



Supplementary Fig. 6. (A) Expression of cytokines (*IL1A*, *IL1B*, *IL2*, *IL4*, *IL6*, *IL10*, *TNF*, *IFNG*, *IL12A*, *IL12B*) by cluster in T/NK subset visualized using a dot plot. (B) Expression of chemokines (*CCL1*, *CCL2*, *CCL3*, *CCL4*, *CCL5*, *CCL7*, *CCL8*, *CCL11*, *CXCL1*, *CXCL2*, *CXCL3*, *CXCL5*, *CXCL6*, *CXCL8*, *CXCL9*, *CXCL10*, *CXCL11*, *CXCL12*, *CXCL13*, *CX3CL*, *XCL1*, *XCL2*) by cluster in the T/NK subset visualized using a dot plot. (C) Expression of cytokines (*IL1A*, *IL1B*, *IL2*, *IL4*, *IL6*, *IL10*, *TNF*, *IFNG*, *IL12A*, *IL12B*) by cluster in the myeloid subset visualized using a dot plot. (D) Expression of chemokines (*CCL1*, *CCL2*, *CCL3*, *CCL4*, *CCL5*, *CCL7*, *CCL8*, *CCL11*, *CXCL1*, *CXCL2*, *CXCL3*, *CXCL5*, *CXCL6*, *CXCL8*, *CXCL9*, *CXCL10*, *CXCL11*, *CXCL12*, *CXCL13*, *CX3CL*, *XCL1*, *XCL2*) by cluster in the myeloid subset visualized using a dot plot. (E) Violin plot comparing the TLS signature scores between MT-cluster1 and MT-cluster2. The TLS signature scores were computed using the AddModuleScore function based on TLS-associated genes. The plot shows a significant difference in the TLS signature scores between the two clusters, with MT-cluster1 exhibiting a higher TLS signature score compared to MT-cluster2.