Examining resistance to immunotherapy in ovarian cancer

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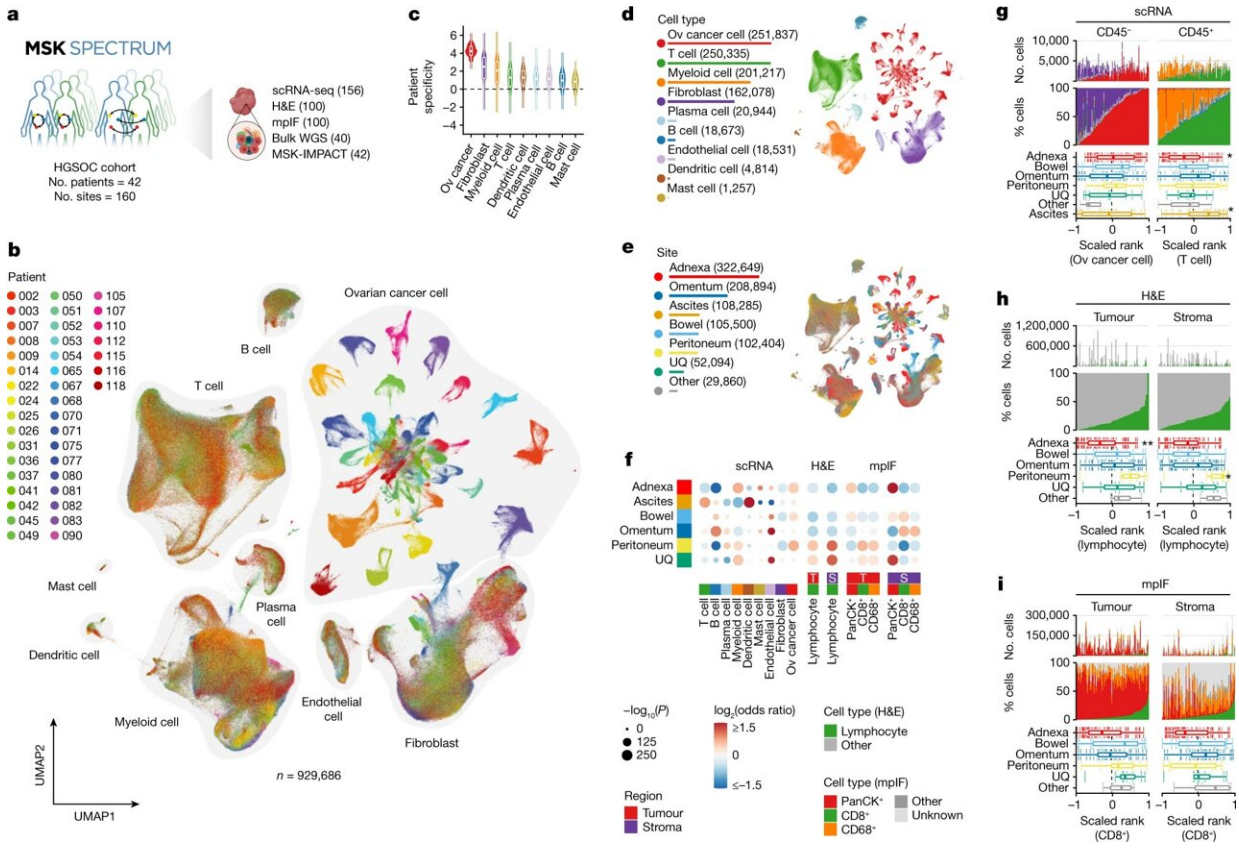

TME of HGSOC at single-cell resolution. **a**, Overview of the MSK SPECTRUM cohort and specimen collection workflow. **b**, UMAP plot of cells profiled by scRNA-seq colored by patient. Cell types are highlighted with gray outlines. **c**, Patient specificity for each cell type. Ov, ovarian. **d**, Number of cells identified per cell type next to a UMAP plot with cells colored by cell type. **e**, Number of cells profiled per tumor site next to a UMAP plot with cells colored by tumor site. UQ, upper quadrant. **f**, Site-specific enrichment of cell type composition in scRNA-seq, H&E and mpIF data fitted using a GLM. GLMs for H&E and mpIF

data were separated by tumor (T) and stroma (S) regions. The color gradient indicates the $\log_2$-transformed odds ratio (red, enrichment; blue, depletion), and sizes indicate the Bonferroni-corrected $-\log_{10}(P$ value). **g**, Cell type composition based on scRNA-seq data for $CD45^-$ and $CD45^+$ samples. Upper panels, absolute and relative cell type numbers; lower panels, box plot distributions of sample ranks with respect to tumor site. **h**, Cell type composition based on H&E with lymphocyte ranks in tumor and stroma. Panels are analogous to those in **g**. **i**, Cell type composition based on mpIF with $CD8^+$ T cell ranks in tumor and stroma. Panels are analogous to those in **g**. For **c** and **g–i**, violin plots and box plots are shown as the median, top and bottom quartiles; whiskers correspond to 1.5× interquartile range (IQR). *P