

Figure S1. (A) Gene mutation status of patients with tuberous sclerosis complex-associated renal angiomyolipoma. (B) The 3D spatial distribution of all patients based on plasma proteomics. AML, angiomyolipoma; TSC, tuberous sclerosis complex; CY, renal cyst; QC, quality control; CY, renal cyst.

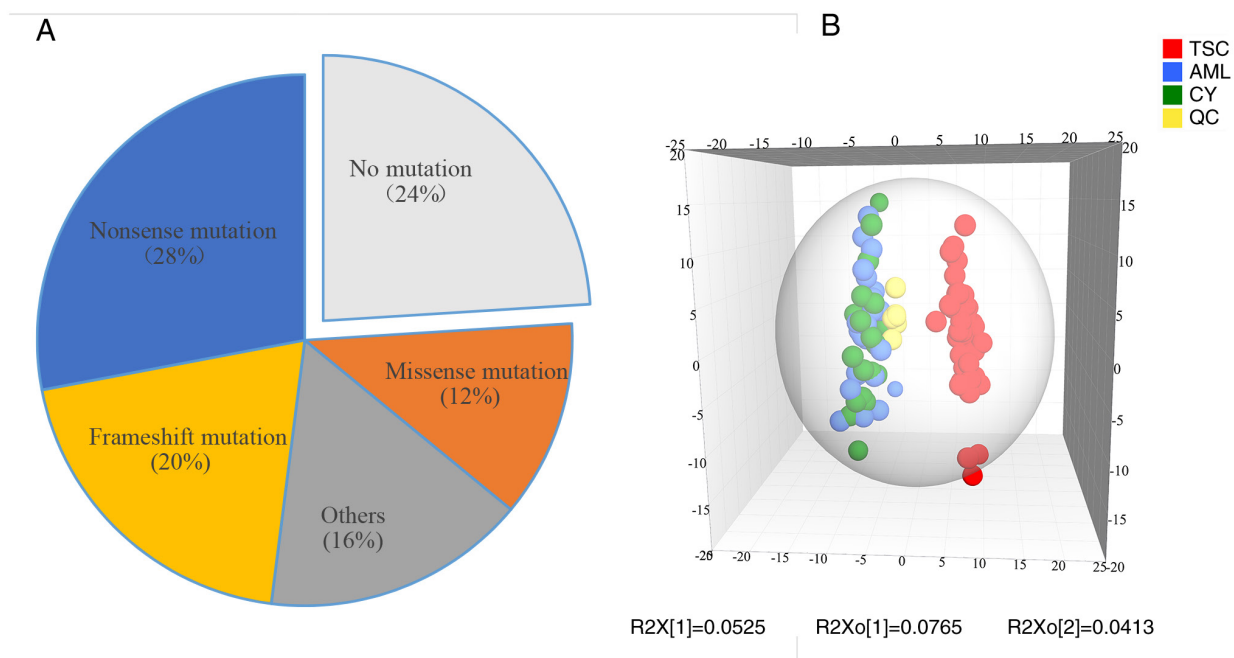


Figure S2. Insignificant immune cell estimation within the tumor microenvironment based on the RNA transcriptome. The estimated cell compositions of (A) NK cells, (B) neutrophils, (C) CD8<sup>+</sup> T cells and (D) monocytic lineage within the TSC-RAML and para-tumor normal tissue microenvironment.

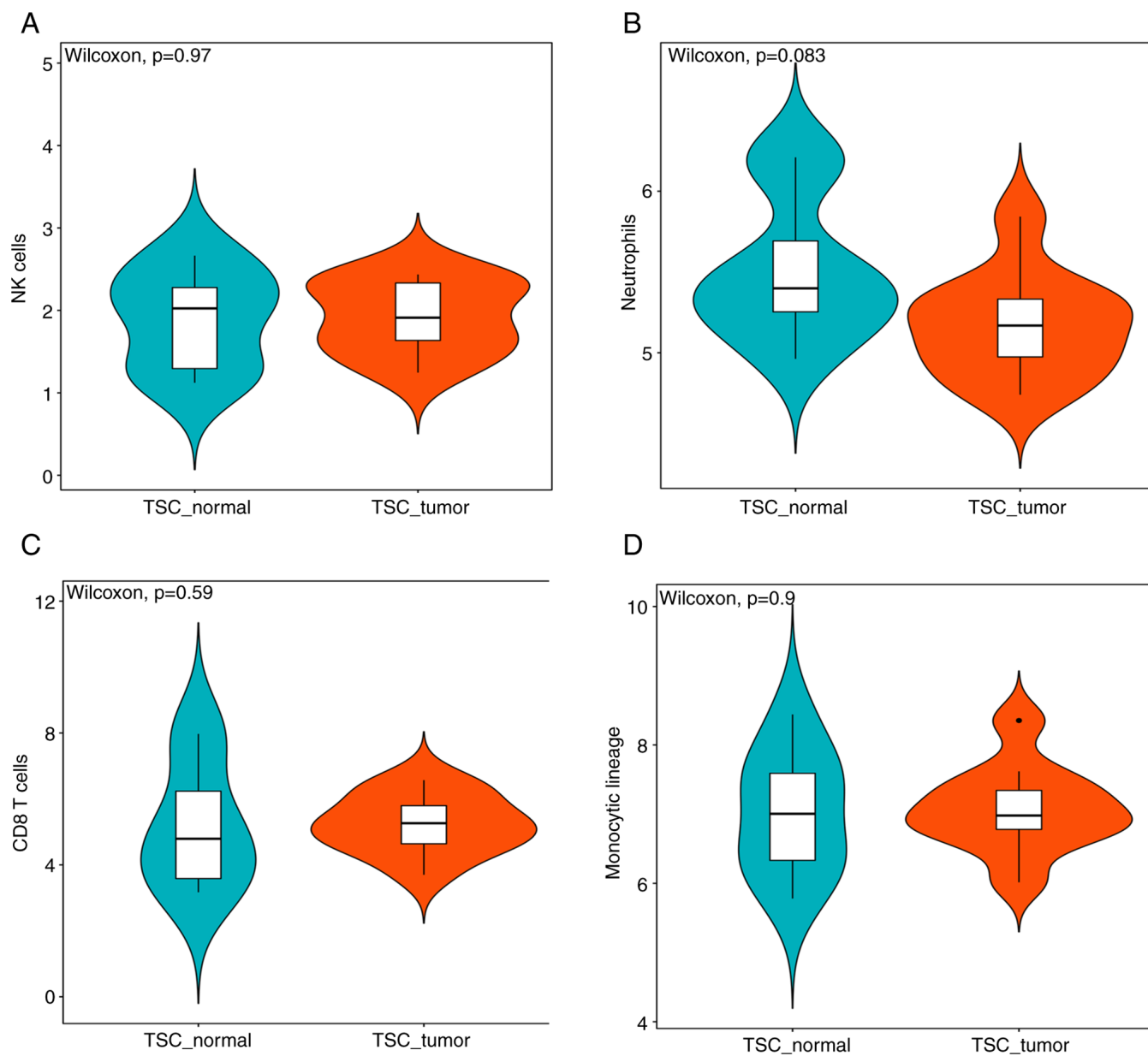


Figure S3. Heatmap of characteristic molecules across various cell types.

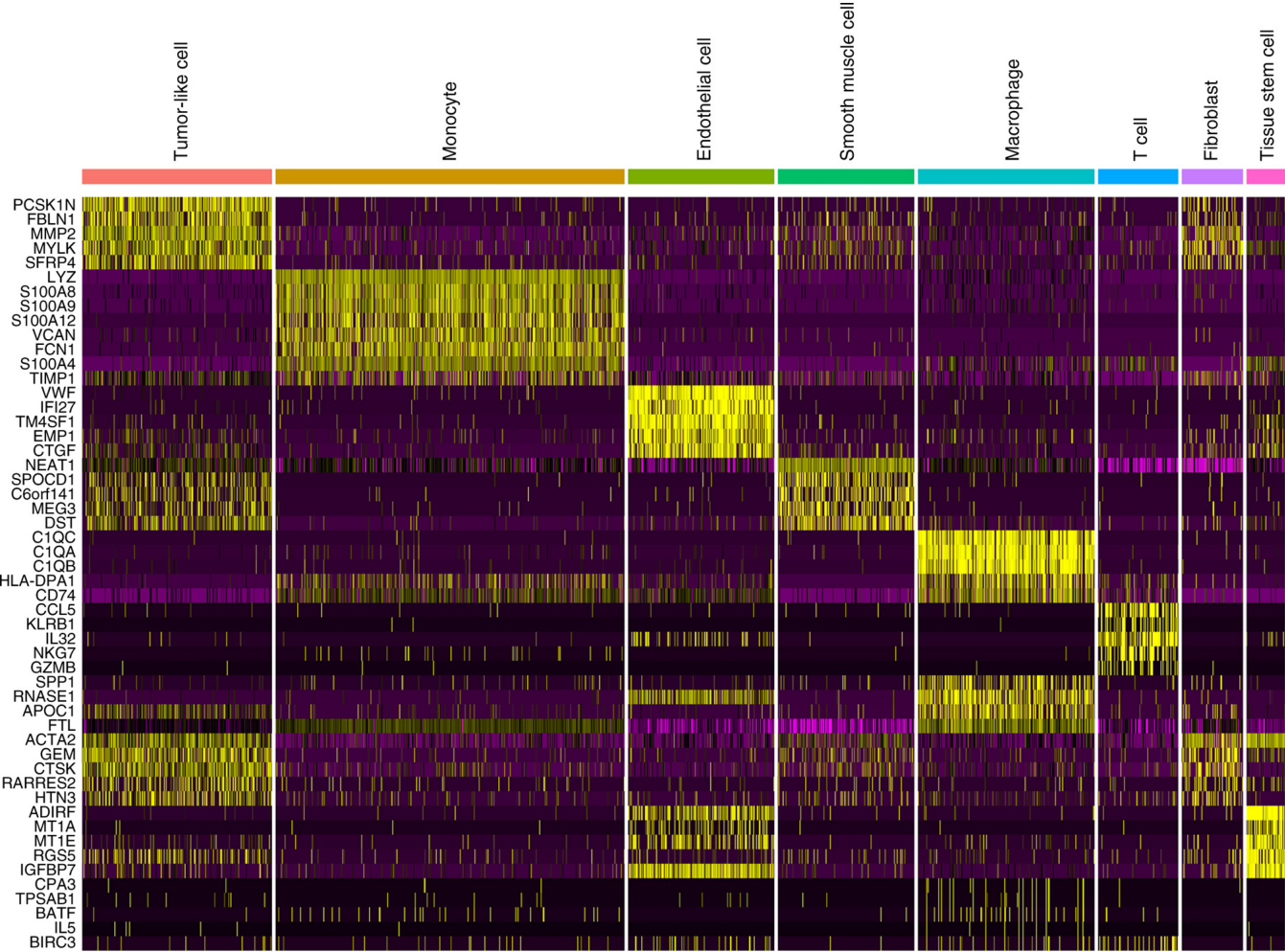


Figure S4. Characteristic RNA expression of TSC1 gene-mutated renal angiomyolipoma tumor-like cells. UMAP, Uniform Manifold Approximation and Projection; TSC, tuberous sclerosis complex.

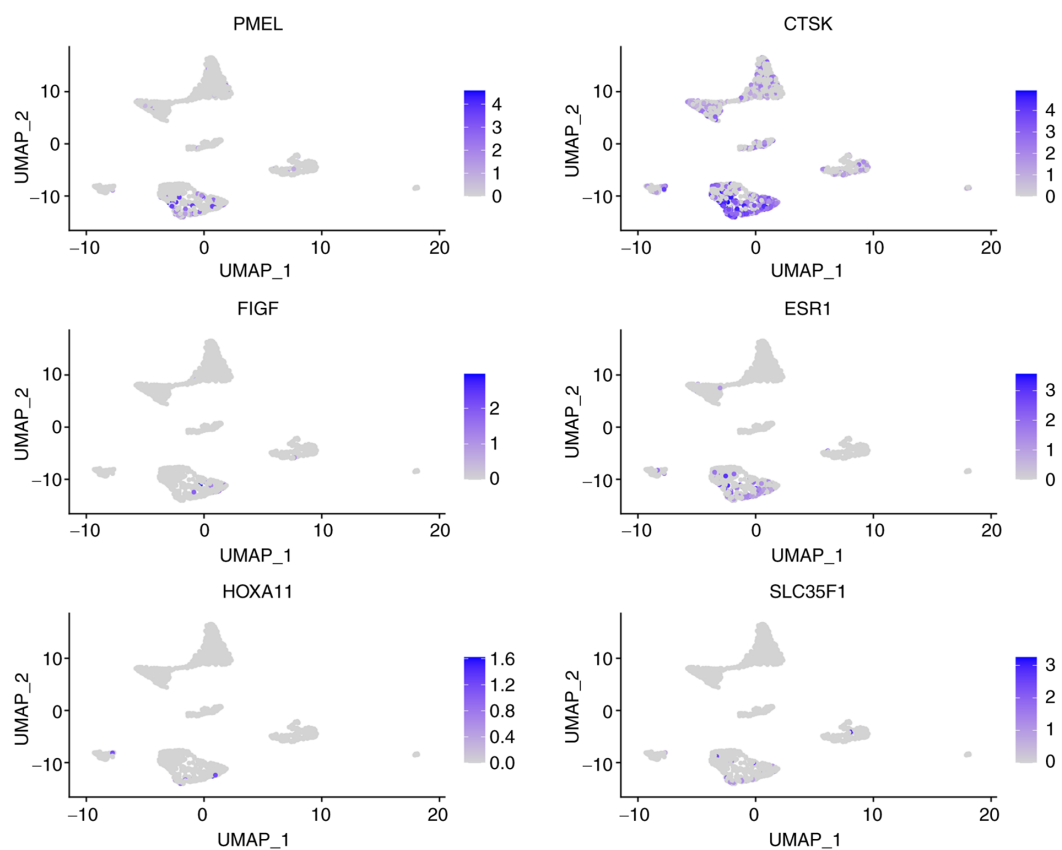
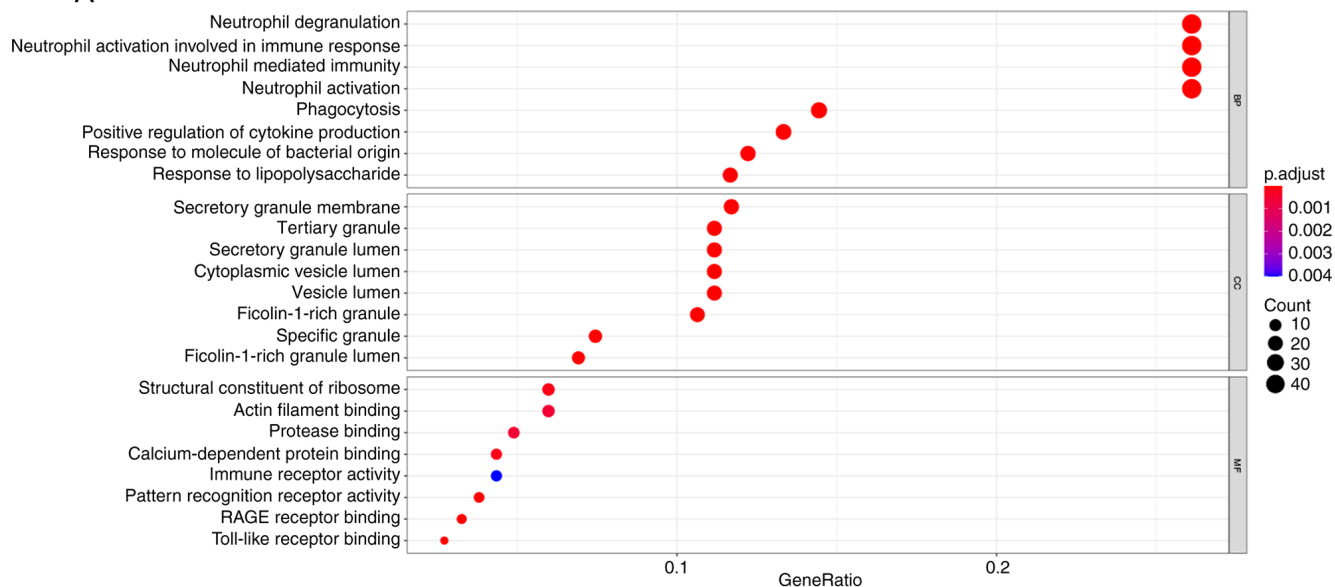


Figure S5. Functional enrichment of monocytes and macrophages within the tumor microenvironment. (A) GO enrichment of differentially expressed genes of monocytes within TSC-RAML tumor microenvironment. (B) GO enrichment of differentially expressed genes of macrophages within the TSC-RAML tumor microenvironment. TSC-RAML, tuberous sclerosis complex-associated renal angiomyolipoma; GO, Gene Ontology; BP, biological process; CC, cellular component; MF, molecular function.

A



B

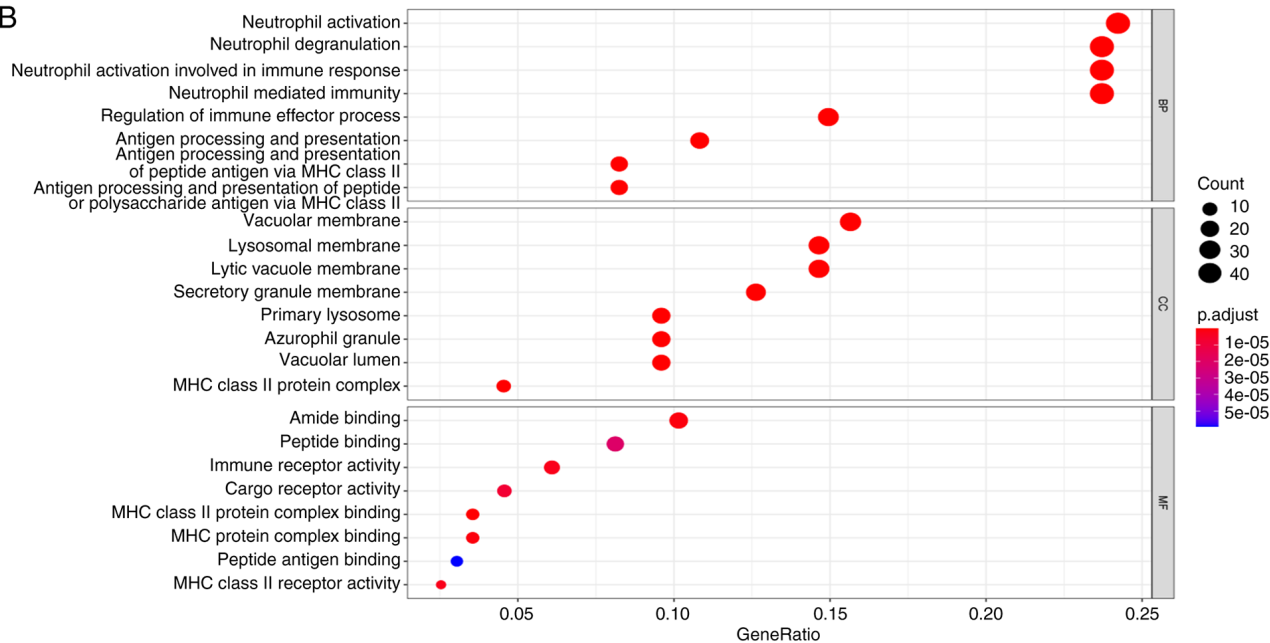


Figure S6. Gene Ontology functional enrichment of fibroblasts within the tumor microenvironment. BP, biological process; CC, cellular component; MF, molecular function.

