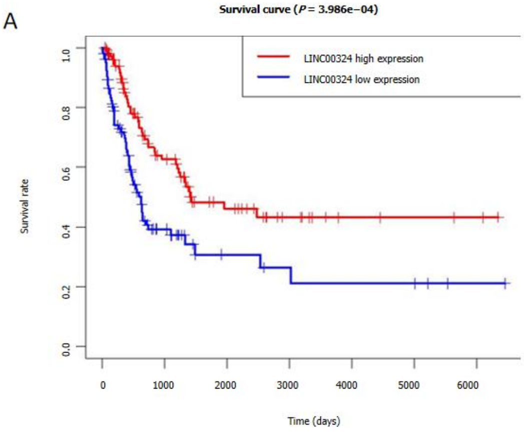
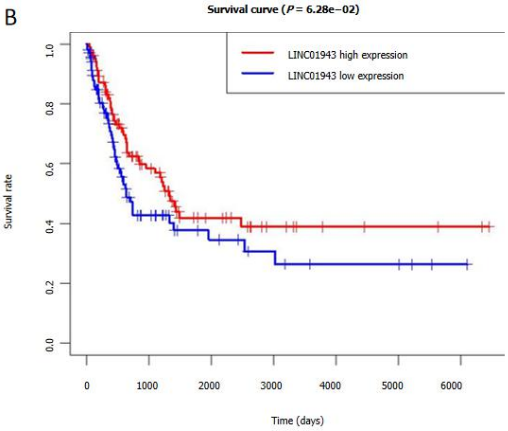
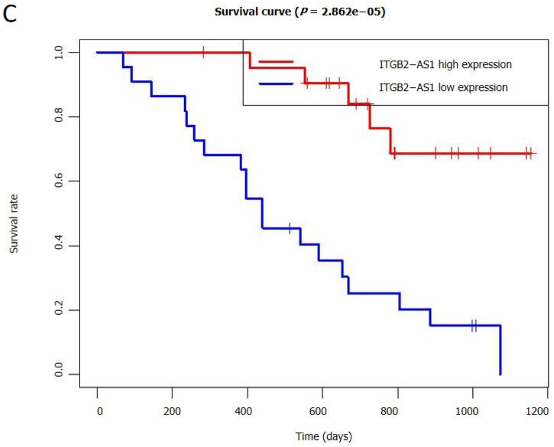
A


Survival curve (P = 3.986e−04)
LINC00324 high expression
LINC00324 low expression
Survival rate
0.0
0.2
0.4
0.6
0.8
1.0
0
1000
2000
3000
4000
5000
6000
Time (days)

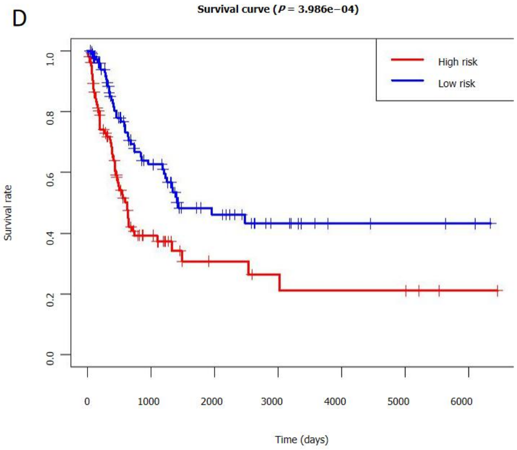
B


Survival curve (P = 6.28e−02)
LINC01943 high expression
LINC01943 low expression
Survival rate
0.0
0.2
0.4
0.6
0.8
1.0
0
1000
2000
3000
4000
5000
6000
Time (days)

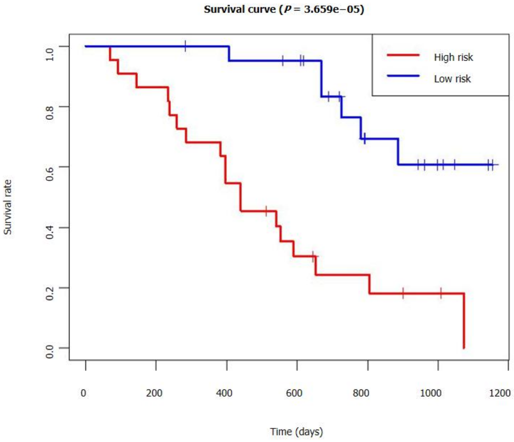
C


Survival curve (P = 2.862e−05)
ITGB2−AS1 high expression
ITGB2−AS1 low expression
Survival rate
0.0
0.2
0.4
0.6
0.8
1.0
0
200
400
600
800
1000
1200
Time (days)

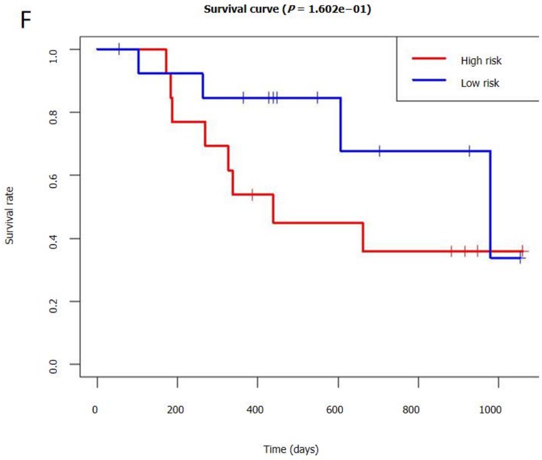
D


Survival curve (P = 3.986e−04)
High risk
Low risk
Survival rate
0.0
0.2
0.4
0.6
0.8
1.0
0
1000
2000
3000
4000
5000
6000
Time (days)

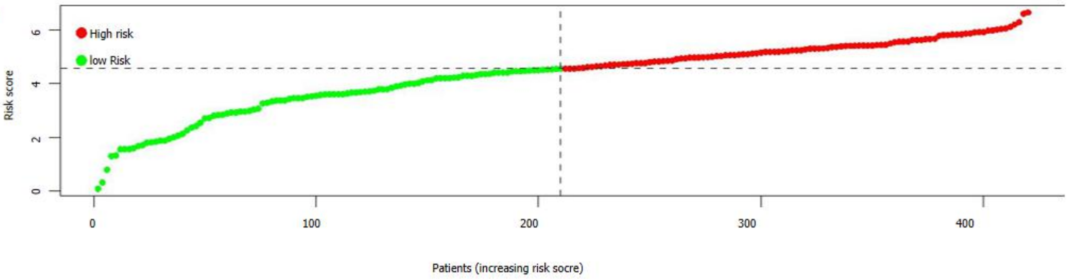
E

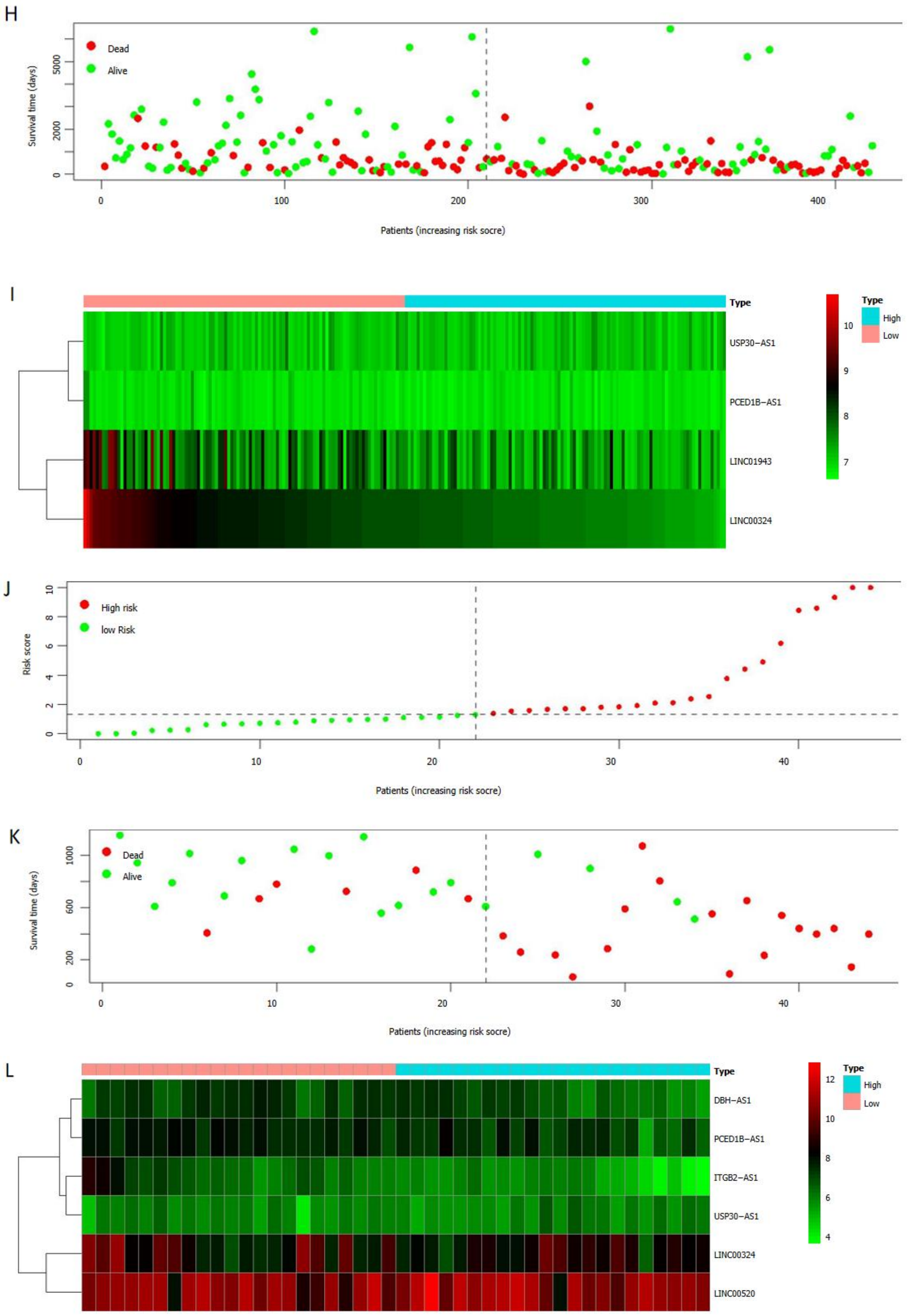

Survival curve (P = 3.659e−05)
High risk
Low risk
Survival rate
0.0
0.2
0.4
0.6
0.8
1.0
0
200
400
600
800
1000
1200
Time (days)

F


Survival curve (P = 1.602e−01)
High risk
Low risk
Survival rate
0.0
0.2
0.4
0.6
0.8
1.0
0
200
400
600
800
1000
Time (days)

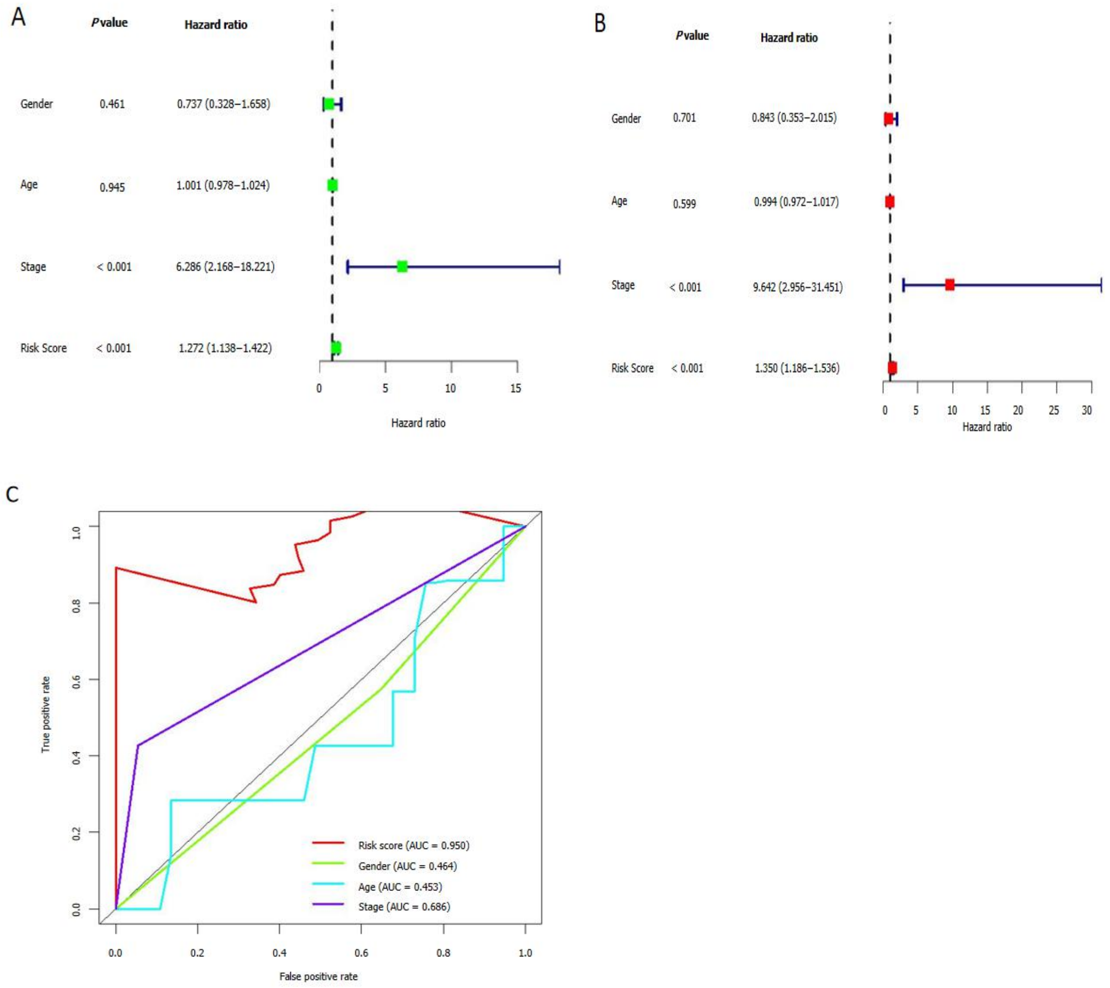
G


High risk
low Risk
Risk score
0
2
4
6
0
100
200
300
400
Patients (increasing risk socre)



Supplementary Figure 1 Prognostic value of risk models from the GSE65904, GSE19234, and GSE78220 datasets for melanoma. A-C: Survival analysis of autophagy-related lncRNA in data sets GSE65904, GSE19234, and GSE78220; D-F: Survival analysis of melanoma risk models from the

GSE65904, GSE19234, and GSE78220 datasets; G: The GSE65904 data set representative risk curve showing samples' risk scores; H: Scatter diagram of survival state of GSE65904. Green dots: Alive; Red dots: dead; I: A representative heat map of GSE65904 shows the expression of specific lncRNAs in different groups. Green and red Represent low expression and high expression, respectively; J: The GSE78220 data set representative risk curve showing samples' risk scores; K: Scatter diagram of survival state of GSE78220. Green dots: Alive; Red dots: dead; L: A representative heat map of GSE78220 shows the expression of specific lncRNAs in different groups. Green and red represent low expression and high expression.



Supplementary Figure 2 Melanoma risk model evaluation of the GSE78220 dataset. A and B: Univariate and multivariate Cox regression analyses for prognostic risk scores and different clinical features; C: ROC curves for risk scores and different clinical characteristics (age, gender and stage).