

## Supplementary Materials

### Supplementary Figure legends

**Figure S1** A flowchart describing the research process.

**Figure S2. WGCNA to identify HCC subtype-specific modules.** A-B Determination of the optimal soft threshold. C-E Construction and visualization of co-expression modules. **WGCNA, weighted gene co-Expression network analysis.**

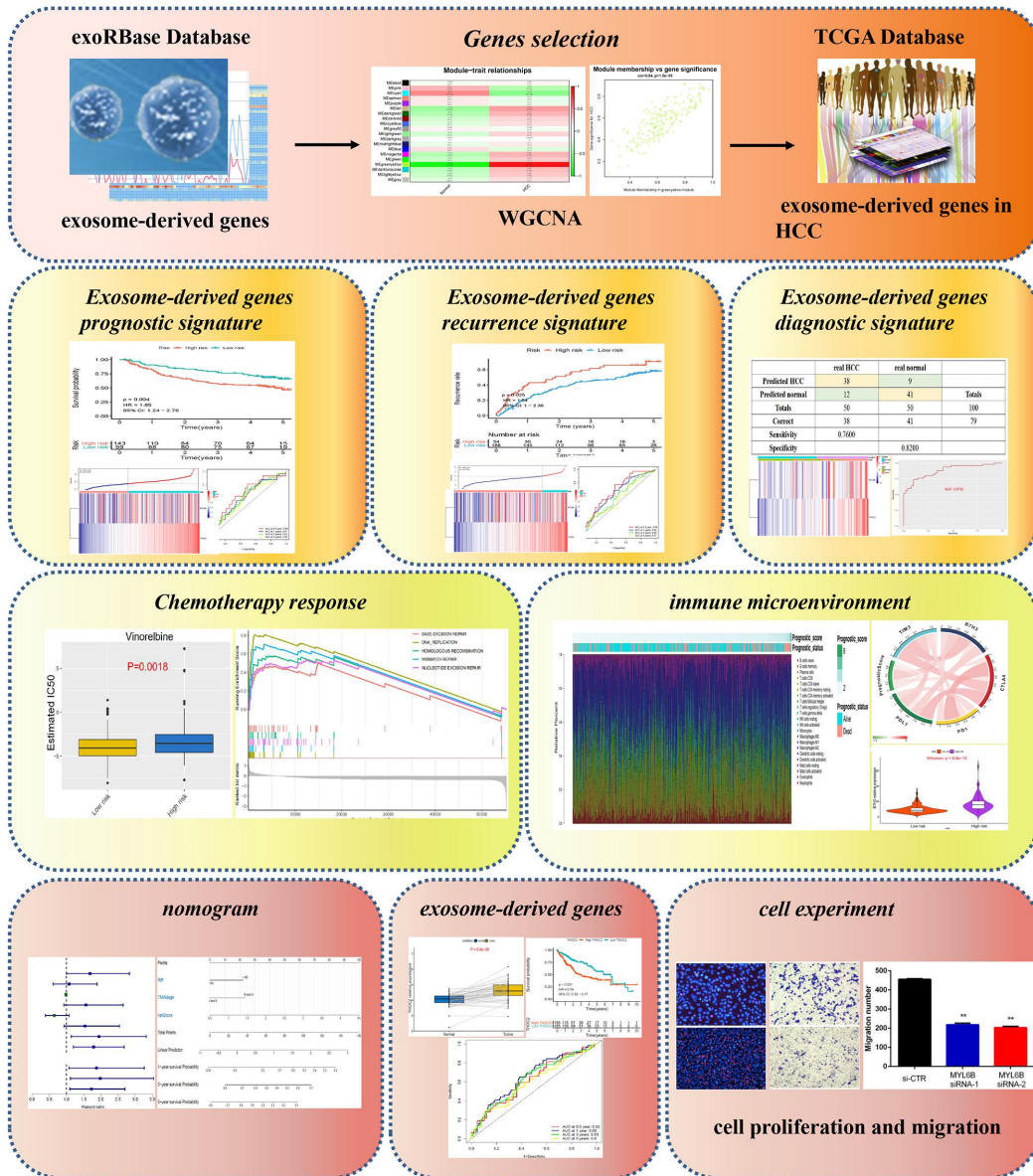
**Figure S3. Correlation between clinical variables and prognostic models.** A Distribution of prognostic risk scores, expression of *MYL6B* and *THOC2* and characteristics of clinical variables. B Prognostic risk of HCC patients with different pathological grades. **\*\*\*\*p < 0.0001(Wilcoxon test).** C HCC patients with vascular tumor invasion had a higher prognostic risk than patients without vascular tumor invasion. **\*p < 0.05(Wilcoxon test).** D There was no significant difference in the prognostic risk of HCC patients with different TNM stages. **NS: not significant.**

**Figure S4. Correlation between clinical variables and the recurrence model.** A Expression of *MYL6B* and *THOC2*, stratification of clinical variables and recurrence risk of HCC patients. B Higher recurrence risk was found in HCC patients with a G3-G4 pathological grade. **\*\*\*\*p < 0.0001(Wilcoxon test).** C Patients with vascular tumor invasion were more likely to experience relapses than patients without vascular tumor invasion. **\*p < 0.05(Wilcoxon test).** D There was no significant difference in recurrence probability among patients with different TNM stages. **NS: not significant.**

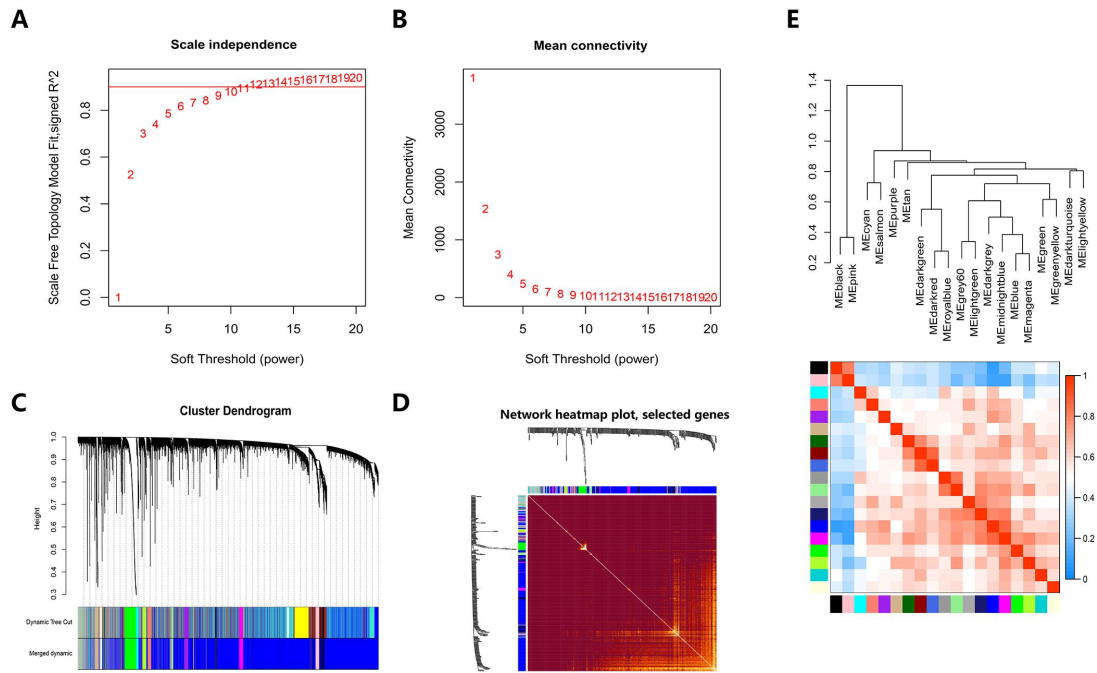
**Figure S5. The impact of *MYL6B* and *THOC2* on the expression of immune checkpoints.** A Interaction between *MYL6B* and immune checkpoints including *PDI*, *B7H3*, *CTLA4* and *TIM3*. B-E Correlation between expression of *MYL6B* and the immune checkpoints. **\*\*p < 0.01, \*\*\*p < 0.001 (Wilcoxon test).** F Interaction between *THOC2* and immune checkpoints including *PDI*, *B7H3*, *CTLA4* and *TIM3*. G-J Association between expression of *THOC2* and the immune checkpoints. **\*p < 0.05, \*\*\*p < 0.001 (Wilcoxon test).**

# Supplementary Figures

## Figure S1



**Figure S2**



**Figure S3**

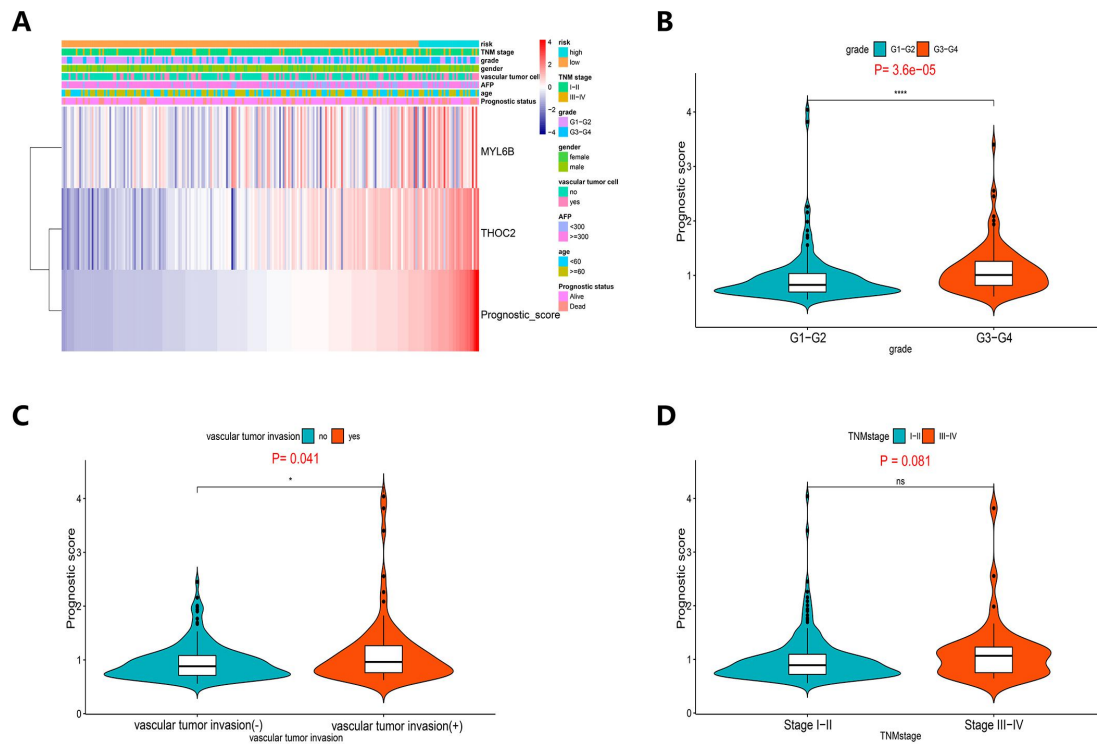
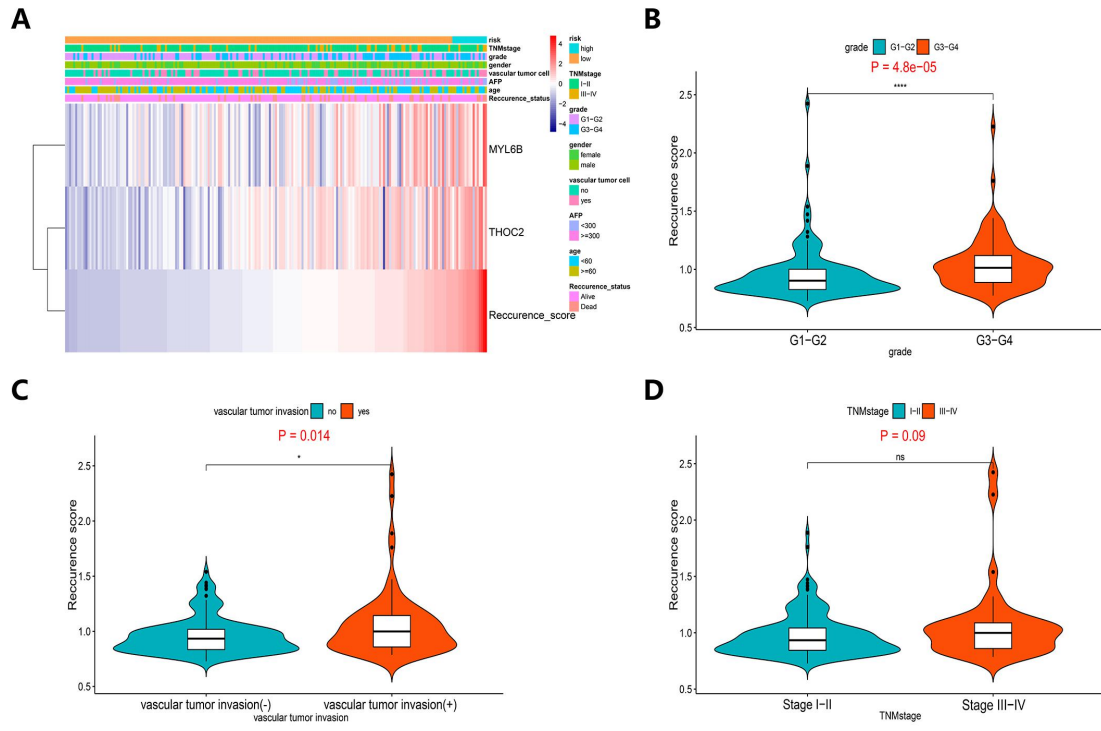
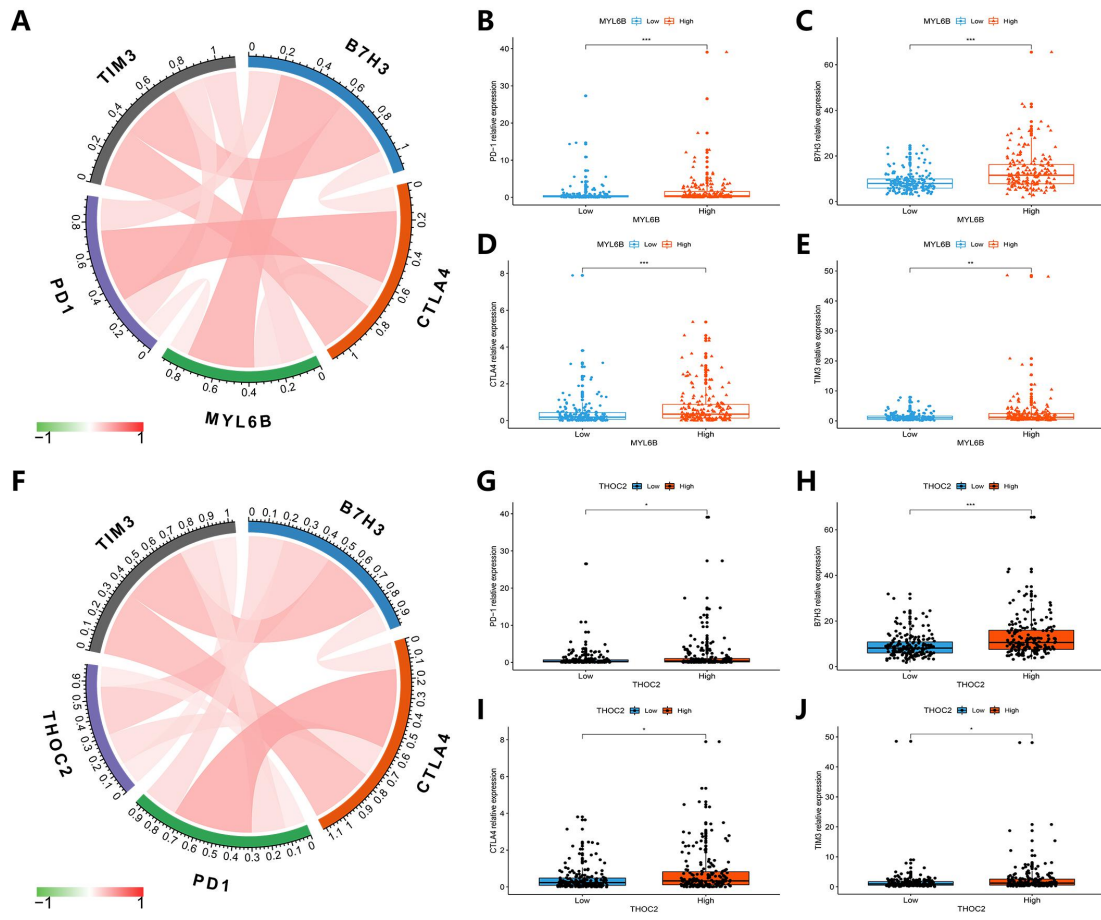


Figure S4



Revised-Figure S5



## Supplementary tables

**Table S1**

### **Patients' baseline character in the three cohorts**

Clinicopathological characterisites	TCGA patients (N=376)		GSE14520 (N=242)		ICGC (N=260)	
	N	%	N	%	N	%
<b>Age(years)</b>						
<60	172	45.7	192	79.3	50	19.2
≥60	204	54.3	50	20.7	210	80.8
<b>Gender:</b>						
Male	254	67.6	211	87.2	192	73.8
Female	122	32.4	31	12.8	68	26.2
<b>vascular cell invasion</b>						
Macro	17	4.5				
Micro	93	24.7				
None	210	55.9				
Unknow	56	14.9				
<b>AFP</b>						
≤300	218	58.0	128	52.9		
>300	65	17.3	110	45.5		
Not available	93	24.7	4	1.6		
<b>Grade</b>						
G1	55	14.6				
G2	180	47.9				

G3	123	32.7				
G4	13	3.5				
Unknow	5	1.3				
<b>TNM staging</b>						
I	175	46.5	96	39.7	40	15.4
II	86	22.9	78	32.2	117	45
III	86	22.9	51	21.1	80	30.8
IV	5	1.3	0	0	23	8.8
Unknow	24	6.4	17	7.0		
<b>Survival status</b>						
Alive	248	66.0	146	60.3	214	82.3
Death	128	34.0	96	39.7	46	17.7
<b>Recurrence status</b>						
Non-recurrence	181	48.2	106	43.8		
Recurrence	143	38.0	136	56.2		
Not available	52	13.8	0	0		

**Table S2**

Univariate Cox regression analyses of the prognostic genes in HCC patients.

id	HR	HR. 95L	HR. 95H	pvalue
CSF2RA	1.085016106	0.939750693	1.252736454	0.265871818
AKAP17A	1.045876105	1.004083617	1.089408102	0.031096742
HNRNPA3	1.028184948	1.013451076	1.043133026	0.00016044
MYL6B	1.021231135	1.000702409	1.042180995	0.042587278

SEMA3F	1.057437643	0.996737462	1.121834397	0.064080386
PLCXD1	0.997441333	0.978588464	1.016657409	0.792440782
SLC25A6	1.001175675	0.999485118	1.002869092	0.172983617
HIST1H4K	0.957755181	0.774365767	1.18457585	0.69061616
THOC2	1.199677191	1.104575089	1.302967428	1.56E-05
F0538757.1	1.376714631	1.097542242	1.726897701	0.005693986
P2RY8	0.877249838	0.77132224	0.997724738	0.046080284
RPL36A	1.000627727	0.988636297	1.012764604	0.918743859
HBA2	0.997399767	0.991430056	1.003405424	0.395303745
PPP2R3B	1.20065909	0.920226131	1.566552179	0.17784813
HSPA1B	1.001139772	0.996963503	1.005333535	0.593276784
TUBB2A	1.004638096	0.997555223	1.011771258	0.199884755
RPL39	1.001659095	0.996903261	1.006437616	0.494806757
SLC38A2	0.99668396	0.988240551	1.005199507	0.444144498
VOPP1	1.050101558	1.008795642	1.093098776	0.016955494

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**Multivariate Cox regression analyses of the prognostic genes in HCC patients**

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<b>id</b>	<b>HR</b>	<b>HR. 95L</b>	<b>HR. 95H</b>	<b>pvalue</b>
MYL6B	1.027678372	1.00614828	1.049669175	0.011492123
THOC2	1.213018758	1.116886377	1.317425423	4.56E-06

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