

Fig. S3

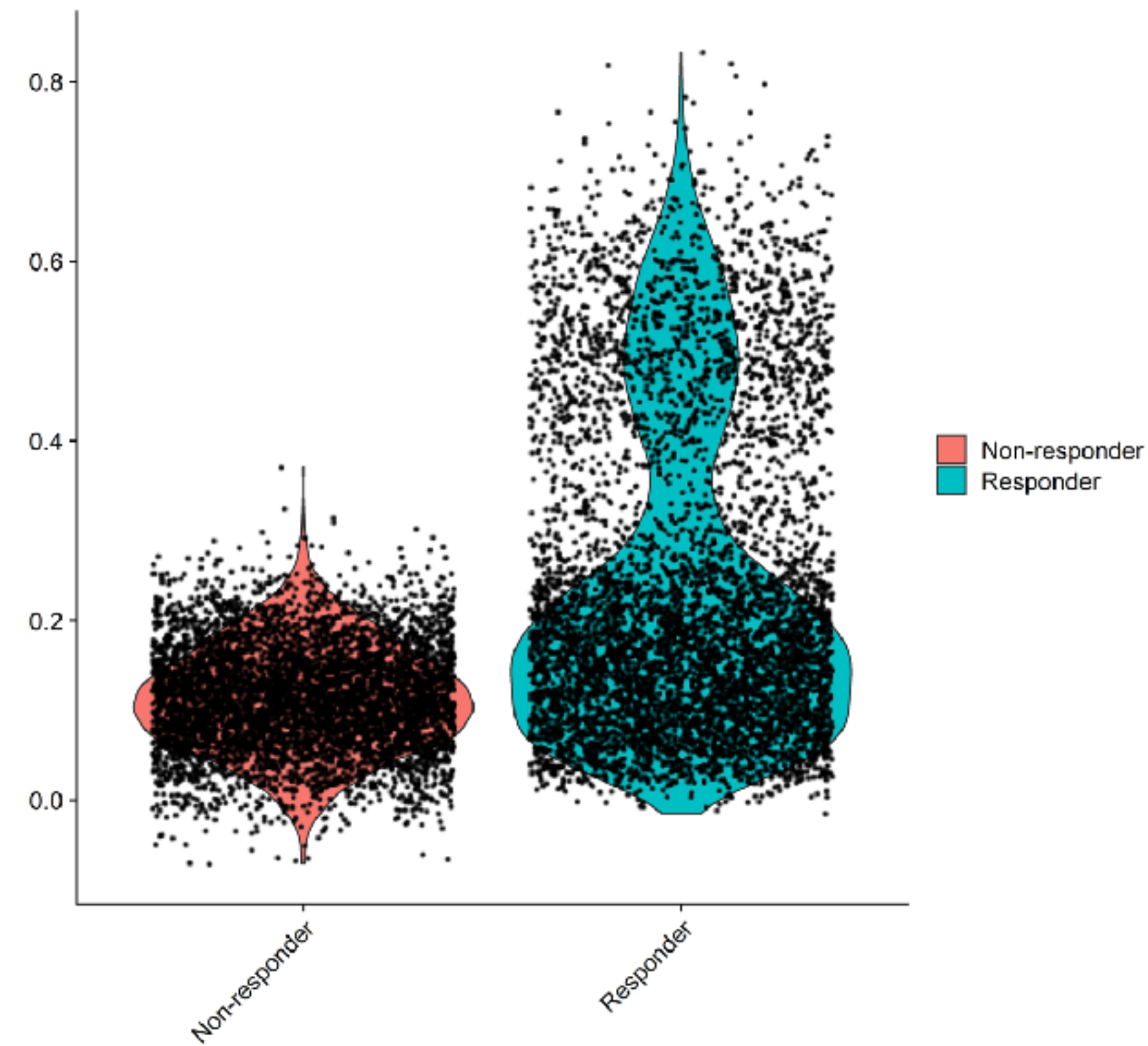


Fig. S2 - Overall expression of the antigen processing and presentation signaling pathway in the subset of spots in the spatial transcriptomics data from non-responders and responders. Using the ModuleScore function from the Seurat Bioconductor/R package, the expression of all the genes in the KEGG antigen processing and presentation pathway was calculated in each spot assigned to tumor regions and a score representative of the averaged expression was determined. The module scores are increased in a significant proportion of tumor spots from responders, suggesting that immune cell recruitment was more efficient in the patients with pathological responses to the neoadjuvant therapy.