

Table S1 qRT-PCR primer sequences

mRNA	Primer sequence
<i>B-actin</i>	Forward: TAGTTGCGTTACACCCTTTCTTG
	Reverse: TCACCTTCACCGTTCAGTTT
<i>RCOR2</i>	Forward: CGCACGCTACAGCAACAAG
	Reverse: CTTGTCTCTACTGTCCACTCGT
<i>PPARGC1A</i>	Forward: TAAAGCGAAGAGTATTTGTCAACAG
	Reverse: GGTCAGAGGAAGAGATAAAGTTGTT
<i>PKM</i>	Forward: CTCCAGGTGAAGCAGAAAGGT
	Reverse: TGCCTTGCGGATGAATGA
<i>RAC3</i>	Forward: CTTTCTGATCTGCTTCTCTCTGG
	Reverse: GCCGCTCAATGGTGCCT
<i>PHF19</i>	Forward: CCCCAGTGACAGATCGAGG
	Reverse: GAGGCAACAAACCAGGCTT
<i>MYBBP1A</i>	Forward: CCTCCCTGTCACGCCTACT
	Reverse: TGGGCTTTCTTCTGGTTGTT
<i>ORC1</i>	Forward: GGACCTGCCAGAGCGAAT
	Reverse: CCAGACAGTGCTGCTACCTTC
<i>EYA2</i>	Forward: GCGATTGTCTGGATAAACTGAA
	Reverse: TTGTGCTGGAGGTGGGTAAG

qRT-PCR, quantitative real-time reverse transcription-polymerase chain reaction; RNA, ribonucleic acid.

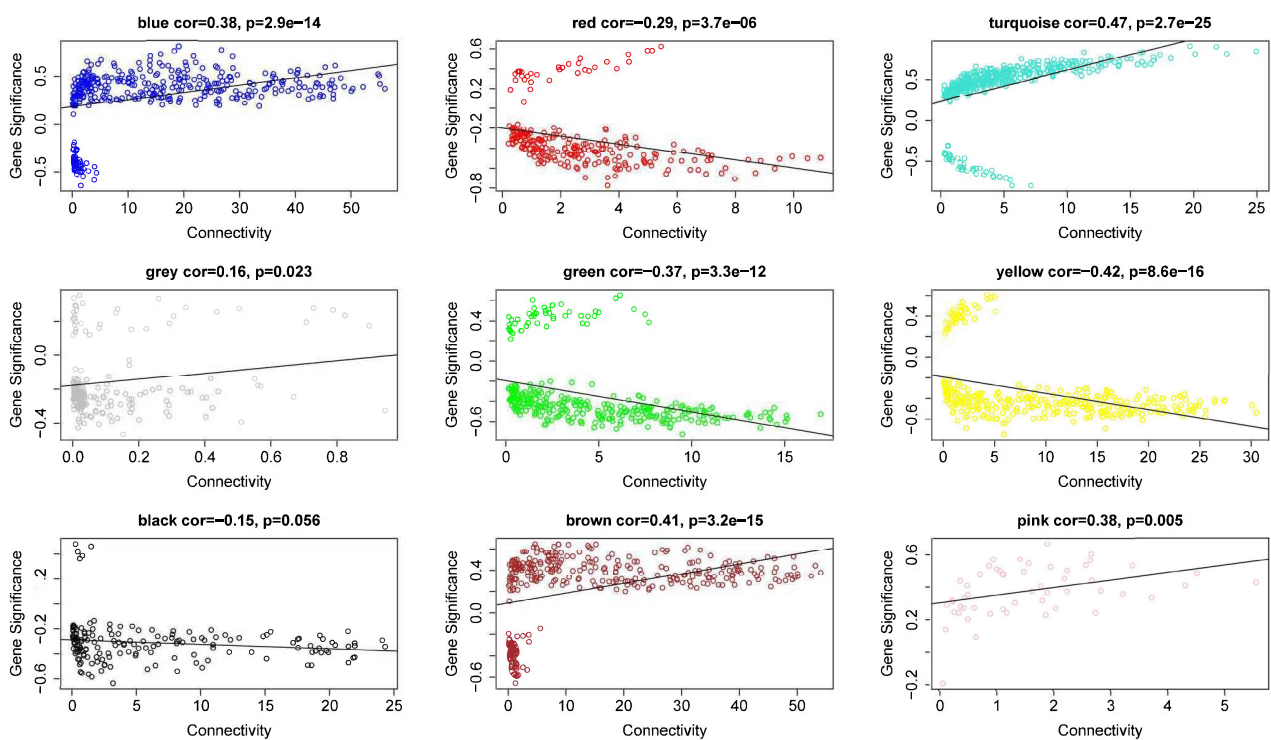


Figure S1 Correlation of modular gene significance with gene linkage in normal traits.

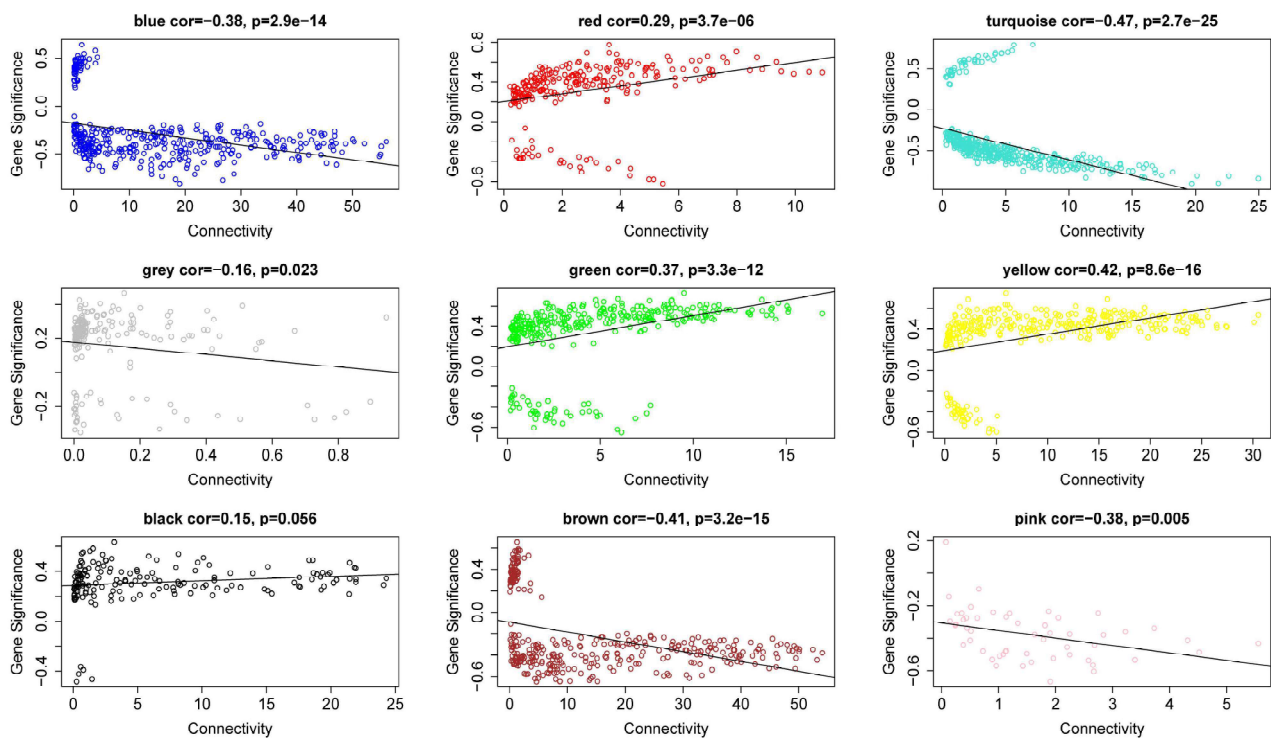


Figure S2 Correlation of modular gene significance with gene linkage in tumor traits.

Table S2 Coef values of the model genes

Gene	Coef
<i>RCOR2</i>	0.021725906
<i>PPARGC1A</i>	-0.050256306
<i>PKM</i>	0.001422719
<i>RAC3</i>	0.007767943
<i>PHF19</i>	0.010947093
<i>MYBBP1A</i>	0.01123364
<i>ORC1</i>	-0.061084477
<i>EYA2</i>	0.041305297

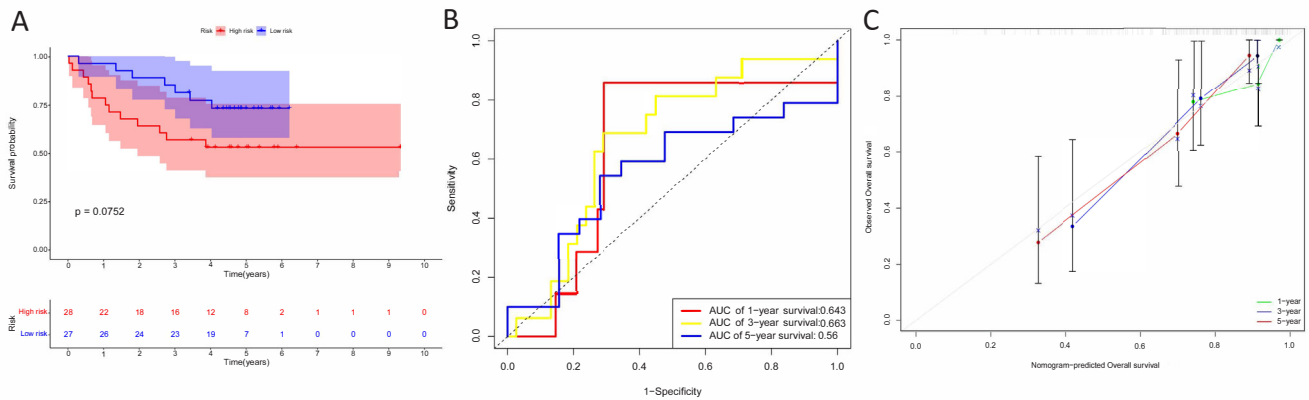


Figure S3 Risk prognosis model validation in GSE17537 data. (A) Survival curve comparing high-risk and low-risk groups by R package “survival”. (B) ROC curve of 1-, 3-, 5-year survival by R package “timeROC”. (C) The calibration curve of the nomogram baseline. ROC, receiver operating characteristic; AUC, area under the curve.