

Supplementary Table S1: The sequence-specific primers of 20 key/hub genes and β -actin.

S. No	Genes	Primer	Primer Sequences
1.	<i>PKM</i>	FP	GCAGCACCTGATTGCCCCG
		RP	CTTCTGTGGGGTCGCTGGTA
2.	<i>PFKP</i>	FP	ACCAACCTGTGTGTGATCGG
		RP	TATCGATCTGGCCGTTCCCTG
3.	<i>PC</i>	FP	CTGCCTCCCCAAATGTCCG
		RP	ACGGATGGCAATCTCACCTCT
4.	<i>PK4</i>	FP	ACTCGGATGCTGATGAACCA
		RP	ACACTCAAAGGCATCTTGGAC
5.	<i>GART</i>	FP	CCCTTGAGGAAGCCAAGAAAGG
		RP	CCTTGTAAGTCAAACCTCCTGGGC
6.	<i>PAICS</i>	FP	TGCAGTCCAAGGACCAGATT
		RP	TGACTTATATGAGGTAAGTCTTCC
7.	<i>PPAT</i>	FP	GCATGTGATCACTCTGGGAC
		RP	CAAGACCCATTCCCTTGTGT
8.	<i>RRM2</i>	FP	ACTATGCTCTCCCTCCGTGT
		RP	CGTGTTCTCCTTGTCGACCA
9.	<i>NME1</i>	FP	CTCAAGCTGTGATACAGGAACCA
		RP	TTTCAGACCAACAAGGCGGA
10.	<i>CTPS1</i>	FP	GCAGTGTGGGCACAATACTCA
		RP	GCACAAAACCTCACCATGCTC
11.	<i>AHCY</i>	FP	ACTCCGTCACCAAGAGCAAG
		RP	CACCATAGCCTGCTACCACC
12.	<i>DHFR</i>	FP	GGCCACCGCTCAGGAATG
		RP	GCTCCTTGTGGAGGTTCTTG
13.	<i>ASNS</i>	FP	CAGAGGTCCAGATGCATTCC
		RP	TCAAAATGCTGTTGCATCTTCT
14.	<i>BCAT1</i>	FP	GTGGTGGGGACTTTTAAGGCTA
		RP	GATGAGCCAGGGTGCAATGA
15.	<i>ACACB</i>	FP	ATCTCGTGAGTCTACCCGGA
		RP	ACATGCTCGGCCTCATAGT
16.	<i>CDK1</i>	FP	CGTCATCCAAATATAGTCAGTCTTC
		RP	ACAATCCCCTGTAGGATTTGG
17.	<i>EGFR</i>	FP	TGGAGGAAAAGAAAGTTTGCCA
		RP	CCAAGGACCACCTCACAGTT
18.	<i>AURKA</i>	FP	GCCATCGGCACCTGAAAATAA
		RP	CCCAGAGGGCGACCAATTT
19.	<i>DEPDC1</i>	FP	TGCCATGAAGTGCCTAGCAA
		RP	GTGATGTAGCCACAAACAACCAA
20.	<i>HMMR</i>	FP	CAATGACCCTTCTGGTTGTGC
		RP	AGCTGAAGCAGGCAAGGTAG
21.	<i>ACTB</i>	FP	TCCCTGGAGAAGAGCTACG
		RP	GTAGTTTCGTGGATGCCACA

Supplementary Table S2: Common 46 MRGs with their function after the intersection of DEGs and MRGs.

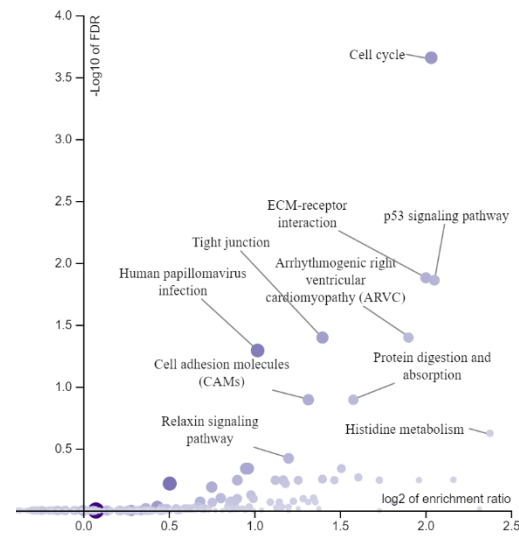
S. No	Genes (MRGs)	Functions of MRGs	Key/hub genes
1.	<i>MAOA</i>	Oxidative deamination of biogenic amines and neurotransmitters into ammonia, aldehydes, and hydrogen peroxide	
2.	<i>GPX3</i>	Reduction of organic hydrogen peroxides and hydrogen peroxide via glutathione	
3.	<i>PDK4</i>	Inhibition of Pyruvate dehydrogenase activity by phosphorylation of pyruvate dehydrogenase subunits PDHA1 and PDHA 2	*
4.	<i>ASPA</i>	Conversion of N –acetyl-L-aspartic acid to aspartate and acetate	
5.	<i>ACACB</i>	Carboxylation of acetyl-CoA to malonyl-CoA	*
6.	<i>CA4</i>	Reversible hydration of carbon dioxide	
7.	<i>MGLL</i>	Conversion of monoacylglycerides to free fatty acids and glycerol	
8.	<i>ACAA2</i>	Catalysis of the last step of the mitochondrial fatty acid beta-oxidation spiral	
9.	<i>HNMT</i>	Inactivation of histamine by transferring a methyl group from S-adenosyl-L-methionine to histamine	
10.	<i>EGFR</i>	Cell surface receptor for binding to members of the epidermal growth factor family, ultimately leading to cell proliferation	*
11.	<i>PC</i>	Carboxylation of pyruvate to oxaloacetate	*
12.	<i>CITED2</i>	Inhibition of transactivation of Hypoxia-inducible factor 1-alpha by competitively binding to p300-CH1	
13.	<i>PTPRG</i>	Tyrosine phosphatase activity and regulation of cell growth, differentiation, mitosis and transformation.	
14.	<i>MAOB</i>	Oxidative deamination of amines and neurotransmitters into ammonia, aldehydes, and hydrogen peroxide	
15.	<i>MSRA</i>	Reduction of methionine sulfoxide to methionine	
16.	<i>HPGD</i>	Metabolism of arachidonic acid	
17.	<i>DHFR</i>	Conversion of dihydrofolate to tetrahydrofolate	*
18.	<i>BCAT1</i>	Reversible transamination of branched-chain alpha-keto acids to branched-chain L-amino acids.	*
19.	<i>PAPSS2</i>	ATP sulfurylase and APS kinase activity in the sulphate activation pathway	
20.	<i>ARG2</i>	Hydrolysis of arginine to ornithine and urea	
21.	<i>GCLM</i>	Glutathione biosynthesis and sulphur metabolism	
22.	<i>SDCI</i>	Linking of the cytoskeleton to the interstitial matrix and regulation of exosome biogenesis.	

23.	<i>RRM2</i>	Biosynthesis of deoxyribonucleotides from corresponding ribonucleotides	*
24.	<i>AURKA</i>	Formation and stabilization at the spindle pole during chromosome segregation	*
25.	<i>CDK1</i>	G2/M transition in eukaryotic cell cycle	*
26.	<i>HMMR</i>	Receptor for Hyaluronic acid and is involved in cell motility	*
27.	<i>KIF20A</i>	Microtubule bundle formation, midbody abscission and regulation of cytokinesis	
28.	<i>PPAT</i>	Formation of phosphoribosylamine from phosphoribosylpyrophosphate	*
29.	<i>PKM</i>	Transfer of phosphoryl group from phosphoenolpyruvate to ADP	*
30.	<i>EGLN3</i>	Hydroxylation of peptidyl-proline to 4-hydroxy-L-proline, activation of cysteine-type endopeptidase activity in apoptosis, and involvement in response to hypoxia.	
31.	<i>GART</i>	De- novo biosynthesis of purine	*
32.	<i>CTPS1</i>	Conversion of uridine triphosphate to cytidine triphosphate	*
33.	<i>VCAN</i>	They are involved in cell adhesion, proliferation, migration, angiogenesis, tissue morphogenesis, and maintenance.	
34.	<i>ASNS</i>	Synthesis of asparagine	*
35.	<i>PAICS</i>	Involved in purine metabolism and biosynthesis of secondary metabolites	*
36.	<i>DEPDC1</i>	Might be involved in the regulation of transcription	*
37.	<i>AHCY</i>	Reversible hydrolysis of S-adenosylhomocysteine to adenosine and homocysteine	*
38.	<i>DSC2</i>	Involved in cell adhesion by mediating the interaction of plaque proteins and intermediate filaments	
39.	<i>SLC7A11</i>	Mediate's exchange of extracellular anionic L-cystine and intracellular L-glutamate across the plasma membrane	
40.	<i>GGCT</i>	Involved in glutathione homeostasis and formation of 5-oxo proline from gamma-glutamyl dipeptides	
41.	<i>LRPPRC</i>	Might be involved in cytoskeletal organisation, vesicular transport and transcriptional regulation	
42.	<i>DNMT3B</i>	De-novo methylation of the genome might be involved in gene silencing	
43.	<i>NME1</i>	Synthesis of nucleoside triphosphates other than ATP.	*
44.	<i>PFKP</i>	Phosphorylation of D-fructose-6-phosphate to fructose-1,6-bisphosphate	*
45.	<i>POLR1B</i>	Transcription of ribosomal RNA genes and production of rRNA	
46.	<i>TDO2</i>	Conversion of L-Tryptophan to N-formyl-L-kynurenine and oxidative cleavage of the indole moiety	

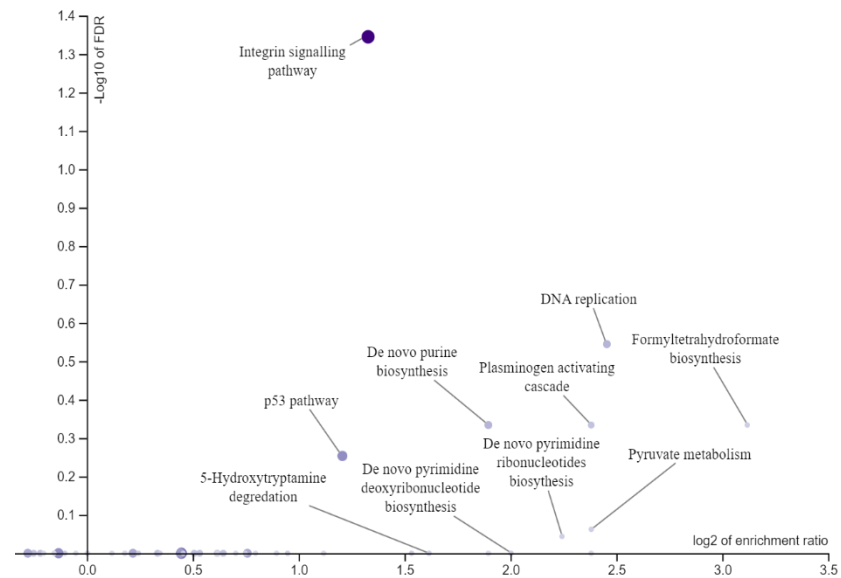
Note: - (*) Indicates the 20 key/hub genes.

Supplementary Figure S1

(A)



(B)

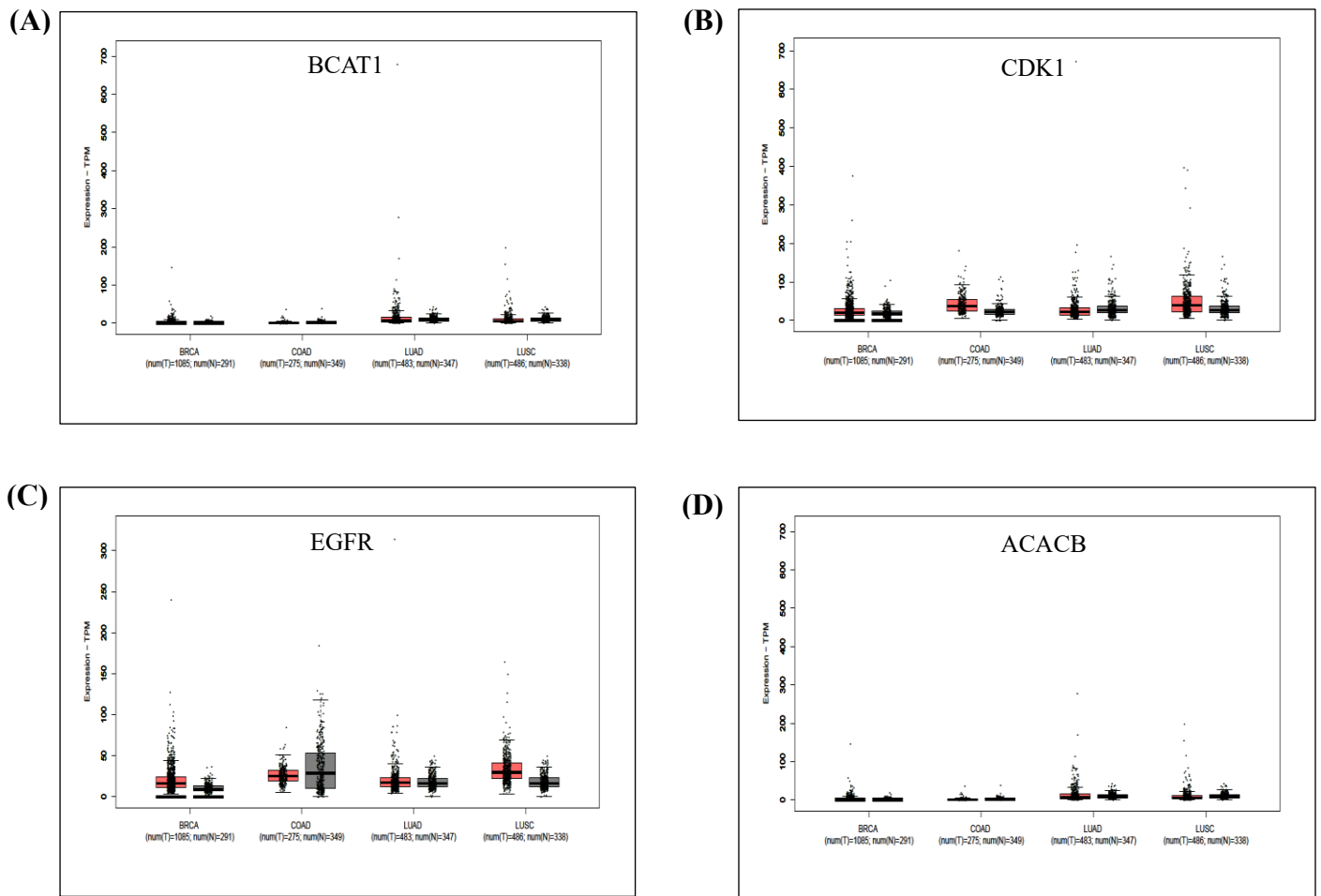


Supplementary Figure S1

Volcano plots depicts the pathways analysis of 540 intersected genes.

The Volcano plots of pathways analysis, The KEGG (A) and PANTHER (B) of 540 DEGs. The top significant terms of KEGG and PANTHER analysis. The enrichment ratio and, the expression of the enriched pathway.

Supplementary Figure S2

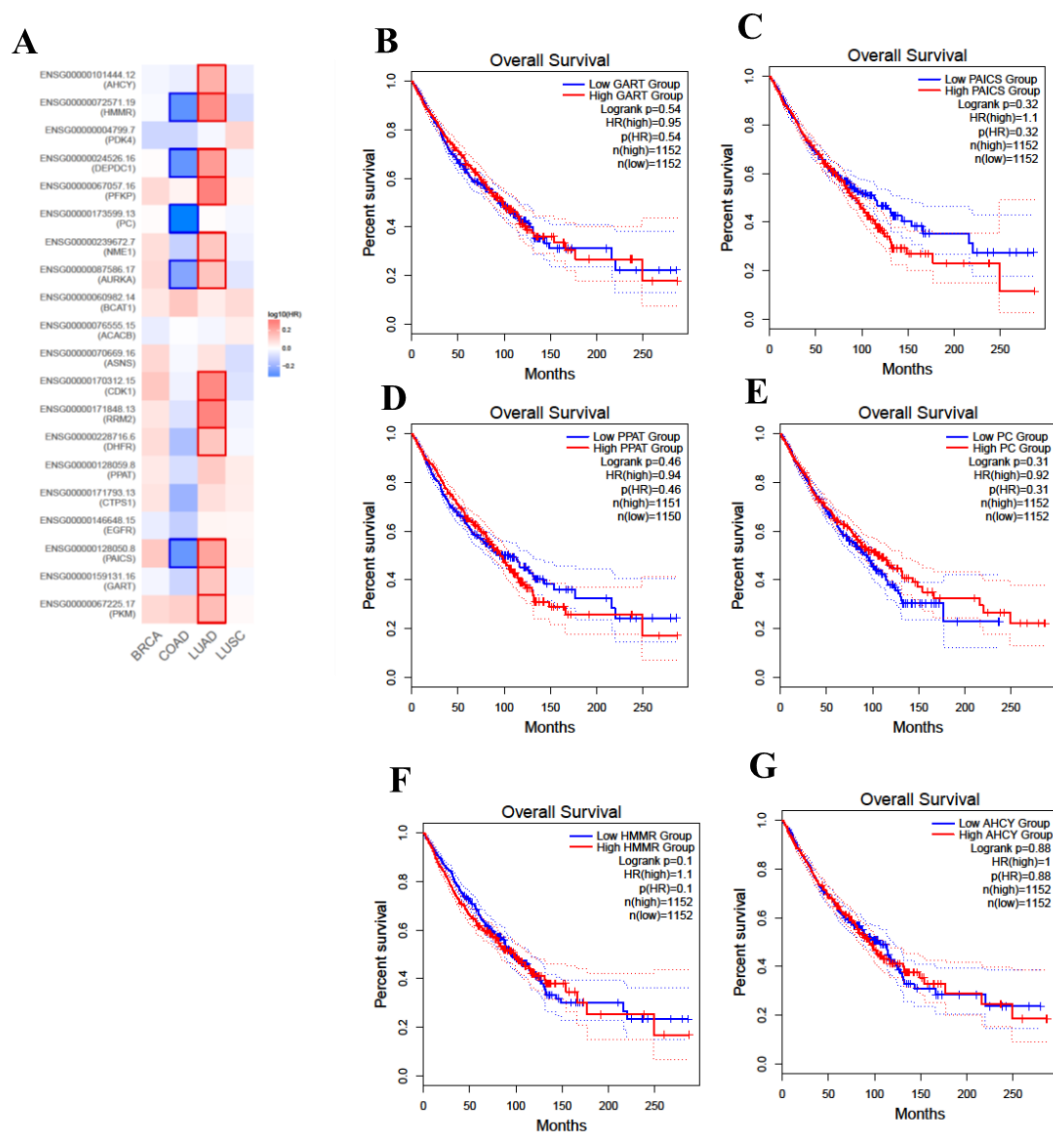


Supplementary Figure S2

Validation of Key/Hub MRGs: - The box plot showing expression level Transcript per million (TPM) of hub MRGs in TCGA cohort between cancer v/s normal patients of BRC, CRC, and LUC on GEPIA database. The red and grey boxes represent cancer and normal tissues, respectively. The p value for the significance *, $P < 0.05$; **, $P < 0.01$; ****, $P < 0.0001$.

(A-D) PC, PFKP, GART, PAICS, BCAT1, CDK1, EGFR and ACACB.

Supplementary Figure S3



Supplementary Figure S3

Overall survival of hub/genes in high-risk patients and low-risk patients.

(A) Risk score evaluation of 20 hub MRG signatures based in TCGA on the GEPIA2 database in BRCA, COAD, LUAD and LUSC. The risk score is plotted in the form of Log10 (HR) on a heatmap.

(B-G) Kaplan-Meier curves of six hub MRGs (GART, PAICS, PPAT, PC, HMMR and AHCY) in TCGA on GEPIA2 database.