MedGenome's genomics solutions for precision medicine
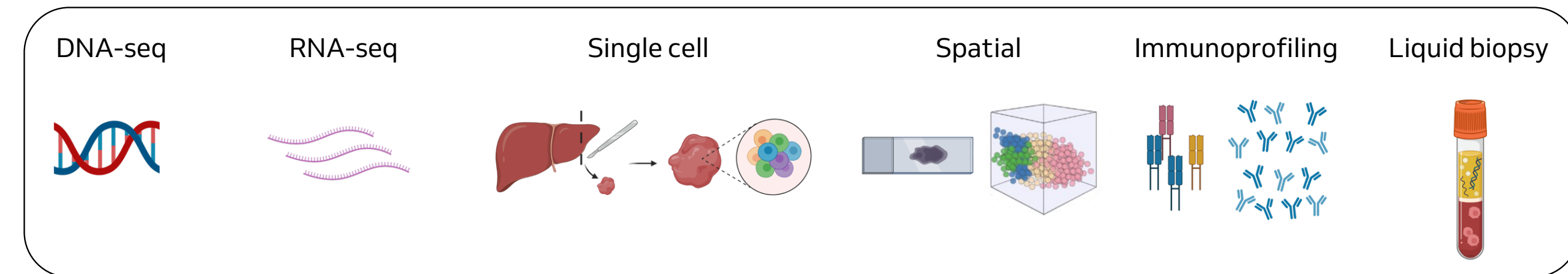
Kushal Suryamohan[1] , Ravi Gupta[2] , Marco Corbo[1] , Ramesh Menon[2], Megha Muraleedharan[1] , Chaitanya E. Ramesh[1], Harsha Gowda[1] , Hiranjith G.H[1] , Vedam L. Ramprasad[2] , Somasekar Seshagiri[1]

[1]MedGenome Inc., Foster City, CA; [2]MedGenome Labs Ltd., Bangalore, India

About us
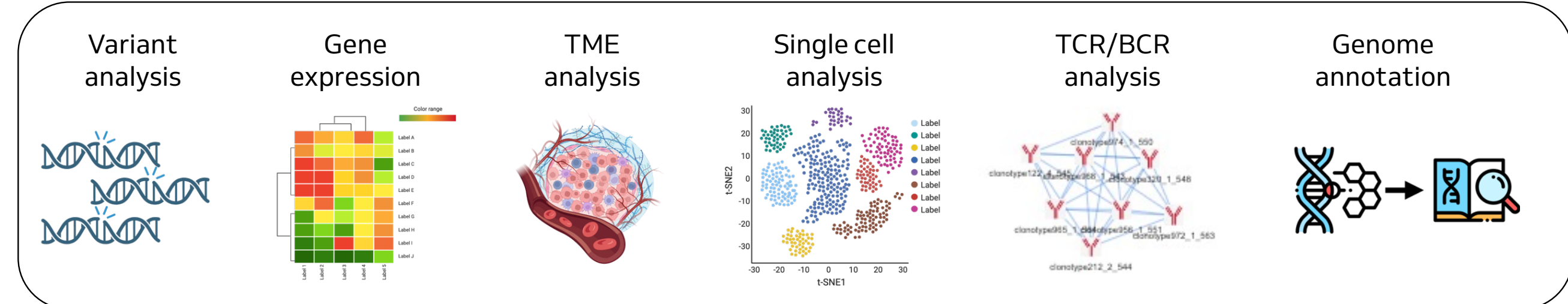
- MedGenome is a leading provider of sequencing and bioinformatics solutions.
- Comprehensive solutions for genome, exome transcriptome and single cell sequencing.
- State-of-the-art laboratories in the US, India, Singapore and Africa with expertise in handling diverse sample types.
- Proprietary technologies including VarMiner, an AI-enabled variant interpretation software, and OncoPeptTUME, an algorithm to classify tumors amenable for immunotherapy.
- Ongoing collaboration with over 5,000 hospitals and clinicians across India and South Asia on multiple genomics projects.
- Founding member of the GenomeAsia 100K consortium to sequence and catalog novel genetic risk

Comprehensive single cell solutions

Analyze data from fresh, frozen or FFPE samples or cryopreserved cells and nuclei. Different data modalities including 3' and 5' gene expression, multiome, CITE-seq and VDJ expression profiling. MedGenome's user-friendly single cell browser allows researchers to easily explore the results and perform tertiary data analysis as well as compare against publicly available single cell datasets.`
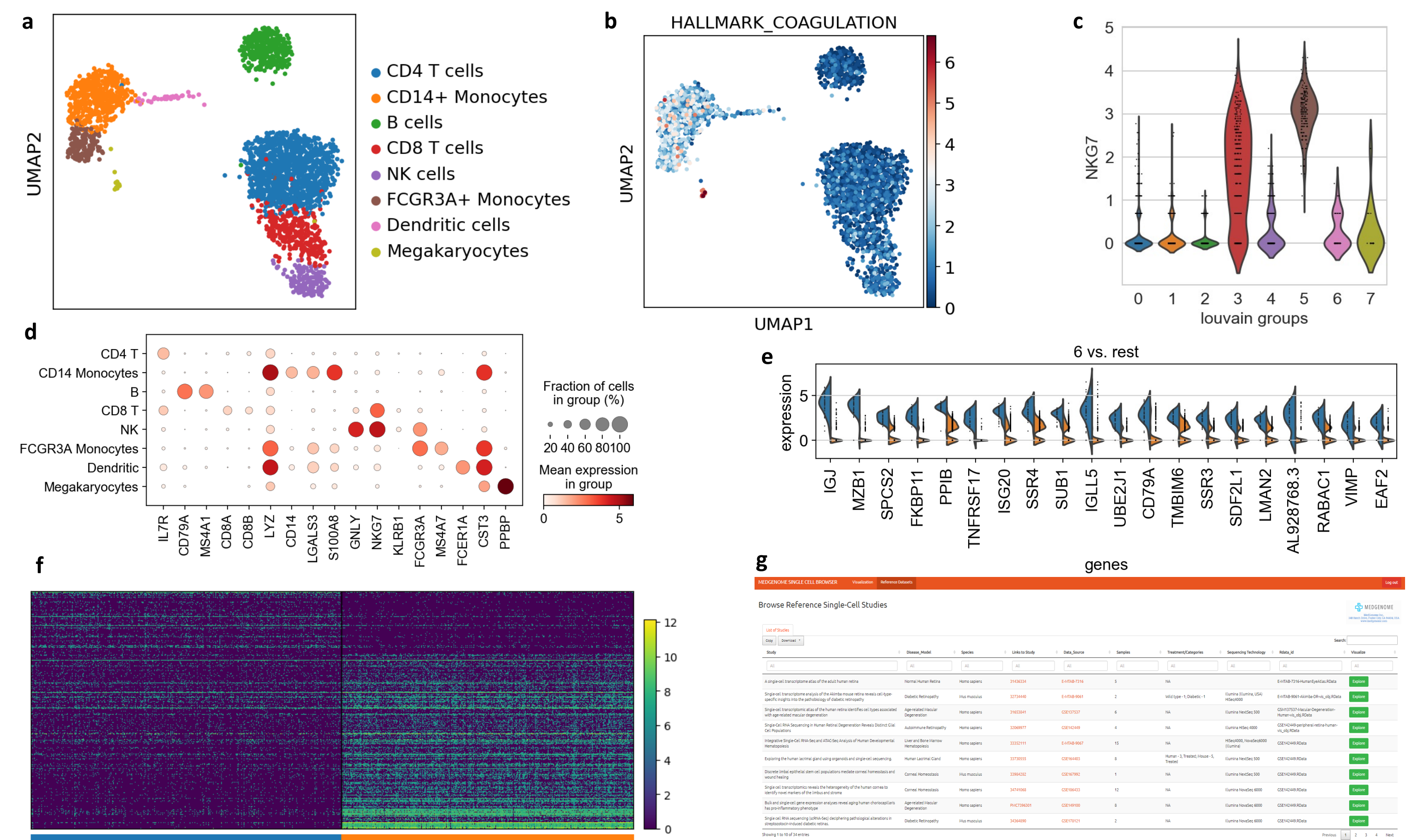
ene expression data annotated by cell type, **b**) UMAP plot showing cells expressing
ed genes, **c**) violin plot showing NKG7 expression in each annotated cell type, **d**)
 by cell type/cluster, **e**) Stacked violin plot comparing expression of marker genes
 emaining clusters, **f**) heatmap of differentially expressed genes between conditions
 wing curated repository of publicly available single cell data.

Immune-seq solutions

 iling bioinformatics workflow generates a comprehensive report including
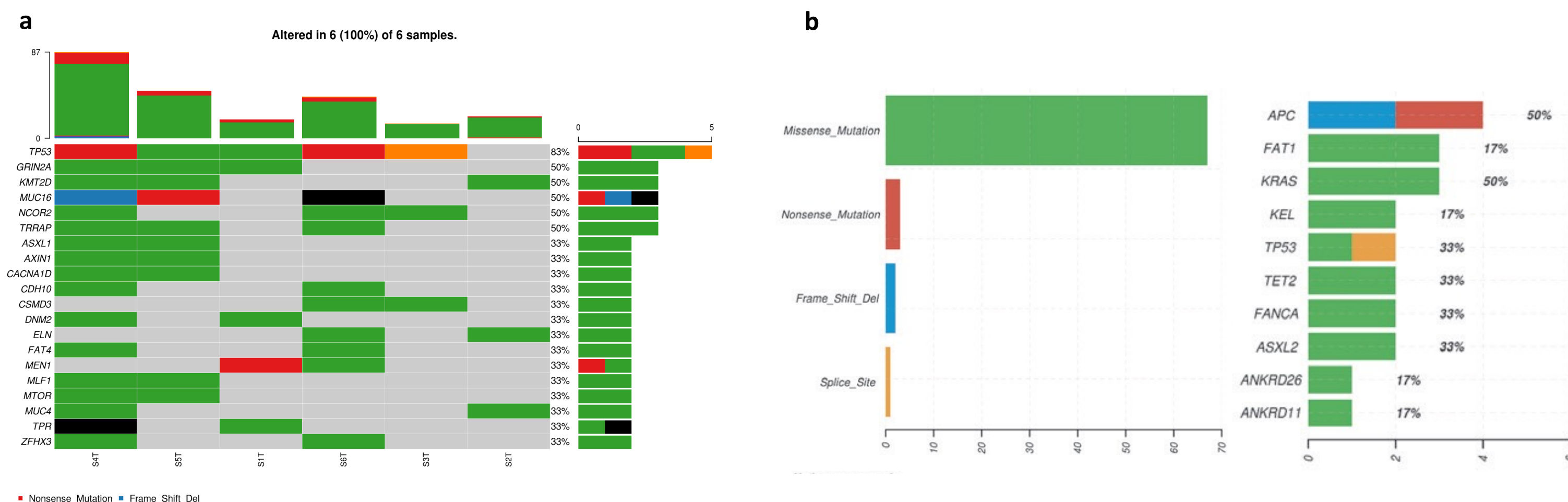 nd light chain antibody sequences and the corresponding clonotype diversity

Figure 2: Example figures from our report. **a)** Oncoplot showing most frequently mutated genes (rows) in each sample (columns) and **b)** Summary plots showing variant classification and top 10 mutated genes.

Figure 5: Plots showing results from single cell BCR/TCR data analysis; **a)** clonotype phylogenetic tree; **b)** Circos plot showing TCR V-J gene usage; **c)** multiple sequence alignment of selected clonotypes
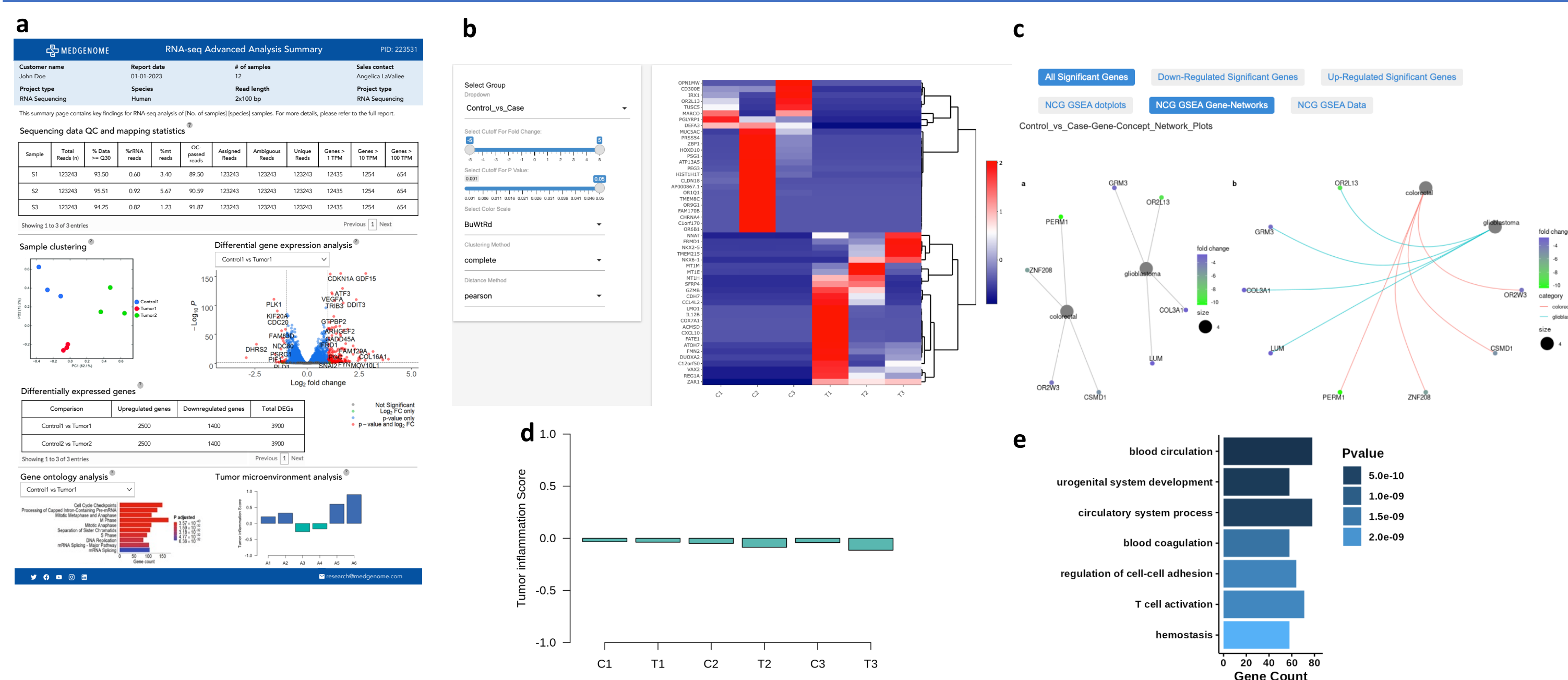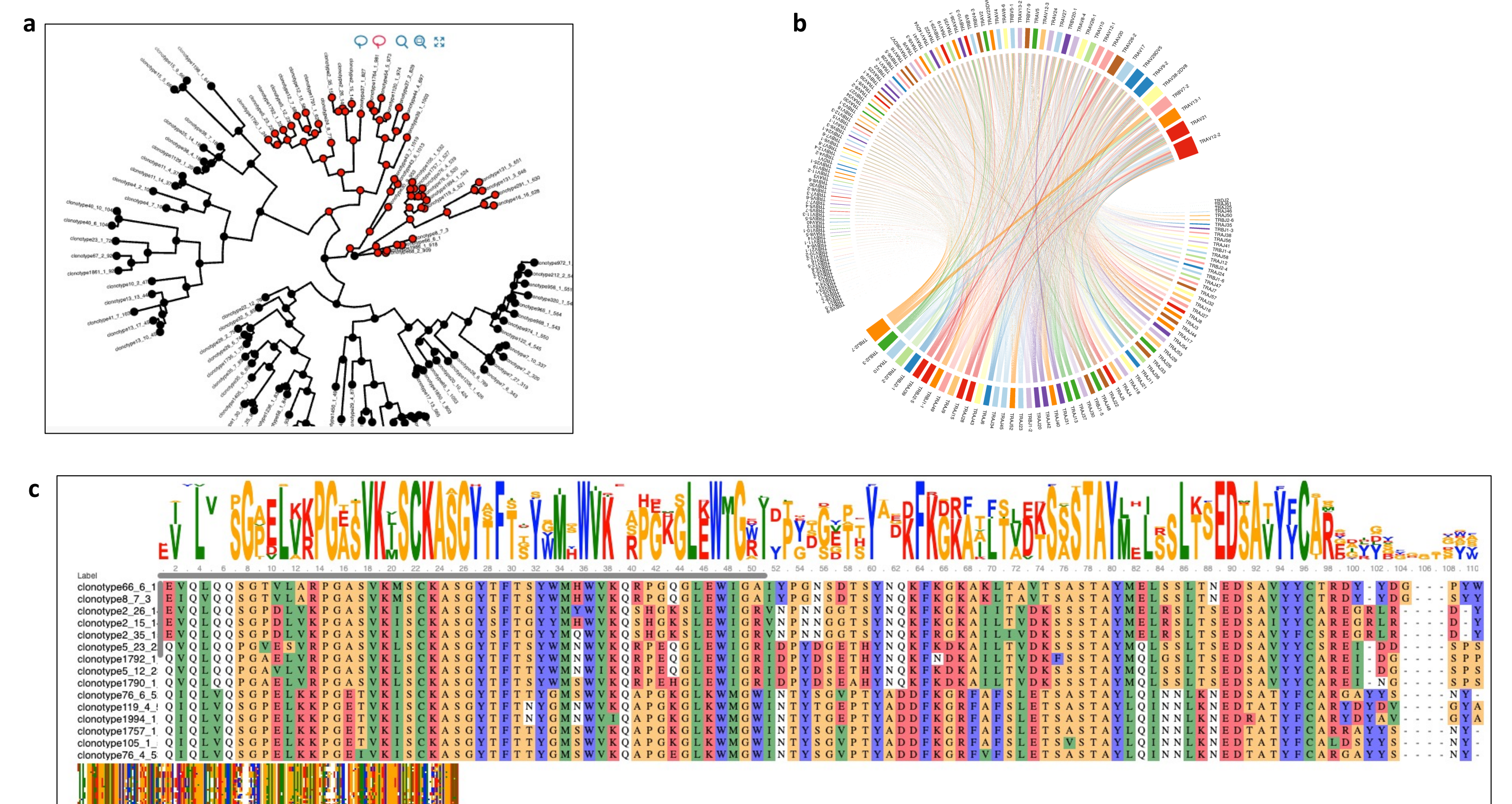
RNA sequencing

Figure 3: Example figures from an interactive MAnGO RNA-seq report. **a)** Summary report page showing key statistics and results including sample clustering, volcano plot of differentially expressed genes, pathway analysis and tumor microenvironment analysis using our proprietary OncoPeptTUME algorithm, **b)** Interactive heatmap to visualize differentially expressed genes between groups, **c)** network diagrams, **d)** Bar plot showing OncoPeptTUME scores for each sample, **e)** Bar plot showing differentially enriched pathways

Immuno-oncology solutions

OncoPeptTUME is a patented algorithm that uses bulk RNA-seq data to **a)** produce a cell-type specific immune score to quantitate the relative proportion of immune cell types present in the complex tumor microenvironment, **b)** assign immunogenicity (via immune score) of tumors and **c)** define immune signatures of different samples.
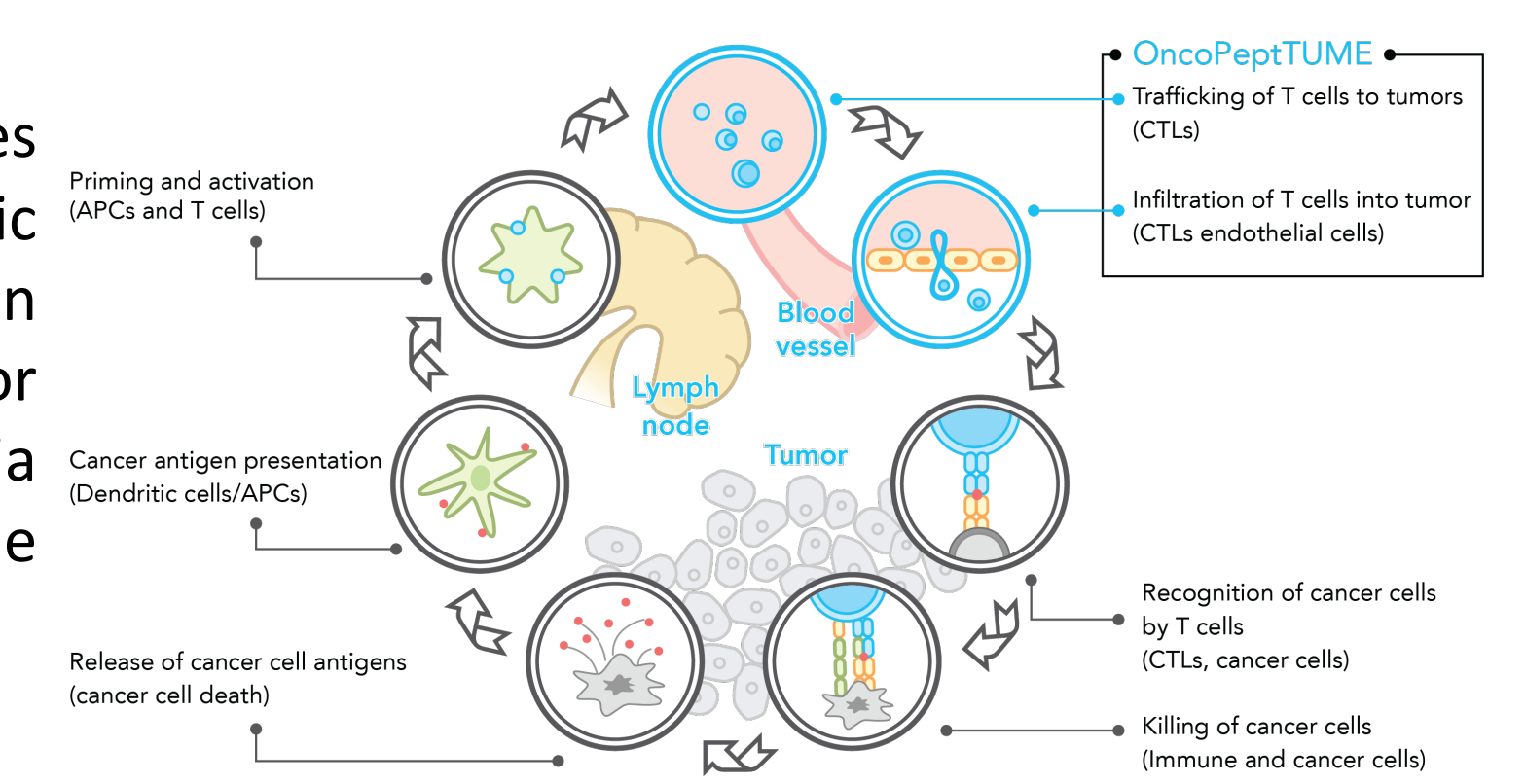

Figure 6: OncoPeptTUME provides critical insights into the role of the tumor microenvironment at different stages of the cancer immunity cycle

Contact us

MedGenome is committed to fast turnaround times to enable researchers to push the frontiers of precision medicine. Let our world class team of lab and bioinformatics scientists support your research needs in basic and early discovery research.

For enquiries, contact: research@medgenome.com