21) |
| SELENOS | CAGCTGCTCGACTGAAAATGC (21) GCATGCTGTCCCACATTTCAA (21) |
| SELENOT | TCAATCCCACACCATCGATCA (21) ACAACGAGCCTGCCAAGAAAG (21) |
| SELENOV | GTGGATTTCGTCATTTCCCATG (21) TTTGAGTCTGACTGCCATCCC (21) |
| SELENOW | GTTTATTGTGGCGCTTGAGGC (21) CCATCACTTCAAAGAACCCGG (21) |
| SEPHS2 | CGGCTCGCTTTTGTCTGAA (20) TCGCGGCTTGTC AATGATC (19) |
| SRPK2 | GCAAAGGACAATGGTGAAGCTGAGG (25) CATCATCATCTTCATCGTCCAGTTGC (26) |
| TXNRD1 | CACAATTGGAATCCACCCTGT (21) GGTTTGCAGTCTTGGAACA (20) |
| TXNRD2 | AGGACATTGCTGGTTCGAAGC (21) GGAATCCCCTGGAAAAACGTT (21) |
| TXNRD3 | CCTTTCCAGTTGCTAGTGC (20) GTGCTACACTCTGGGCAACA (20) |
| VCP | GCCTTGAATGAAGTAGGGTAT(21) GTTGGGTCTGTTGGTTGC (18) |
| β -actin | TCTGGCACACACCTTCTACAATG (24) AGCACAGCCTGGATAGCAACG (21) |