

Fig S1 The analysis process of this study

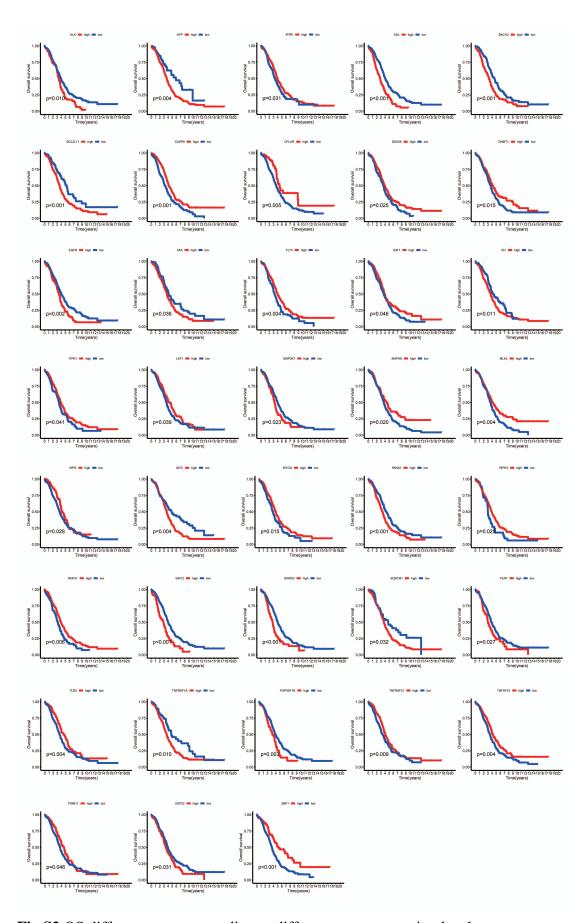


Fig S2 OS differences corresponding to different gene expression level.

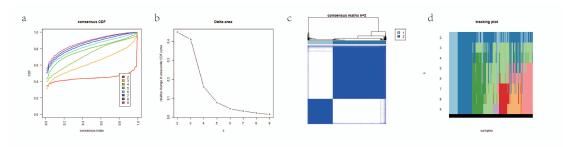


Fig S3 Consensus clustering analysis

(a) Uniform clustering cumulative distribution function (CDF), k = 2-9 (k represents the number of clusters). (b) The change of area under CDF curve with k = 2-9. (c) The samples were divided into two clusters when k=2. (d) Tracking plot of the cluster when k=2.

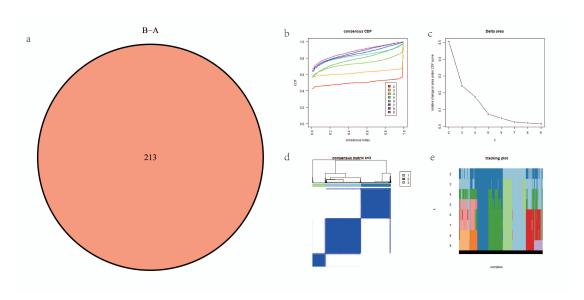


Fig S4 Consensus clustering analysis

- (a) Venn diagram showing the similar parts between NRGclustr A and NRGcluster B.
- (b) Uniform clustering cumulative distribution function (CDF), k = 2-9 (k represents the number of clusters). (c) The change of area under CDF curve with k = 2-9. (d) The samples were divided into three clusters when k=3. (e) Tracking plot of the cluster when k=3.

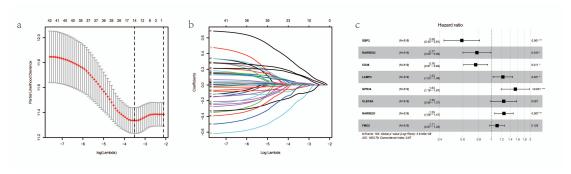


Fig S5 Identifying representative candidate prognostic genes (a-b) The LASSO regression analysis and partial likelihood deviance on the prognostic genes. (c) Forest plot of multivariate cox regression analysis for prognostic genes.

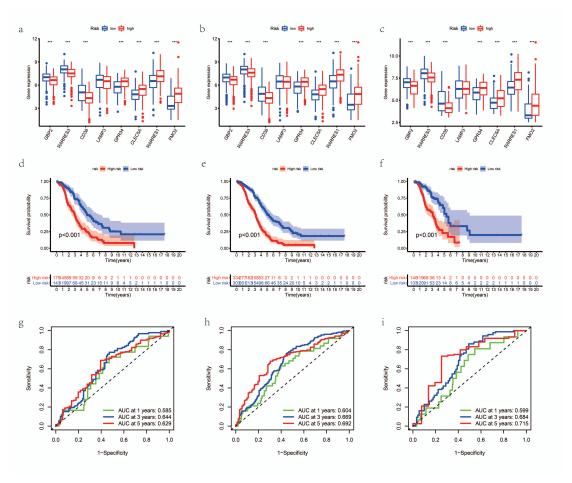


Fig S6 Validation of the prognostic model based on NRG score Different expression of the 8 NRGs between high-and low-risk groups in testing set (a), all set(b) and GEO set(c). Kaplan–Meier analysis of the survival probability between the two groups in testing set(d), all set(e) and GEO set(f). ROC curves to predict the sensitivity and specificity of 1-, 3- and 5-year survival according to the NRG_score in testing set(g), all set(h) and GEO set(i).

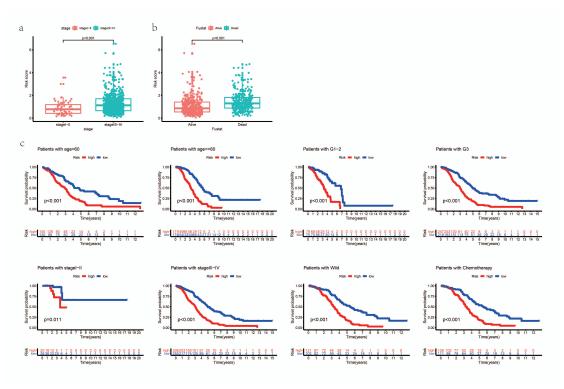


Fig S7 Clinical correlation analysis and stratified analysis of the model Comparison of risk scores of different stages (a) and fustat (b). (c) Survival analysis of OV patients with different clinical characteristics.

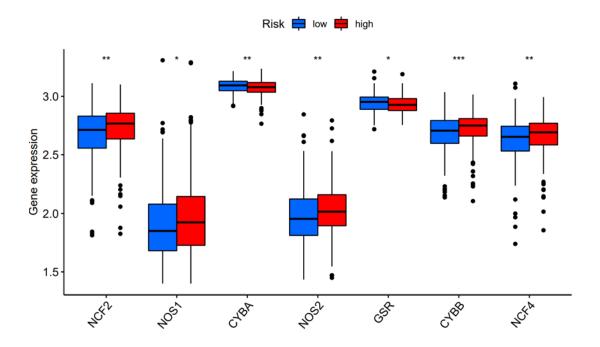


Fig S8 Expression levels of oxidative stress-related genes in high and low risk groups. *P<0.05, **P<0.01, ***P<0.001.

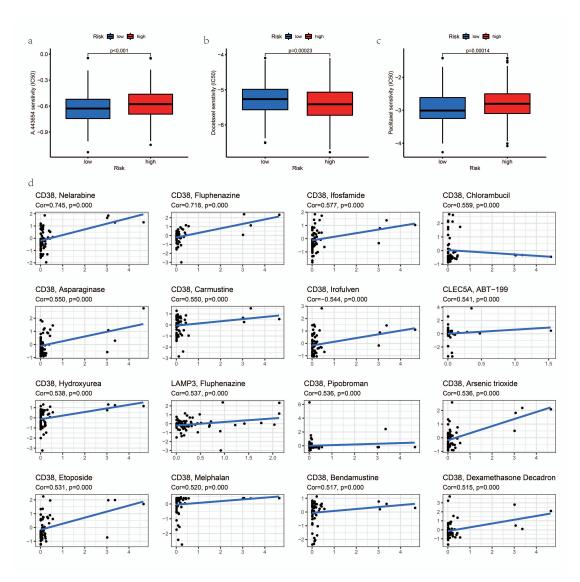


Fig S9 Analysis of drug sensitivity

The difference of IC50 of A.443654(a), docetaxel(b) and paclitaxel (c) in high and low risk groups. (d) Correlation between common drugs and 8 genes.

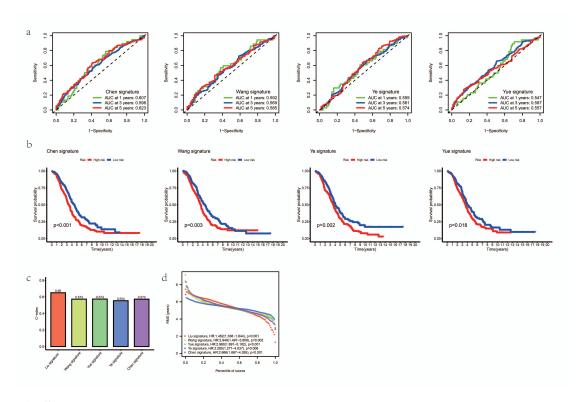


Fig S10 Comparison of our risk model with other established models

(a) ROC curves of four other published gene-signatures. (b) KM curves of four other published gene-signatures. (c) Concordance index (C-index) of the prognostic risk models. (d) Restricted mean survival (RMS) time curve of all five prognostic risk models.

Table S1 The clinical characteristics of OV patients in the TCGA and GEO databases.

Covariates	Type	Total
age	<=60	463(55.38%)
age	>60	473(44.62%)
grade	G1&G2	188(22.48%)
grade	G3	648(77.52%)
stage	StageI&II	84(10.05%)
stage	StageIII&IV	752(89.95%)
fustat	Alive	434(51.91%)
fustat	Dead	402(48.09%)