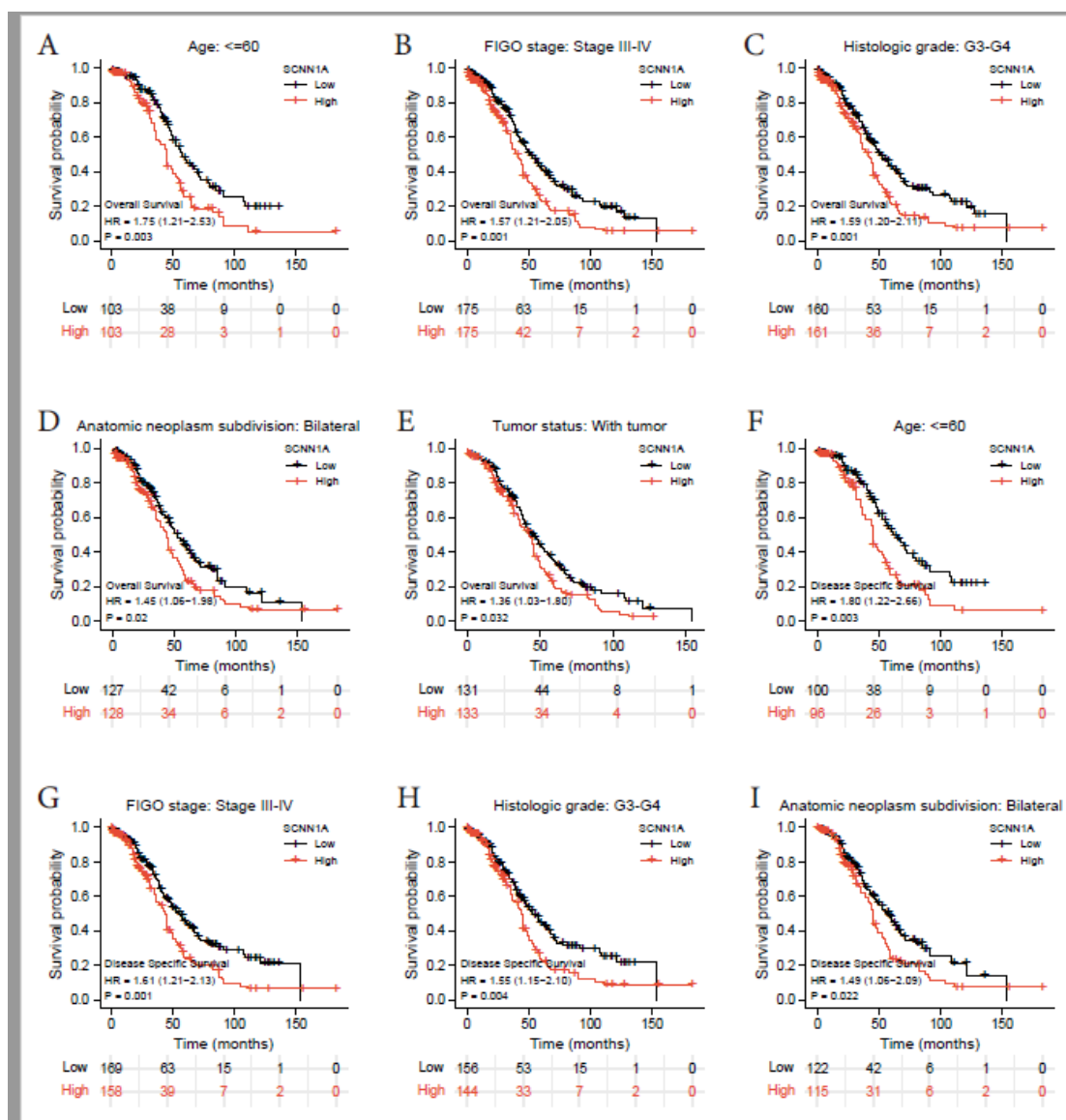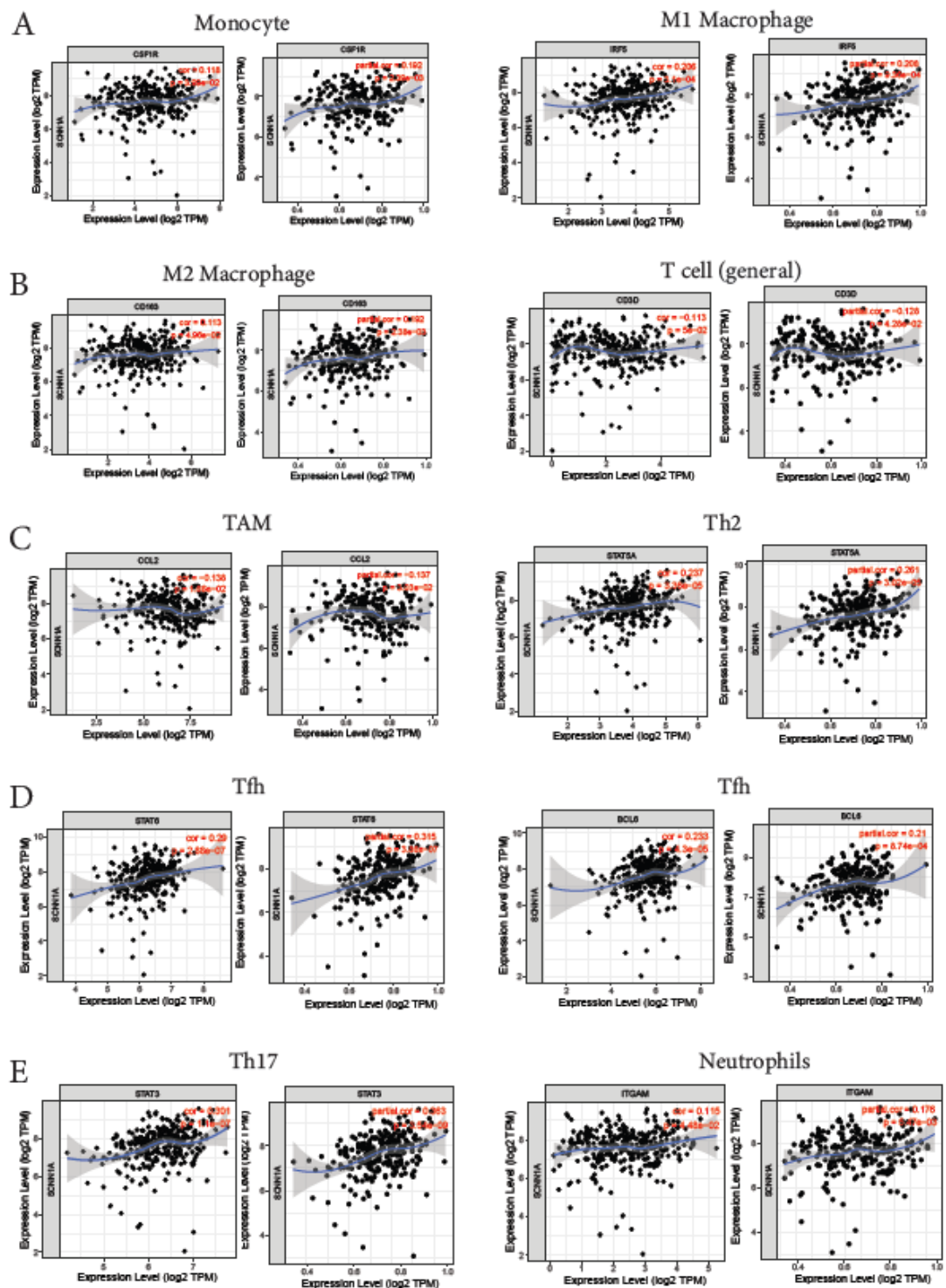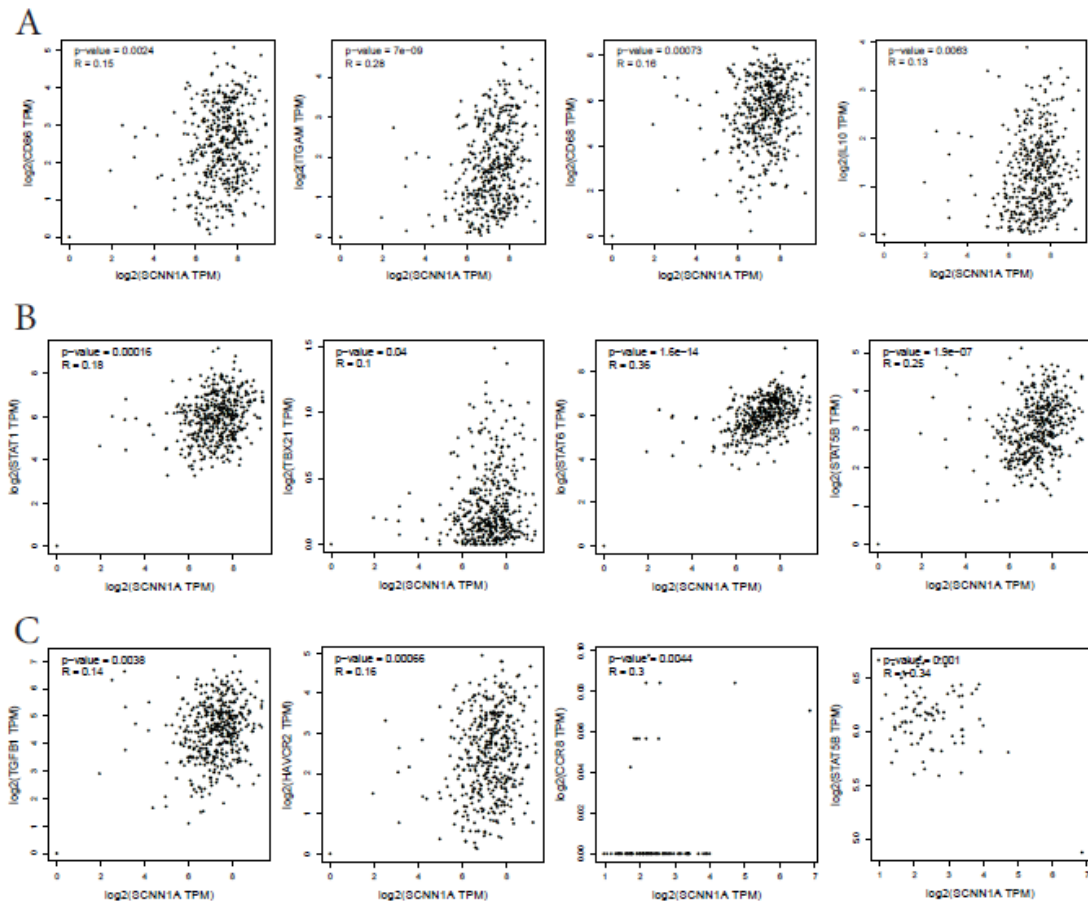## Supplementary Figures

Supplementary Figure 1 Kaplan-Meier survival curves of high- and low- *SCNN1A* expression

in different subgroups of ovarian cancer patients.

(A-E) Overall survival curves of age(≤60), stage III-IV, grade G3-G4, anatomic neoplasm

subdivision(bilateral), tumor status(with tumor) subgroups between *SCNN1A*-high ang -low

patients with OV. (F-I) Disease specific survival curves of age(≤60), stage III-IV, grade G3-G4,

anatomic neoplasm subdivision(bilateral) subgroups between *SCNN1A*-high ang -low patients

with OV.

Supplementary Figure 2 Correlation analysis between *SCNN1A* expression and immunological

marker set in ovarian cancer. (A-E) Scatterplots of correlations between *SCNN1A* expression

and gene markers of immune cells. Markers include *CSF1R*(*CD115*) of monocyte, *IRF5* of M1

Macrophage, *CD163* of M2 Macrophage, *CD3D* of T cell(general), *CCL2* of TAM, *STAT5A* of

Th2, *STAT6* and *BCL6* of Tfh, *STAT3* of Th17, *ITGAM*(*CD11b*) of neutrophils. TAM, tumor-

associated-macrophages. *P* < 0.05 is considered as significant.

Supplementary Figure 3

Correlation analysis between *SCNN1A* and marker genes of immune cells in GEPIA. Markers

include *CD86* of monocyte, *ITGAM*(*CD11b*) of neutrophils, *CD68* and *IL-10* of TAM, *STAT1* and

TBX21(*T-bet*) of Th1, *STAT6* of Th2, CCR8, *STAT5B* and *TGF-β*(*TGFB1*) of Treg, TIM-

3(HAVCR2) of T cell exhaustion. TAM, tumor-associated-macrophages. *P* < 0.05 is considered

as significant.