

Figure S1.

Figure S1. Diagram of analysis.

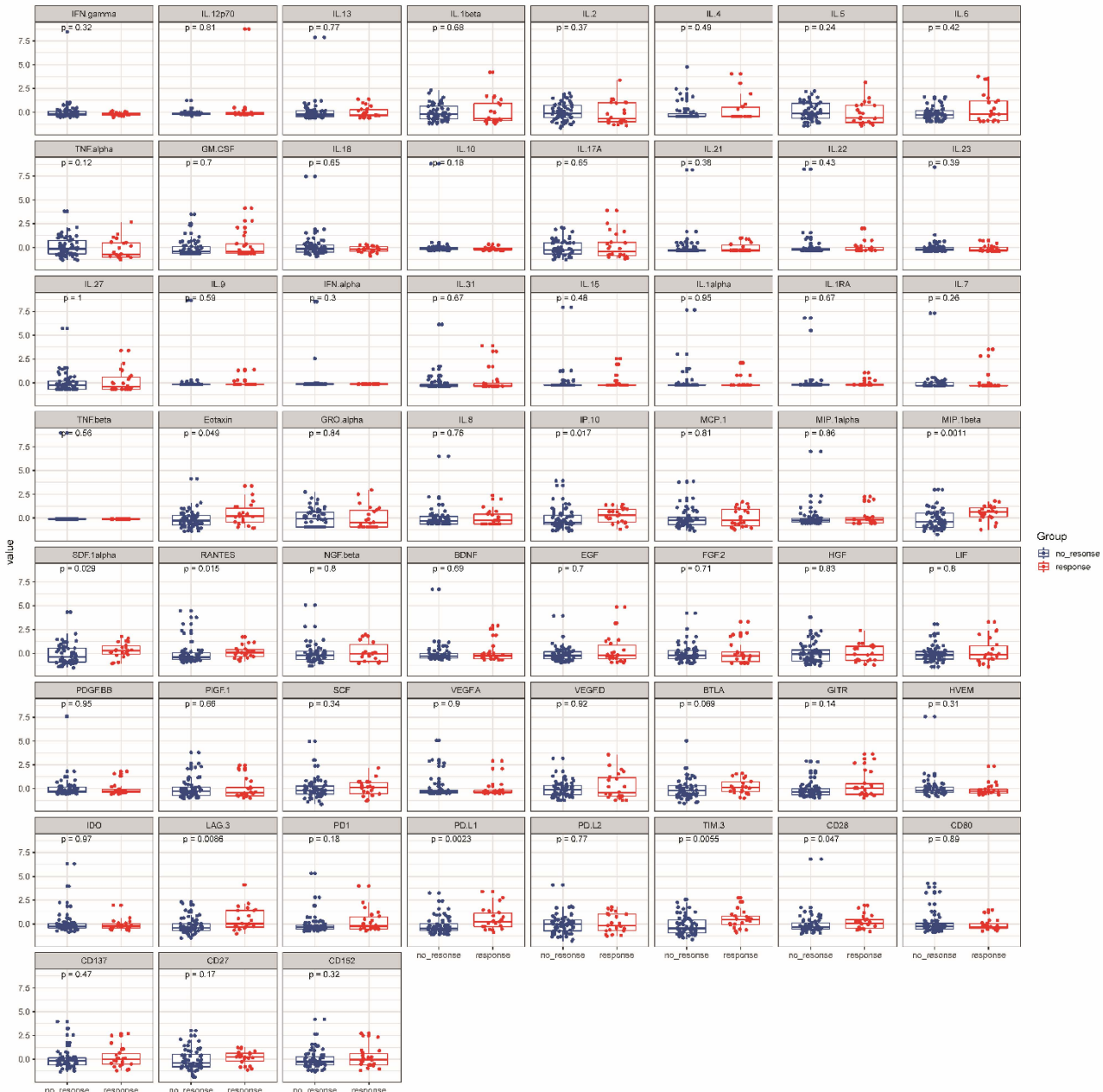


Figure S2.

Figure S2. The expression levels (standardized z-scores) of serological cytokines in the discovery cohort.

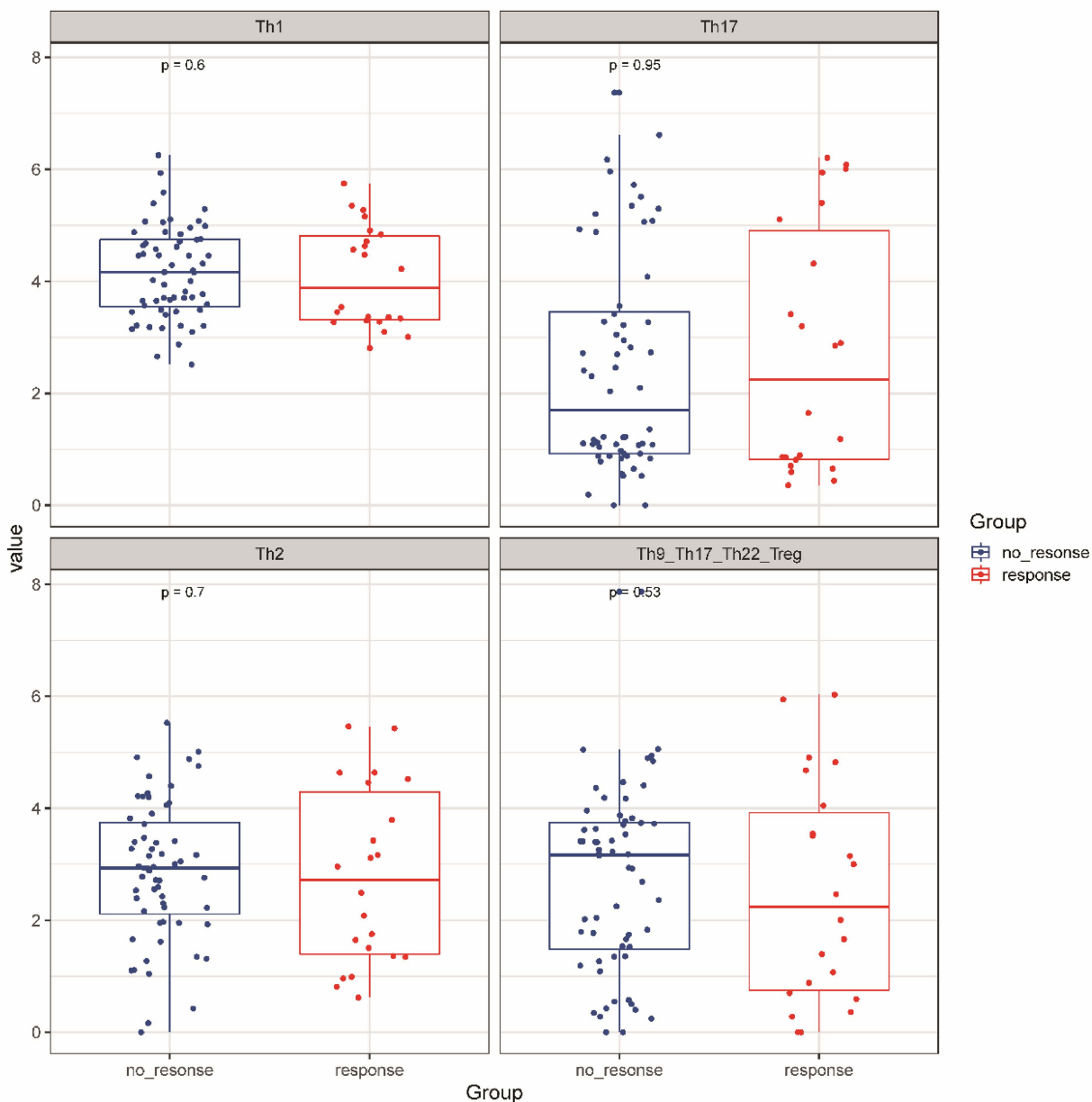
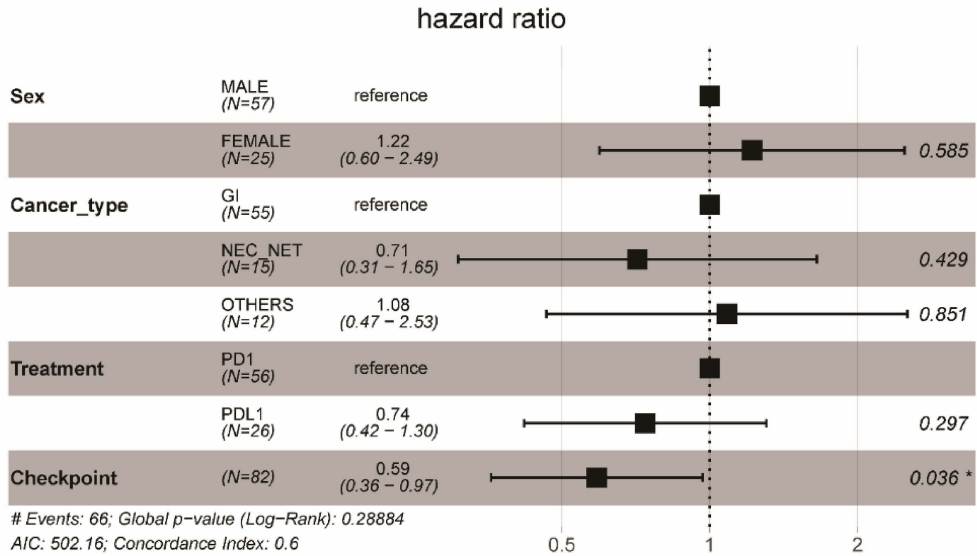


Figure S3.

Figure S3. The expression levels of serological signatures (Th1, Th2, Th17 and Th9/Th17/Th22/Treg cytokines) in the discovery cohort.

A.



B.

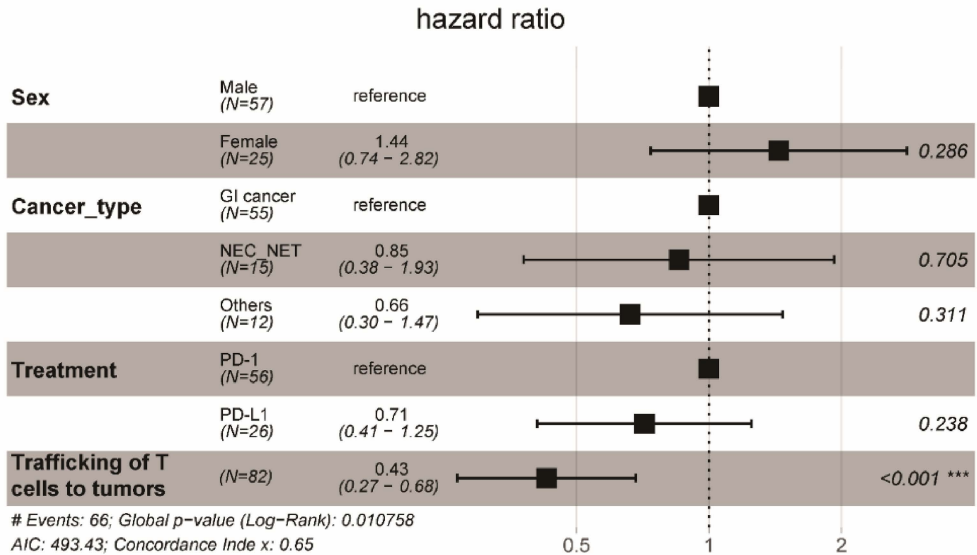


Figure S4

Figure S4. Survival analysis of cytokine signatures in the discovery cohort.

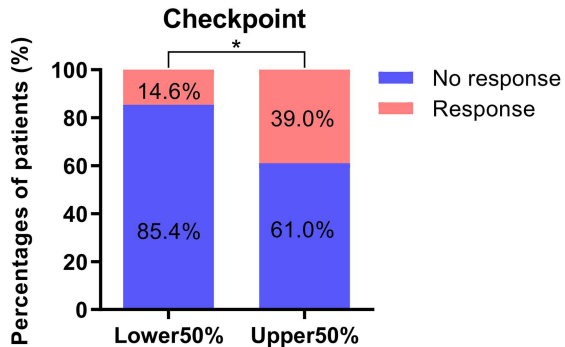
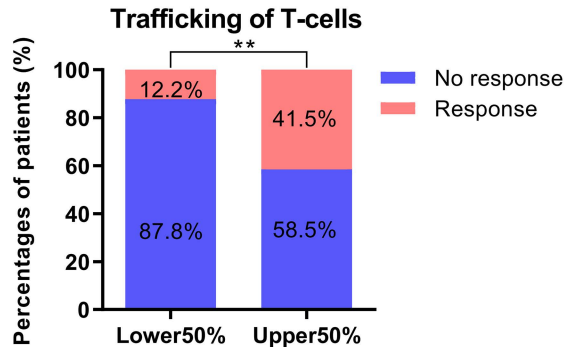
A.**B.****Figure S5**

Figure S5. Higher signature levels correlated with increased response rate in the discovery cohort. A,B. Response rates (CR/PR) in higher versus lower checkpoint signature (A) or trafficking of T-cells signature (B). Median value of each signature was used as the cut point.



Figure S6.

Figure S6. The expression levels (standardized z-scores) of serological cytokines in the validation cohort.

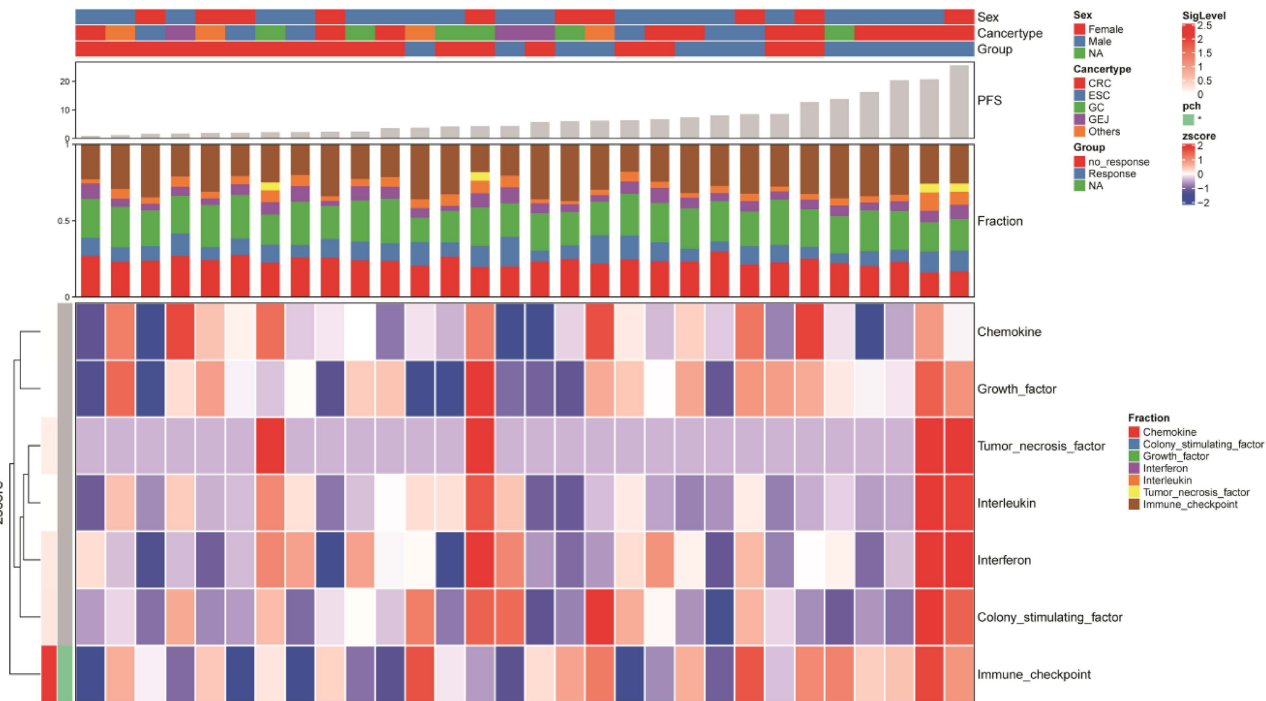


Figure S7

Figure S7. Classification and exploration of cytokine clusters in the validation cohort.

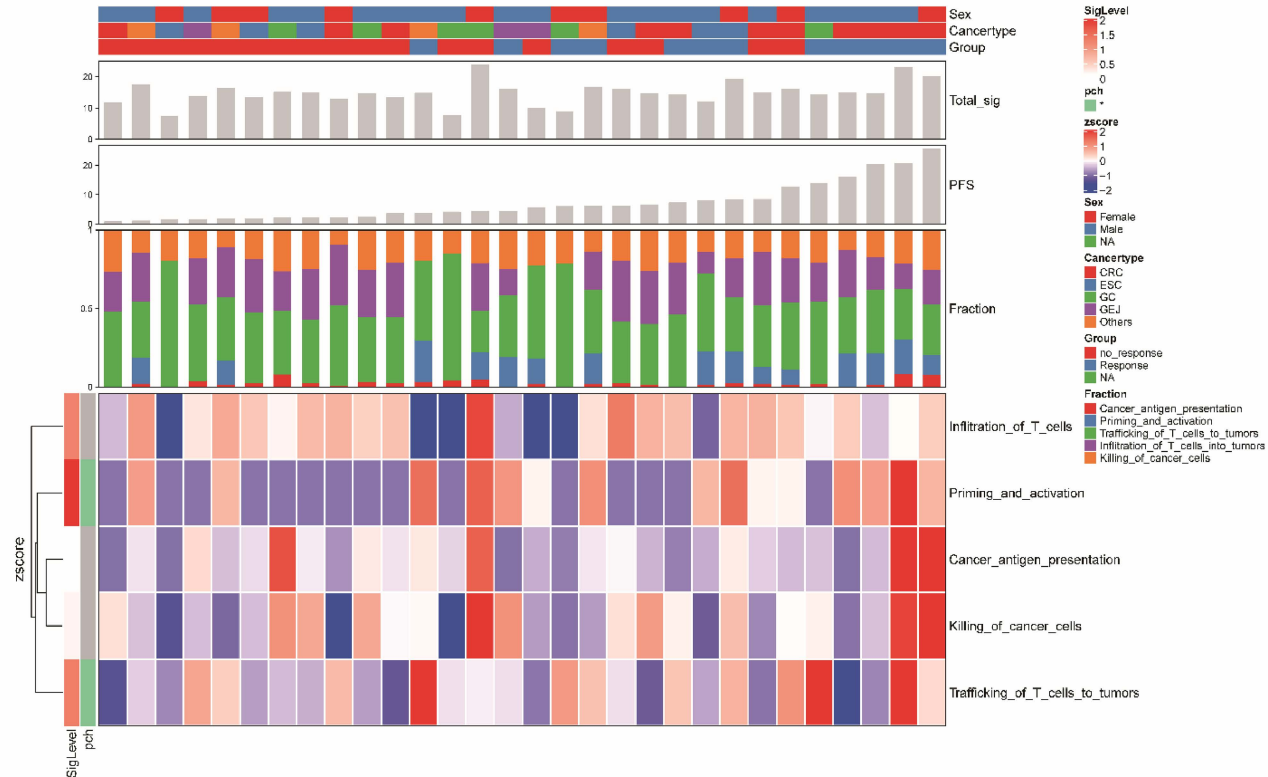


Figure S8

Figure S8. Functional characterization of cytokine signatures in the validation cohort.