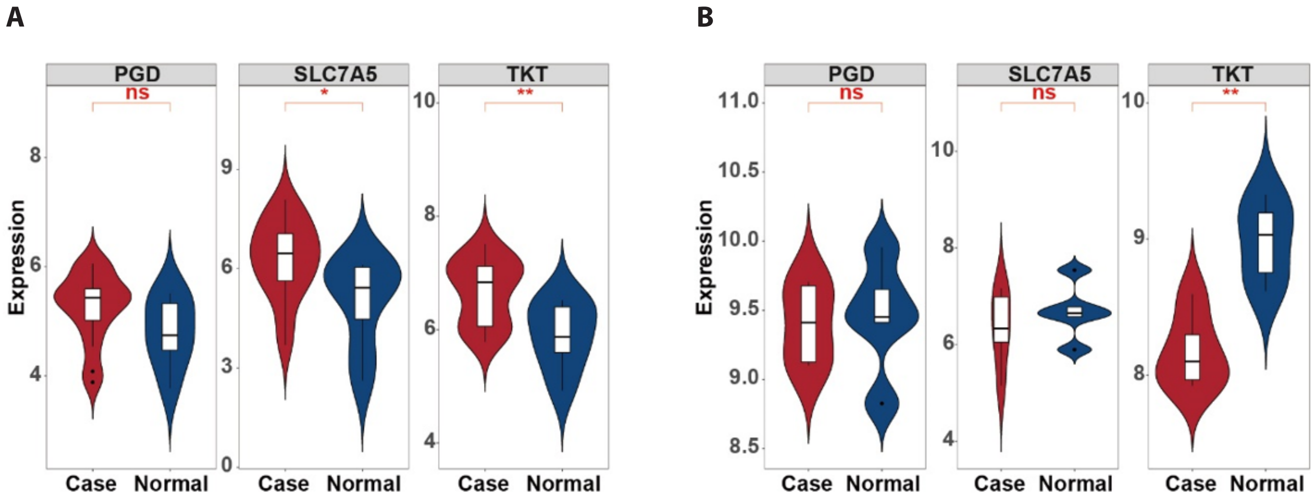
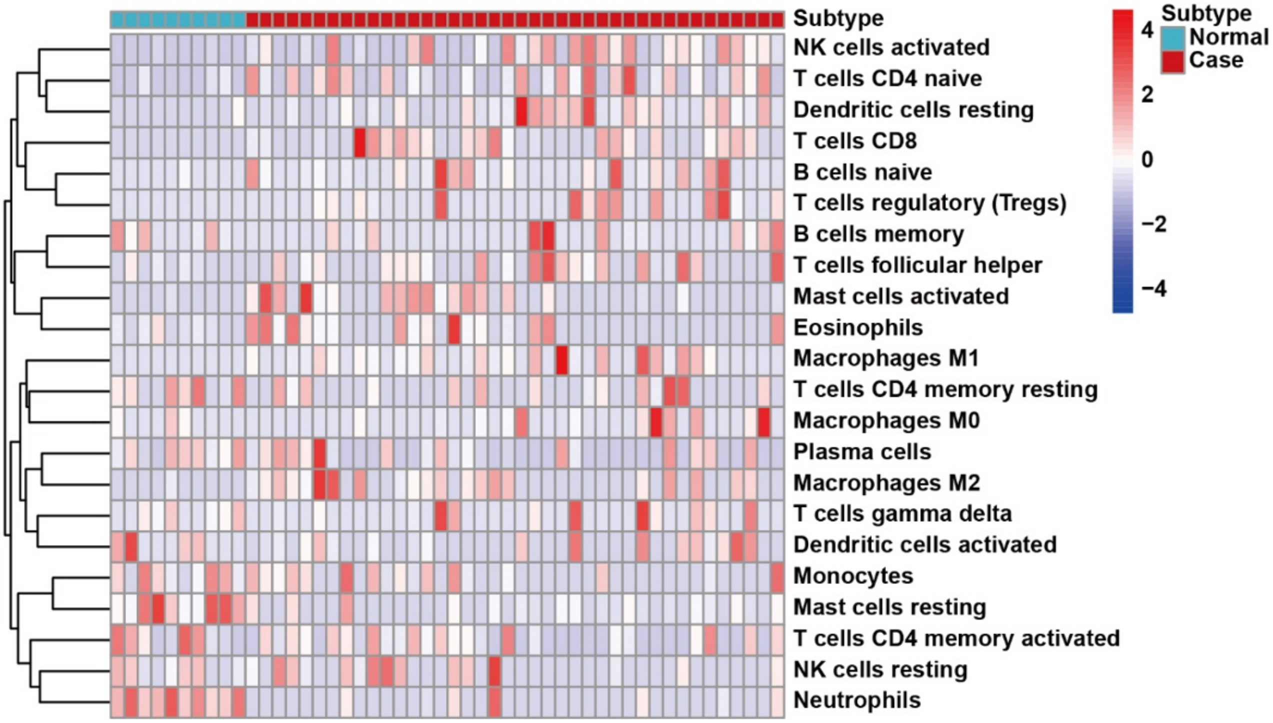
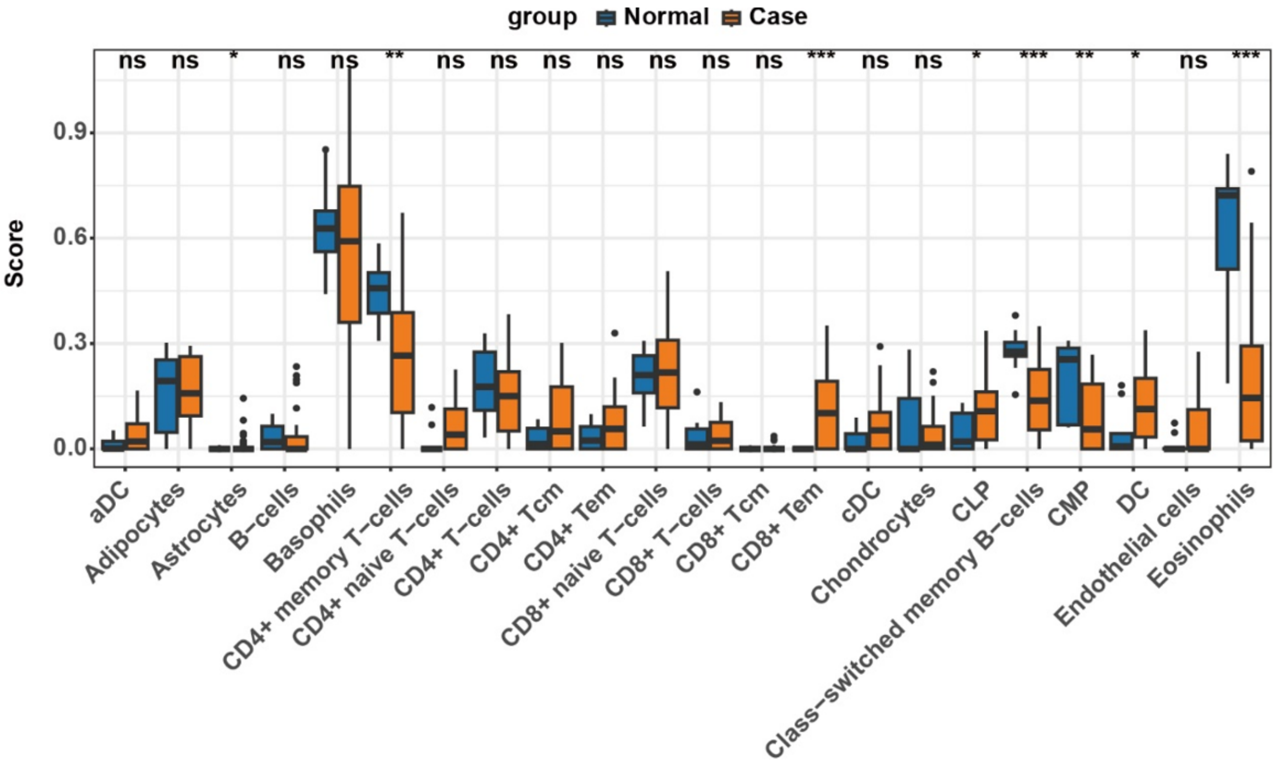


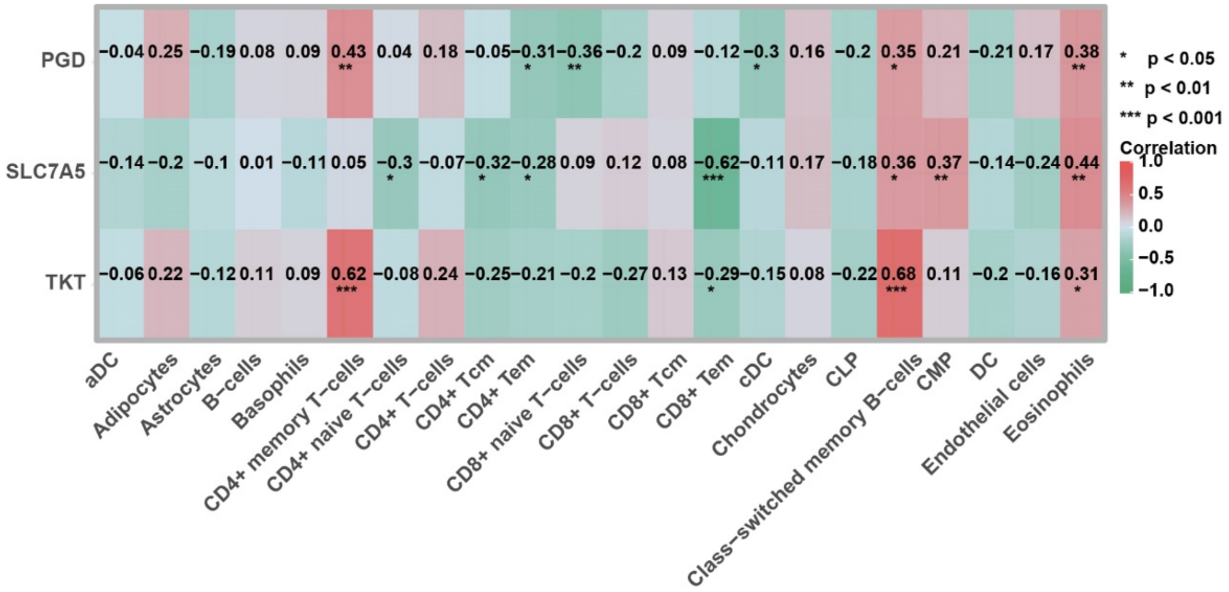
Supplementary Fig. 1. Expression pattern of the feature genes in rheumatoid arthritis (RA). (A) Expression of *PGD, SLC7A5,* and *TKT* between RA cases and normal control in dataset GSE77298. (B) Expression of *PGD, SLC7A5,* and *TKT* between RA cases and normal control in dataset GSE1919. ns, not significant. *$p < 0.05$, **$p < 0.01$.



Supplementary Fig. 2. Immune cells infiltration in osteoarthritis (OA) by xCell algorithm. Relative abundance of 22 immune cells infiltration in OA and normal samples. The left part represents normal samples, the right part represents OA samples, red represents upregulation and blue represents downregulation.



Supplementary Fig. 3. Immune cells infiltration in osteoarthritis (OA) by xCell algorithm. Comparison of 22 immune cells infiltration between OA and normal control, bule represents normal samples and orange represent OA samples. ns, not significant. $^*p < 0.05$, $^{**}p < 0.01$, $^{***}p < 0.001$.



Supplementary Fig. 4. Immune cells infiltration in osteoarthritis (OA) by xCell algorithm. Correlation of *PGD, SLC7A5*, and *TKT* to immune cells infiltration in OA. Red represents positive correlation, green represents negative correlation. ns, not significant. *p < 0.05, **p < 0.01, ***p < 0.001.