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Retrospective Study

Why *MUC16* mutations lead to a better prognosis: A study based on The Cancer Genome Atlas gastric cancer cohort

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Abstract

BACKGROUND

MUC16, encoding cancer antigen 125, is a frequently mutated gene in gastric cancer. In addition, *MUC16* mutations seem to result in a better prognosis in gastric cancer. However, the mechanisms that lead to a better prognosis by *MUC16* mutations have not yet been clarified.

AIM

To delve deeper into the underlying mechanisms that explain why *MUC16* mutations signal a better prognosis in gastric cancer.

METHODS

We used multi-omics data, including mRNA, simple nucleotide variation, copy number variation and methylation data from The Cancer Genome Atlas, to explore the relationship between *MUC16* mutations and prognosis. Cox regression and random survival forest algorithms were applied to search for hub genes. Gene set enrichment analysis was used to elucidate the molecular mechanisms. Single-sample gene set enrichment analysis and "EpiDISH" were used to assess immune cells infiltration, and "ESTIMATE" for analysis of the tumor microenvironment.

RESULTS

Our study found that compared to the wild-type group, the mutation group had a better prognosis. Additional analysis indicated that the *MUC16* mutations appear to activate the DNA repair and p53 pathways to act as an anti-tumor agent. We also identified a key gene, *NPY1R* (neuropeptide Y receptor Y1), which was

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significantly more highly expressed in the *MUC16* mutations group than in the *MUC16* wild-type group. The high expression of *NPY1R* predicted a poorer prognosis, which was also confirmed in a separate Gene Expression Omnibus cohort. Further susceptibility analysis revealed that *NPY1R* might be a potential drug target for gastric cancer. Furthermore, in the analysis of the tumor microenvironment, we found that immune cells in the mutation group exhibited higher anti-tumor effects. In addition, the tumor mutation burden and cancer stem cells index were also higher in the mutation group than in the wild-type group.

CONCLUSION

We speculated that the *MUC16* mutations might activate the p53 pathway and DNA repair pathway; alternatively, the tumor microenvironment may be involved.

Key Words: Gastric cancer; *MUC16* mutation; Cancer antigen 125; Prognosis; The Cancer Genome Atlas; Gene Expression Omnibus

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Core Tip: Our study utilized multi-omics data from The Cancer Genome Atlas, by analyzing these data, we found that the *MUC16* mutations may activate the p53 pathway and DNA repair pathway on the one hand, on the other hand, the tumor microenvironment may be involved, with higher tumor killer cells and lower stromal score together building the unique tumor microenvironment of the mutation group.

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INTRODUCTION

As the fourth most common cancer worldwide, gastric cancer is a major cause of cancer-related death[1]. Currently, the number of new gastric cancer cases reported globally accounts for 5.7% of all cancer cases, with 8.2% of patients dying as a result[2]. In China, there were approximately 679100 new cases, with 498000 deaths in 2015. The five-year survival rate of patients with gastric cancer is less than 25% due to resistance to chemotherapy drugs and tumor recurrence[3,4].

MUC16 is a type I transmembrane mucin that encodes cancer antigen 125 (CA-125). It consists of a C-terminal domain, a tandem repeat region, and an extracellular N-terminal section, of which CA-125 is part of the tandem repeat domain. In ovarian cancer, CA-125 is used to monitor cancer progression[5]. Previous studies have shown that *MUC16* mutations are associated with a longer survival time in patients with gastric cancer, although the reasons for this are not well understood.

Our study aimed to explore in greater depth the underlying mechanisms as to why *MUC16* mutations lead to a better prognosis in patients with gastric cancer.

MATERIALS AND METHODS

Acquisition of patient data

We obtained multi-omics data, including mRNA, methylation, and simple nucleotide variation (SNP) data from The Cancer Genome Atlas (TCGA) (<https://portal.gdc.cancer.gov/>) and copy number variation (CNV) data from the University of California Santa Cruz (<http://xena.ucsc.edu/>) for gastric cancer patients, and we also downloaded the matching clinical data. The mRNA data of a separate gastric cancer cohort (GSE62254) and its corresponding clinical data were obtained from the

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Tumor mutation burden scores

Tumor mutation burden (TMB) is generally defined as the total number of replacement and insertion/deletion (indel) mutations per basic group in the exon coding region of the assessed gene in a tumor cell's genome. In our study, the following formula was used to calculate TMB: the numbers of mutations/length of exons (38 mb).

Cancer stem cell

As research on tumors has progressed, growing numbers of academics have begun to recognize the heterogeneity of tumors and have proposed the cancer stem cell hypothesis. They argue that the tumor cells, even in the same tumor tissue, can be divided into different clusters, one of which is cancer stem cells[6,7]. Malta *et al*[8] proposed two cancer stem cell indices, mRNasi and mDNasi. The former reflects gene expression and the latter reflects epigenetic features, using a one-class logistic regression machine learning algorithm based on transcriptomic and epigenetic feature set information. For this reason, we also used their calculated mRNasi in our study.

Acquisition of differentially expressed genes and construction of a model

To investigate differentially expressed genes due to *MUC16* mutations, we first classified the TCGA cohort into the *MUC16* mutation group and the *MUC16* wild-type group and then analyzed them using 'edgeR' (an R package), where we defined $\log_{2}FC > 1$ ($\log_{2}FC < -1$) and false discovery rate (FDR) < 0.05 as differentially expressed genes in these two groups. To validate the GEO cohort, the differentially expressed genes obtained in TCGA were taken to intersect with all genes in the GEO cohort. The intersected genes were used in our subsequent model construction.

We used univariate Cox regression to identify prognostically related genes, where we took $P < 0.05$ as the cutoff value and ranked the importance of the obtained genes using a random survival forest algorithm ($nrep = 100$, $nstep = 5$). We defined genes with relative importance > 0.65 as our target genes. The entire random survival forest algorithm was implemented using the two R packages "randomForestSR" and "randomSurvivalForest".

Estimation of immune cells infiltration

Two different methods were applied to estimate the infiltration of immune cells according to the type of data; for mRNA data, we used single-sample gene set enrichment analysis (ssGSEA) to calculate the infiltration of 28 different immune cells and EpiDISH was used for methylation data, to estimate the infiltration of six different immune cells.

Gene set enrichment analysis

Gene set enrichment analysis (GSEA) was performed to elucidate molecular mechanisms and pathways using two different tools to achieve this. In the case of multiple genes, we used the "clusterProfiler" (an R package). For a single gene, we used javaGSEA v. 4.0 software based on the data from C2 (c2.cp.kegg.v7.1.symbols).

Assessment of immune score, tumor purity, and stromal score

In order to evaluate the immune score, tumor purity, and stromal score, we analyzed the TCGA cohort using ESTIMATE (an R package). The ESTIMATE algorithm was designed by Yoshihara *et al*[9] to calculate stromal score and immune score in tumor tissues using expression data. In recent years, this algorithm has been used in tumors such as breast cancer and glioblastoma multiforme and has shown unique appeal[10-12]. The Kruskal-Wallis test compared stromal and immune scores in the *MUC16* mutation group and the *MUC16* wild-type group.

Statistical analysis

Continuous variables between the two groups were compared utilizing the Wilcoxon rank-sum test, and the Kruskal-Wallis test applied to compare more than two categories. Kaplan-Meier survival analysis was performed and tested using the log-rank test. Heatmaps and correlation matrices were plotted using "pheatmap" and "corrplot" packages, respectively, and "maftools" was used to analyze somatic mutation profiles. We completed all statistical analyses using R software (version 3.6.2). All P values are two-sided and $P < 0.05$ is considered statistically significant.

RESULTS

***MUC16* mutations in relation to prognosis and TMB**

We obtained 437 samples of gastric cancer patients containing mutation data in TCGA and visualized them using maftools. We found that the top ten mutations in the TCGA cohort were *TTN*, *TP53*, *MUC16*, *LRP1B*, *SYNE1*, *ARID1A*, *CSMD3*, *FAT4*, *FLG*, and *PCLO* (Figure 1A). In the mutation types analysis, we observed that missense mutations were predominant and that C>T was the most common SNV class (Supplementary Figure 1A). Supplementary Figure 1B shows the correlation between the top 20 mutations.

Following further survival analysis of the 389 samples with complete survival data, we noted that only *MUC16* ($P = 0.020$) had a strong correlation with prognosis (Figure 1B). The *MUC16* mutation group had a better prognosis, and after calculating the TMB, a significantly higher TMB score was found in the *MUC16* mutation group than in the *MUC16* wild-type group (Figure 1C).

***MUC16* mutations and the tumor microenvironment**

We obtained three scores of immune score, tumor purity, and stromal score in the TCGA cohort using ESTIMATE (Figure 2A-C). The Wilcoxon test was applied to evaluate the differences between the *MUC16* mutation group and the *MUC16* wild-type group. We found that the *MUC16* mutation group differed from the *MUC16* wild-type group in the stromal score, in that the wild-type group exhibited a higher stromal score, while there was no significant difference between an immune score and tumor purity. The results showed that the *MUC16* mutation group demonstrated a higher cancer stem cell index when we introduced the previously calculated cancer stem cell index (Figure 2D). Thus, we inferred that when the stromal score was too high, and the cancer stem cell index too low, it might impact prognosis.

In addition, we calculated the infiltration of 28 different immune cells using ssGSEA, and the data showed that activated CD4T cells and CD56dimNK cells were more abundant in the mutation group, but effector memory CD4T cells and plasmacytoid dendritic cells were more enriched in the wild-type group compared to the *MUC16* wild-type group (Figure 2E).

Differentially expressed genes and drug sensitivity

To explore the differentially expressed genes, we combined the mRNA data from TCGA, which we divided into the *MUC16* mutation group and the *MUC16* wild-type group and analyzed them using "edgeR". We defined $\log_{2}FC > 1$ ($\log_{2}FC < -1$) and $FDR < 0.05$ as the differentially expressed genes in these two groups and intersected with all genes in the GEO cohort (Figure 3A), and then further screened genes associated with prognosis using univariate Cox, with $P < 0.05$ in univariate Cox analysis as input genes for the random survival forest algorithm. The random survival forest algorithm was used to further define and analyze the data, and the genes with relative importance greater than 0.65 were defined as our target genes. Finally, the gene *NPY1R* (neuropeptide Y receptor Y1) was obtained (Figure 3B-C).

Next, we attempted to predict possible drug targets for *NPY1R* by browsing the Genomics of Drug Sensitivity in Cancer (<https://www.cancerrxgene.org/>) database and downloading the relevant data. We analyzed the relationship between the expression of *NPY1R* and the IC_{50} (natural log half maximal inhibitory concentration) values of several targeted drugs in gastric cancer cell lines. A positive correlation between *NPY1R* expression and IC_{50} value implied increased drug resistance in gastric cancer cell lines. Conversely, it implied that the drug could inhibit the expression of *NPY1R*. Three drugs that showed a strong negative correlation with *NPY1R* expression were obtained, including WH-4-023, WZ-184, and Roscovitine (Figure 3D).

Prognosis and GSEA analysis

We used the TCGA cohort as a training group with the median value of *NPY1R* as a cutoff value and divided the TCGA cohort into high-risk and low-risk groups. The GEO cohort was used as external validation to test our model. Kaplan-Meier survival analysis showed that high expression of *NPY1R* led to poorer prognosis, whether in the TCGA cohort or the GEO cohort (Figure 4A and B). Moreover, the frequency of poorer prognosis was higher in the high-risk group (Figure 4C-F).

GSEA was used to elucidate molecular mechanisms and pathways. The Kyoto Encyclopedia of Genes and Genomes enrichment (KEGG) showed that the low-risk group showed more enrichment on DNA repair, while the high-risk group showed little enrichment, whether in the TCGA cohort or the GEO cohort (Figure 4G-H).

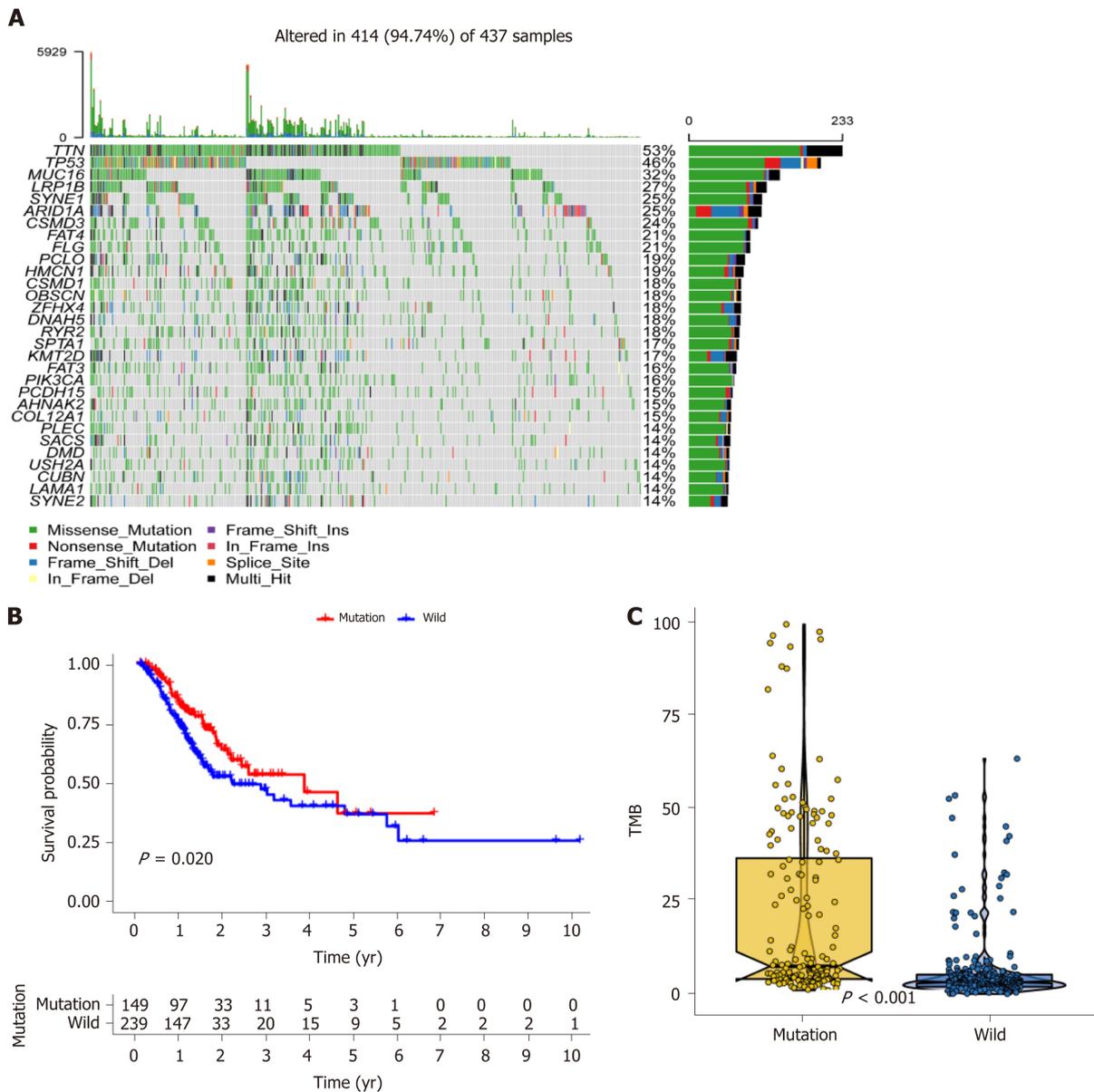


Figure 1 *MUC16* mutations in relation to prognosis and tumor mutation burden. A: Waterfall plot showing the mutation information for each gene. Each color represents a type of mutation; B: Kaplan-Meier survival analysis was used to assess prognosis, with red representing the mutation group and blue representing the wild-type group; C: Boxplot showing the tumor mutation burden scores in the two groups. TMB: Tumor mutation burden.

NPY1R and immune infiltration

To further explore the relationship between *NPY1R* and immune infiltration, we used EpiDISH to evaluate the infiltration of six immune cells based on methylation data. The percentage of six immune cells in each sample is shown in the plots (Figure 5A). Next, we divided them into the high-risk group and the low-risk group according to the median value of *NPY1R*, and the Wilcoxon test was applied to compare whether there was a difference in immune cell infiltration between the two groups. The results were visualized in violin plots.

We found that the contents of B cells and CD4T cells were higher in the high-risk group than in the low-risk group. However, natural killer (NK) cells and neutrophils were more abundant in the low-risk group (Figure 5B). We also plotted the correlation matrix of these six immune cells. In the correlation matrix, we noted that CD4T cells negatively correlated with neutrophils and CD8T cells, and B cells also showed a negative correlation with NK cells (Figure 5C). At the same time we plotted the heatmap to show the contents of these six immune cells between the two groups (Figure 5D).

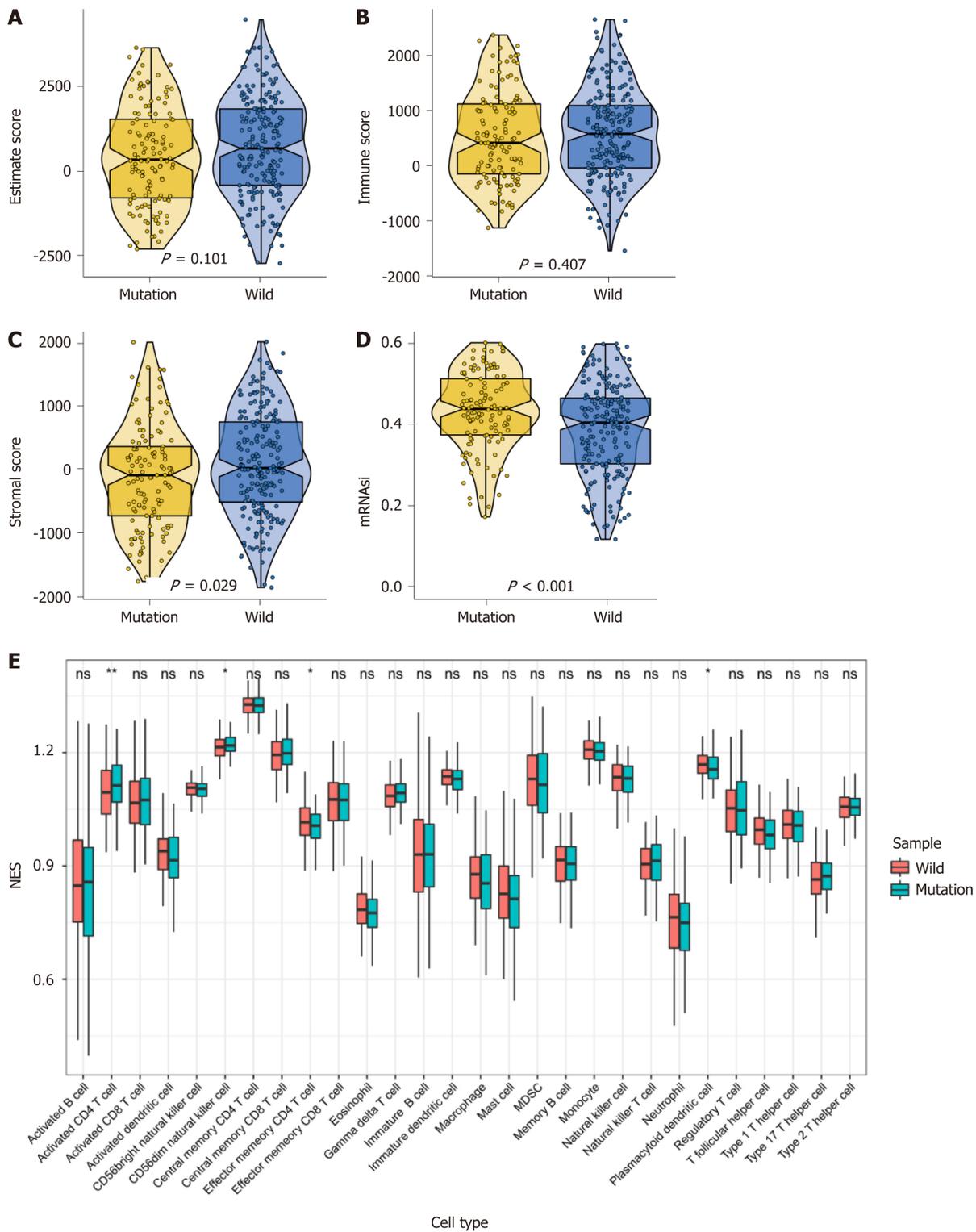


Figure 2 *MUC16* mutations and the tumor microenvironment. A-C: Violin plot showing tumor purity, immune score, and stromal score, respectively; D: Boxplot showing the difference in cancer stem cell index between the two groups; E: The infiltration of 28 immune cells in tumors was assessed using single-sample gene set enrichment analysis, red represents the mutation group and blue represents the wild-type group.

MUC16 mutations and CNVs

To explore the relationship between *MUC16* mutations and CNVs, we downloaded CNV data. The two groups were divided similarly, according to *MUC16* mutation status. Using the χ^2 test, we assessed whether there was a difference in CNV between the two groups, and we defined $P < 0.05$ as differential CNVs, displayed by the circle plot (Figure 6A). The circle plot illustrates CNVs at chromosomal locations. The relationship between CNV and mRNA expression was further analyzed.

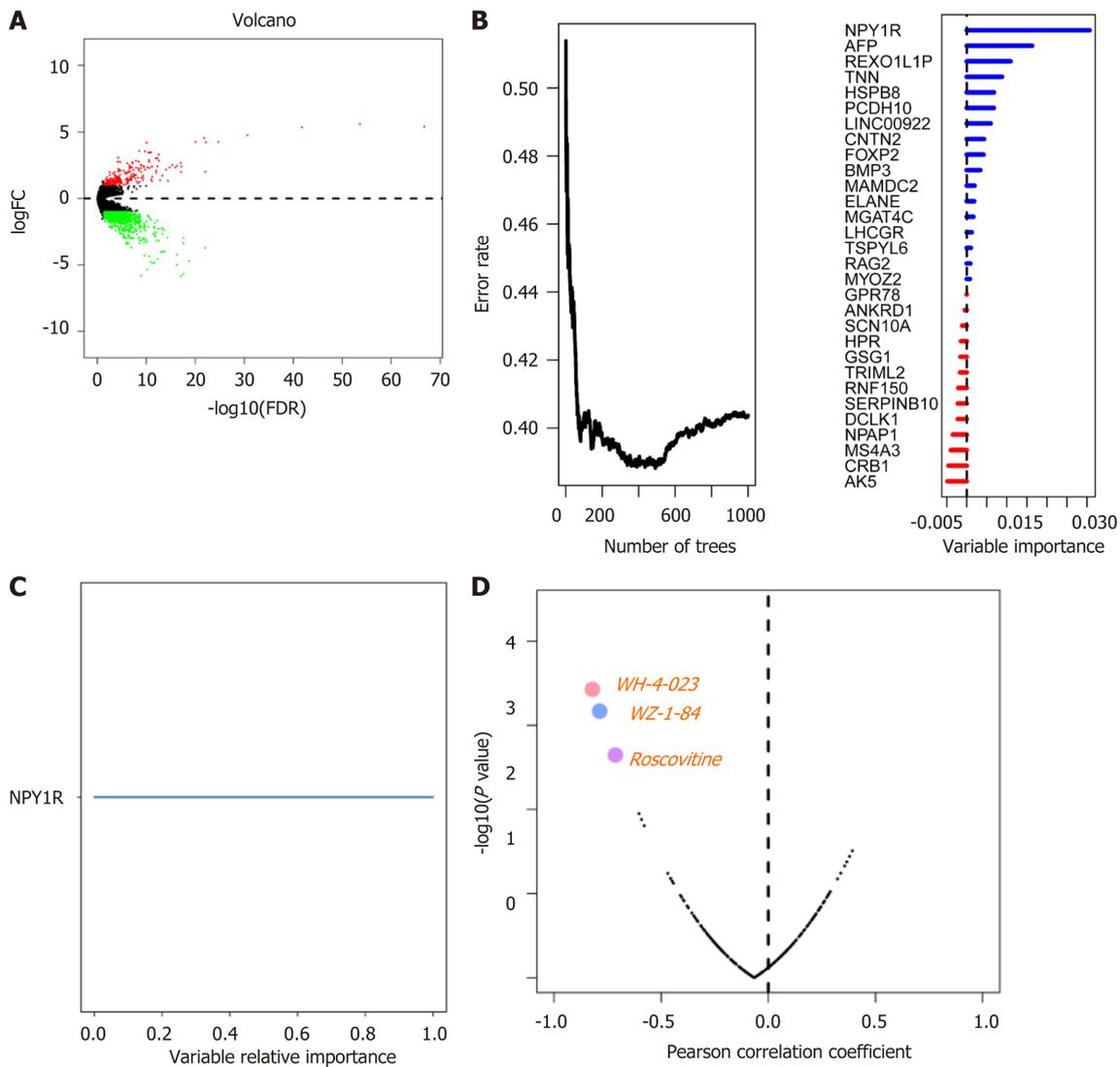


Figure 3 Differentially expressed genes and drug sensitivity. A: Volcano plot showing differentially expressed genes between the *MUC16* mutation group and the *MUC16* wild-type group, up-regulated genes are in red, down-regulated genes are in green, and black represents genes that are not differentially expressed; B: Error rate for the data as a function of the classification tree and out-of-bag importance values for the predictors; C: Genes of relative importance greater than 0.65; D: The plot showing the correlation between *NPY1R* expression and the sensitivity of gastric cancer cell lines to various drugs, with the three most negatively correlated drugs being WH-4-023, WZ-184, and Roscovitine. NPY1R: Neuropeptide Y receptor Y1.

We assessed this using the Kruskal-Wallis test: $P < 0.05$ was defined as the differential. In particular, we found that inhibitor of growth gene 2 (*ING2*), with its CNV gain and deletion, mRNA expression also changed, and that *ING2* is involved in DNA damage repair (Figure 6B and C).

In addition, we undertook GSEA to utilize differential CNVs and used the cluster-Profiler to perform enrichment analysis and visualize the results. KEGG pathways showed enrichment in colorectal cancer, B-cell receptor signaling pathways, apoptosis-multi-species, apoptosis, and p53 signaling pathways (Figure 7A). GO analysis seemed to be more focused on the two processes of apoptosis and anti-apoptosis (Figure 7B-D).

DISCUSSION

MUC16 (OMIM606154) is the most frequently mutated gene in gastric cancer and the prognosis of the mutation group was better than that of the wild-type group. However, it is not well understood why the mutation in *MUC16* leads to a better prognosis[5]; thus, we explored the possible mechanisms through multi-omics data, including SNP, CNV, mRNA, and methylation data.

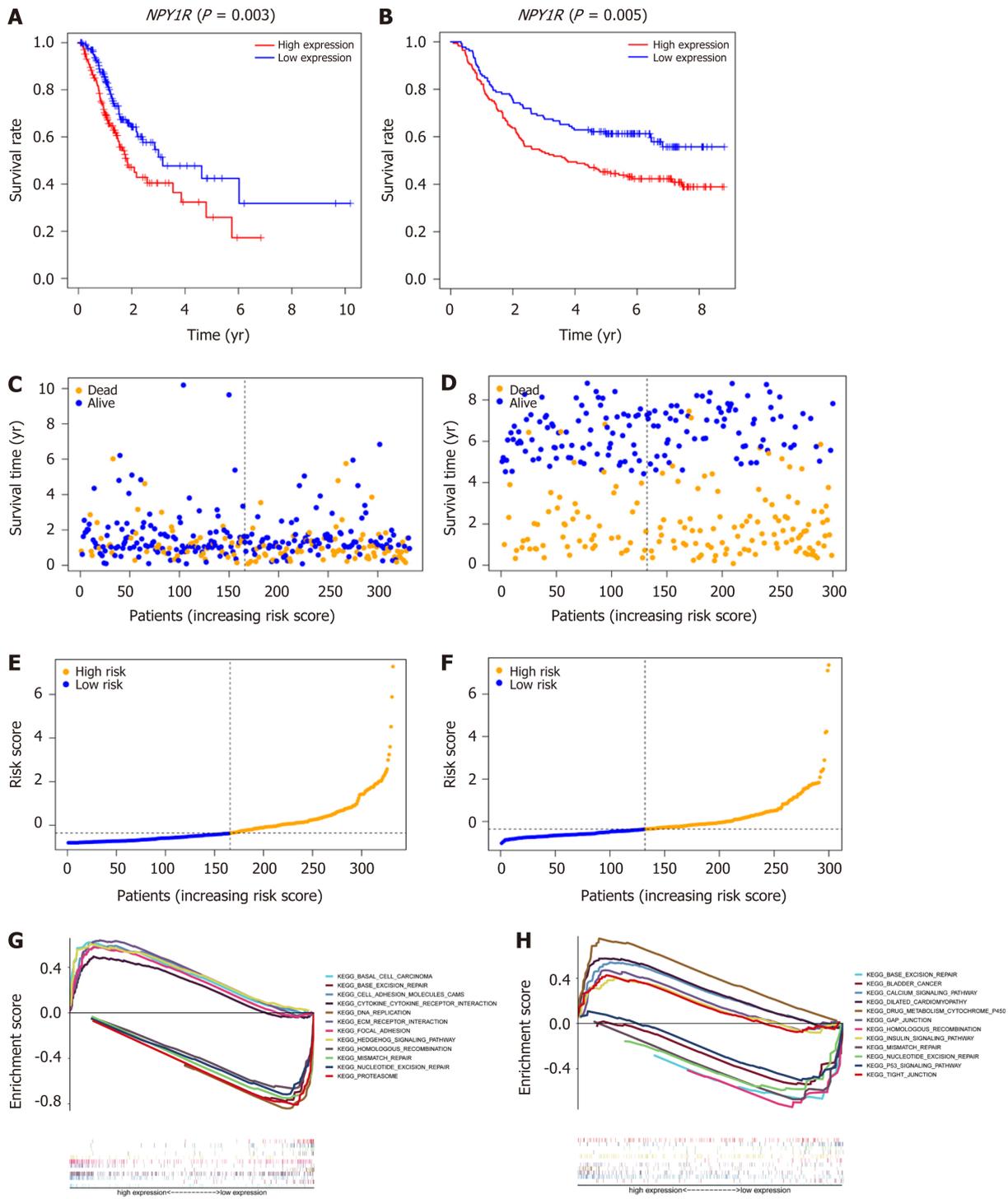


Figure 4 Prognosis and gene set enrichment analysis. A and B: Kaplan-Meier survival analysis for The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO) cohorts, respectively; C and D: Overall survival time distribution in the TCGA cohort and GEO cohort; E and F: Distribution of risk scores in TCGA and GEO cohorts; G and H: Gene set enrichment analysis in the TCGA and GEO cohorts, respectively. The plots on the left are the TCGA cohort and the plots on the right are the GEO cohort. *NPY1R*: Neuropeptide Y receptor Y1.

We first analyzed the gene mutation landscape in the TCGA cohort, and found that *MUC16* had the third-highest mutation frequency, after *TTN* and *TP53*, and was dominated by missense mutations. Survival analysis showed that the *MUC16* mutation group had a better prognosis than the wild-type group. Moreover, we found higher TMB scores in the mutation group. As a marker for predicting immune checkpoint blockade, TMB has shown unique prognostic value in immunotherapy in several tumors and was included in the National Comprehensive Cancer Network (NCCN) guidelines for non-small cell lung cancer in 2019[13-16]. Studies in melanoma, neuroendocrine cervical cancer, and colorectal cancer have also found that patients

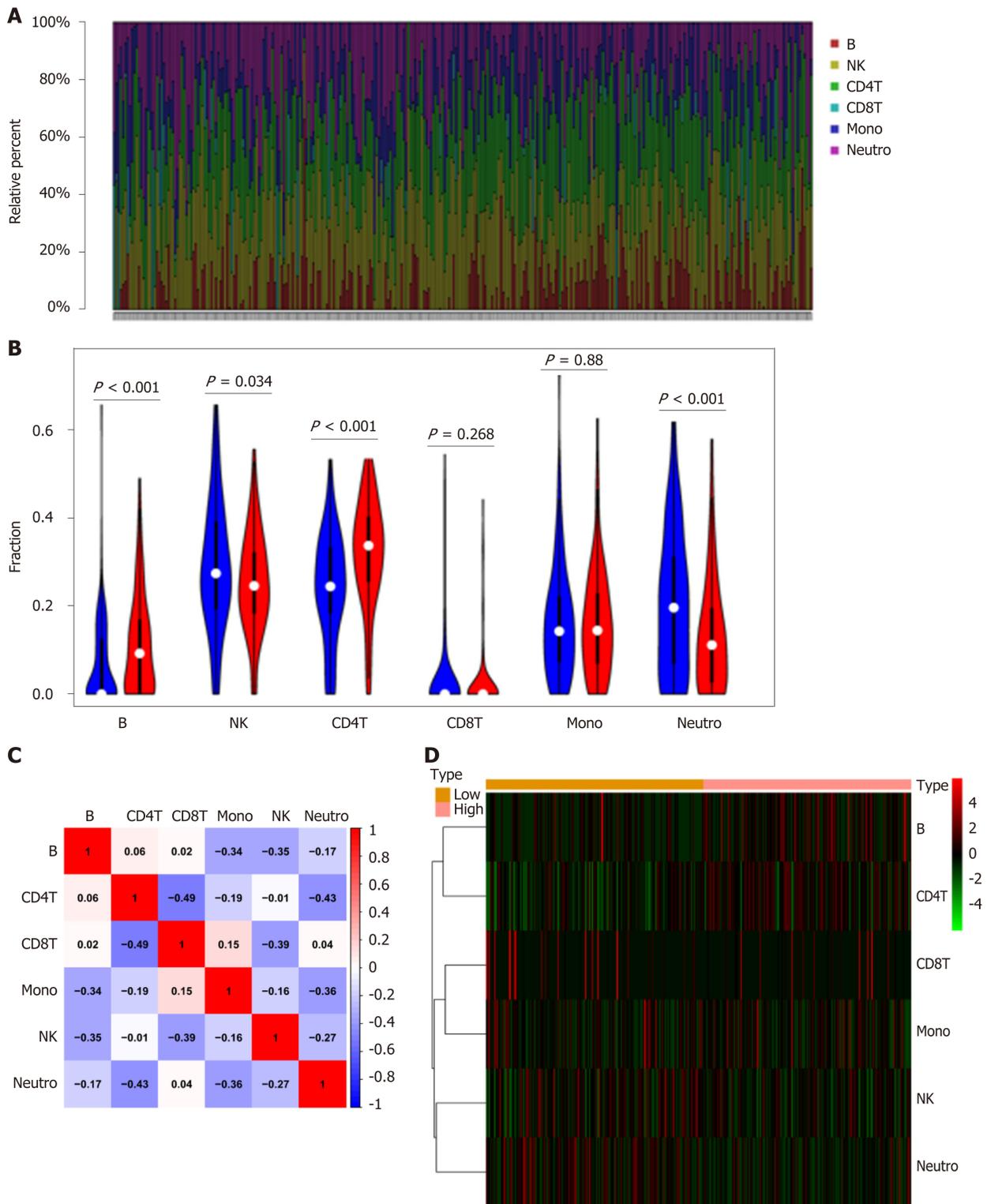


Figure 5 *NPY1R* and immune infiltration. A: The 6 immune cell types in each sample are shown in bar plots; B: The violin plot showing the differences in 6 immune cell types between the two groups; C: The correlation matrix demonstrated the correlations of 6 immune cell types; D: Heatmap revealing the distribution of 6 immune cell types in the two groups. NK: Natural killer; Mono: Monoclonal; Neutro: Neutrophil.

with high TMB scores have a better prognosis after treatment with immune checkpoint inhibitors (ICI)[15,17-19]. Therefore, we speculated that the *MUC16* mutation group is more likely to benefit from ICI treatment.

We also investigated the tumor microenvironment and found no statistically significant differences in the remaining immune score and tumor purity, except for the stromal score, which was higher in the *MUC16* wild-type group. Thus, a higher stromal score seems to predict a worse prognosis, and Gong *et al*[20] also found that a

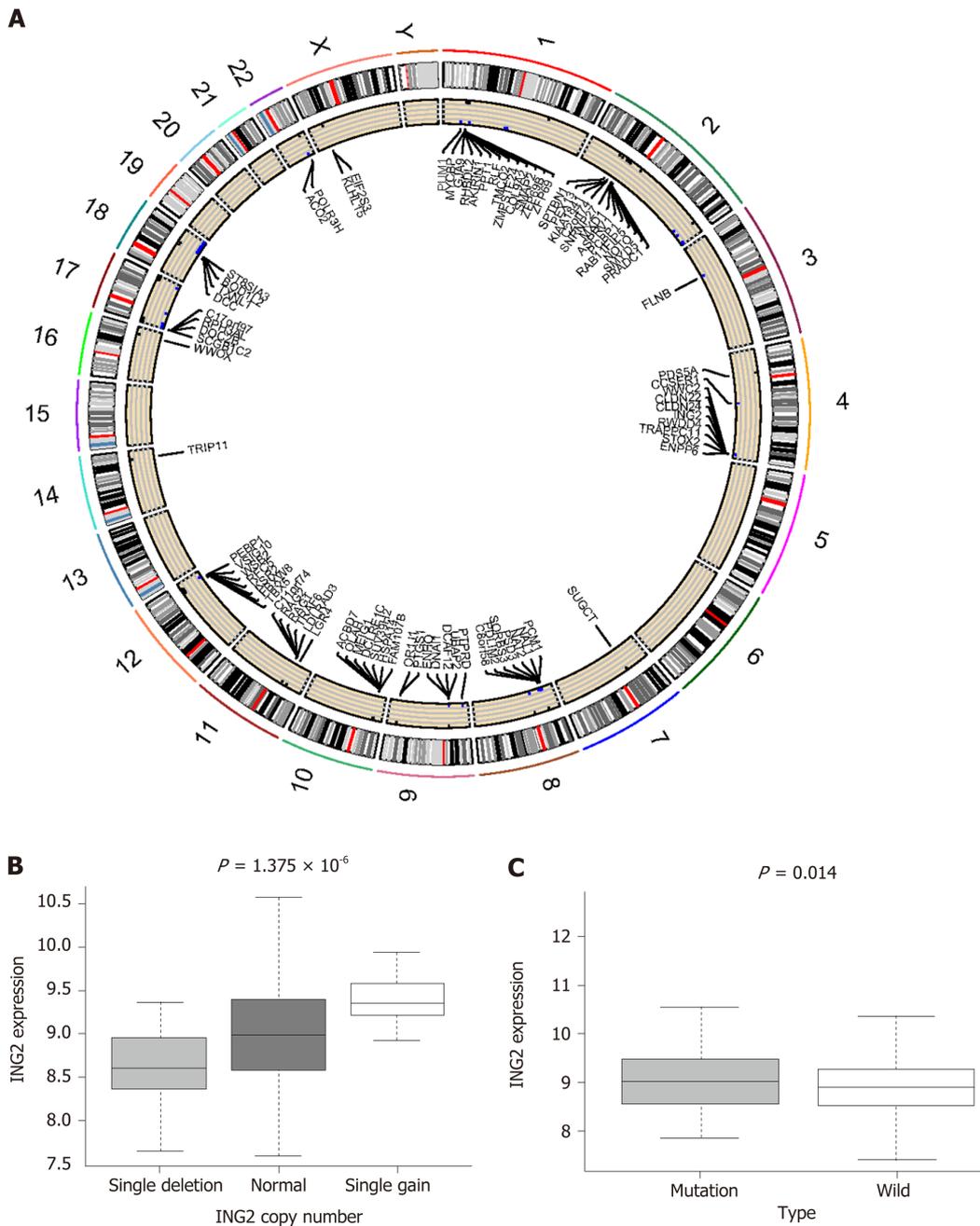
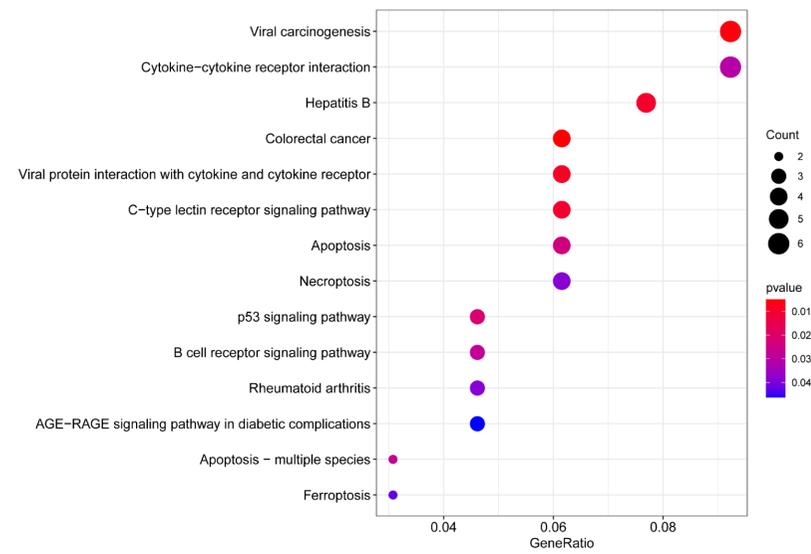
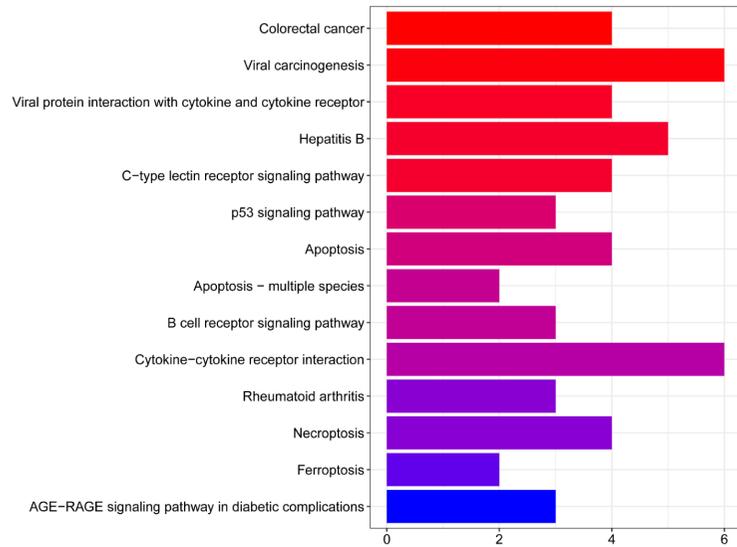


Figure 6 *MUC16* mutations and copy number variations. A: The circle plot shows the location of differential copy number variations in the chromosome; B and C: The left boxplot shows the relationship between *ING2* (inhibitor of growth gene 2) gain and deletion and the mRNA expression, the right boxplot shows the differential expression of *ING2* in the *MUC16* mutation and wild-type groups. *ING2*: Inhibitor of growth gene 2.

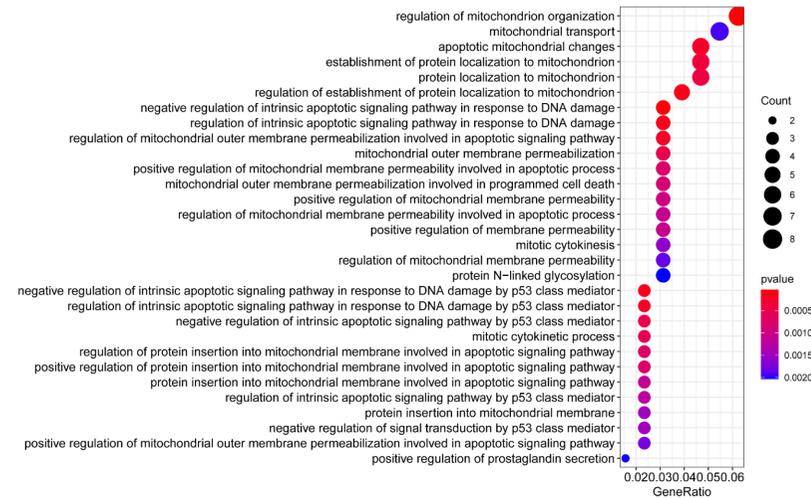
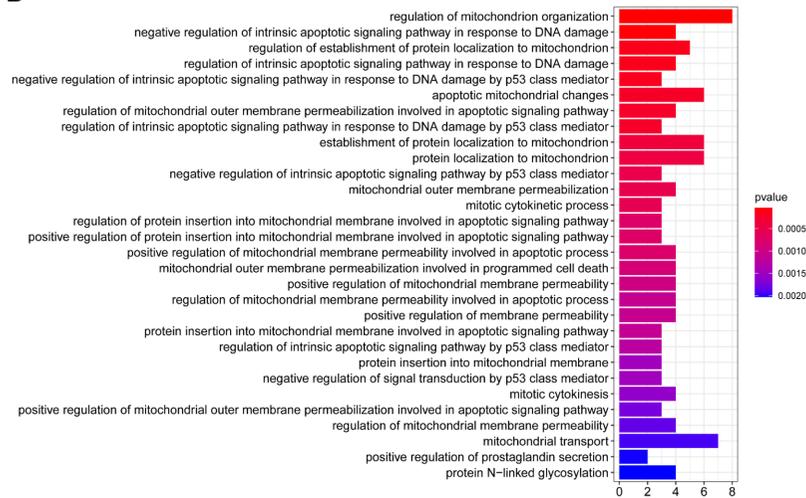
higher stromal score was always associated with poor prognosis in patients with melanoma. mRNAsi in the *MUC16* mutation and wild-type groups was also compared, and mRNAsi was found to be much higher in the mutation group than in the wild-type group. Previous studies have shown that cancer stem cells appear to be associated with tumor recurrence and drug resistance in bladder cancer; therefore, more in-depth studies are needed on the relationship between mRNAsi and gastric cancer[21].

Additionally, in assessing the infiltration of 28 immune cells, we found that activated CD4T cells and CD56dimNK cells were more abundant in the mutation group, whereas effector memory CD4T cells and plasmacytoid dendritic cells were more abundant in the wild-type group. Several studies have shown that CD4T cells are useful for tumor suppression. Belisle *et al*[22] found that in ovarian cancer, *MUC16* specifically binds to CD56dimNK cells, thereby causing immunosuppression, and a similar situation occurred in our study. It has been suggested that plasmacytoid dendritic cells may contribute to the development of Tregs in a colorectal cancer-

A



B



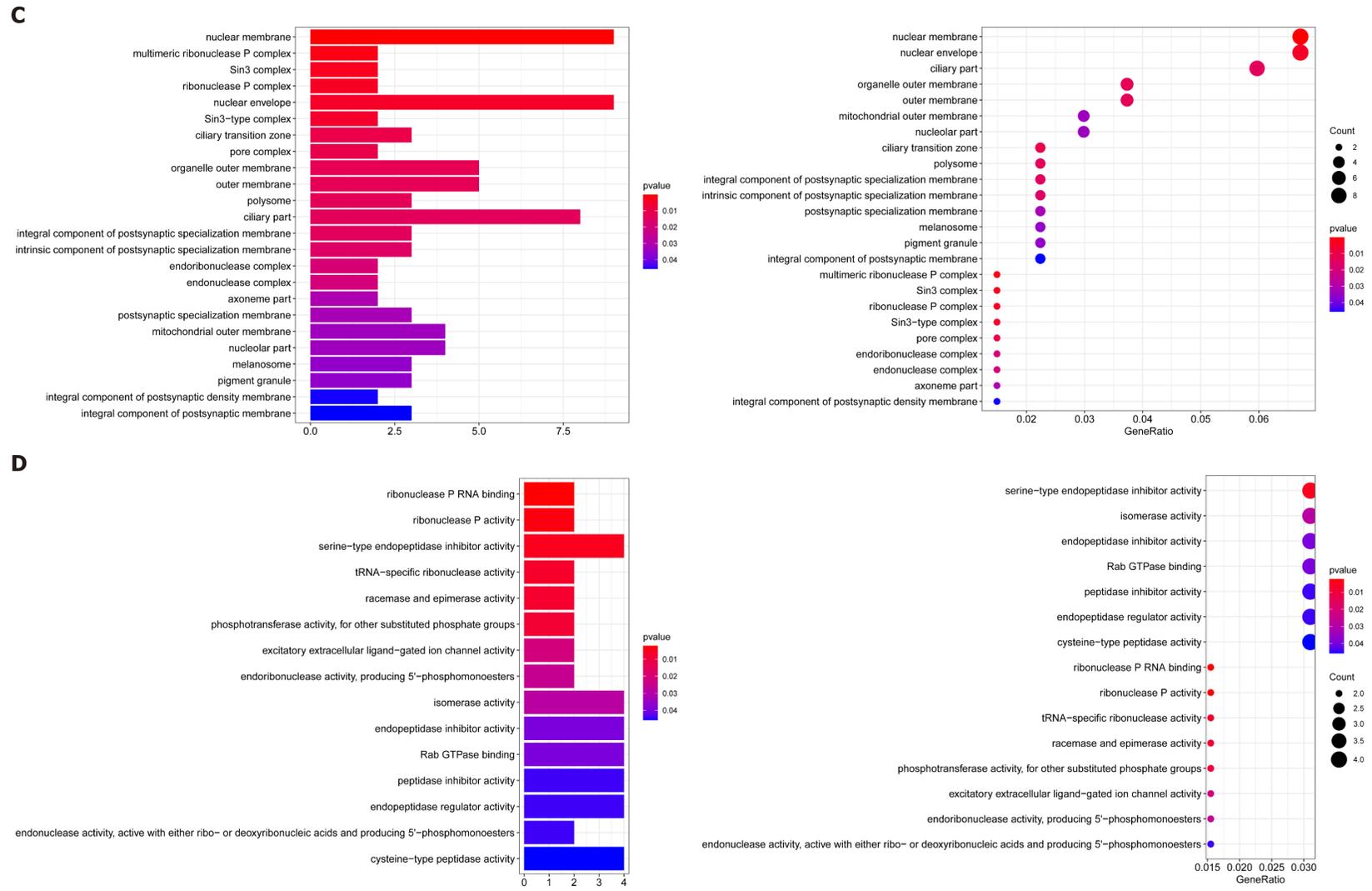


Figure 7 Gene set enrichment analysis. A: Kyoto Encyclopedia of Genes and Genomes enrichment results of the differential copy number variations; B-D: Gene Ontology enrichment results of the differential copy number variations.

resistant environment, thus leading to a poor prognosis[23]. The *MUC16* mutation group exhibited higher tumor-killing cells and lower immunosuppression cells; thus, we speculate that the infiltration of immune cells may also be a non-negligible factor contributing to better prognosis in the mutation group than the wild-type group.

In the subsequent analysis, we applied the random survival forest algorithm and Cox regression to investigate the differentially expressed genes associated with prognosis due to *MUC16* mutations. After screening, we found *NPY1R*, which belongs to the G protein-coupled receptor superfamily. It encodes a transmembrane protein that functions as neuropeptide Y (NPY, a neurotransmitter), and peptide YY (PYY, a gastrointestinal hormone). It has been suggested that *NPY1R* has a unique role in gastric acid secretion and anti-tumorigenesis[24,25].

We noted that high *NPY1R* expression was always associated with a poor prognosis in the study of *NPY1R* and breast cancer, where Liu *et al*[26] found that high *NPY1R* expression was associated with a poorer prognosis. There, immune infiltration based on methylation data showed that NK cells – neutrophils – were more evident in the low *NPY1R* expression group, while there were more B cells and CD4T cells in the high expression group. NK cells act as tumor-killing cells, leading to a better prognosis. In addition, neutrophils potentially influence the clinical outcome of gastric cancer by modulating immune response; it has been shown that enriched neutrophils can induce NK cell activation through receptor-ligand interaction and interleukin 18 production[27-29]. It has also been pointed out that CD4T may be involved in breast tumor progression[30] and that B cells may be associated with a better prognosis of the esophagogastric junction[31].

As we discovered that high expression of *NPY1R* was associated with worse outcomes, we hypothesized that if we could reduce the expression of *NPY1R*, then we might be able to improve the prognosis; thus, we have identified a drug that has the potential to benefit patients with high *NPY1R* expression: Roscovitine.

Roscovitine, is a selective cyclin-dependent kinase inhibitor. Iseki *et al*[32] found that it inhibited the growth of gastric cancer cells. Roscovitine has been reported in many articles to increase p53, and p53 also enhances the effects of Roscovitine[32-34]. Interestingly, our GSEA analysis showed that the *NPY1R* low expression group had more DNA repair pathways and p53 pathways, while it was rarely present in the *NPY1R* high expression group. A similar result emerged when further KEGG and GO analyses were performed on differential CNVs, which were more involved in the p53 pathway, B-cell response pathway in the *MUC16* mutation group, while GO analysis showed that they were more enriched in p53-mediated apoptosis and anti-apoptosis. This may suggest that the *MUC16* mutation may activate the p53 pathway and DNA damage repair, leading to a better prognosis. Therefore, we speculate that the use of Roscovitine may be able to increase p53 expression to promote apoptosis in tumor cells, and perhaps also inhibit *NPY1R* expression, which may be a possible direction for patients with high *NPY1R* expression. Also, when examining the differences in CNVs between the wild-type group and the mutation group, we found that *ING2*, with its CNV gain and deletion, mRNA expression also changed. *ING2*, a member of the *ING* protein family, contains a highly conserved plant homeodomain and nuclear localization sequences[35,36]. In addition, *ING2* is involved in DNA damage repair. It is considered to be a tumor suppressor gene. The expression of *ING2* is decreased in several cancers including lung cancer, hepatocellular carcinoma, and breast cancer[37-39]. As a tumor suppressor gene, we found higher expression in the mutation group, suggesting that the high expression of *ING2* in the mutation group may indicate stronger DNA damage repair.

Therefore, we speculate that the *MUC16* mutation may activate the p53 pathway and DNA repair pathway on the one hand, and the immune microenvironment may also be involved on the other hand, with higher tumor killer cells and fewer tumor suppressor cells jointly constructing the tumor immune microenvironment of the mutation group. Perhaps, it is these characteristics exhibited by the mutation group that makes their prognosis better.

CONCLUSION

Using multi-omics data, we investigated possible mechanisms leading to a better prognosis of *MUC16* mutations from different aspects, and the results implied that the immune microenvironment and DNA repair are possible underlying mechanisms. More importantly, we also identified a gene – *NPY1R* – that was significantly differentially expressed in the *MUC16* mutation group and the *MUC16* wild-type group, and

also discovered a potential drug – Roscovitine – that inhibits *NPY1R* expression and may even improve the prognosis of gastric cancer patients.

ARTICLE HIGHLIGHTS

Research background

MUC16 is a frequently mutated gene in gastric cancer and the *MUC16* mutations seem to result in a better prognosis in gastric cancer. Unfortunately, the mechanism that leads to a better prognosis with *MUC16* mutations is less clear.

Research motivation

Among gastric cancer patients, *MUC16* mutations were associated with better prognosis; however, the mechanism of this is not well understood.

Research objectives

To explore in greater depth the underlying mechanisms as to why *MUC16* mutations lead to a better prognosis in gastric cancer patients.

Research methods

Based on gastric cancer data from The Cancer Genome Atlas (TCGA) and Gene Expression Omnibus (GEO), which were performed to explore the relationship between *MUC16* mutations and prognosis, Cox regression and random survival forest algorithms were applied to search for hub genes. Gene set enrichment analysis was used to elucidate the molecular mechanisms. Single sample gene set enrichment analysis and EpiDISH were used to assess immune cells infiltration, and ESTIMATE analyzed the tumor microenvironment.

Research results

Our study shows that *MUC16* mutations appear to activate the DNA repair and p53 pathways and act as an anti-tumor agent. We also identified a key gene, *NPY1R* (neuropeptide Y receptor Y1), with high expression of *NPY1R* predicting a poorer prognosis, which was confirmed in a separate GEO cohort. Further susceptibility analysis also revealed that *NPY1R* might be a potential drug target for gastric cancer. In analyzing the tumor microenvironment, we found that immune cells in the mutation group exhibited higher anti-tumor effects. In addition, the tumor mutation burden and cancer stem cells index were also higher in the mutation group.

Research conclusions

By analyzing the gastric cancer data from TCGA and GEO, we speculate that the *MUC16* mutation may activate the p53 pathway and DNA repair pathway on the one hand. On the other hand, the tumor microenvironment may be involved, with higher tumor killer cells and lower stromal scores together building the unique tumor microenvironment in the mutation group.

Research perspectives

In gastric cancer patients, *MUC16* mutations predict a better prognosis.

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