

CORRECTION

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# Correction to: *SNCA* correlates with immune infiltration and serves as a prognostic biomarker in lung adenocarcinoma

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**Correction:** *BMC Cancer* 22, 406 (2022)  
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Following publication of the original article [1], the authors identified an error in the order of the figures. The correct order is given below. The original article [1] has been corrected.

Figs. 1, 2, 3, 4, 5, 6, 7 and 8

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## Reference

1. Zhang X, Wu Z, Ma K. *SNCA* correlates with immune infiltration and serves as a prognostic biomarker in lung adenocarcinoma. *BMC Cancer*. 2022;22:406. <https://doi.org/10.1186/s12885-022-09289-7>.

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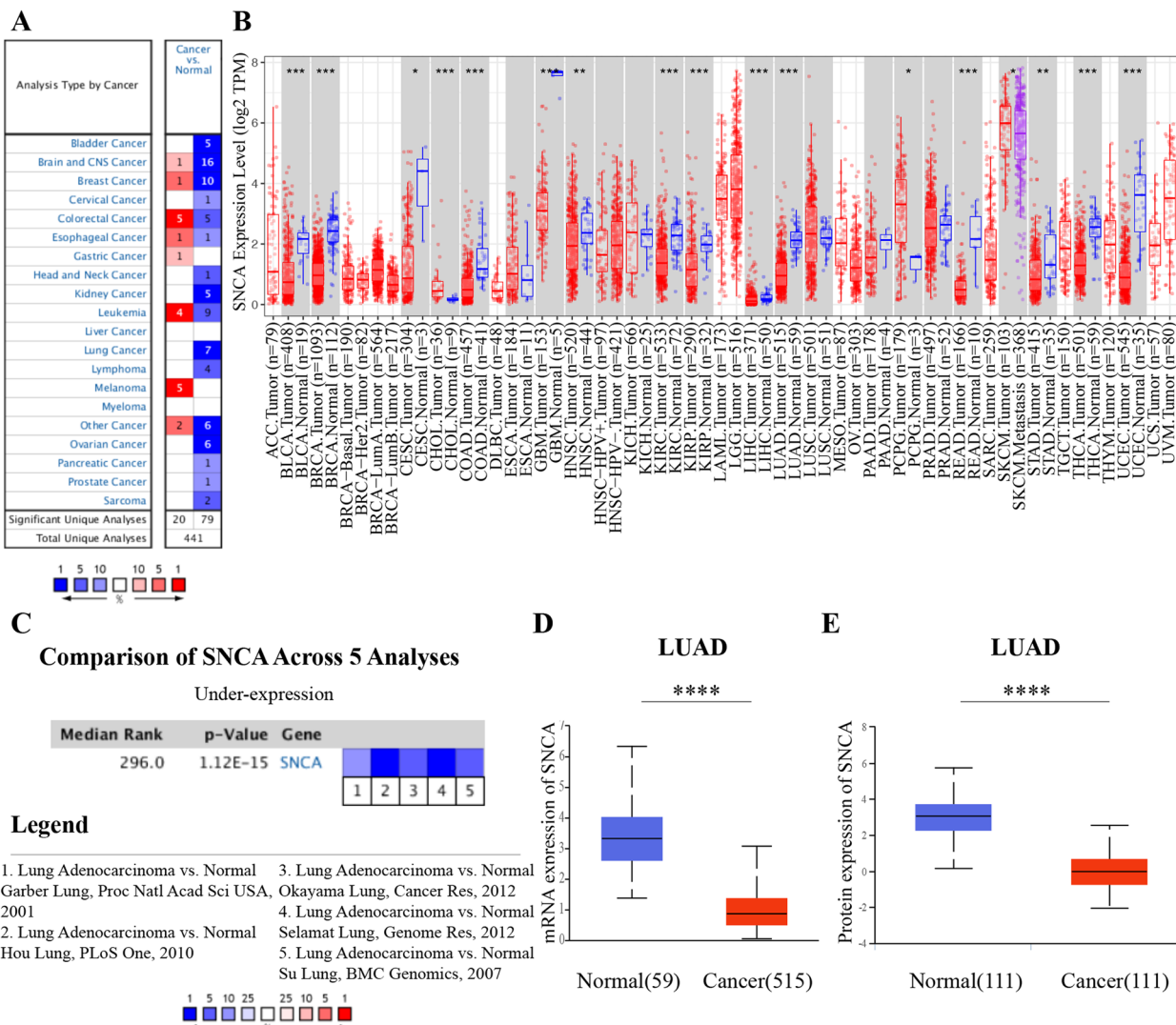
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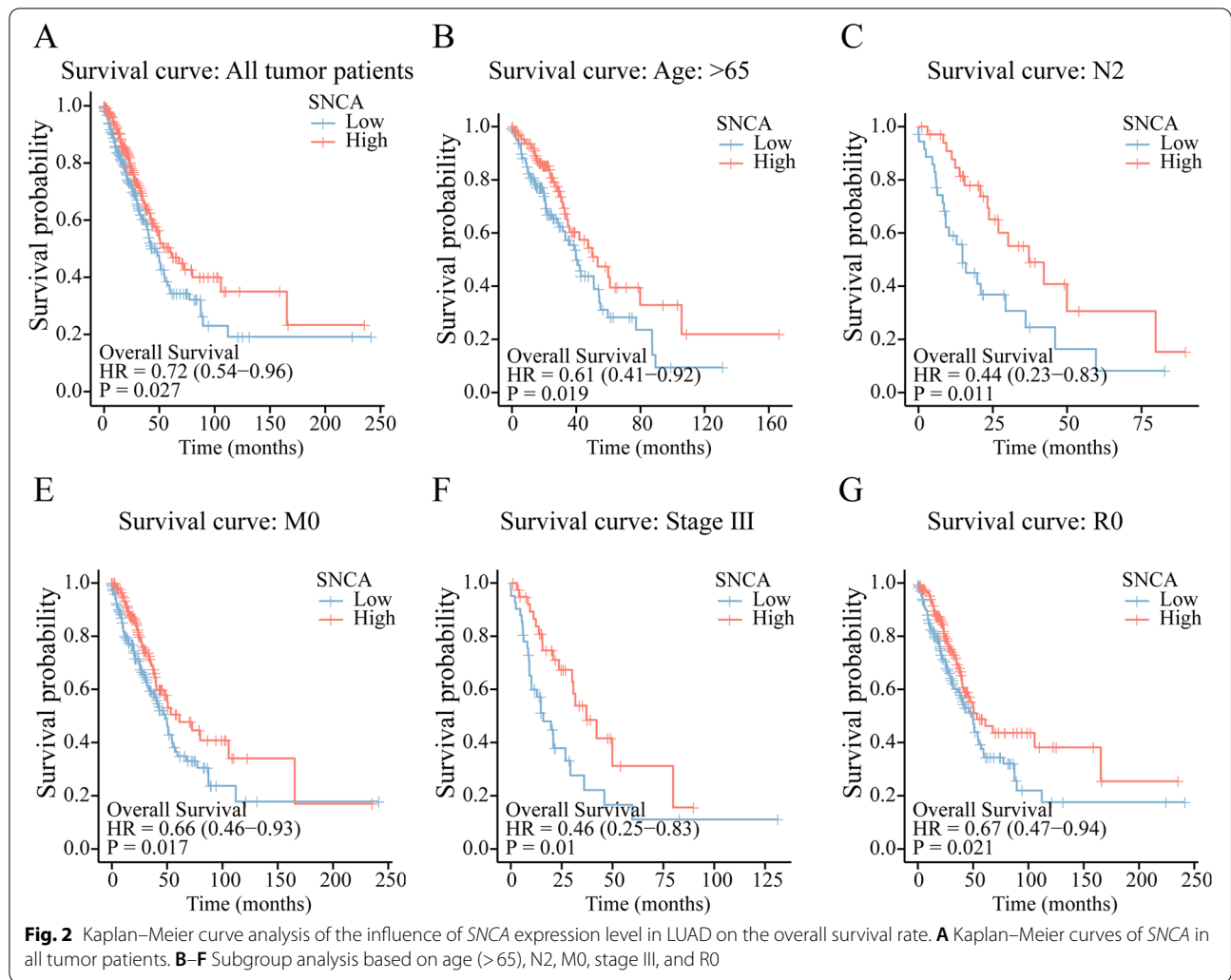
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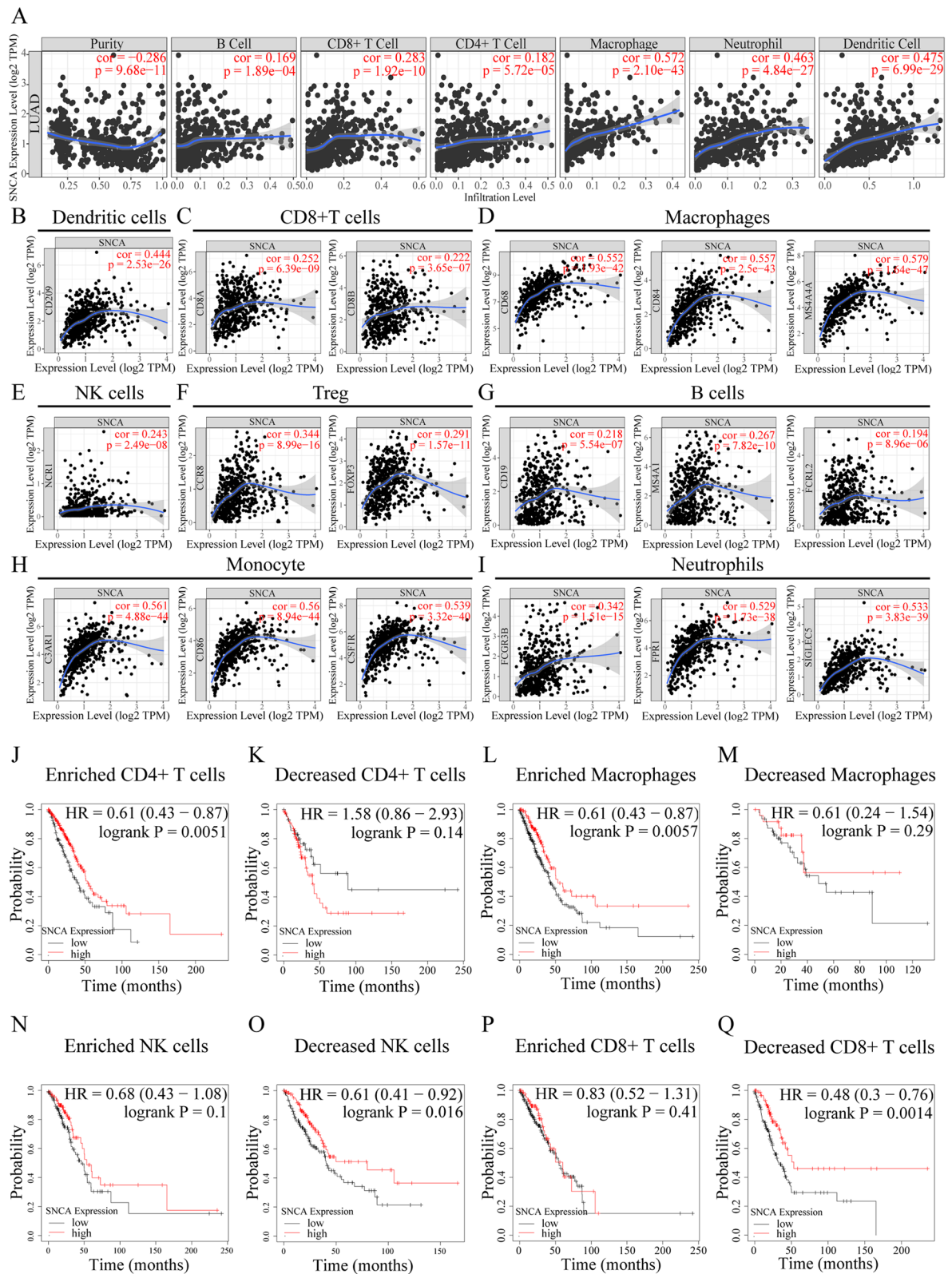


**Fig. 1** The expression of *SNCA* in different tumors was analyzed in OncoPrint and TIMER databases. **A** OncoPrint database was used to analyze the expression of *SNCA* gene in Pan-cancer species. Note: red represents upregulation of the target gene, while blue represents downregulation of the target gene. Threshold parameter: *p*-value is 0.01, fold change is 1.5. **B** The analysis of the expression level of *SNCA* in different tumors in TCGA through TIMER database. **C** Meta-analysis of *SNCA* expression was performed using five LUAD sequencing data sets through OncoPrint database. **D** UALCAN database analysis of the mRNA expression level of *SNCA* in LUAD (\*\*\*\* *P* < 0.0001). **E** According to the analysis of UALCAN database, the protein expression level of *SNCA* in LUAD (\*\*\*\* *P* < 0.0001)



(See figure on next page.)

**Fig. 3** The correlation analysis between SNCA expression and immune infiltration, and the Kaplan–Meier survival curves of SNCA expression based on different immune cell subsets in LUAD. **A** The correlation between SNCA expression and the level of immune infiltration of B cells, CD8+ T cells, CD4+ T cells, macrophages, neutrophils, and dendritic cells in LUAD. **B–I** Correlation analysis of SNCA expression and the markers of dendritic cells, CD8+ T cells, macrophages, NK cells, regulatory T cells, neutrophils, B cells, monocytes, and neutrophils in LUAD. **J–Q** Relationship between SNCA expression and prognosis of LUAD in different immune cell subgroups (enriched / decreased CD4+ T cells, enriched / decreased macrophages, enriched / decreased NK cells, enriched / decreased CD8+ T cells).  $P < 0.05$  was considered statistically significant

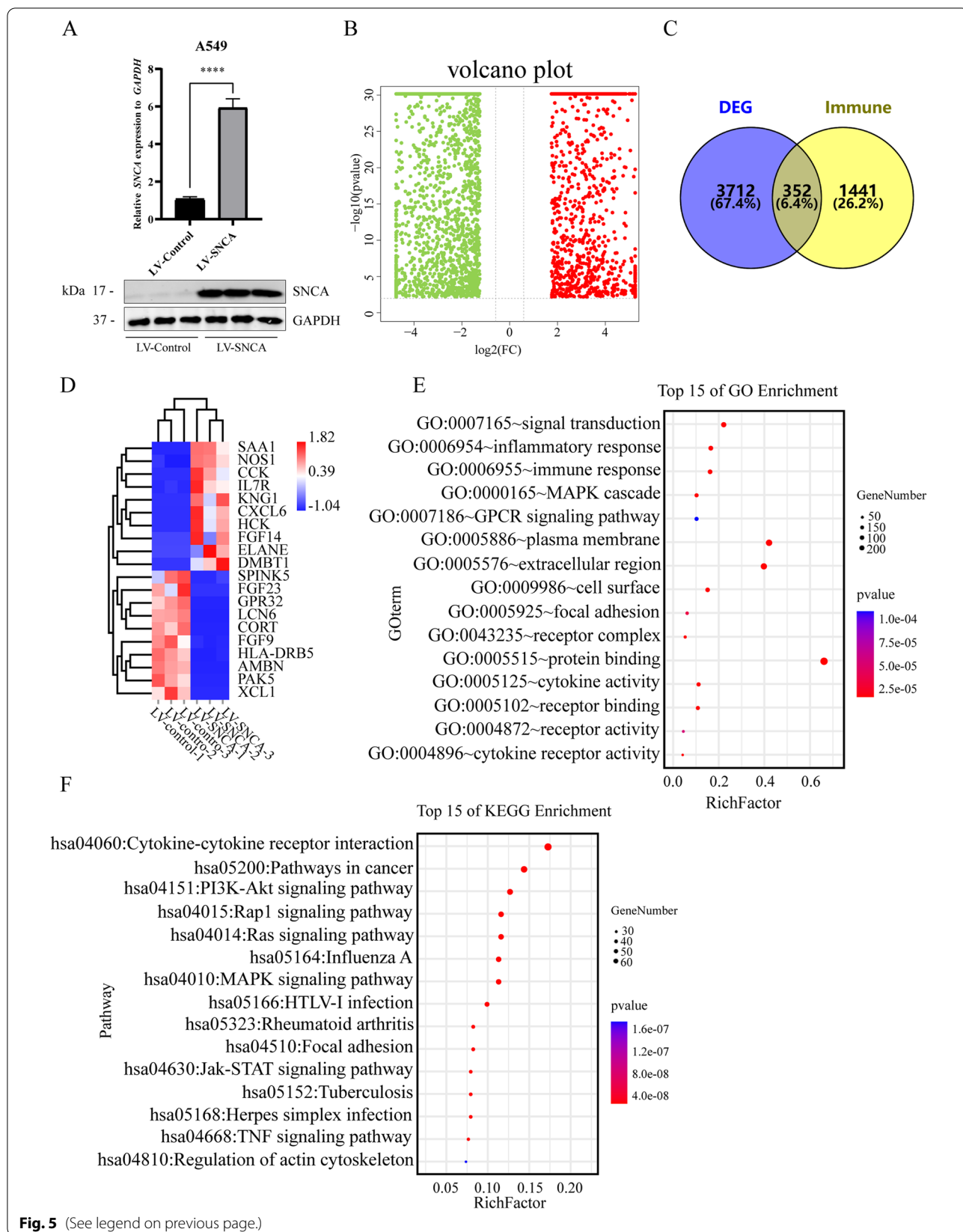


**Fig. 3** (See legend on previous page.)

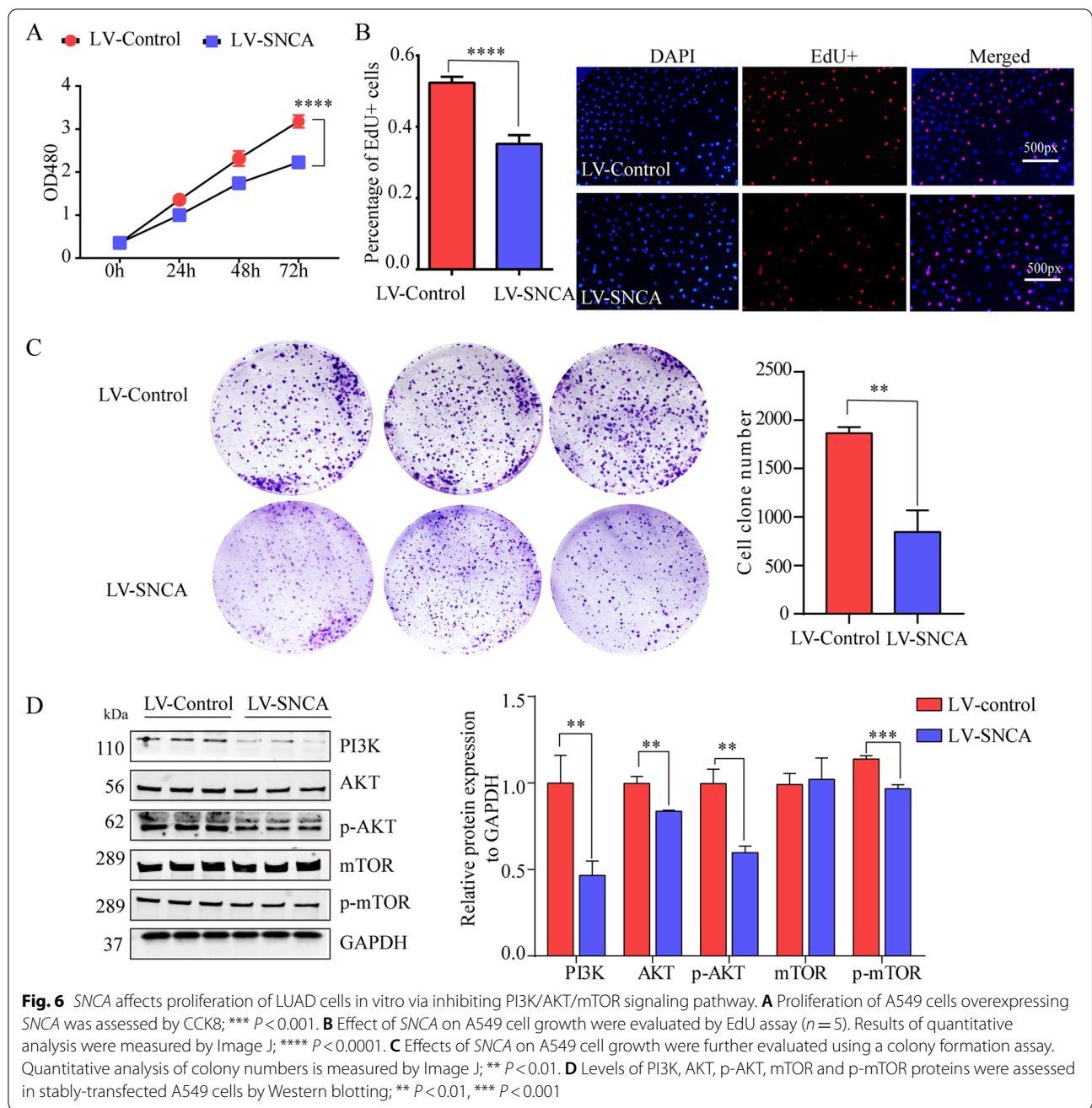


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**Fig. 5** Genes related to immune regulation by *SNCA* in LUAD. **A** mRNA and protein levels of *SNCA* in the A549 cell line overexpressing *SNCA* were detected. **B** Volcanic map distribution of DEGs. Red dots are upregulated genes, and green dots are downregulated genes. **C** *SNCA*-regulated immune-related DEGs were obtained by Wayne analysis between the obtained DEGs and immune-related genes from Immport Resource. **D** Heat map showing the top 20 upregulated and top 20 downregulated immune-related DEGs. **E** GO analysis of immune-related DEGs, including five BP items, CC items, and MF items from top to bottom. **F** KEGG analysis of the top 15 immune-related DEGs (\*\*\*\*  $P < 0.0001$ )



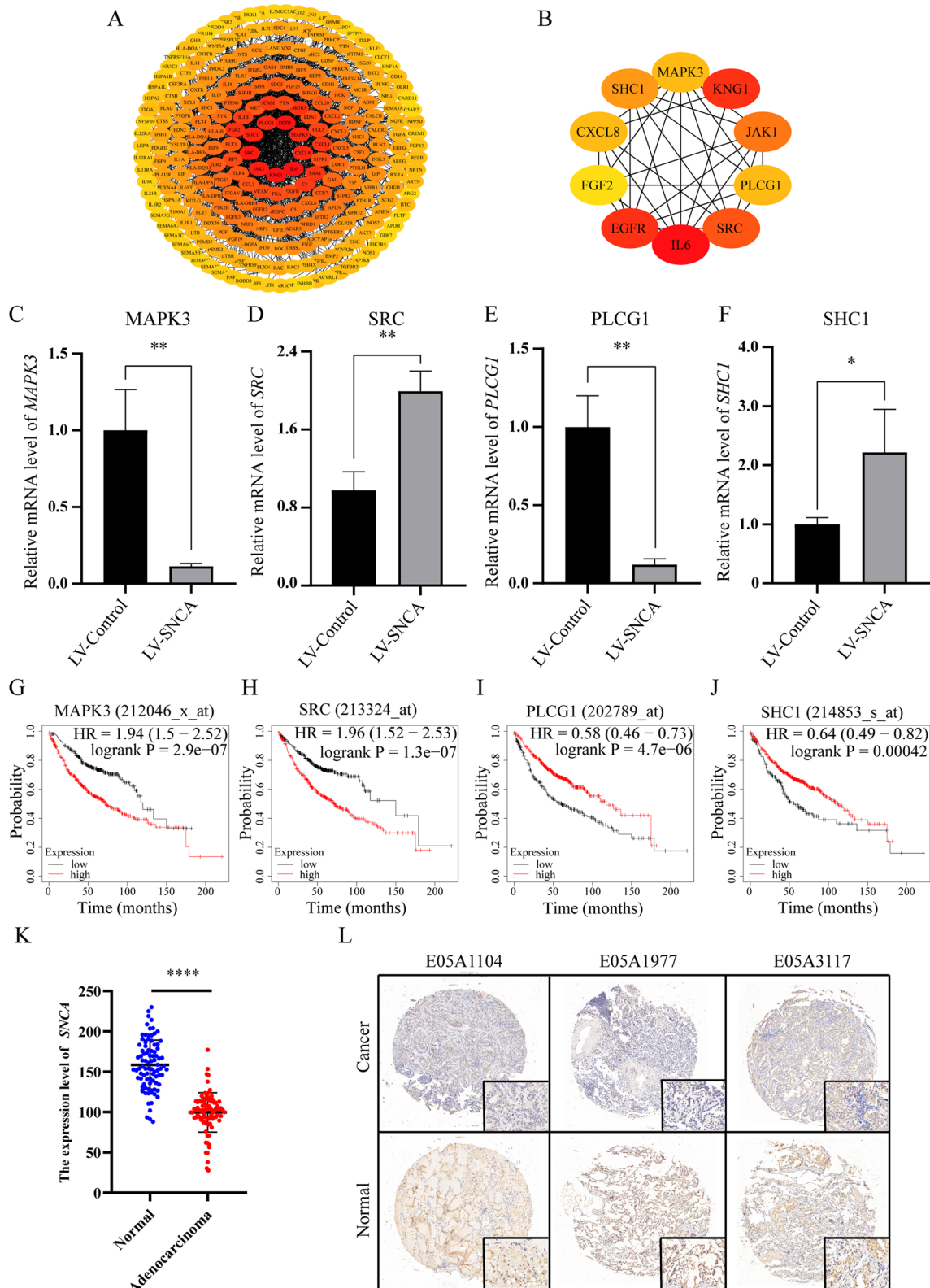
**Fig. 5** (See legend on previous page.)



**Fig. 6** SNCA affects proliferation of LUAD cells in vitro via inhibiting PI3K/AKT/mTOR signaling pathway. **A** Proliferation of A549 cells overexpressing SNCA was assessed by CCK8; \*\*\*  $P < 0.001$ . **B** Effect of SNCA on A549 cell growth were evaluated by EdU assay ( $n = 5$ ). Results of quantitative analysis were measured by Image J; \*\*\*\*  $P < 0.0001$ . **C** Effects of SNCA on A549 cell growth were further evaluated using a colony formation assay. Quantitative analysis of colony numbers is measured by Image J; \*\*  $P < 0.01$ . **D** Levels of PI3K, AKT, p-AKT, mTOR and p-mTOR proteins were assessed in stably-transfected A549 cells by Western blotting; \*\*  $P < 0.01$ , \*\*\*  $P < 0.001$

(See figure on next page.)

**Fig. 7** The screening of the key genes and analysis of SNCA in LUAD clinical samples. **A** Protein interaction network constructed by immune-related DEGs through Cytoscape. The orange node is the node with high degree, and the yellow node is the node with low degree. **B** The interaction network diagram of 10 node genes with the highest degree screened by Cytohubba application in Cytoscape. **C–F** qPCR method was used to verify the expression of four central genes in SNCA-overexpressing A549 cell line. **G–J** Kaplan–Meier curve was used to analyze the prognosis of four central genes in LUAD. **K** Statistical analysis of SNCA immunostaining score in clinical samples, \*\*\*\*  $P < 0.0001$ . **L** Immunohistochemical images of SNCA in clinical samples



**Fig. 7** (See legend on previous page.)



