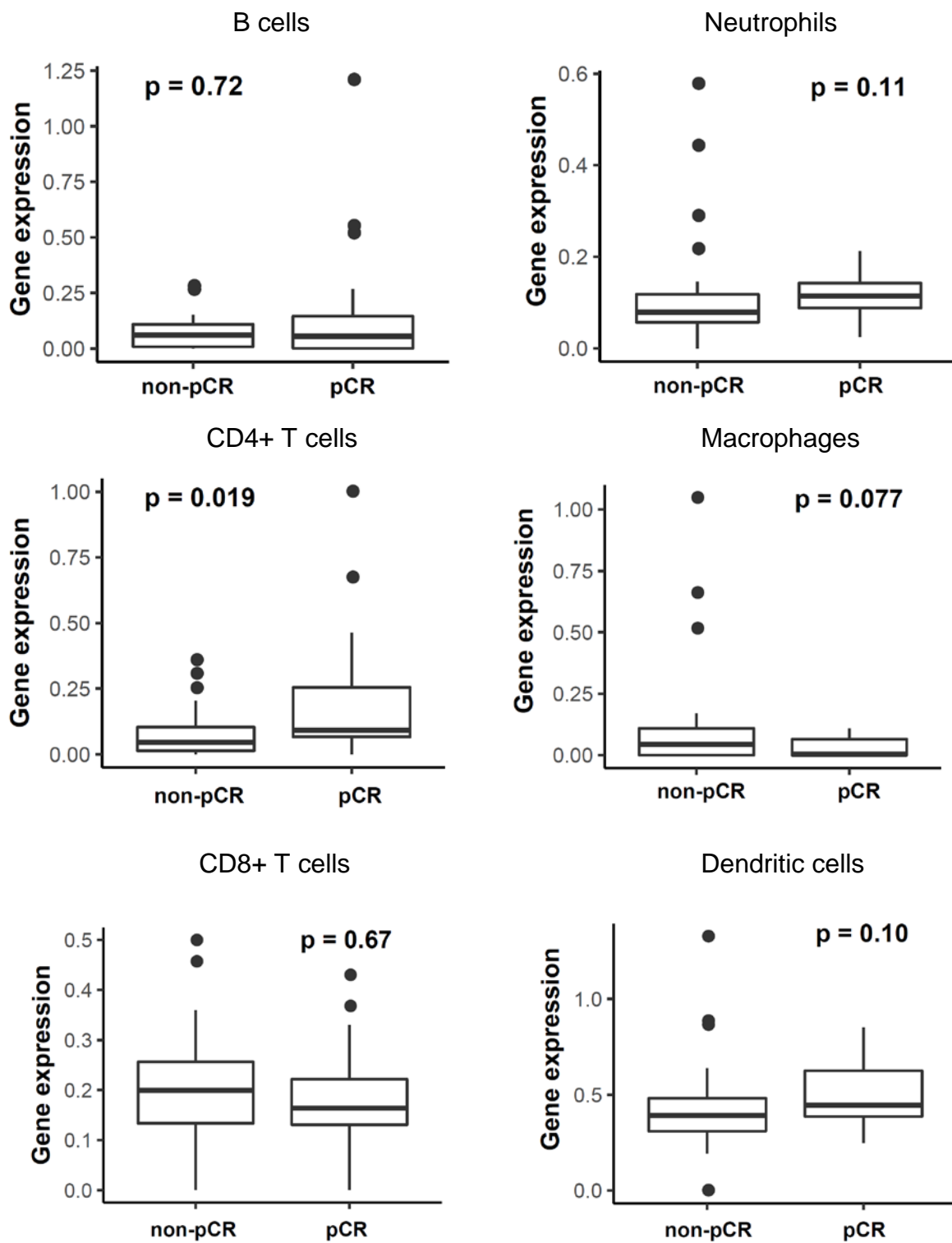
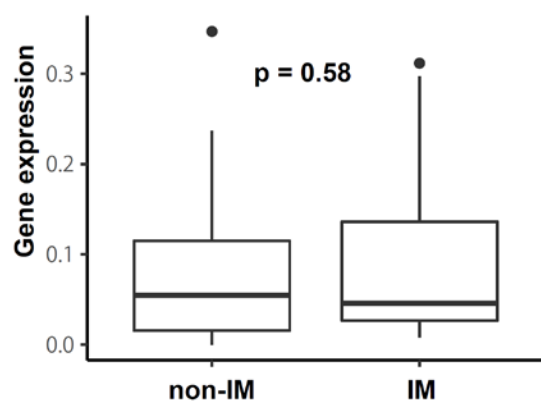


**Figure S1.** Gene expression of immune cell populations in the tumor microenvironment in patients with primary triple-negative breast cancer positive (immunomodulatory; IM) and negative (non-IM) for the 27-gene IO signature by TIMER algorithm. Boxes indicate 25th percentile, median, and 75th percentile. Each dot corresponds to one patient.

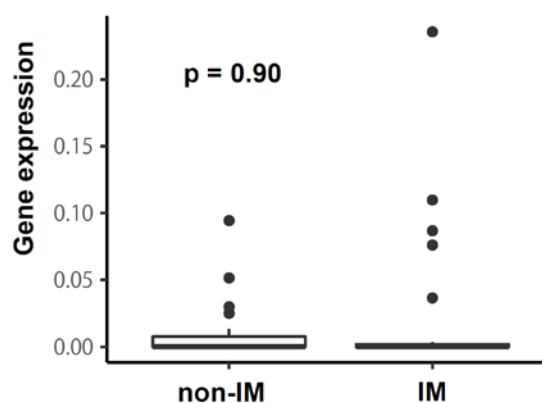


**Figure S2..** Gene expression of immune cell populations in the tumor microenvironment in patients with a pathological complete response (pCR) or without a pCR (non-pCR) by TIMER algorithm.

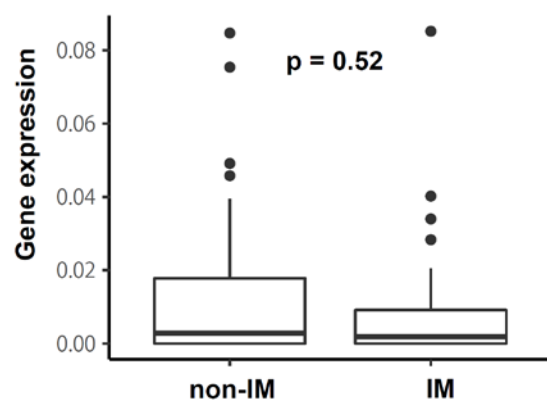
Naïve B cells



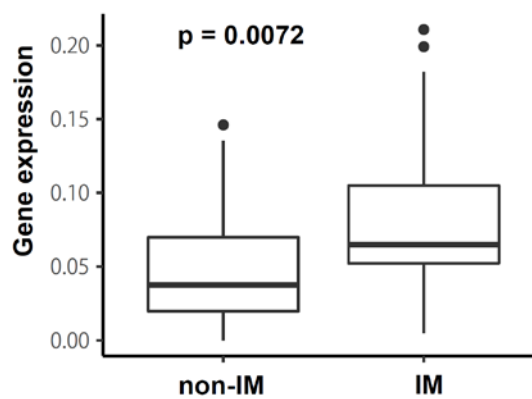
Memory B cells



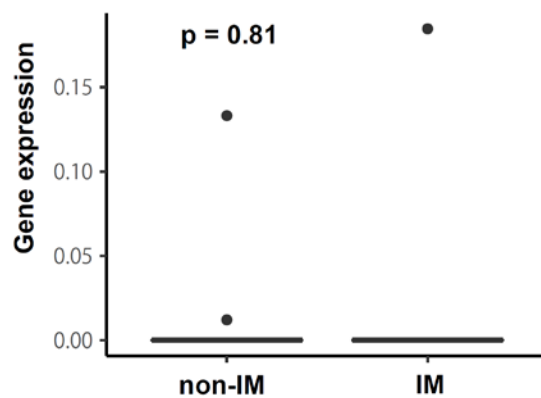
Plasma B cells



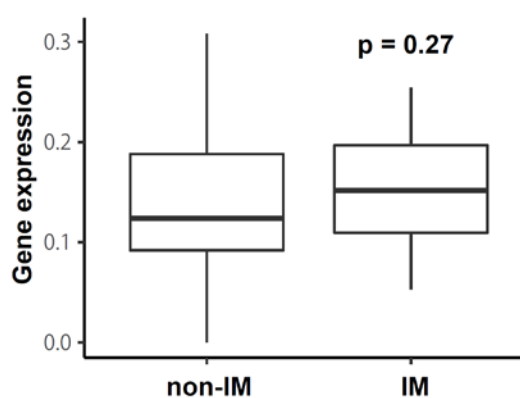
CD8+ T cells



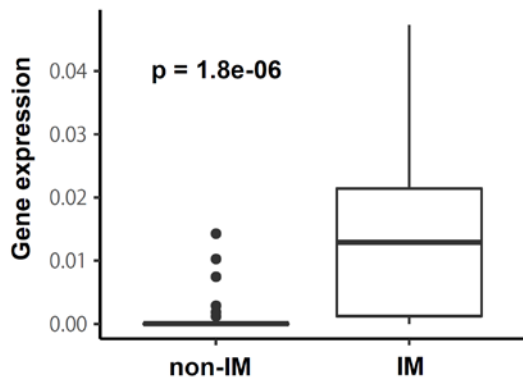
Naïve CD4+ T cells



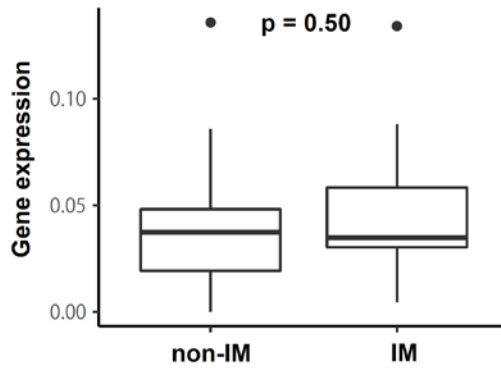
Resting memory CD4+ T cells



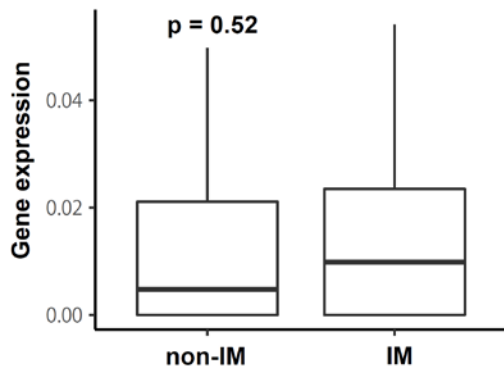
Activated memory CD4+ T cells



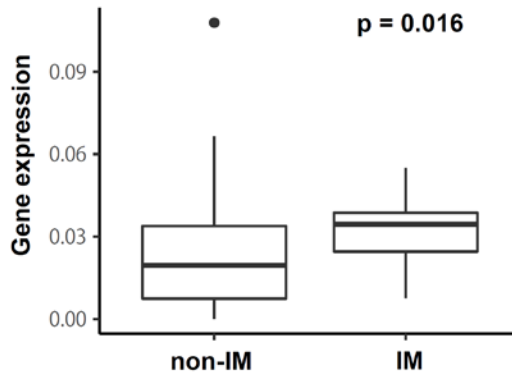
Follicular T helper cells



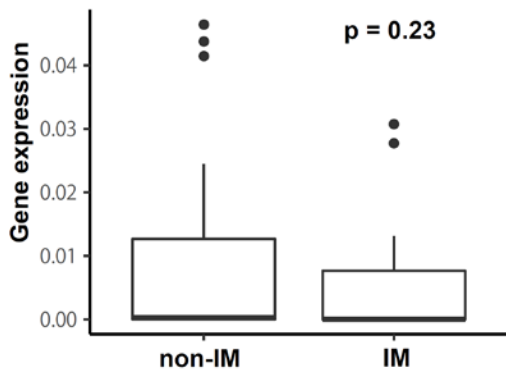
Regulatory T cells



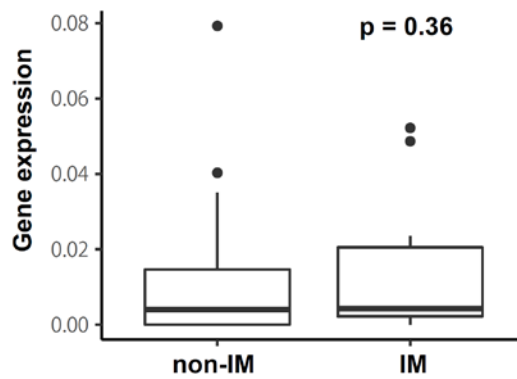
Resting NK cells



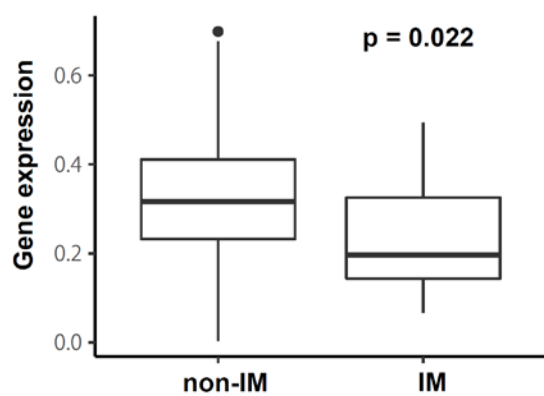
Activated NK cells



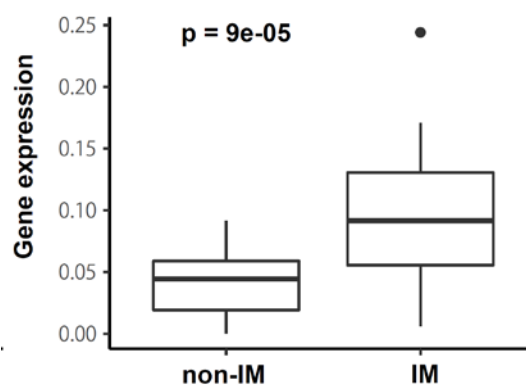
Monocytes



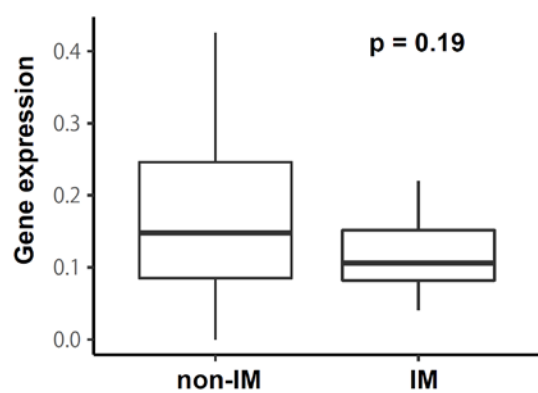
M0 macrophages



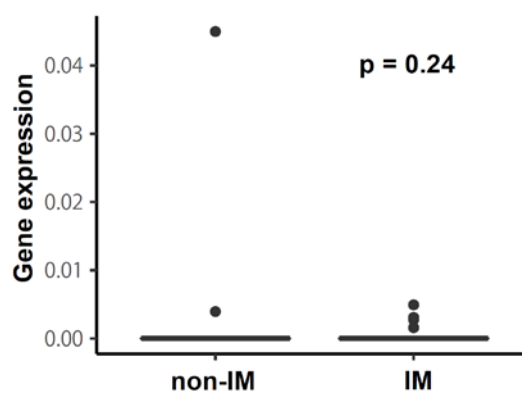
M1 macrophages



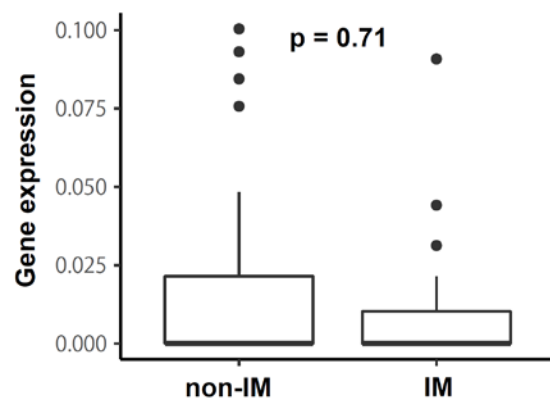
M2 macrophages



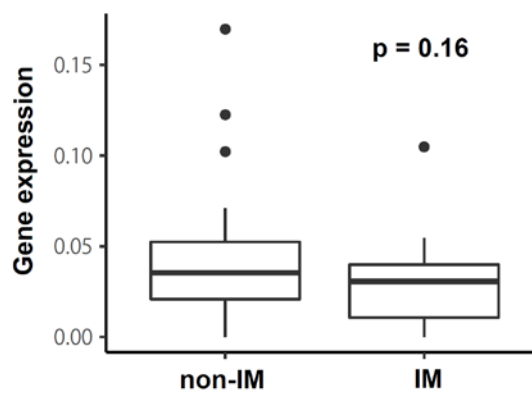
Resting dendritic cells

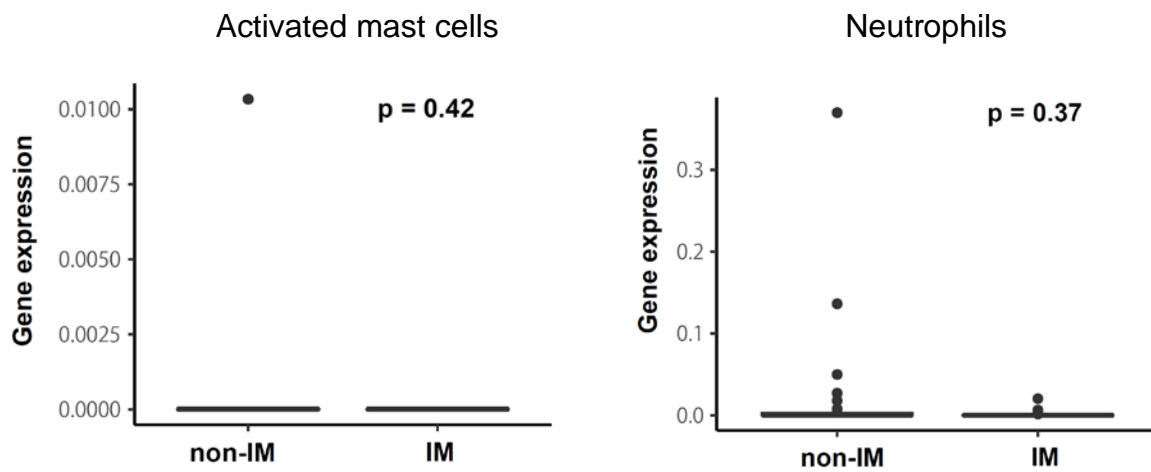


Activated dendritic cells



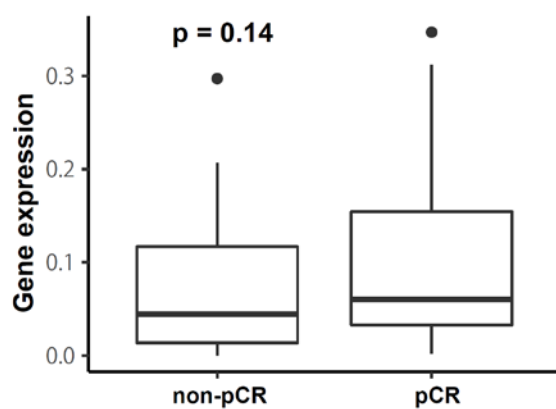
Resting mast cells



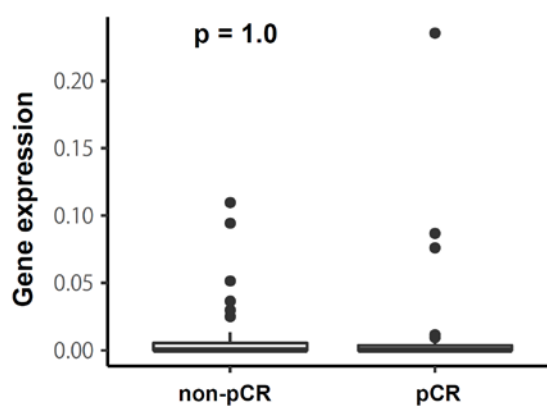


**Figure S3.** Gene expression of immune cell populations in the tumor microenvironment in patients with primary triple-negative breast cancer positive (immunomodulatory; IM) and negative (non-IM) for the 27-gene IO signature by CIBERSORT algorithm.

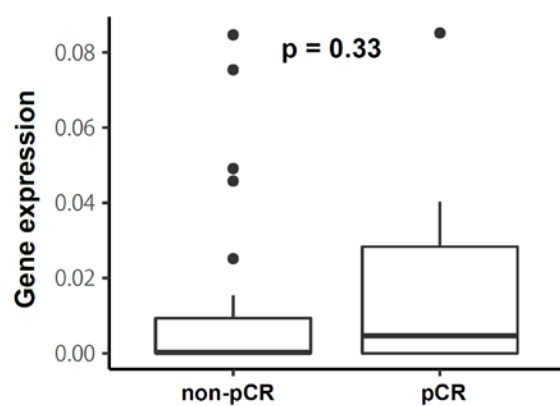
Naïve B cells



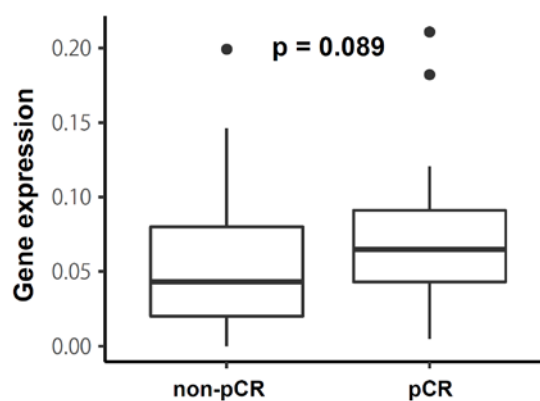
Memory B cells



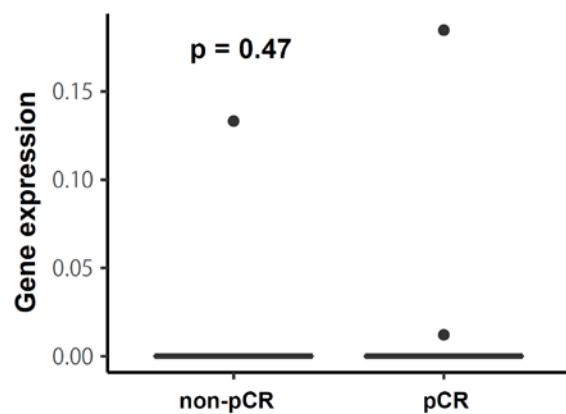
Plasma cells



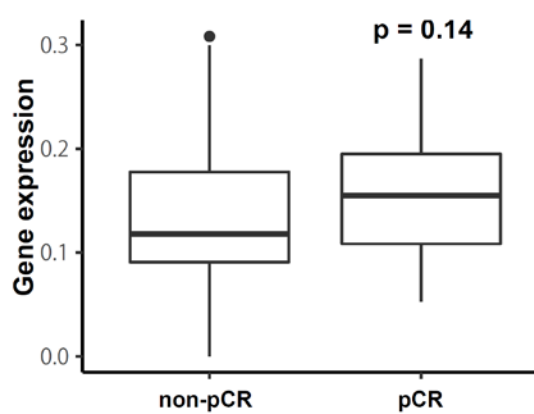
CD8+ T cells



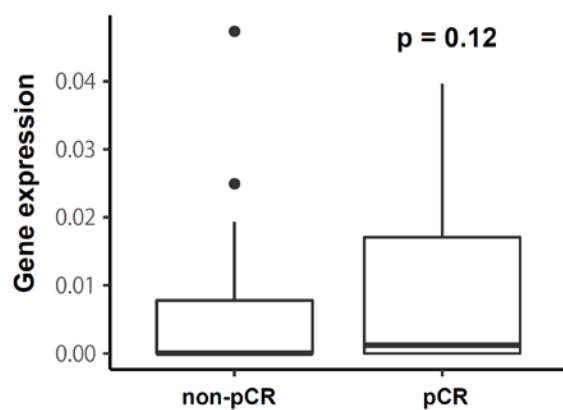
Naïve CD4+ T cells



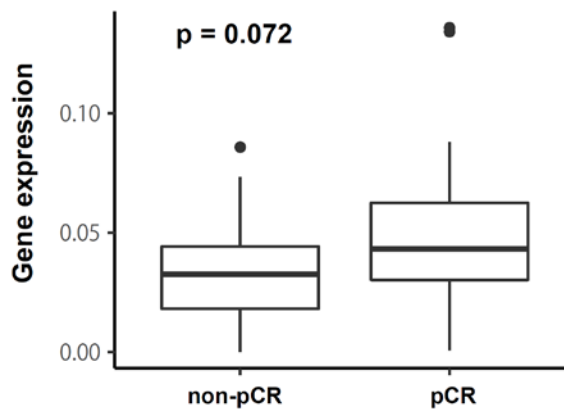
Resting memory CD4+ T cells



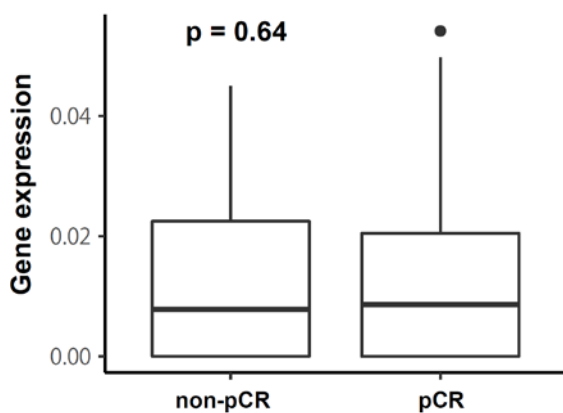
Activated memory CD4+ T cells



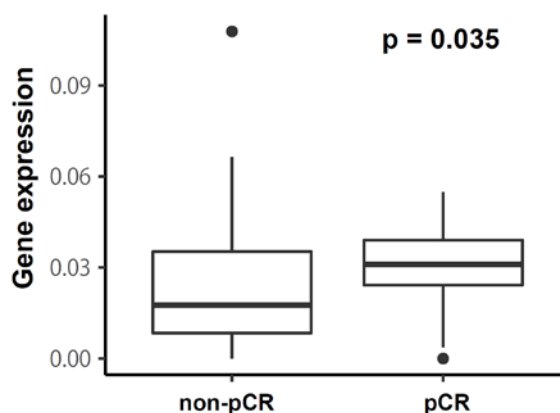
Follicular T helper cells



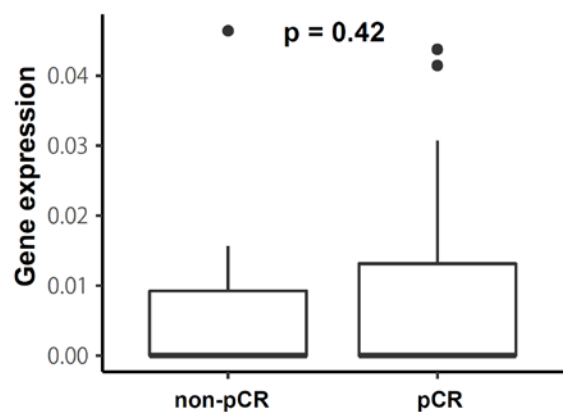
Regulatory T cells



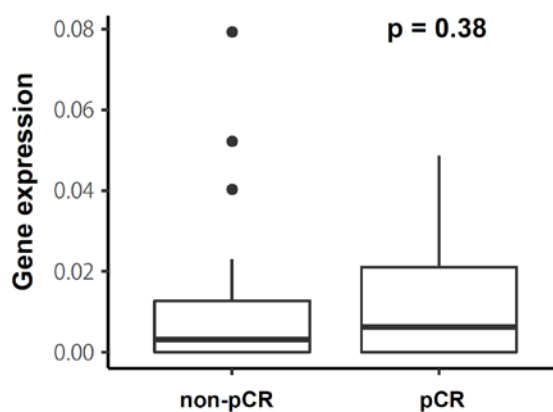
Resting NK cells



Activated NK cells

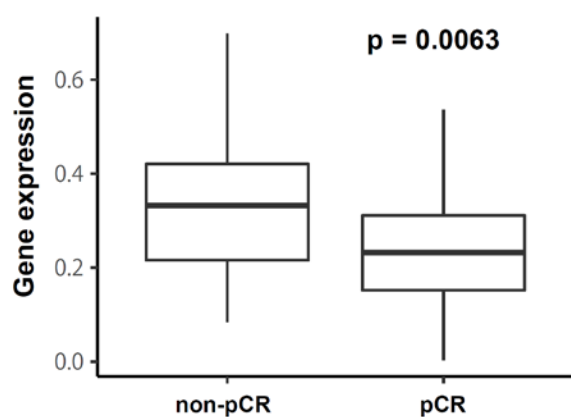


Monocytes

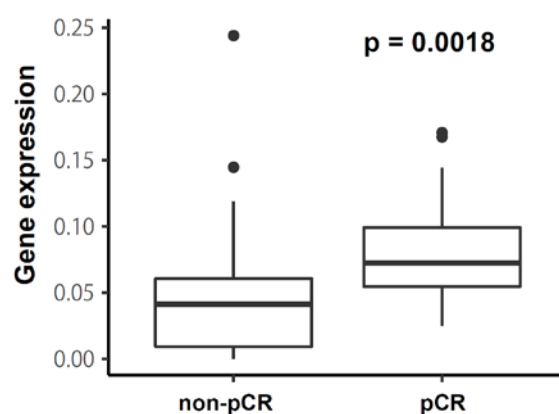




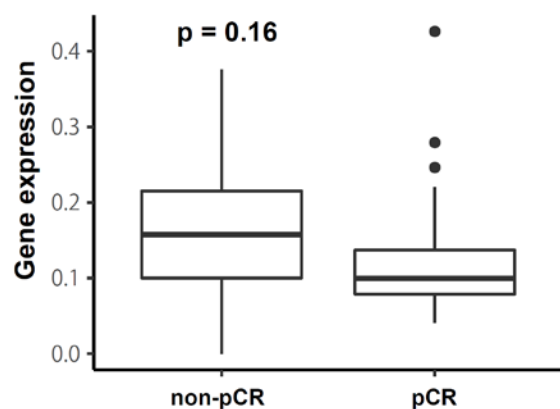
M0 macrophages



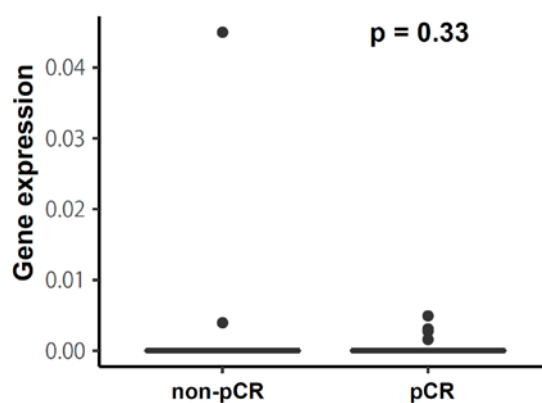
M1 macrophages



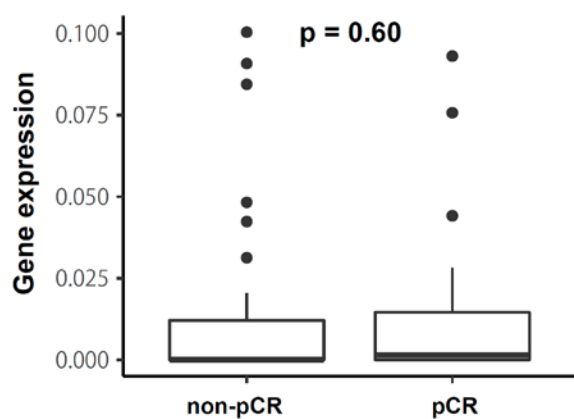
M2 macrophages



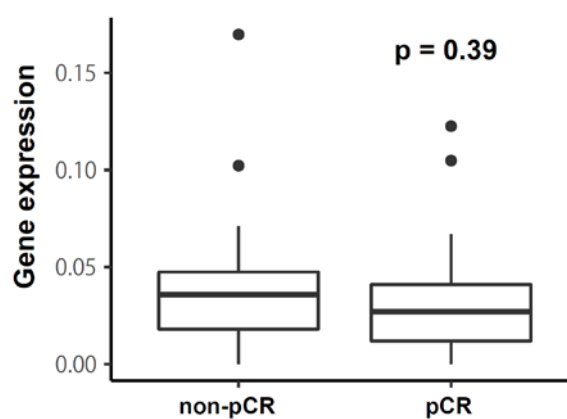
Resting dendritic cells

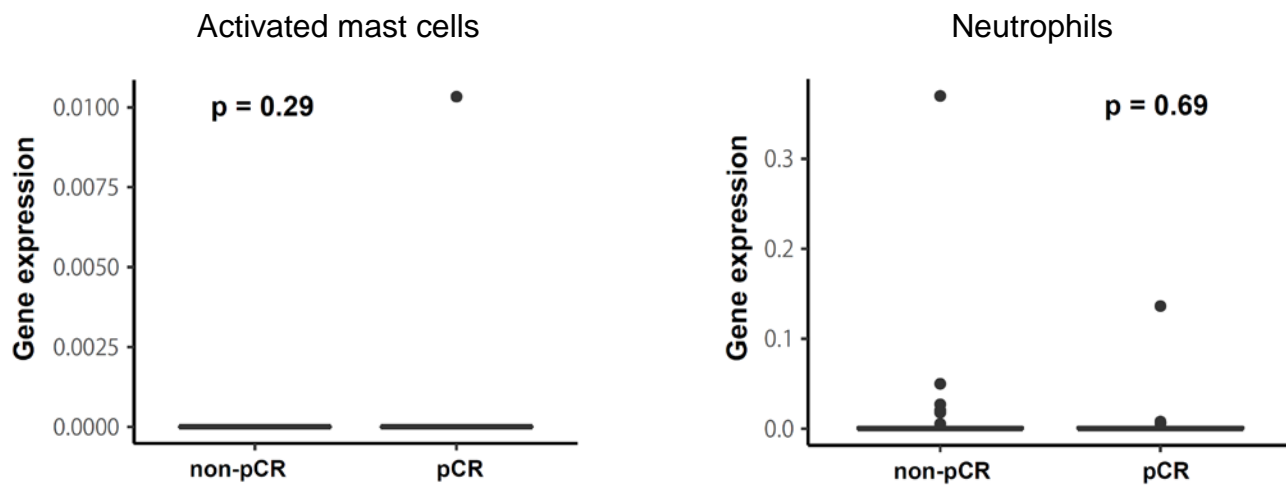


Activated dendritic cells

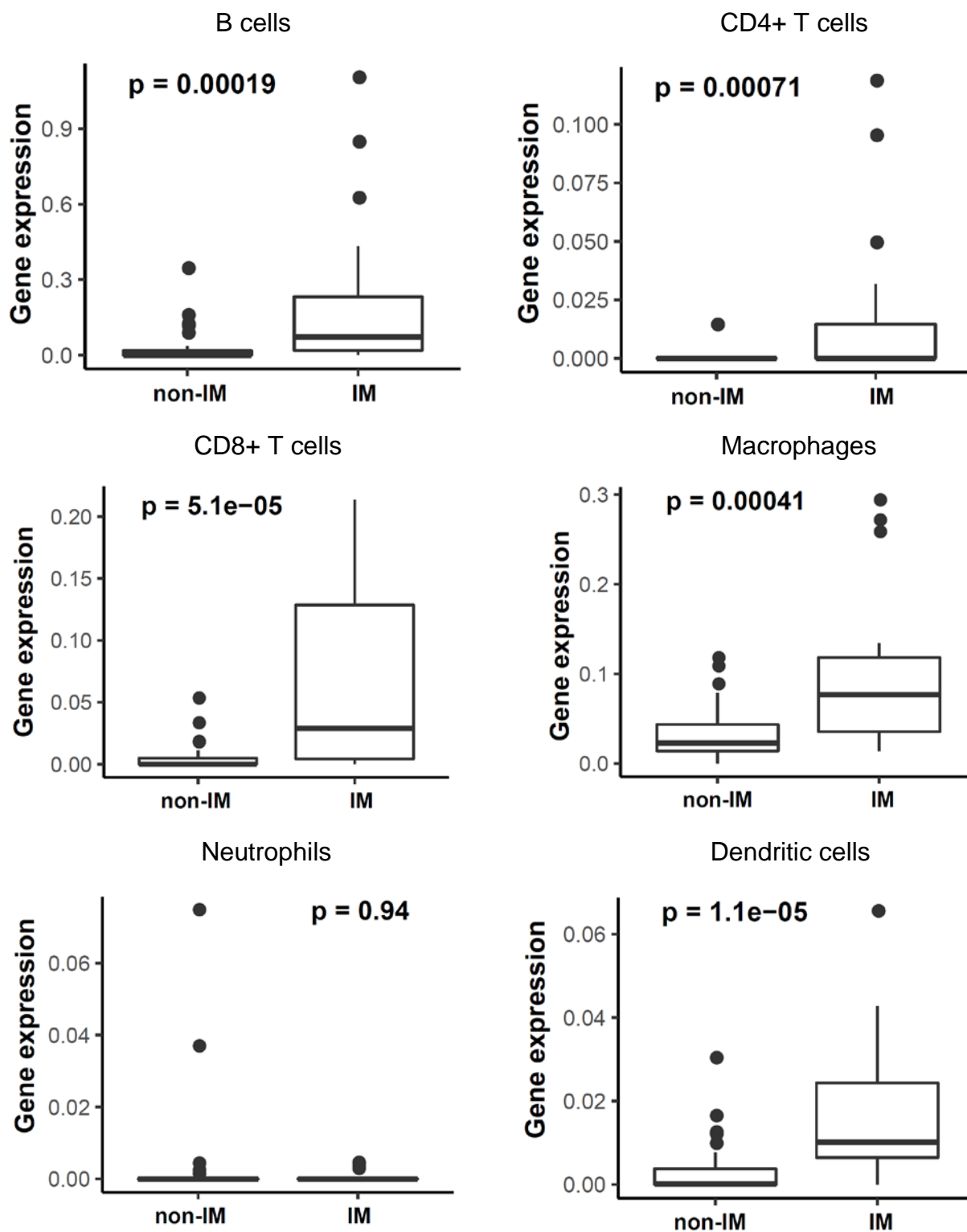


Resting mast cells

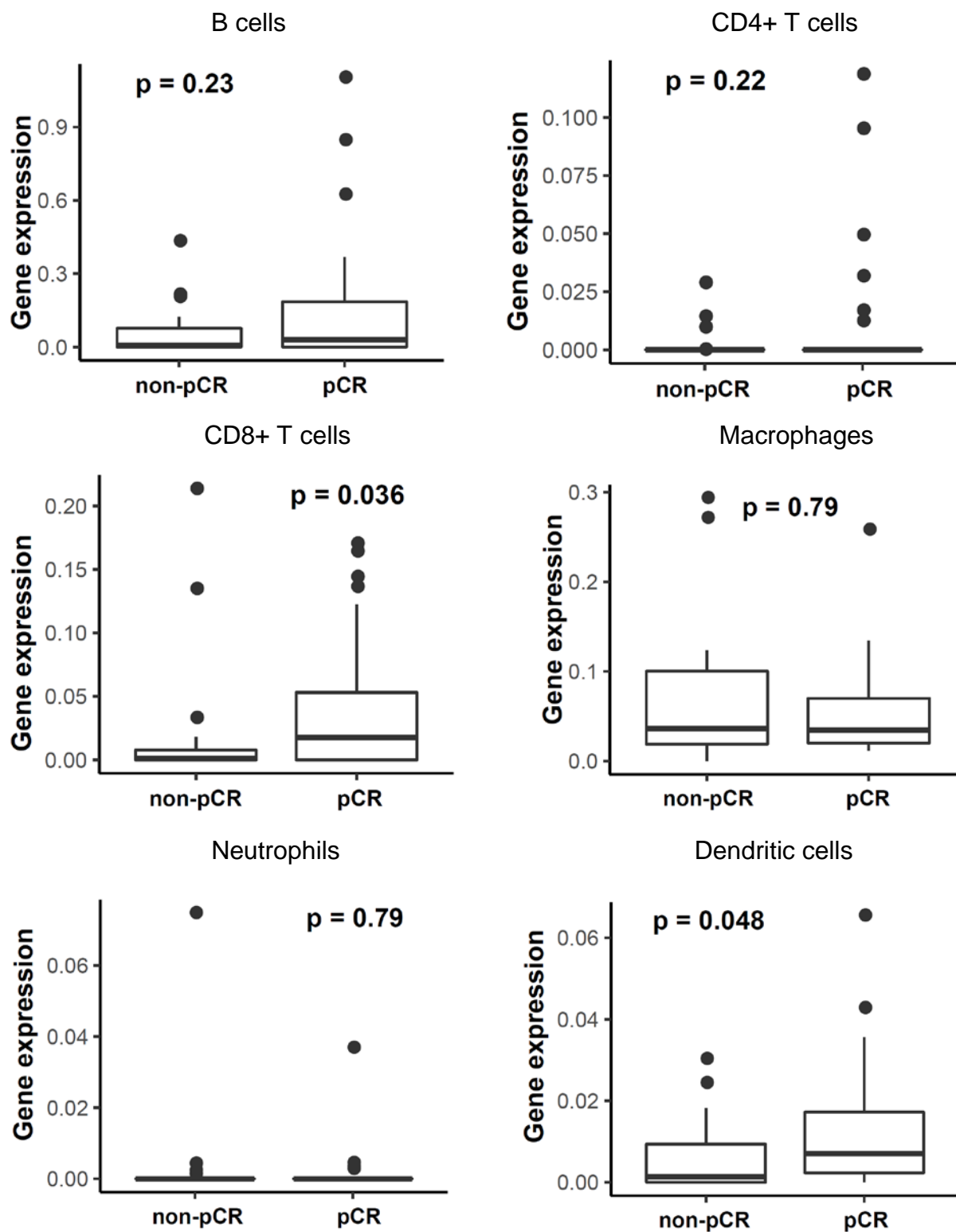




**Figure S4.** Gene expression of immune cell populations in the tumor microenvironment in patients with a pathological complete response (pCR) or without a pCR (non-pCR) by CIBERSORT algorithm.



**Figure S5.** Gene expression of immune cell populations in the tumor microenvironment in patients with primary triple-negative breast cancer positive (immunomodulatory; IM) and negative (non-IM) for the 27-gene IO signature by xCell algorithm.



**Figure S6.** Gene expression of immune cell populations in the tumor microenvironment in patients with a pathological complete response (pCR) or without a pCR (non-pCR) by xCell algorithm.