



Research article

Systematic analysis of lncRNA gene characteristics based on PD-1 immune related pathway for the prediction of non-small cell lung cancer prognosis

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Supplementary

Table S1. Clinical data for the NSCLC samples used in the study.

Clinical Features	TCGA	GSE31210	GSE50081	GSE19188
Survival status				
0 (survival)	602	191	106	32
1 (dead)	391	35	75	50
Gender				
Female	398			23
Male	595			59
T Stage				
T1	281		57	
T2	553		122	
T3	115		2	
T4	41			
TX	3			
N Stage				
N0	640		129	
N1	221		52	
N2	109			
N3	7			
NX	16			
M Stage				
M0	737		181	
M1	31			
MX	225			
Stage				
I	509		127	
II	277		54	
III	163			
IV	32			
X	12			
Age				
≤ 65	426		59	
> 65	552		122	
NA	15			

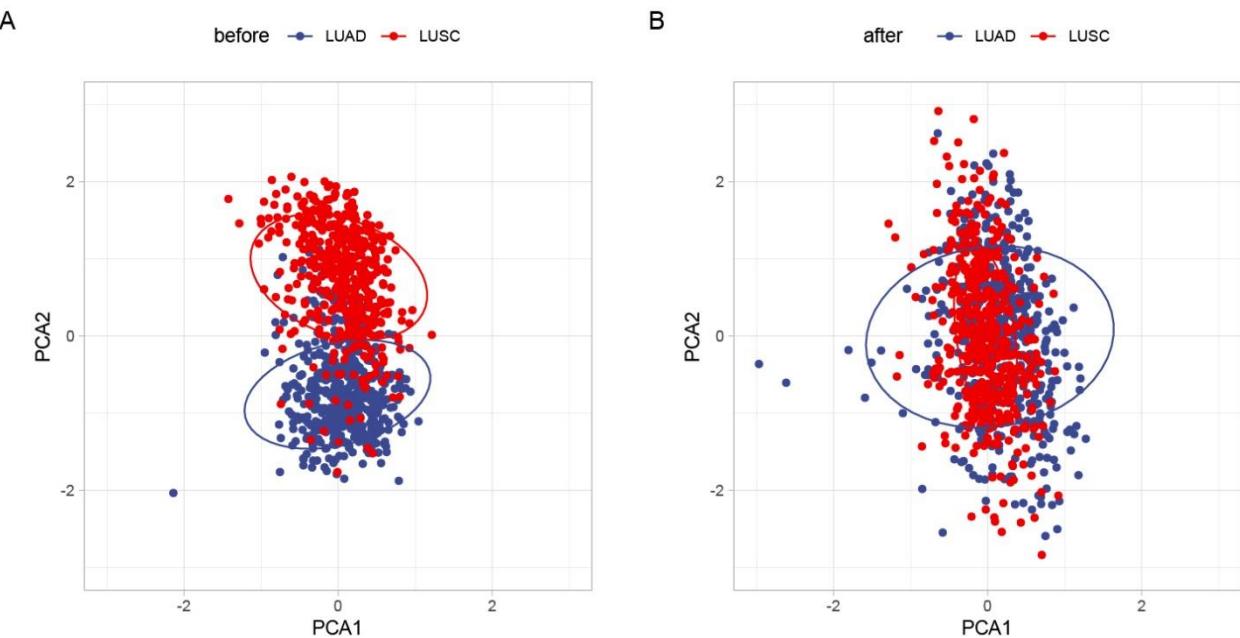


Figure S1. Principal components analysis (PCA) chart for eliminating the batch effect.

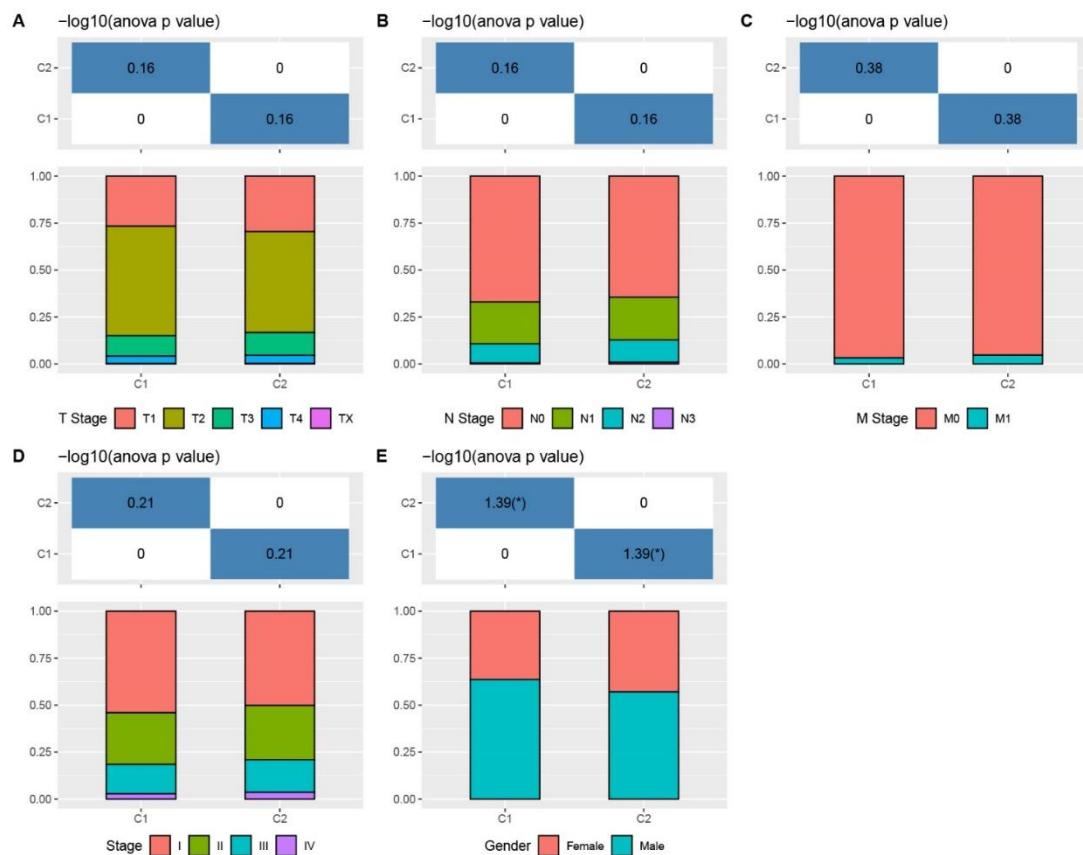


Figure S2. Differences noted in the distribution of various clinical parameters in the C1 and C2 molecular subtypes derived from the TCGA dataset, where (A) T stage; (B) N stage; (C) M stage; (D) stage and (E) gender.

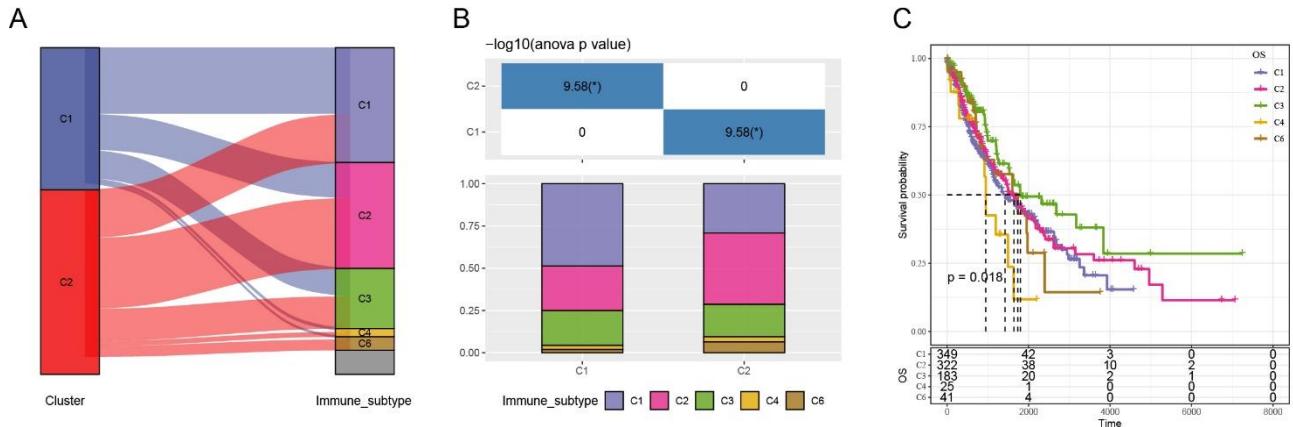


Figure S3. Distribution of the immune subtypes. (A) Sanggi diagram between molecular typing and the prevailing subtypes; (B): Distribution of immune subtypes amongst the various molecular types; (C): Survival curves for the existing immune subtypes.

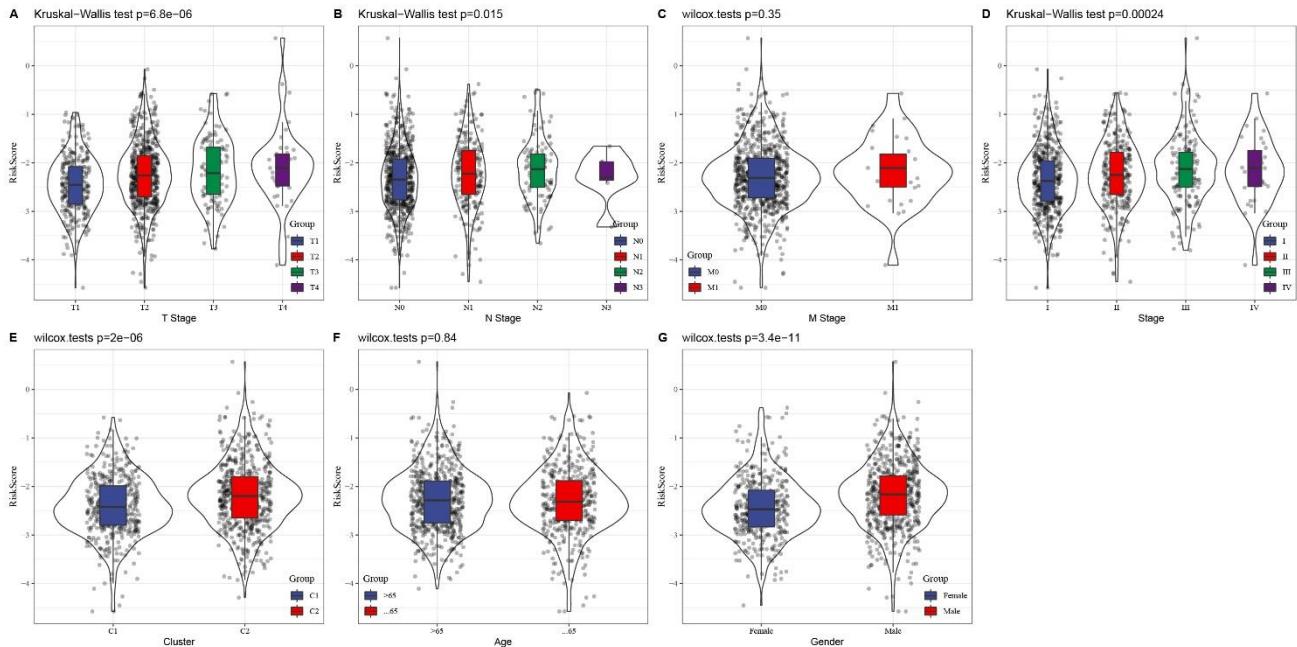


Figure S4. Comparison of the distribution of the risk score among the clinical feature groups derived from the TCGA, where (A) T stage, (B) N stage, (C) M stage, (D) stage, (E) molecular subtypes, (F) age, and (G) gender.

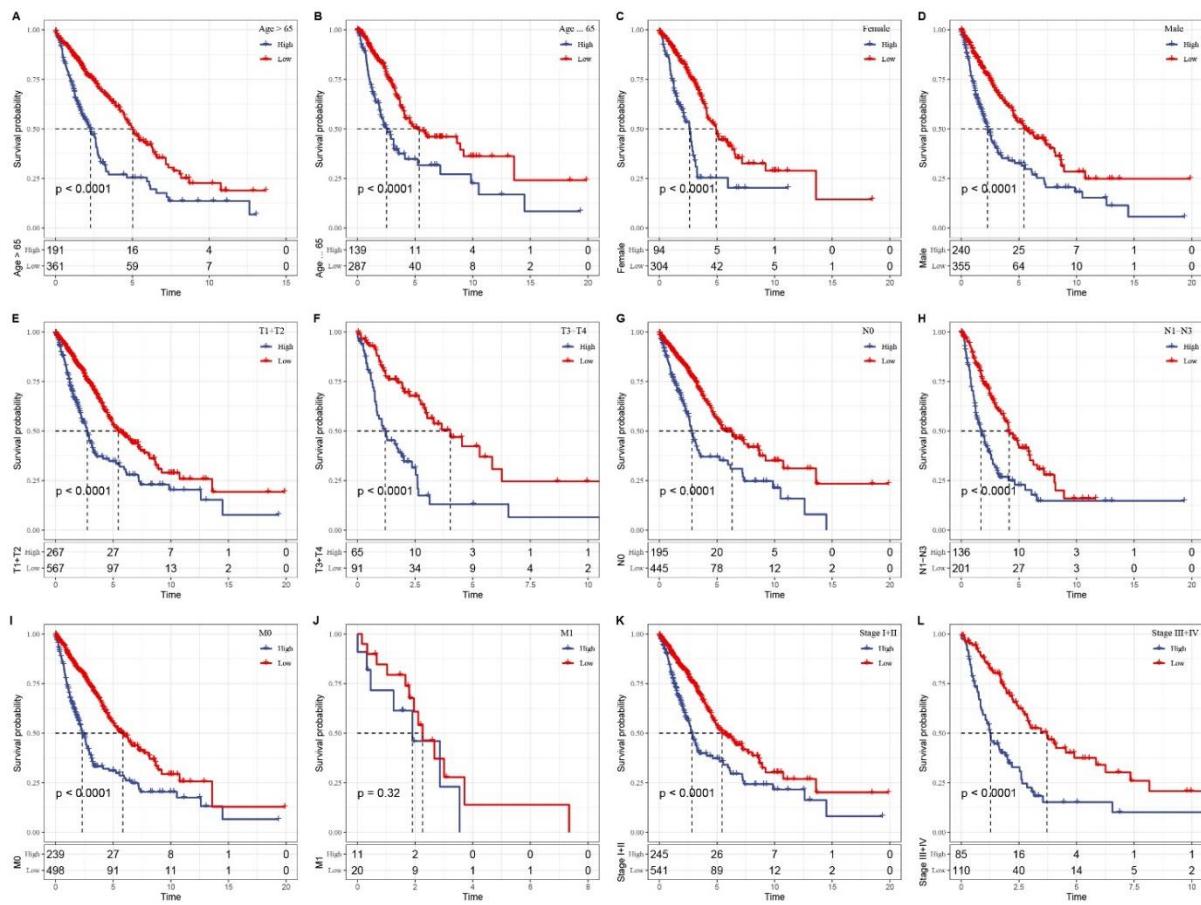


Figure S5. Survival curves for the TCGA risk groups according to different clinical characteristic groups.