

**Comprehensive Analysis of the Expression Profiles of Long Non-Coding RNAs
with Associated ceRNA Network Involved in the Colon Cancer Staging and
Progression**

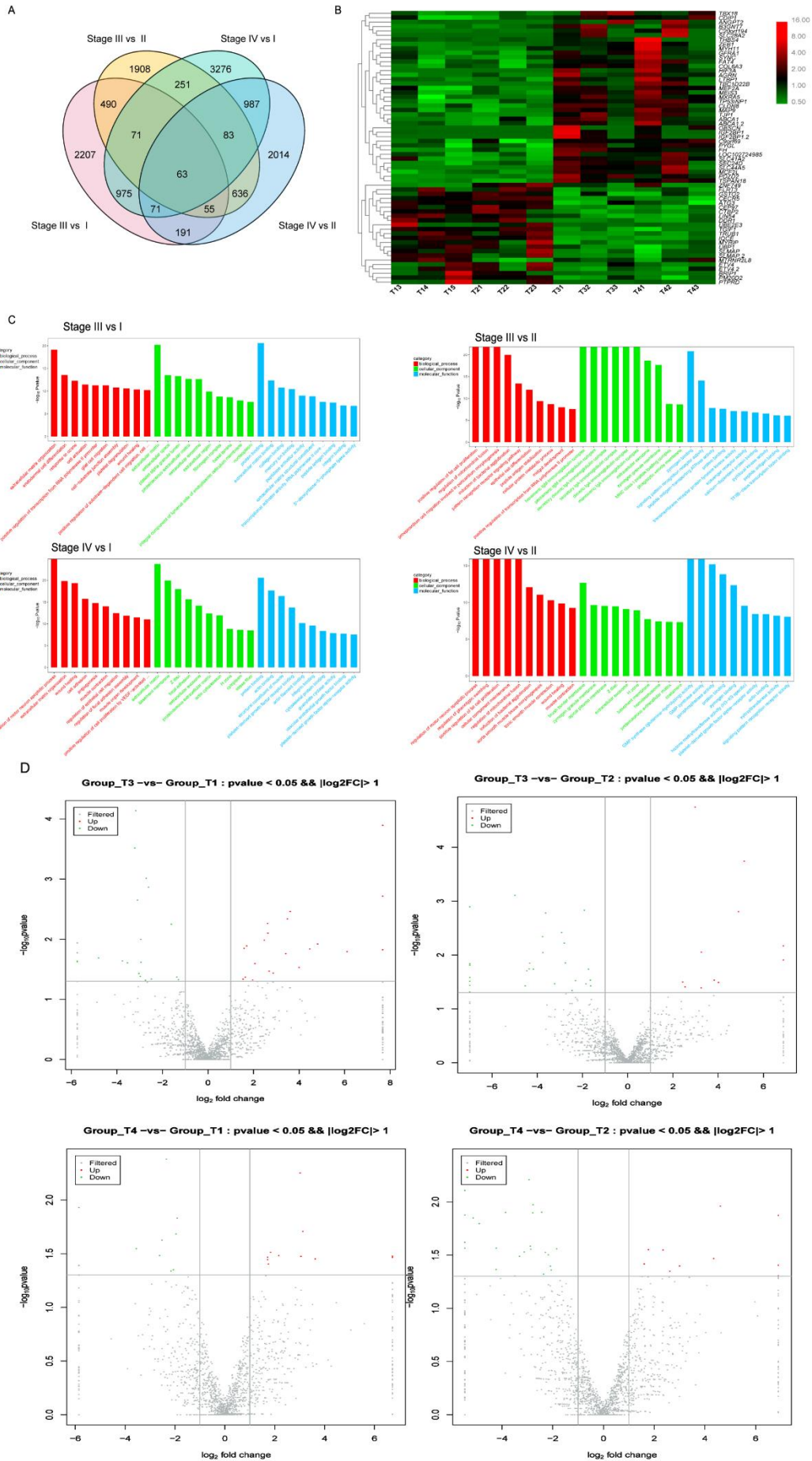
Meini Wu^{1#}, Wenliang Li^{2#}, Fengchang Huang², Jing Sun¹, Kang ping Li², Jiandong Shi¹, Jingyu Yang², Jianfang Li¹, Yanhan Li¹, Ningzhu Hu¹, YunZhang Hu^{1*}

¹Department of vaccinology, Institute of Medical Biology, Chinese Academy of Medical Sciences and Peking Union Medical College, Kunming, 650118 China;

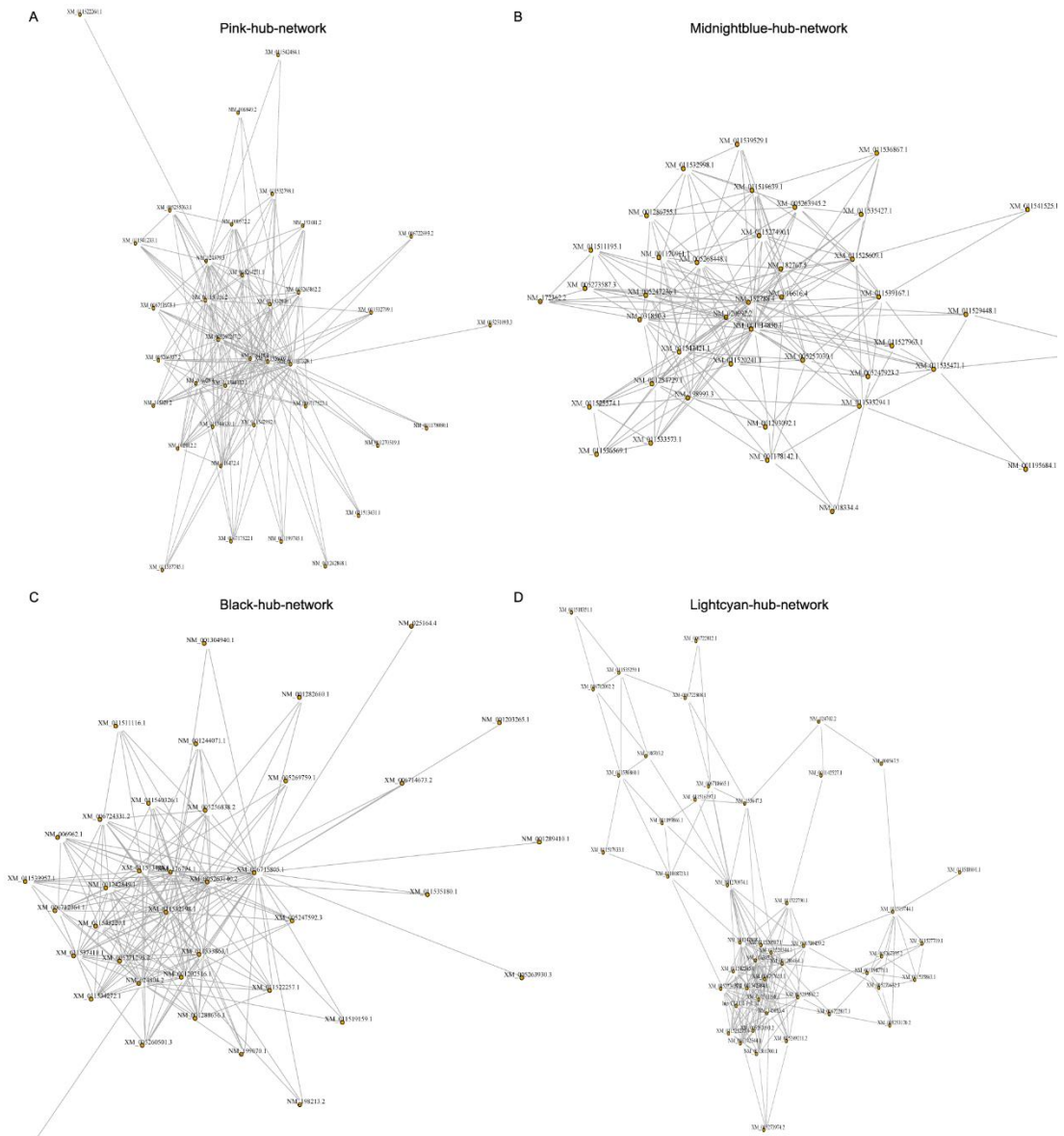
²Department of Surgical Oncology, First Affiliated Hospital of Kunming Medical University, Kunming, China;

#Equal contributors

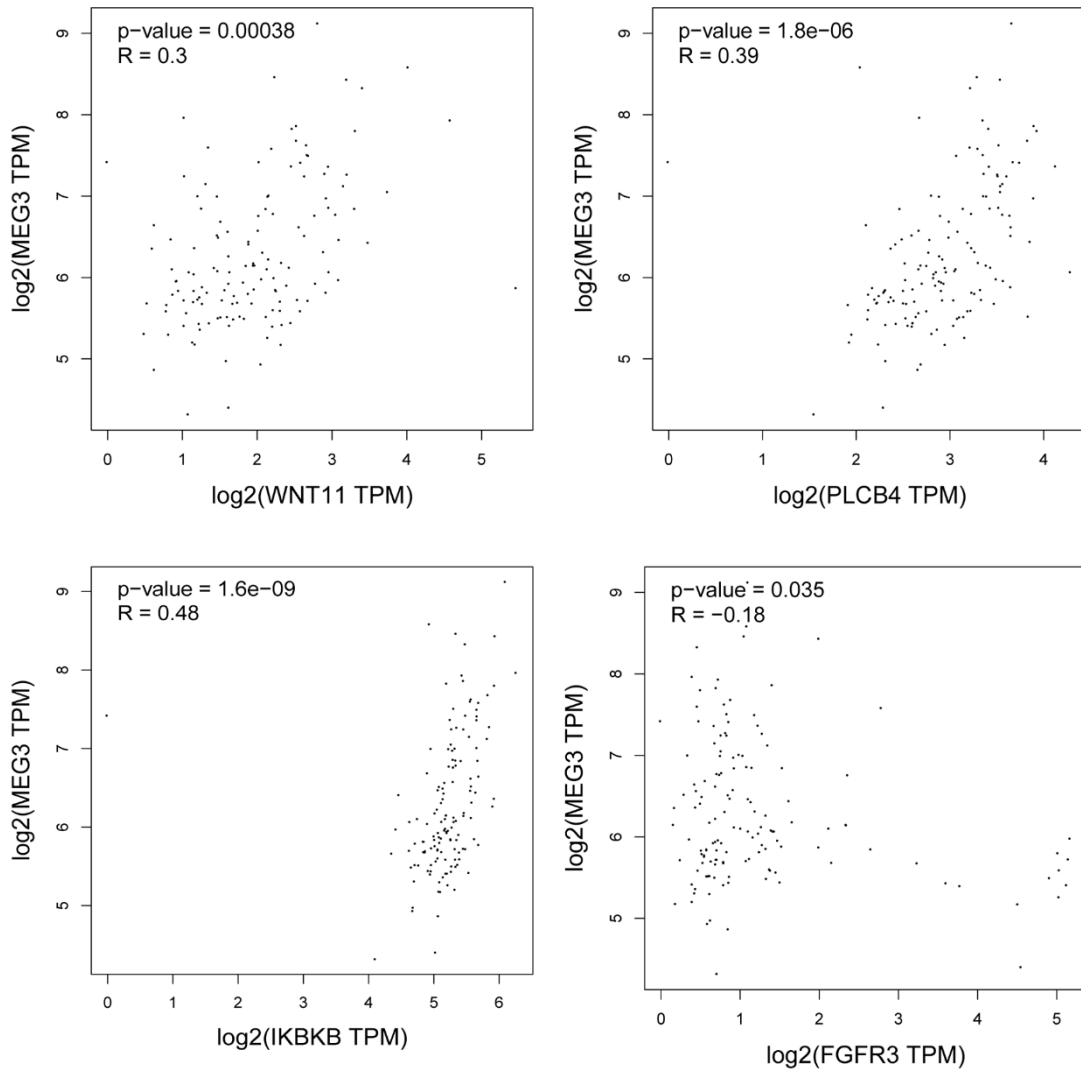
*Corresponding author: Dr. Yunzhang Hu



Supplement 1 Differentially expressed (DE) mRNAs and miRNAs between the stage III/IV tumor tissue and stage I/II tumor tissue. (A) Venn diagram analysis of DEmRNAs at stage III vs stage I, stage III vs stage II, stage IV vs stage I, and stage IV vs stage II of CC (B) Heatmaps of DEmRNAs in stage III/IV tumor. (C) Gene Ontology analysis of DEmRNAs. Red rectangle represents biological process (BP), green rectangle represents cellular component and blue rectangle represents molecular function (MF). (D) Volcano plot of DE miRNAs at stage III vs stage I, stage III vs stage II, stage IV vs stage I, and stage IV vs stage II of CC.



Supplement 2 Module core gene analysis of model pink, midnightblue, black and lightcyan.



Supplement 3 The expressed relationship between lncRNA MEG3 and mRNA Wnt11, PLCB4, IKBKB and FGFR3 was analysis using the TCGA database.

Supplement 4 Demographic and clinical characteristics of colorectal cancer patients (n=40) involved in real time PCR.

Characteristics	patients, n (range)
Age	64 (41-80)
Sex	
F	24
M	16
Stage	
I	10
II	10
III	10
IV	10
T stage	
T1	3
T2	10
T3	8
T4	19
N stage	
N0	23
N1	10
N2	7
M stage	
M0	30
M1	10
N	
+	25
-	15
V	
+	12
-	28
MLH1	
+	31
-	9
MSH2	
+	39
-	1
MSH6	
+	40
-	0
PMS2	
+	35

Supplement 5 Primer sequences used in this study.

Gene name	Primer sequence
MEG3-1-F	5' GCTGAAGAAGCTGCGGATGGAA 3'
MEG3-1-R	CCGTGGCTGTGGAGGGATT 3'
hsa-miR-324-5p RT	5' GTCGTATCCAGTGCCTGTCGTGGAGTCGGCAATTGCACTGG ATACGACCACCAAT 3'
hsa-miR-324-5p F	5' ATATACTCGCATCCCCTAGGGC 3'
hsa-miR-324-5p R	5' AGTGCGTGTCTGGAGTCG 3'
WNT11-F	5' TTGACCTGGAGAGAGGGACC 3'
WNT11-R	5' AGGAGCATCGGAAAAGTTGG 3'
FGFR3-F	5' GTGCTCAAGACGGCGGGC 3'
FGFR3-R	5' GCCACGCAGAGTGATGAGAAAA 3'
PLCB4-F	5' TGAAGGCAAGGAAGGACAGGT 3'
PLCB4-R	5' CCACTGCAGACACAACTATCCG 3' 1
IKBKB-F	5' TGGCACAATCAGGAAACAGGT 3'
IKBKB-R	5' GGGTGGGTCAGCCTTCTCAT 3'
GAPDH -F	5' AGAAGGCTGGGGCTCATT 3'
GAPDH -R	5' TGCTAAGCAGTTGGTGGTG 3'
U6-F	5' CGATACAGAGAAGATTAGCATGGC 3'
U6-R	5' AACGCTTCACGAATTTGCGT 3' 3'