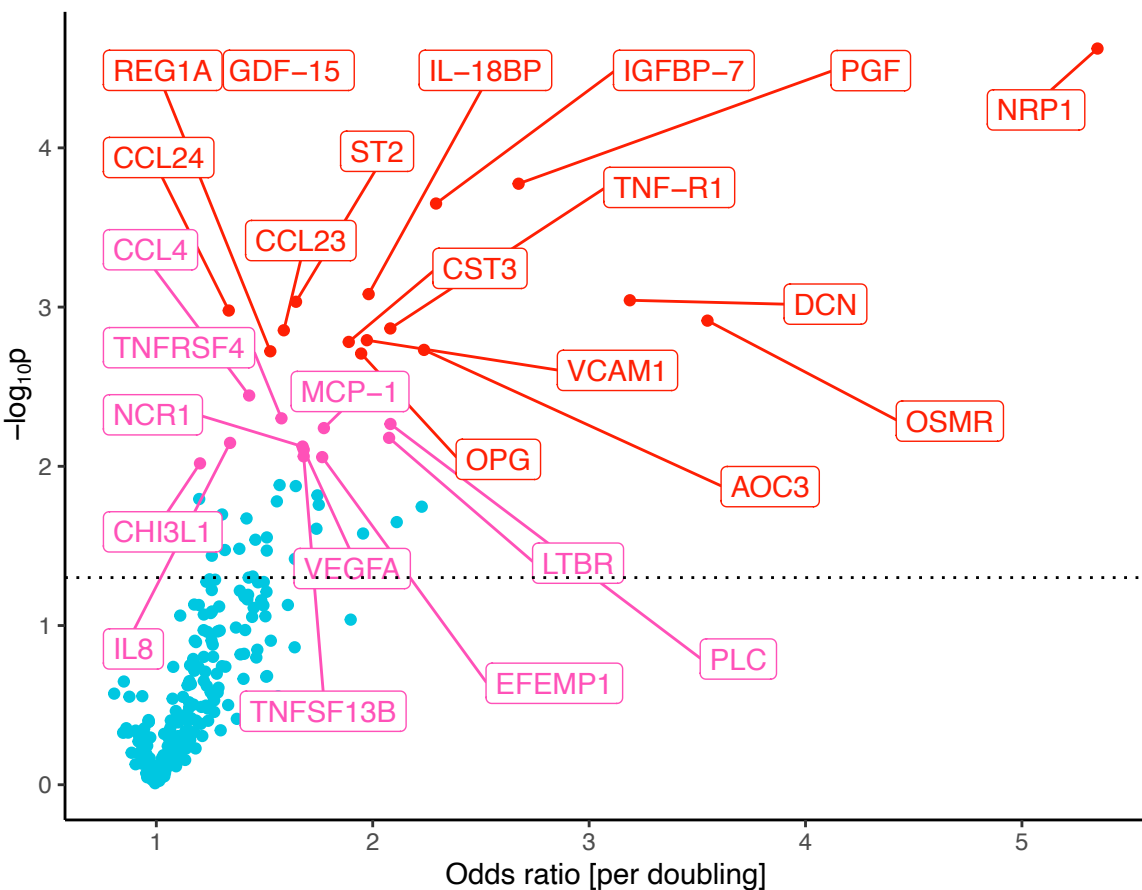
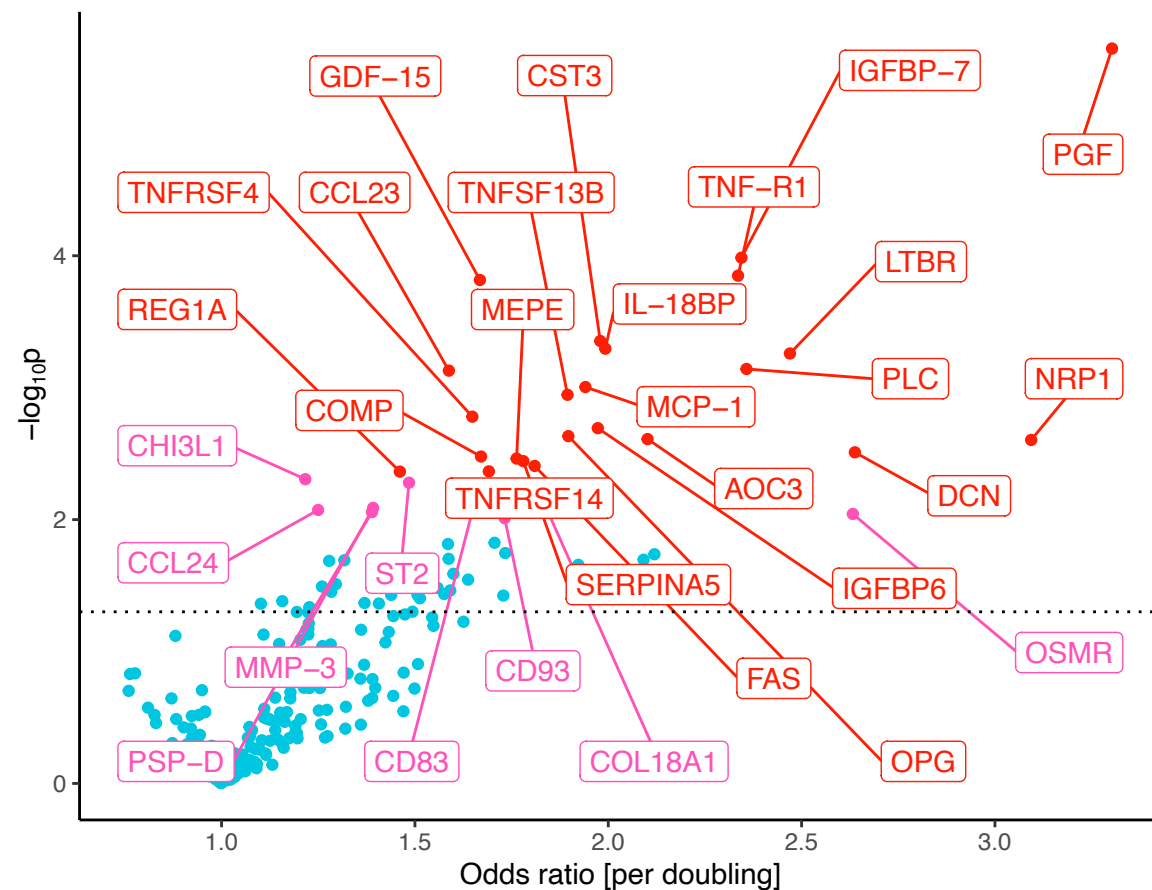


Association between proteomic markers and CAD outcomes

Presence of coronary calcium



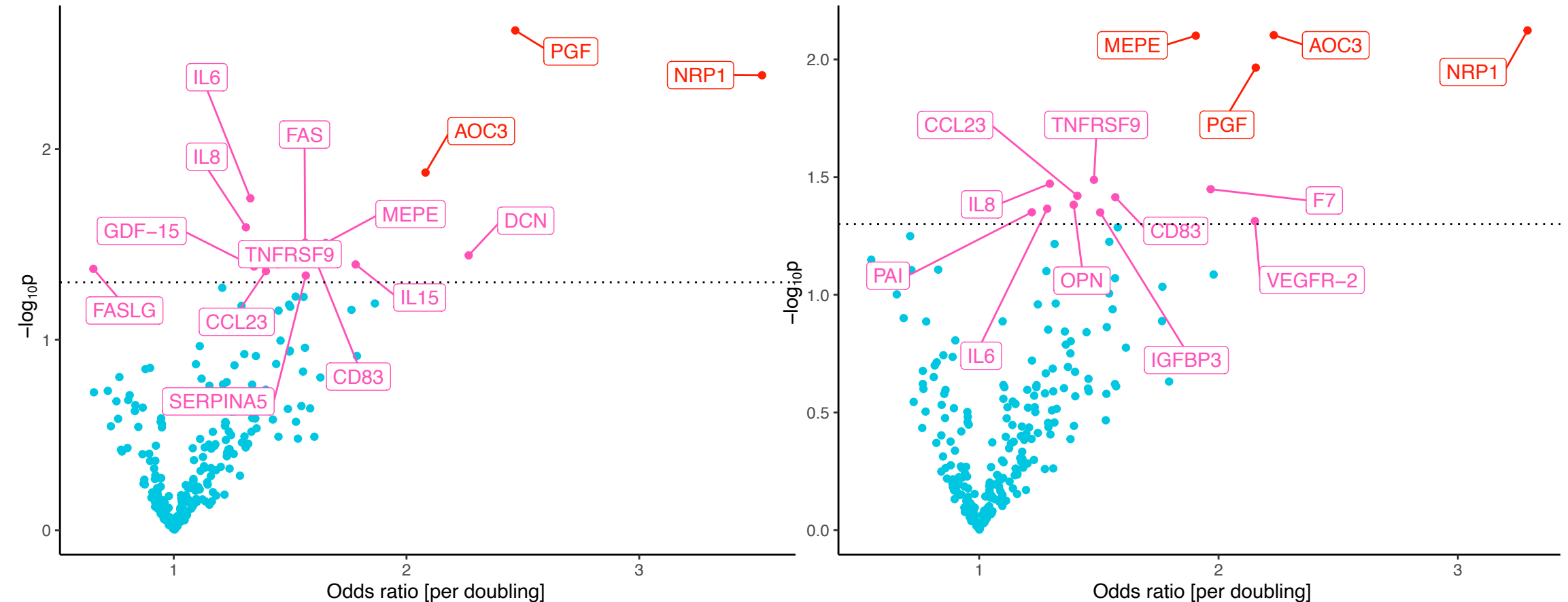
Presence of coronary plaque



Association between proteomic markers and vulnerable plaque

Unadjusted

ASCVD adjusted



Supplementary Figure 2

Nominal p-value threshold*

● ≤ 0.01 ● < 0.05 ● ≥ 0.05

*: All FDR adjusted p > 0.1

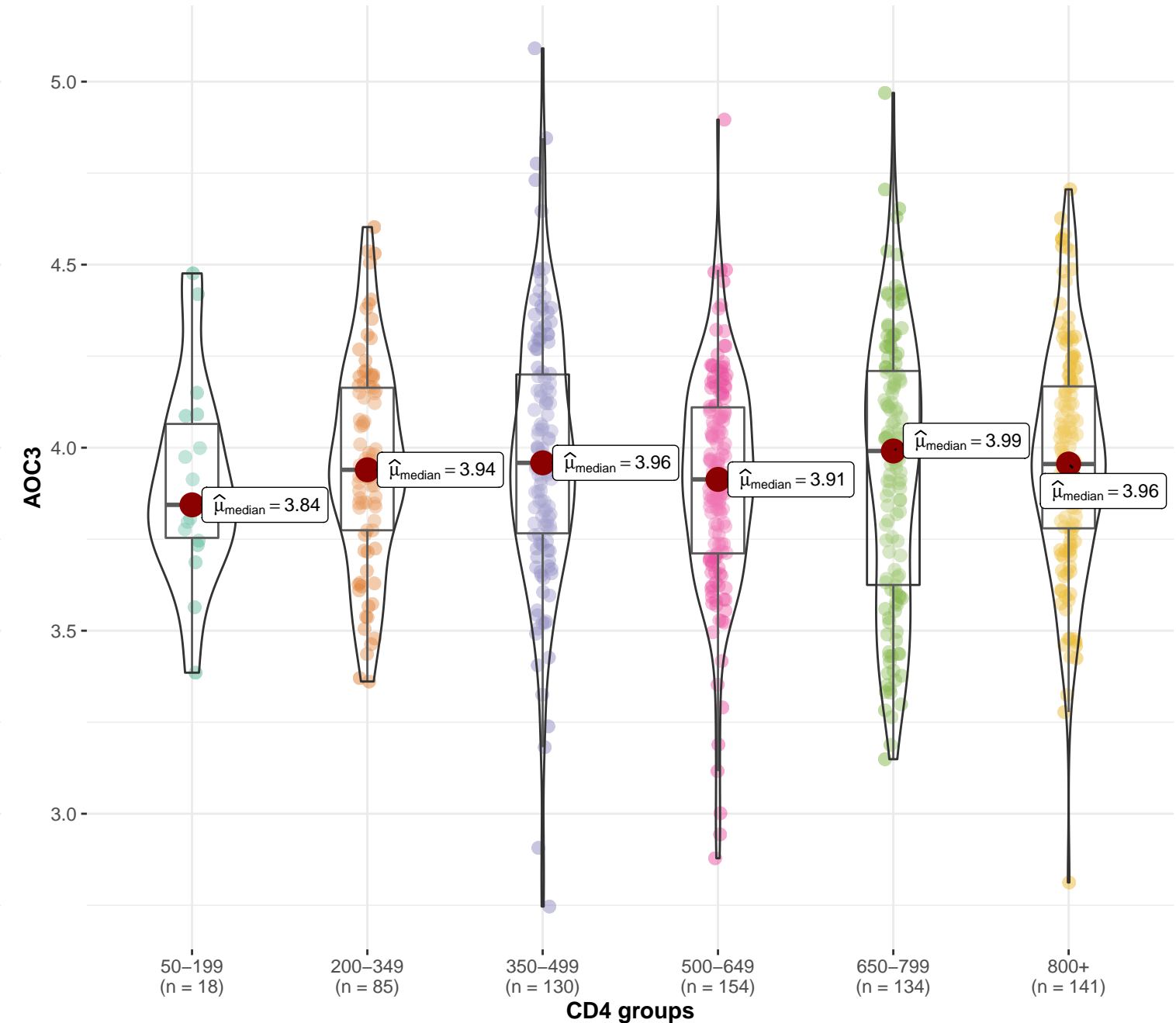
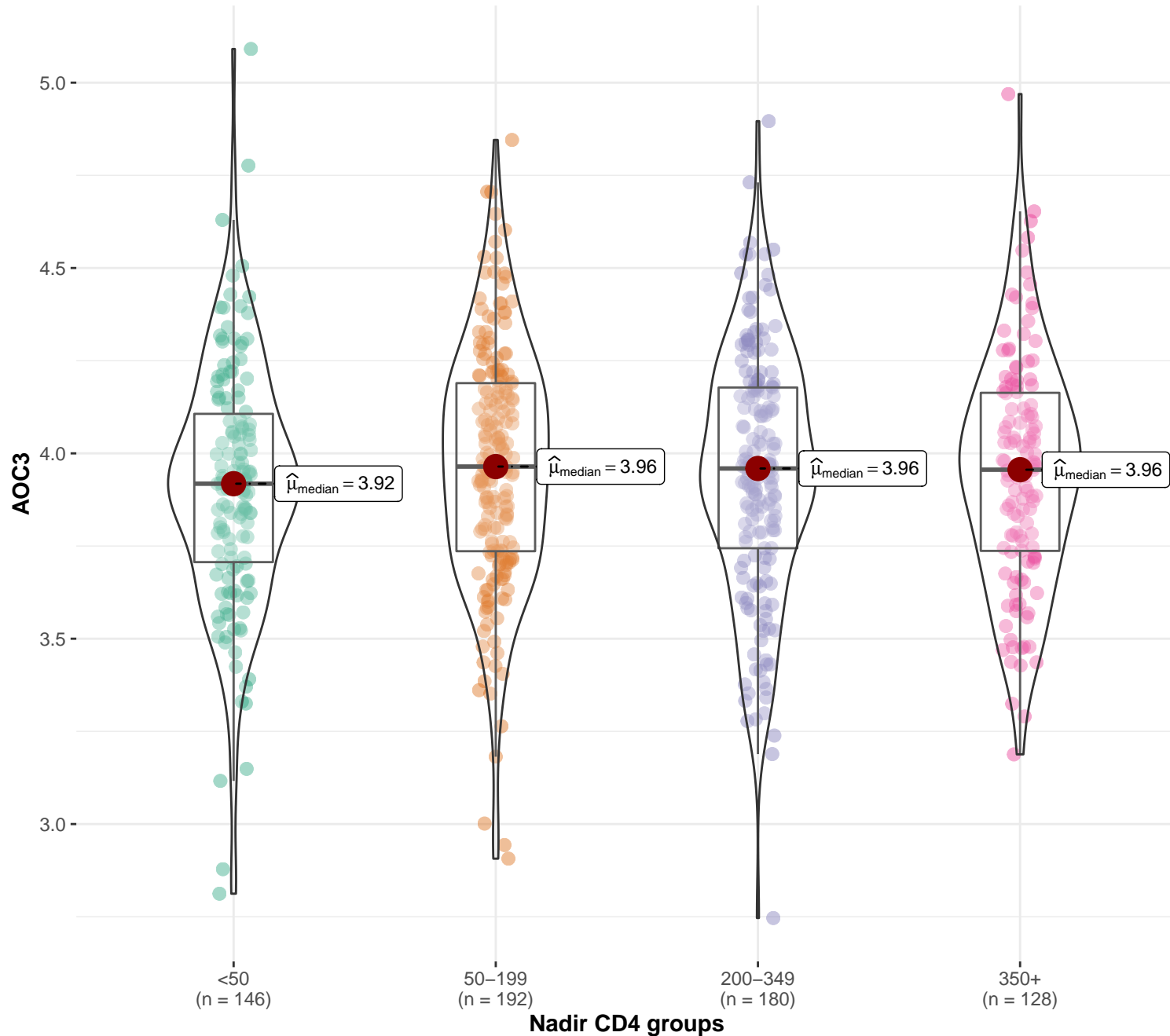
Distribution of AOC3 across different CD4 groups

Distribution of AOC3 across nadir CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(3) = 2.45, p = 0.484, \hat{\epsilon}^2_{\text{ordinal}} = 3.80\text{e-}03, \text{CI}_{95\%} [1.12\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of AOC3 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 4.14, p = 0.530, \hat{\epsilon}^2_{\text{ordinal}} = 6.26\text{e-}03, \text{CI}_{95\%} [3.45\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Pairwise test: **Dunn test**; Comparisons shown: **only significant**

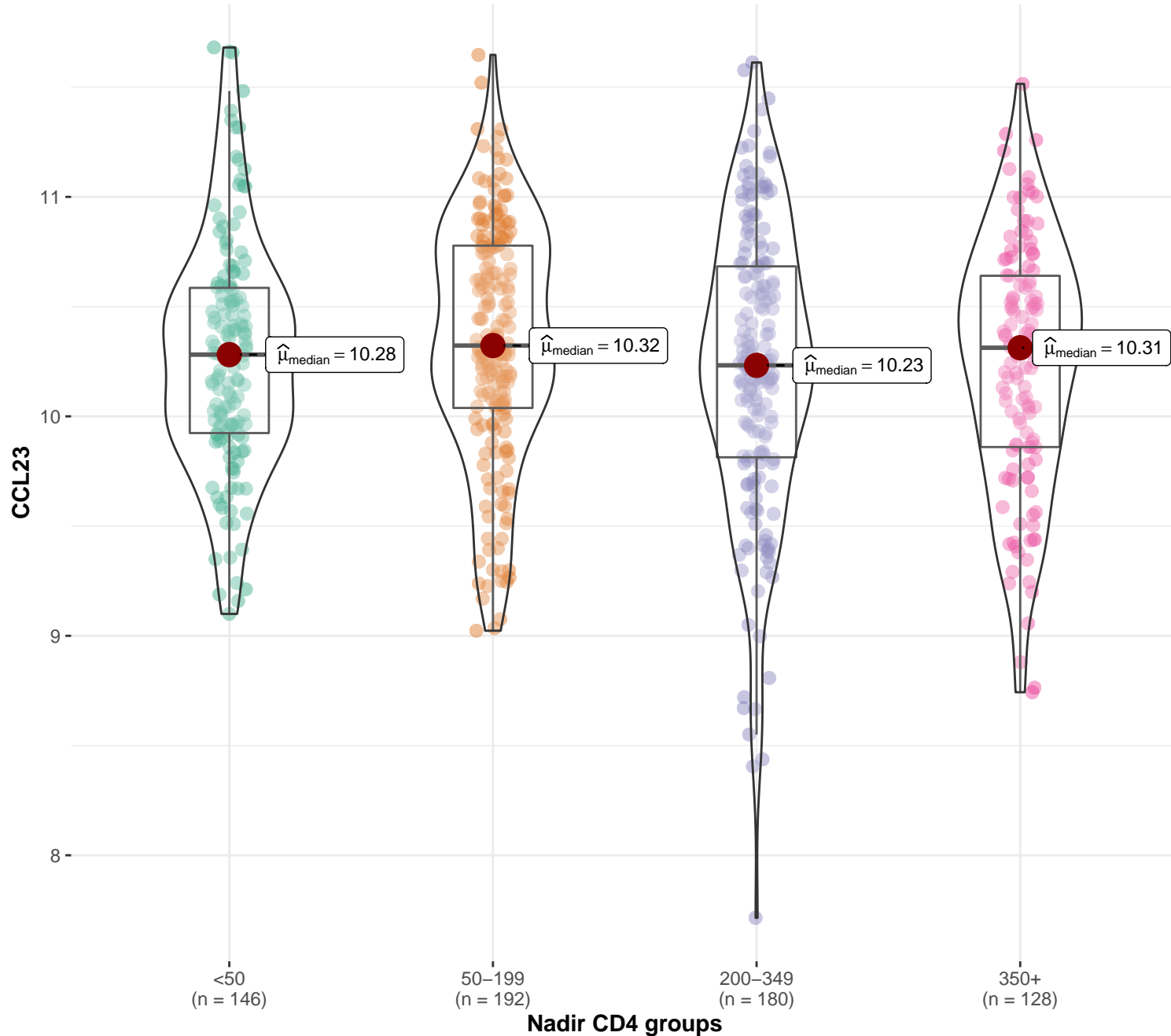
Distribution of CCL23 across different CD4 groups

Distribution of CCL23 across nadir CD4 groups

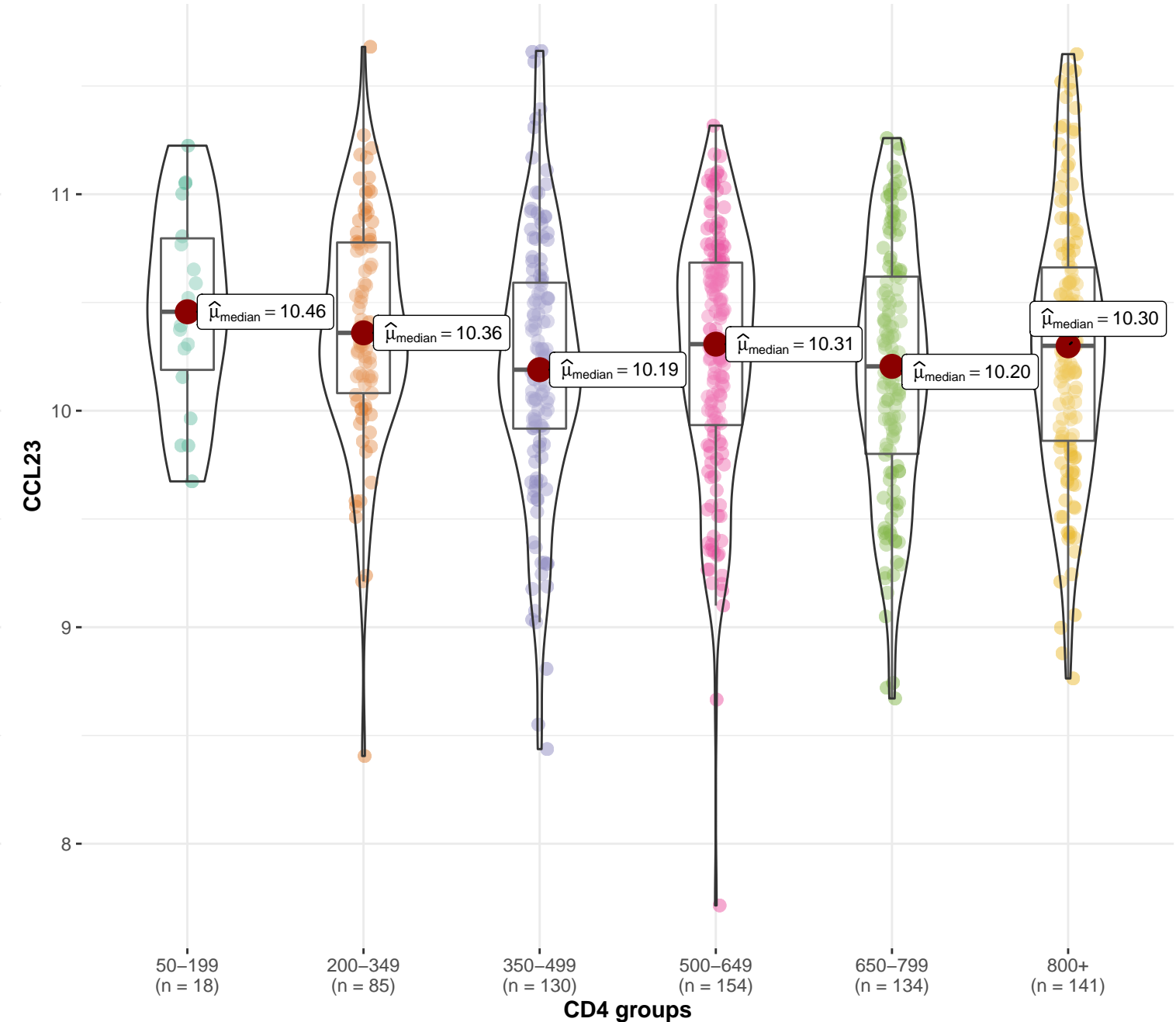
$\chi^2_{\text{Kruskal-Wallis}}(3) = 4.46, p = 0.216, \hat{\epsilon}^2_{\text{ordinal}} = 6.91\text{e-}03, \text{CI}_{95\%} [2.02\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of CCL23 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 10.16, p = 0.071, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, \text{CI}_{95\%} [6.47\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

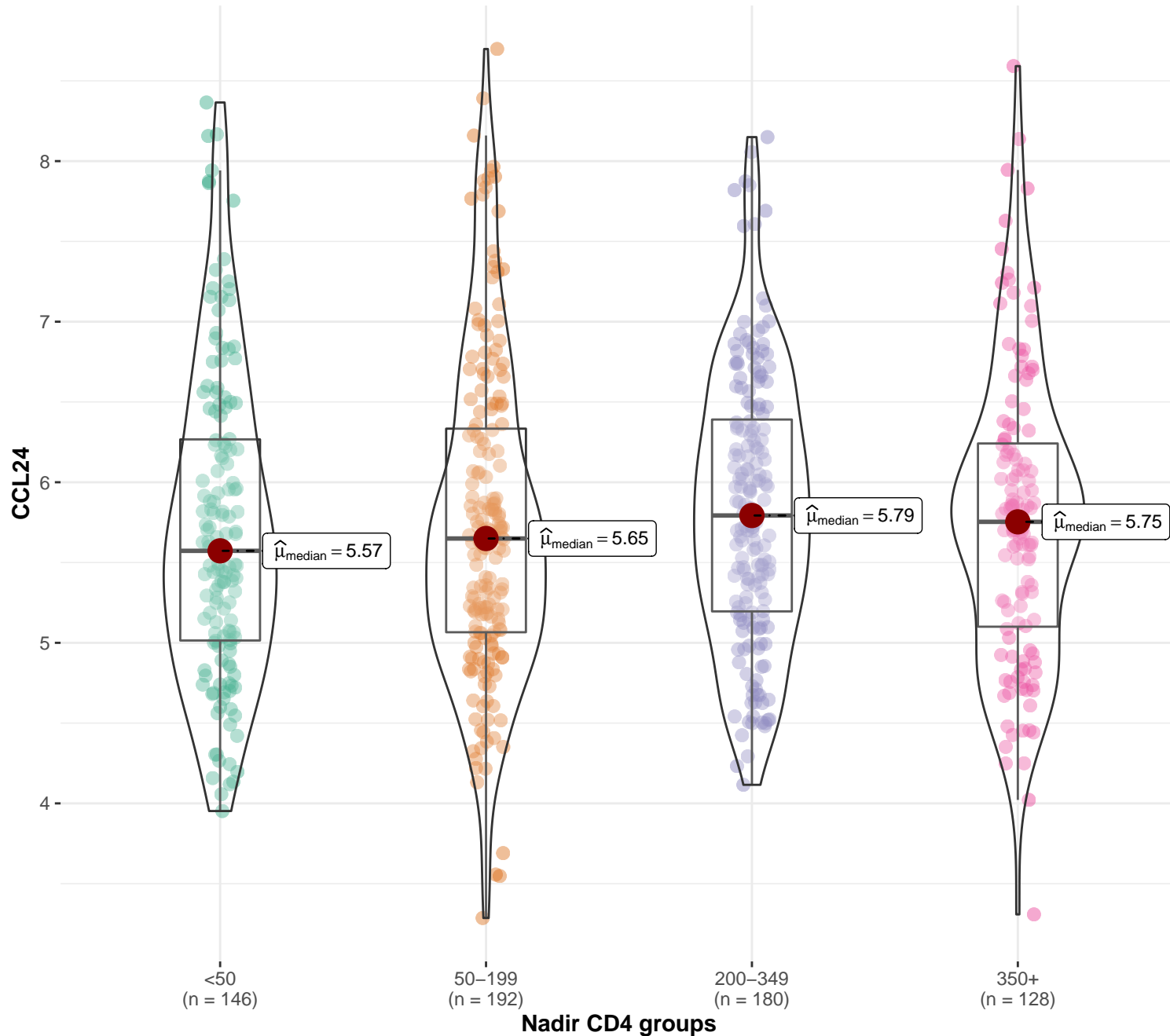
Distribution of CCL24 across different CD4 groups

Distribution of CCL24 across nadir CD4 groups

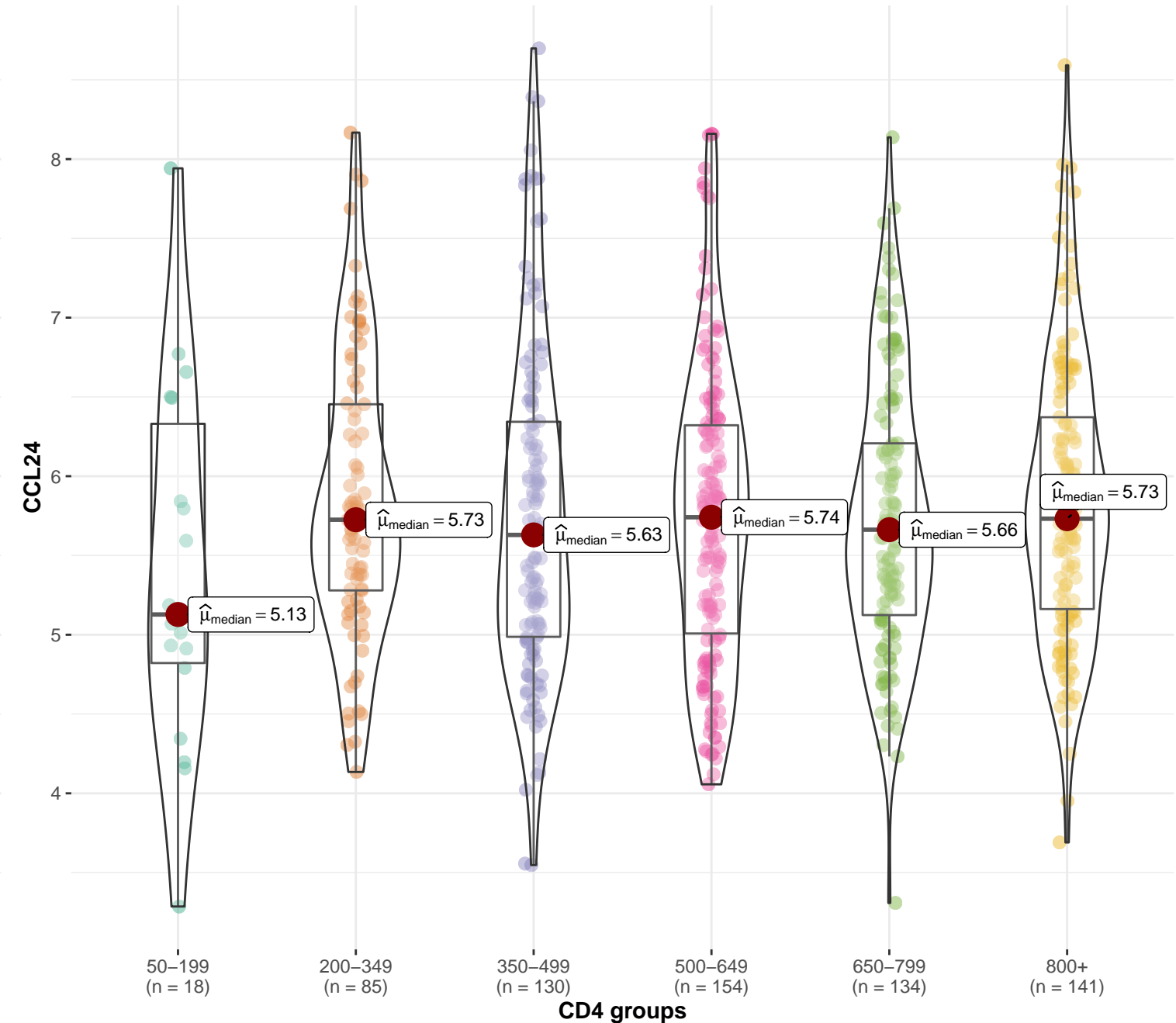
$\chi^2_{\text{Kruskal-Wallis}}(3) = 3.32, p = 0.345, \hat{\epsilon}^2_{\text{ordinal}} = 5.14\text{e-}03, \text{CI}_{95\%} [2.64\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of CCL24 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 4.52, p = 0.477, \hat{\epsilon}^2_{\text{ordinal}} = 6.84\text{e-}03, \text{CI}_{95\%} [4.64\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

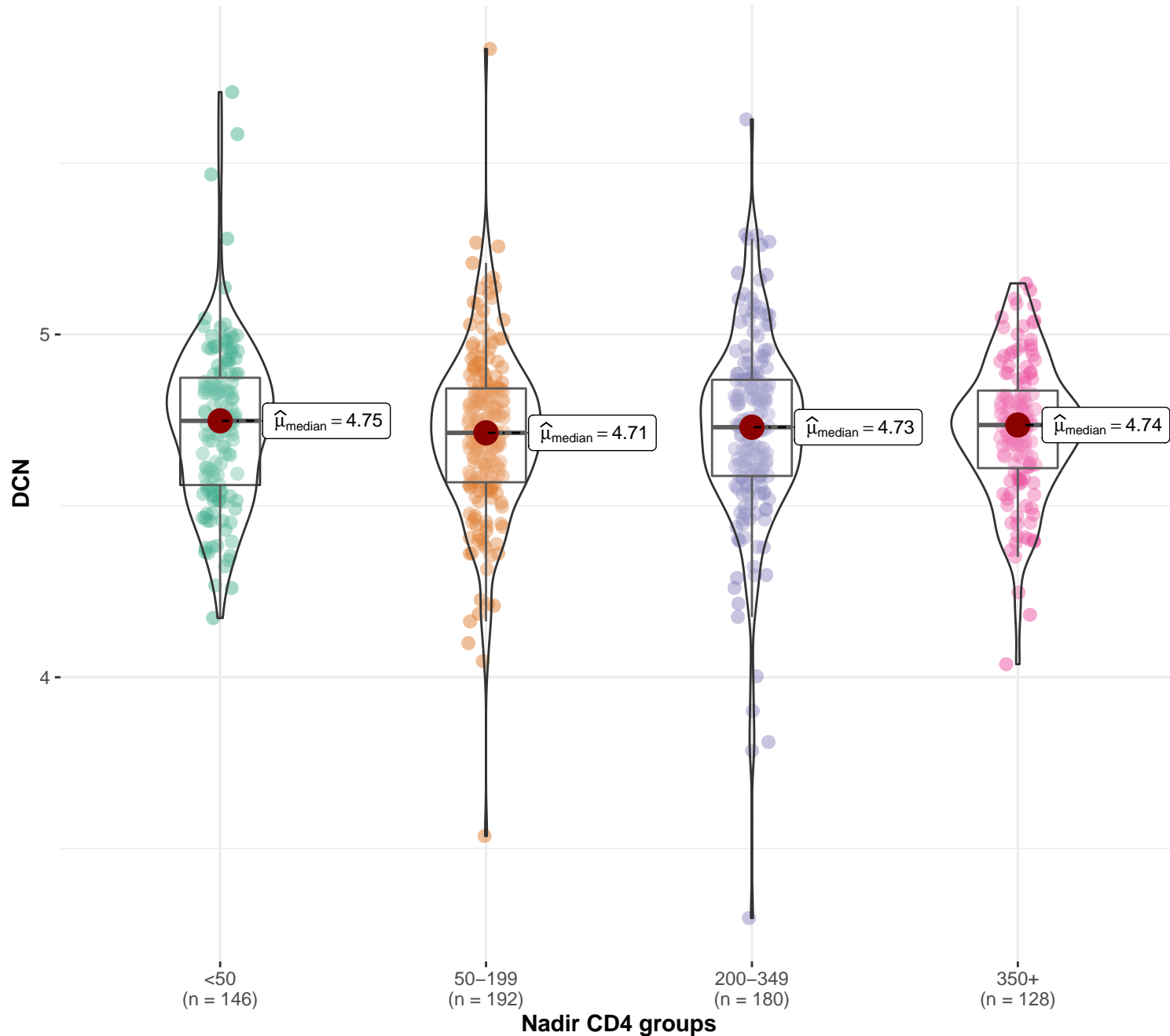
Distribution of DCN across different CD4 groups

Distribution of DCN across nadir CD4 groups

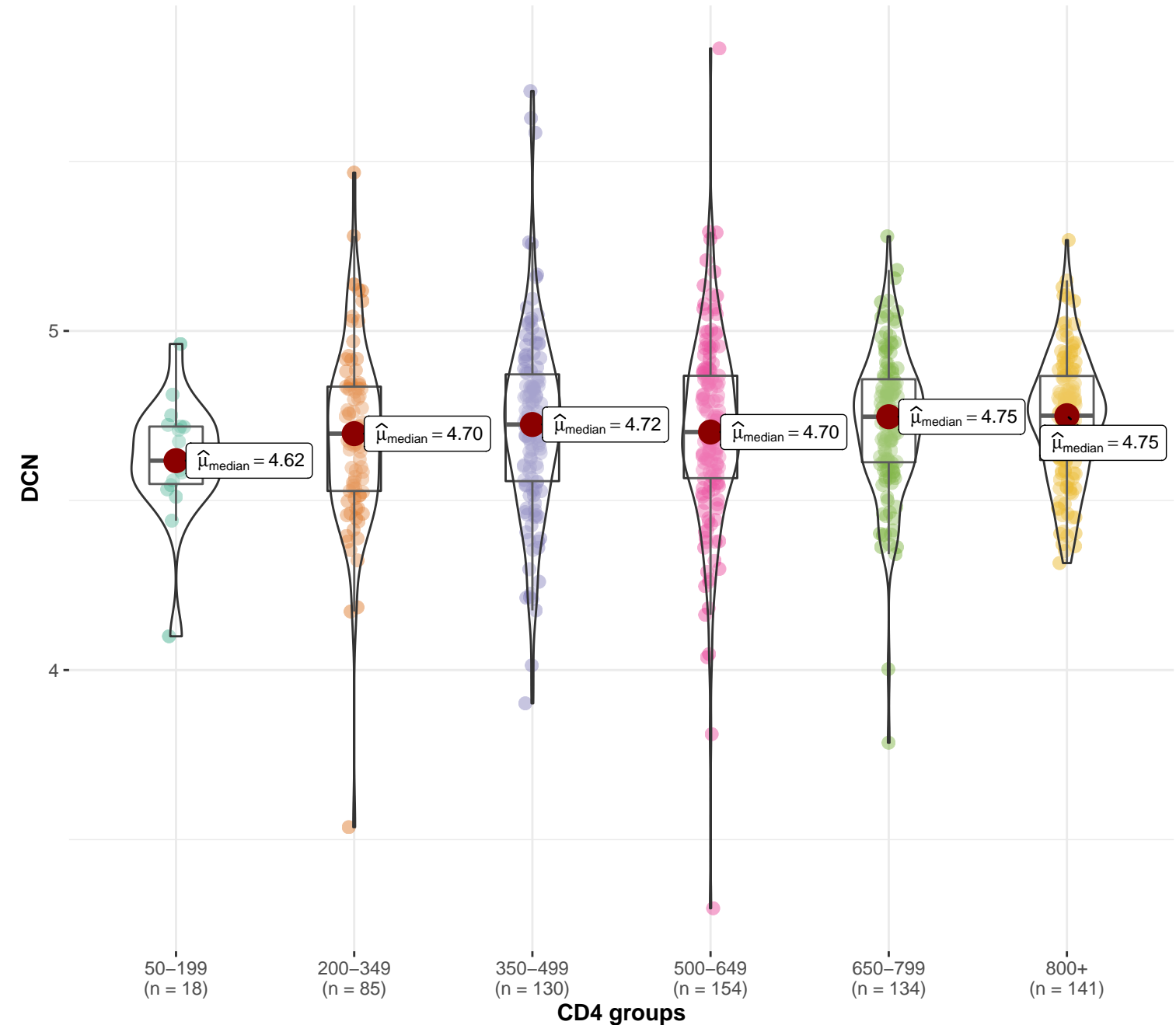
$\chi^2_{\text{Kruskal-Wallis}}(3) = 0.89, p = 0.828, \hat{\epsilon}^2_{\text{ordinal}} = 1.38\text{e-}03, \text{CI}_{95\%} [1.01\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of DCN across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 8.60, p = 0.126, \hat{\epsilon}^2_{\text{ordinal}} = 0.01, \text{CI}_{95\%} [7.57\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

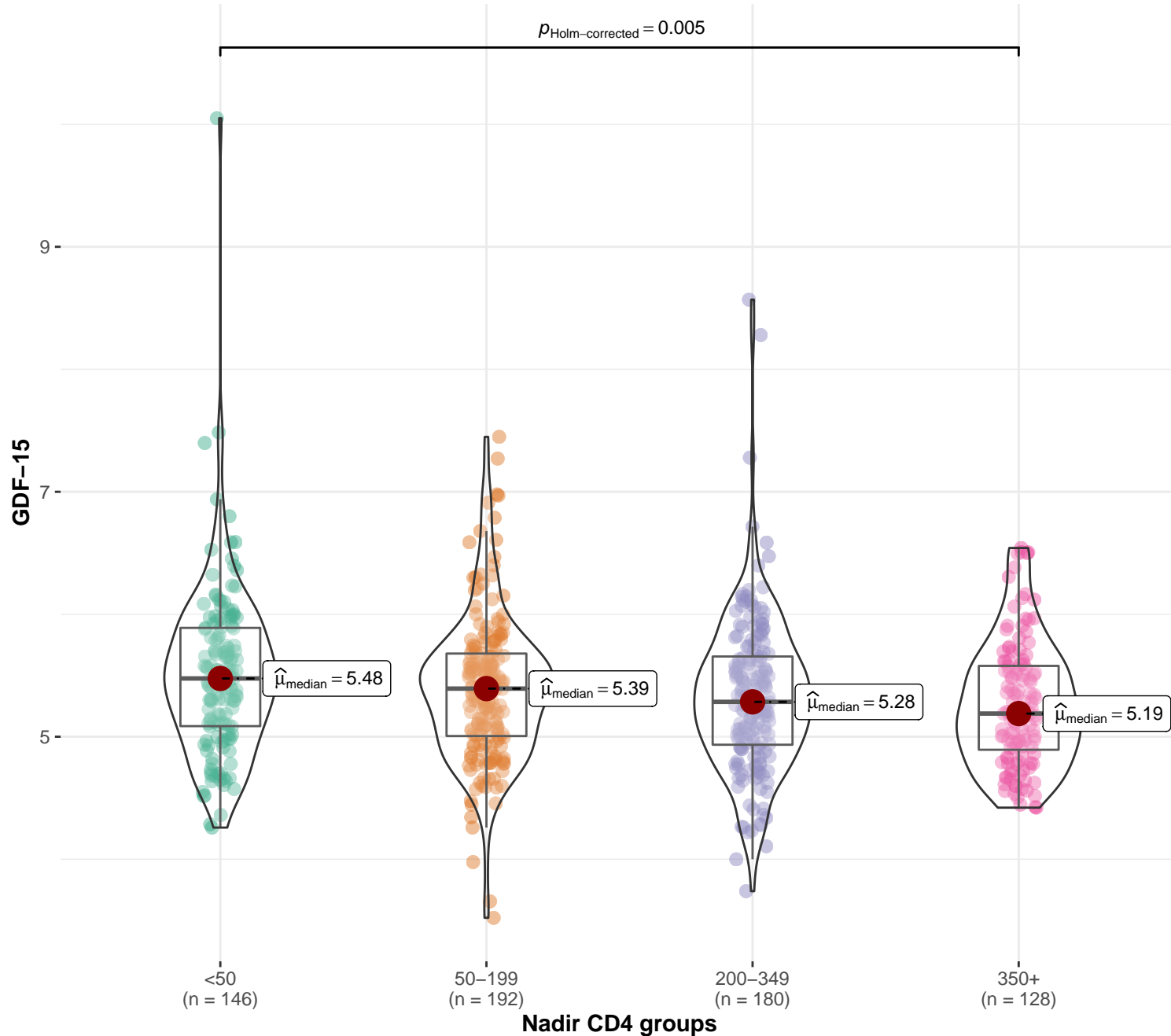
Distribution of GDF-15 across different CD4 groups

Distribution of GDF-15 across nadir CD4 groups

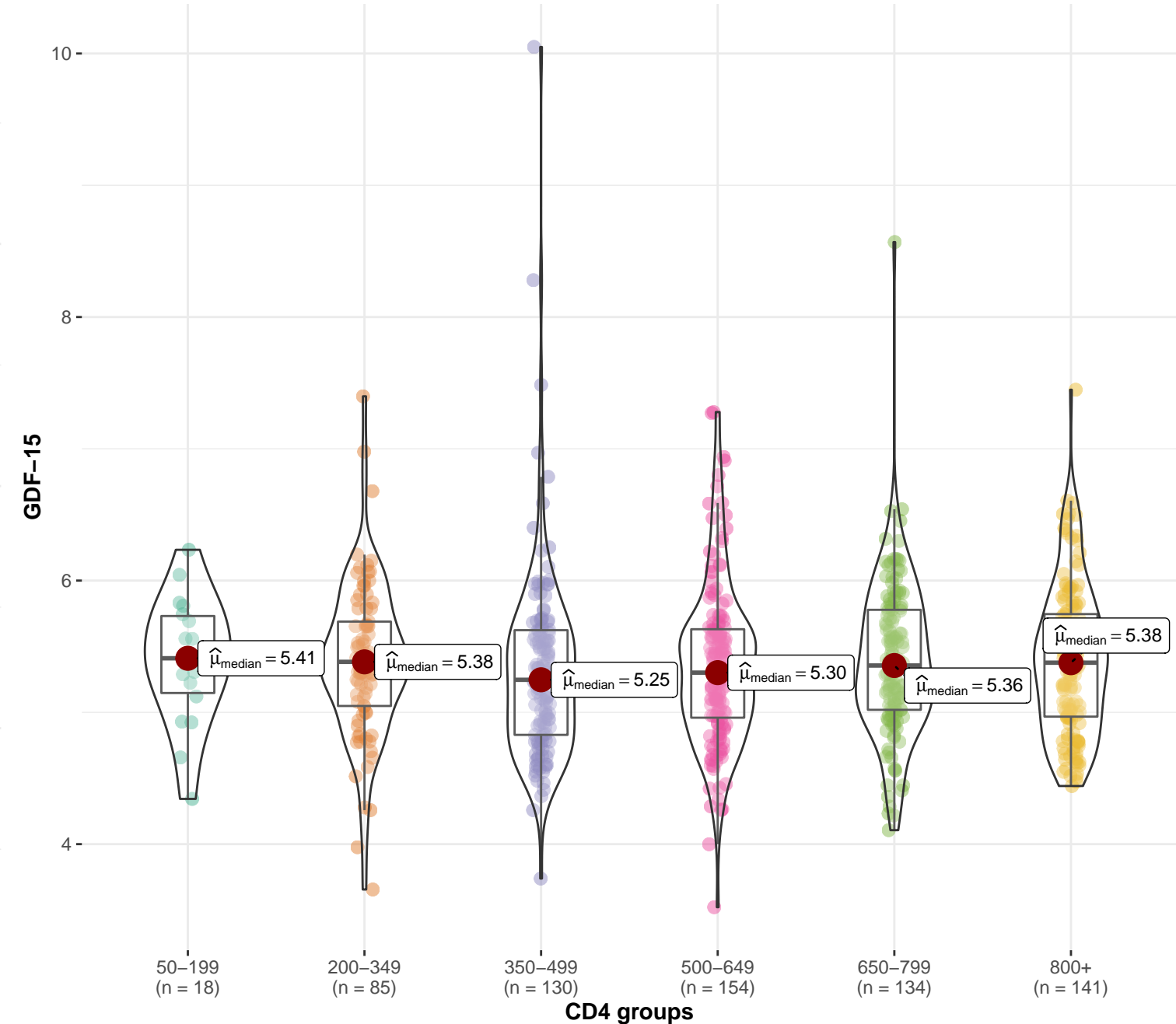
$\chi^2_{\text{Kruskal-Wallis}}(3) = 12.49, p = 0.006, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, \text{CI}_{95\%} [7.50\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of GDF-15 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 4.90, p = 0.429, \hat{\epsilon}^2_{\text{ordinal}} = 7.41\text{e-}03, \text{CI}_{95\%} [2.83\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

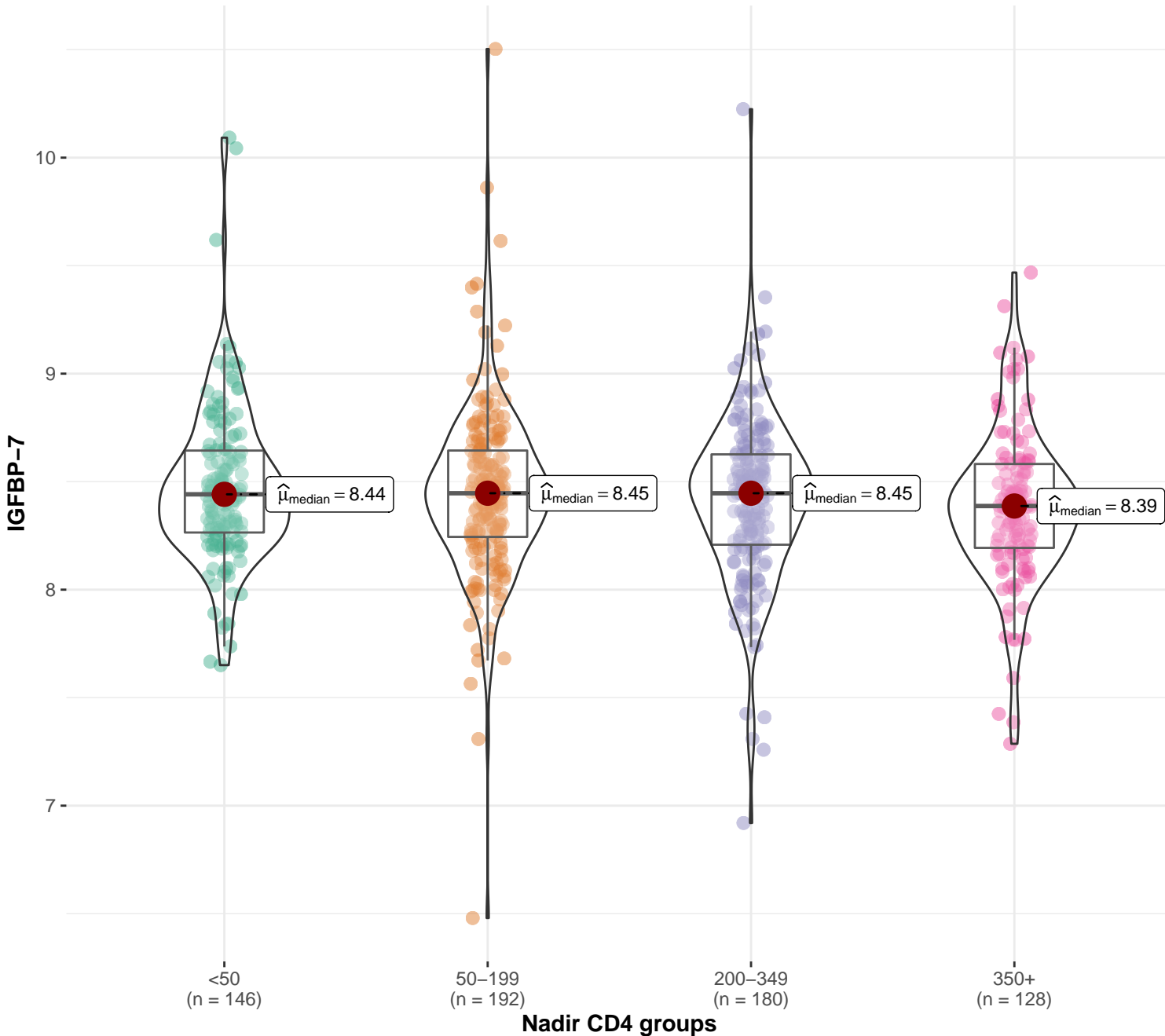
Distribution of IGFBP-7 across different CD4 groups

Distribution of IGFBP-7 across nadir CD4 groups

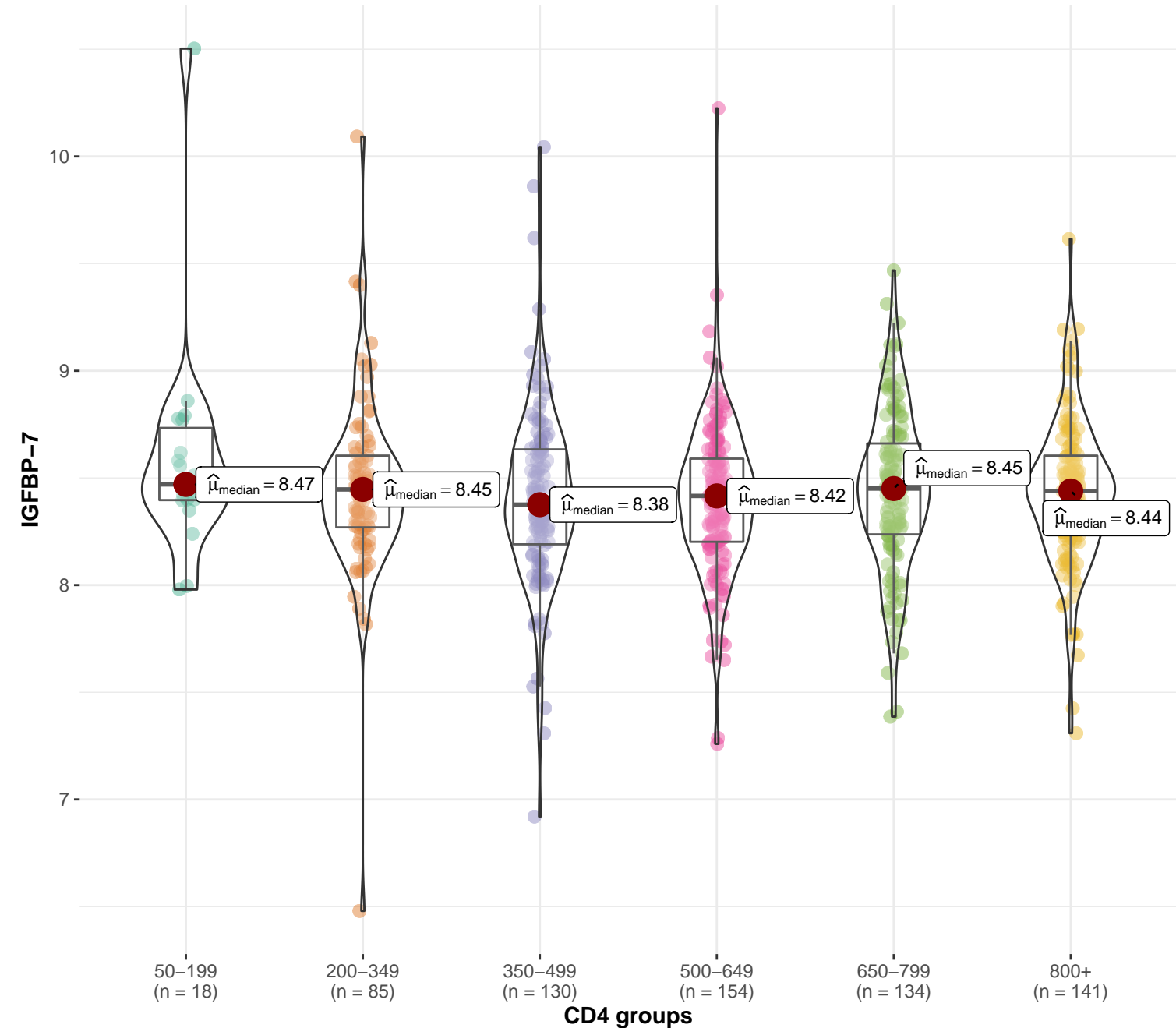
$\chi^2_{\text{Kruskal-Wallis}}(3) = 4.13, p = 0.248, \hat{\epsilon}_{\text{ordinal}}^2 = 6.40\text{e-}03, \text{CI}_{95\%} [1.60\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of IGFBP-7 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 3.50, p = 0.623, \hat{\epsilon}_{\text{ordinal}}^2 = 5.30\text{e-}03, \text{CI}_{95\%} [4.41\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

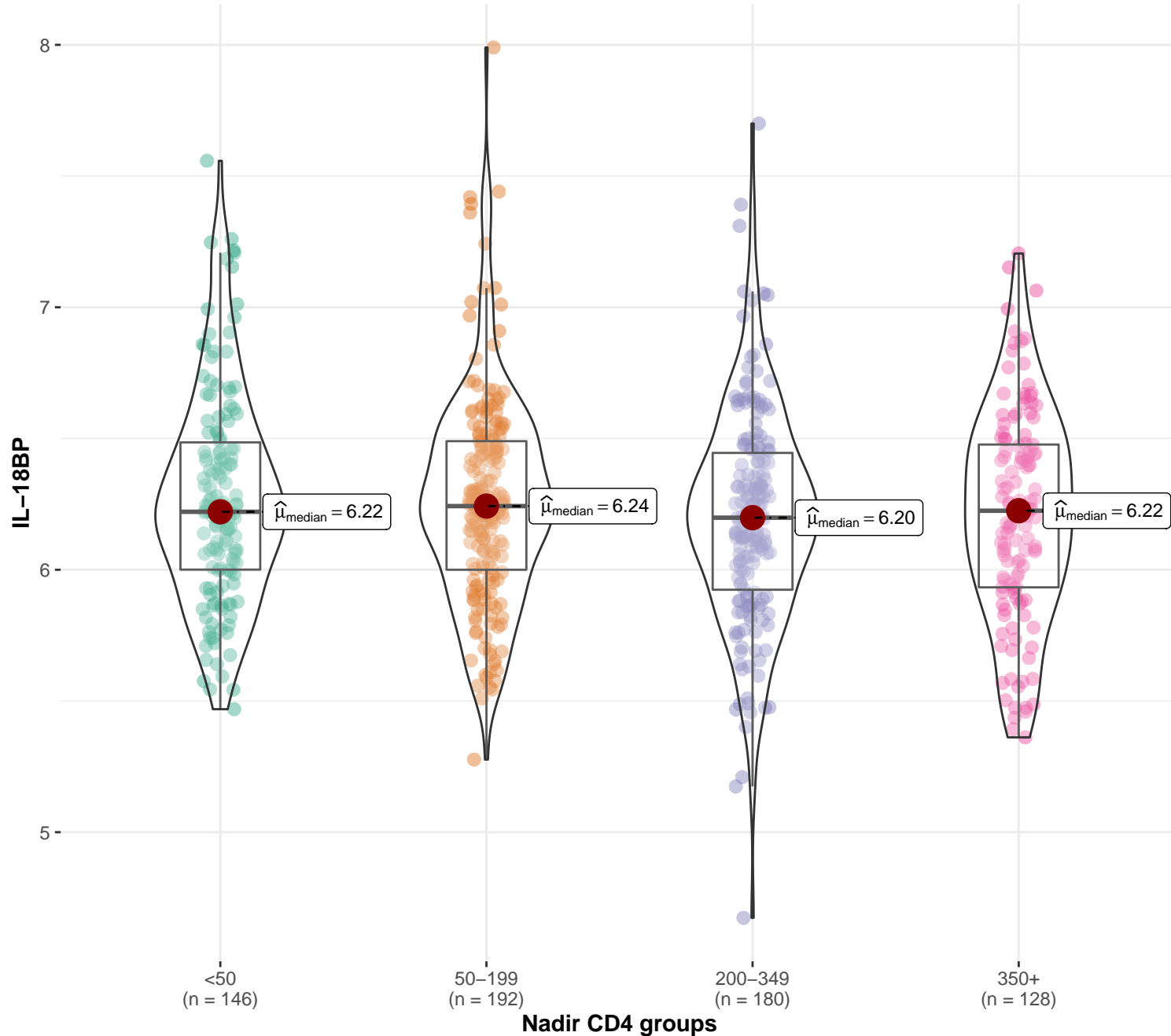


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of IL-18BP across different CD4 groups

Distribution of IL-18BP across nadir CD4 groups

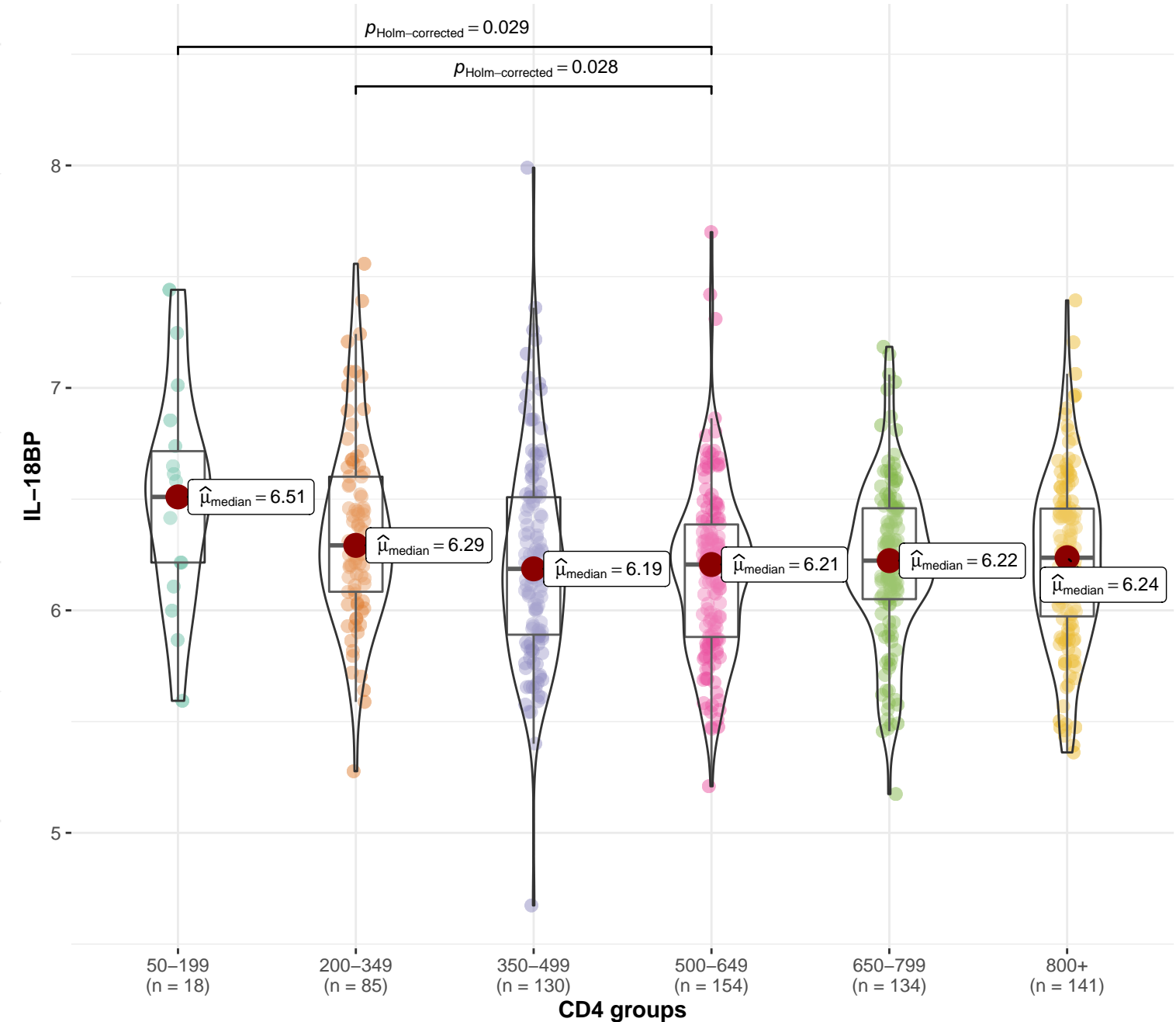
$\chi^2_{\text{Kruskal-Wallis}}(3) = 2.38, p = 0.498, \hat{\epsilon}^2_{\text{ordinal}} = 3.69\text{e-}03, \text{CI}_{95\%} [1.07\text{e-}03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of IL-18BP across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 17.06, p = 0.004, \hat{\epsilon}^2_{\text{ordinal}} = 0.03, \text{CI}_{95\%} [0.01, 1.00], n_{\text{obs}} = 662$

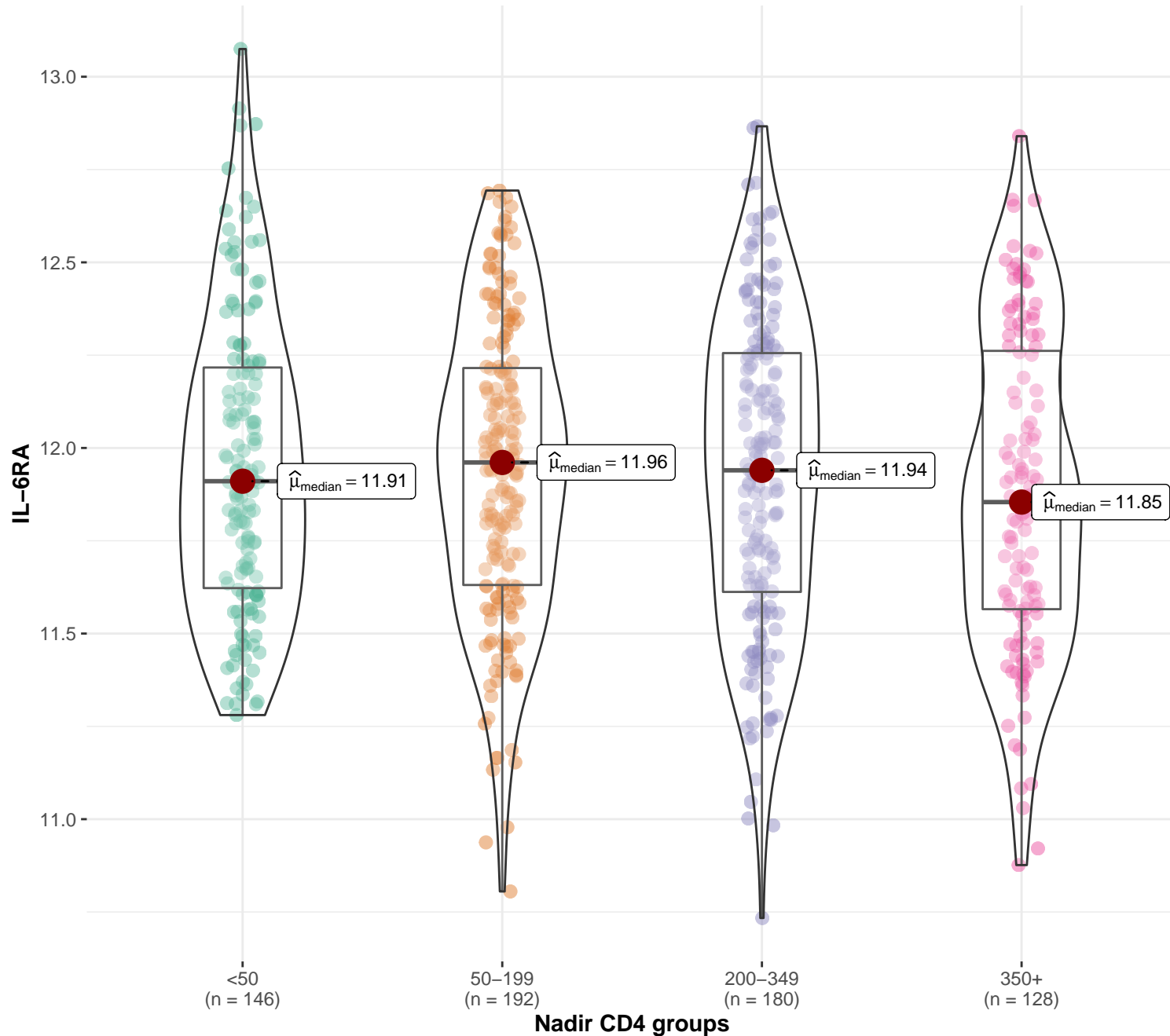


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of IL-6RA across different CD4 groups

Distribution of IL-6RA across nadir CD4 groups

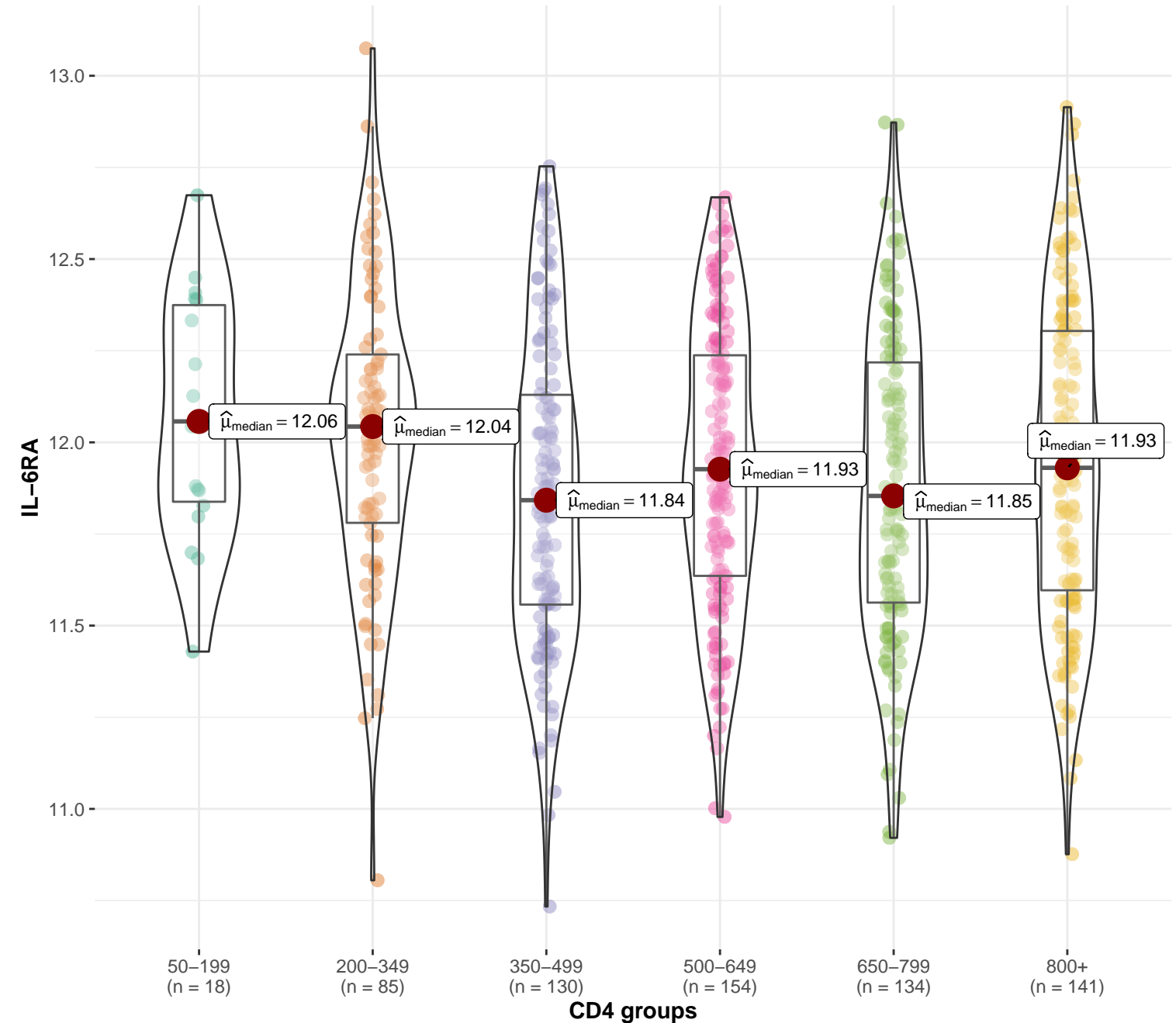
$\chi^2_{\text{Kruskal-Wallis}}(3) = 2.79, p = 0.424, \hat{\epsilon}^2_{\text{ordinal}} = 4.33\text{e-}03, \text{CI}_{95\%} [1.32\text{e-}03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of IL-6RA across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 11.52, p = 0.042, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, \text{CI}_{95\%} [0.01, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

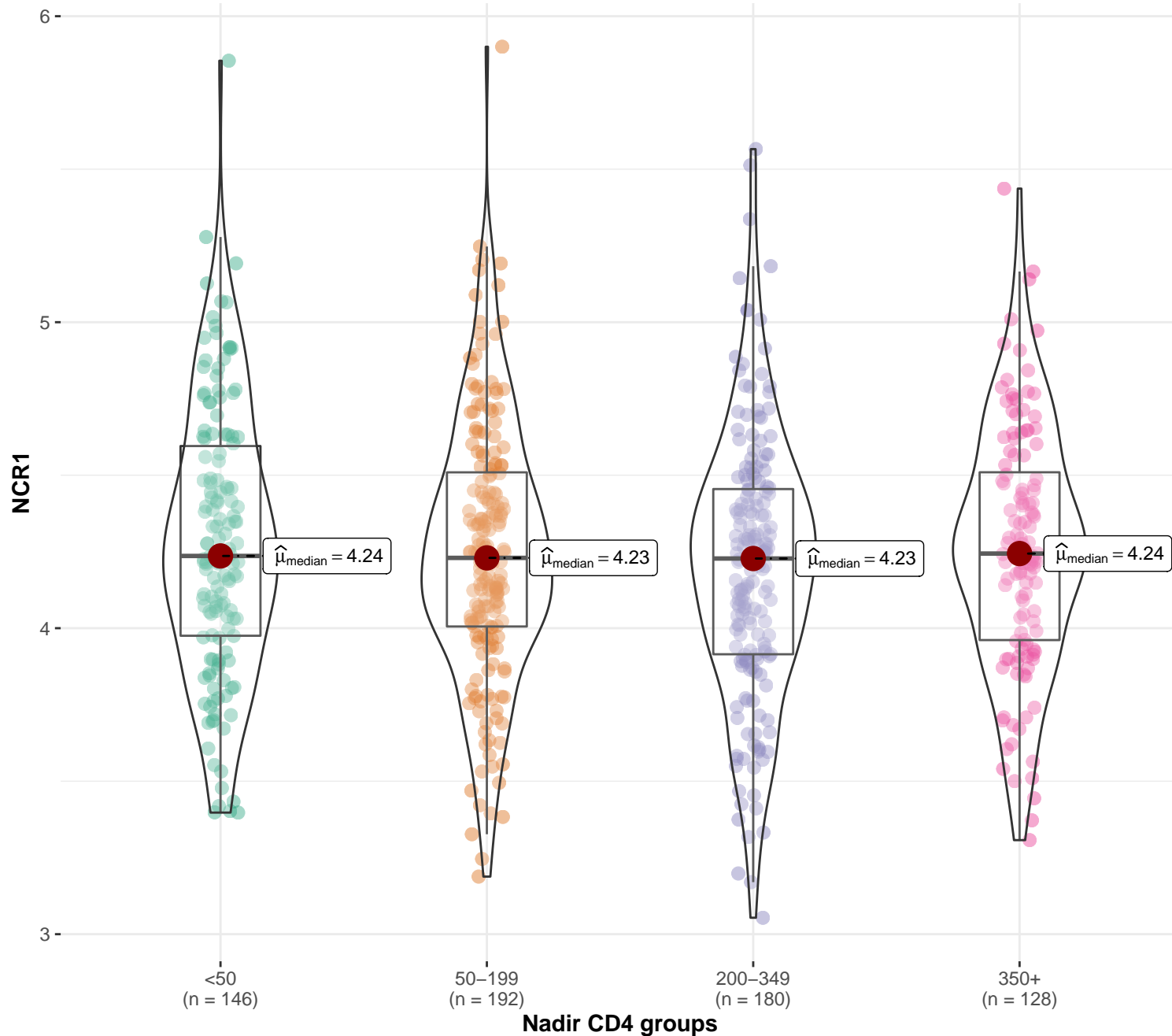
Distribution of NCR1 across different CD4 groups

Distribution of NCR1 across nadir CD4 groups

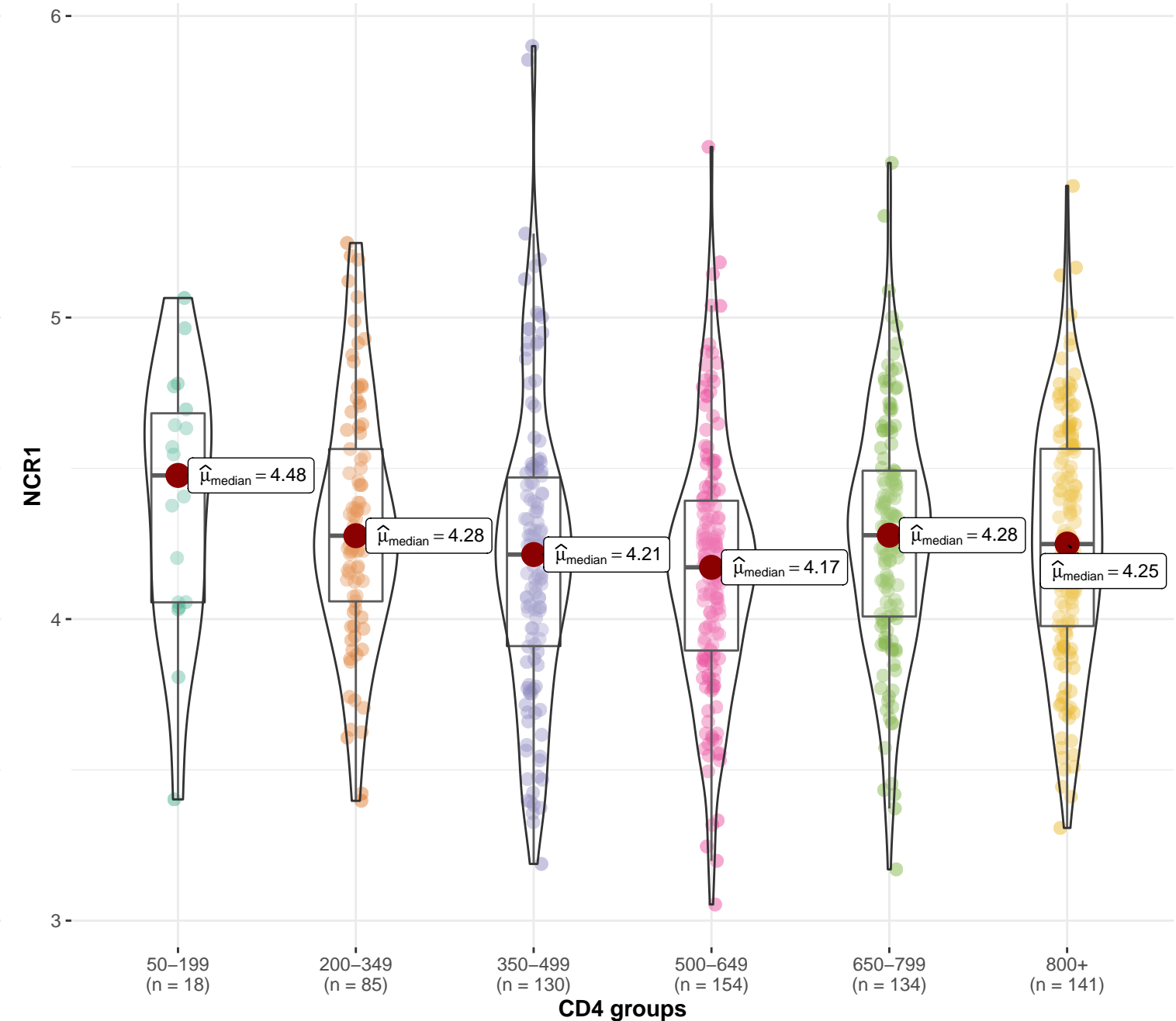
$\chi^2_{\text{Kruskal-Wallis}}(3) = 2.36, p = 0.501, \hat{\epsilon}^2_{\text{ordinal}} = 3.66\text{e-}03, \text{CI}_{95\%} [1.40\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of NCR1 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 11.94, p = 0.036, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, \text{CI}_{95\%} [9.59\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

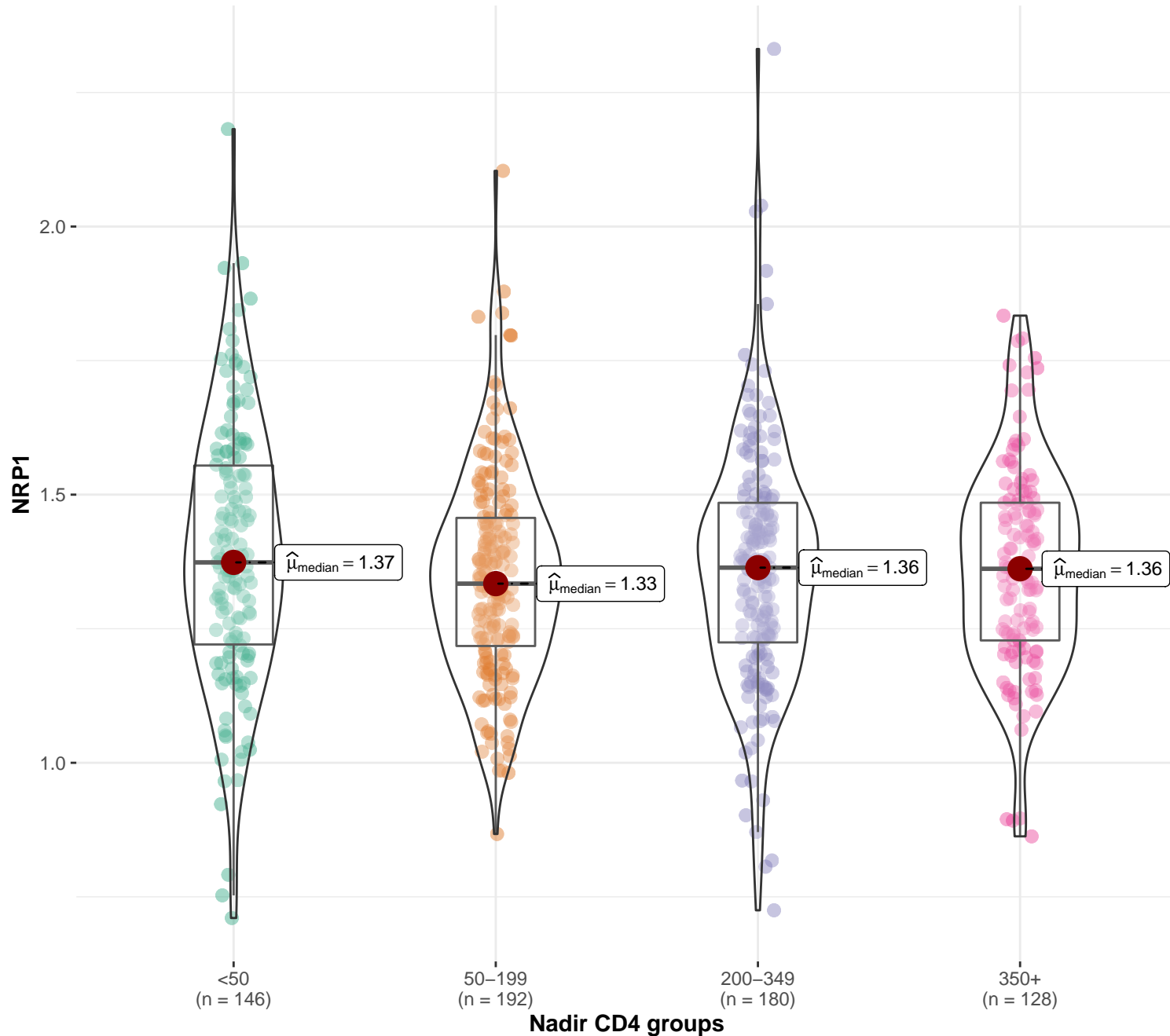
Distribution of NRP1 across different CD4 groups

Distribution of NRP1 across nadir CD4 groups

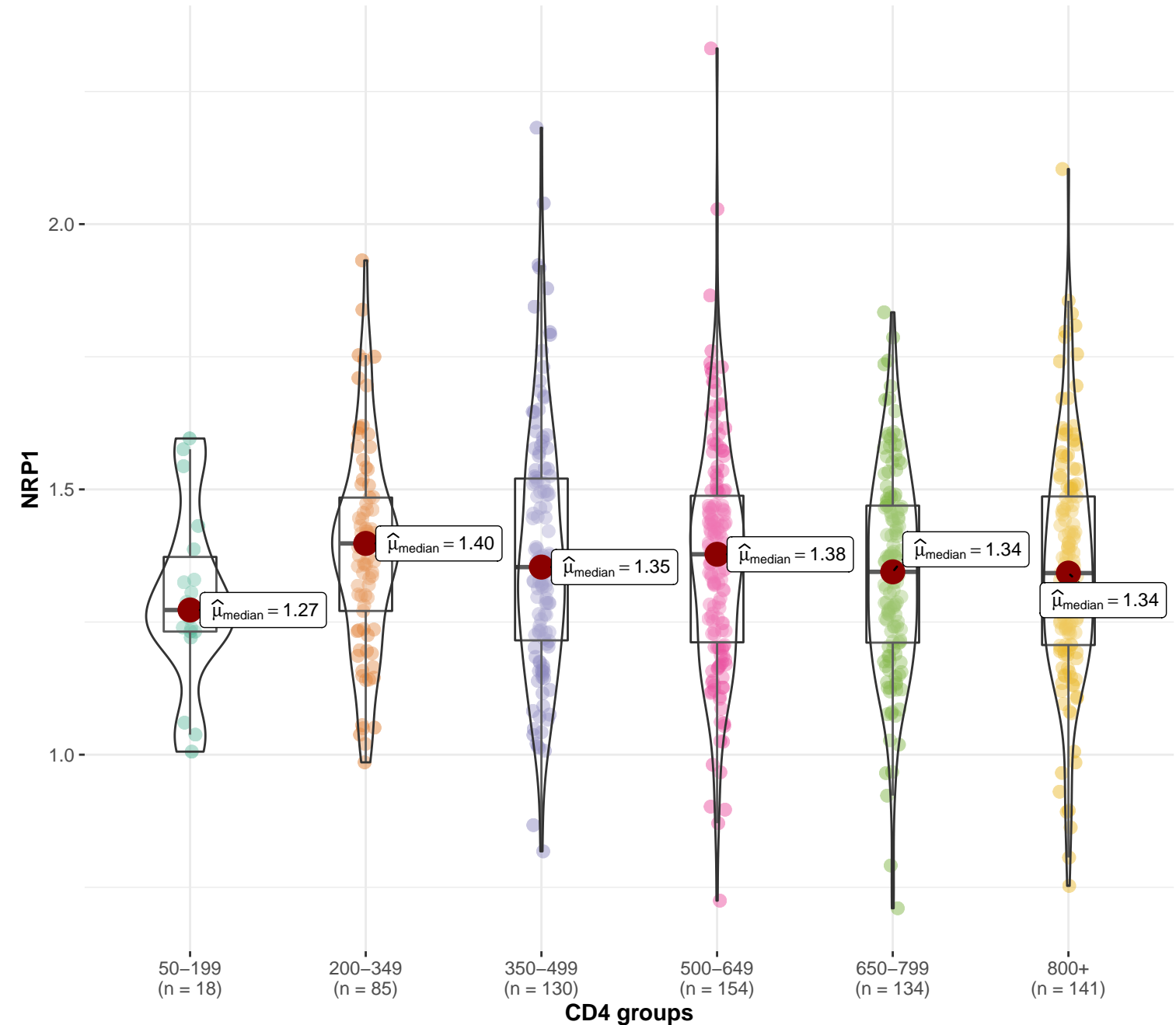
$\chi^2_{\text{Kruskal-Wallis}}(3) = 3.84, p = 0.280, \hat{\epsilon}^2_{\text{ordinal}} = 5.95\text{e-}03, \text{CI}_{95\%} [1.31\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of NRP1 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 4.43, p = 0.490, \hat{\epsilon}^2_{\text{ordinal}} = 6.70\text{e-}03, \text{CI}_{95\%} [4.30\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

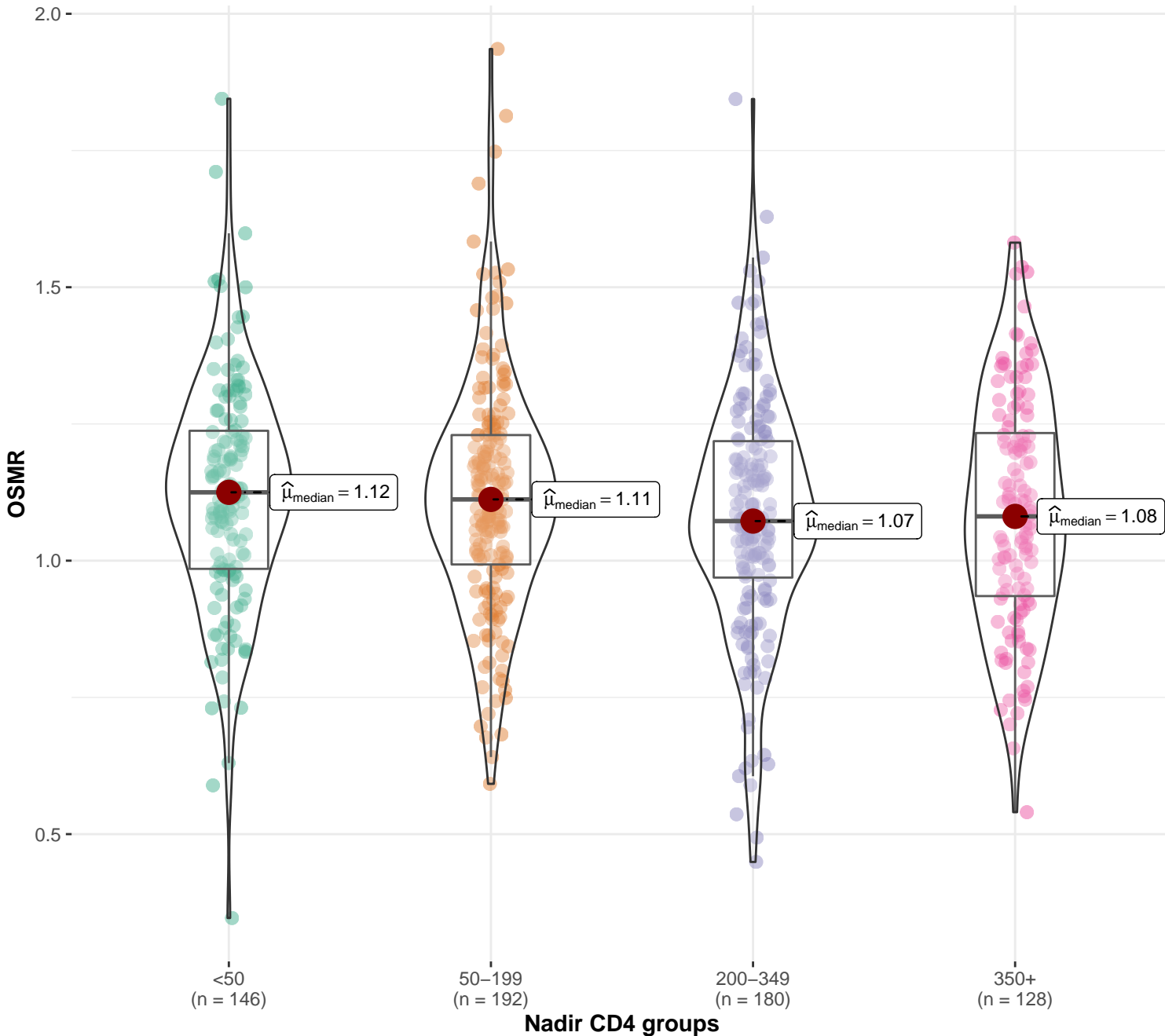


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of OSMR across different CD4 groups

Distribution of OSMR across nadir CD4 groups

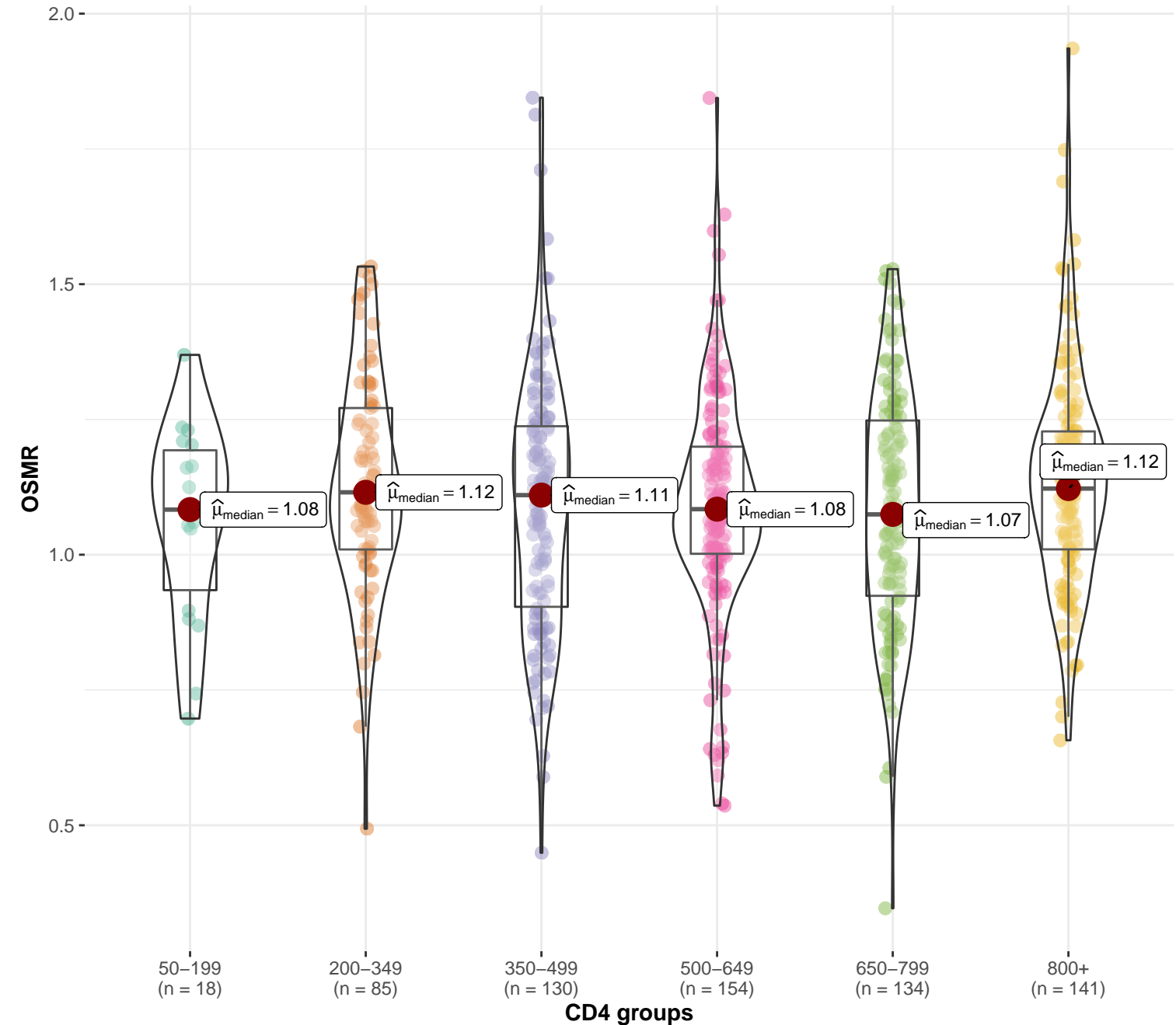
$\chi^2_{\text{Kruskal-Wallis}}(3) = 3.82, p = 0.282, \hat{\epsilon}^2_{\text{ordinal}} = 5.92e-03, CI_{95\%} [1.48e-03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of OSMR across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 6.28, p = 0.280, \hat{\epsilon}^2_{\text{ordinal}} = 9.50e-03, CI_{95\%} [4.48e-03, 1.00], n_{\text{obs}} = 662$

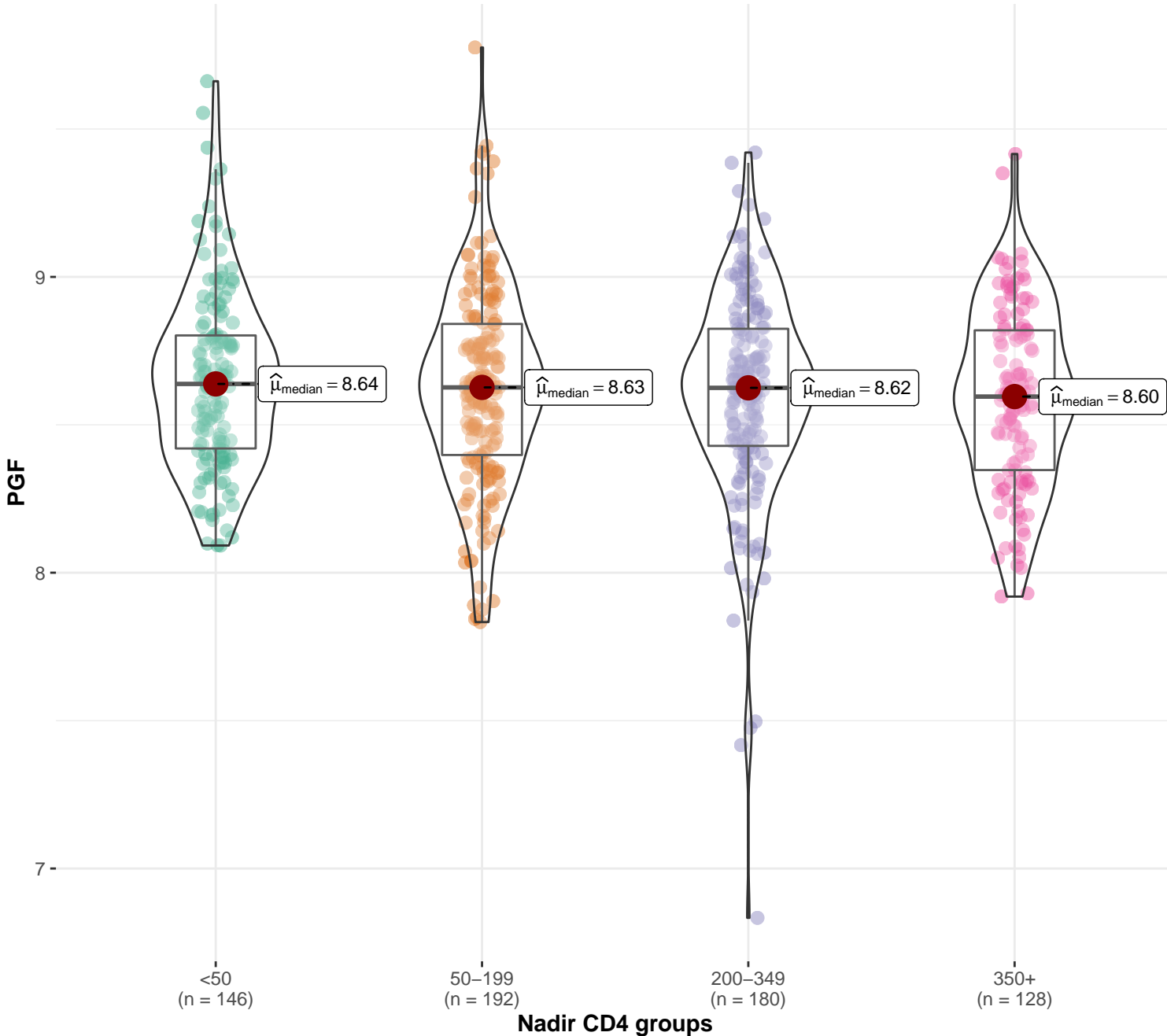


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of PGF across different CD4 groups

Distribution of PGF across nadir CD4 groups

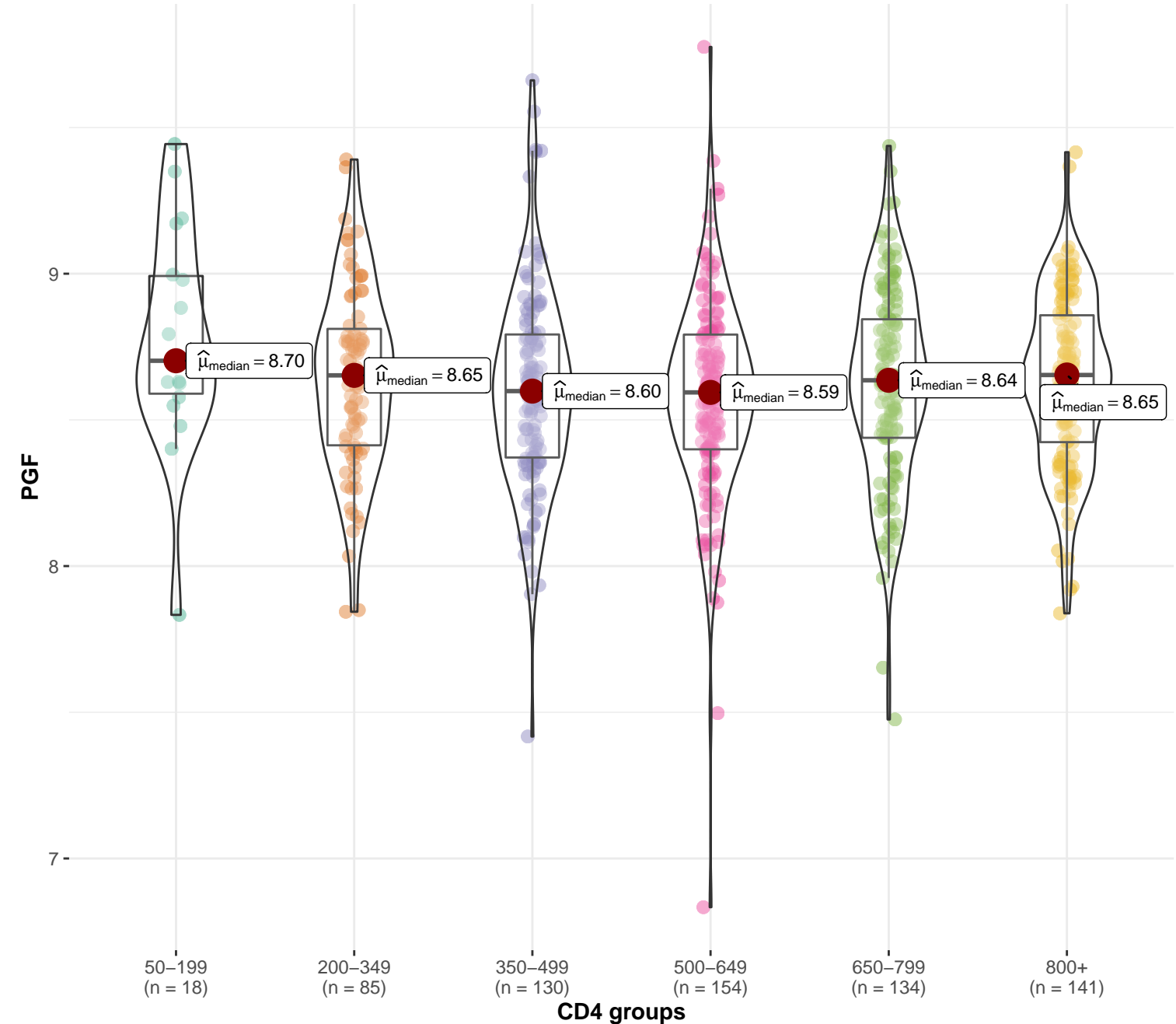
$\chi^2_{\text{Kruskal-Wallis}}(3) = 1.63, p = 0.654, \hat{\epsilon}^2_{\text{ordinal}} = 2.52\text{e-}03, \text{CI}_{95\%} [1.28\text{e-}03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of PGF across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 7.52, p = 0.184, \hat{\epsilon}^2_{\text{ordinal}} = 0.01, \text{CI}_{95\%} [5.11\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

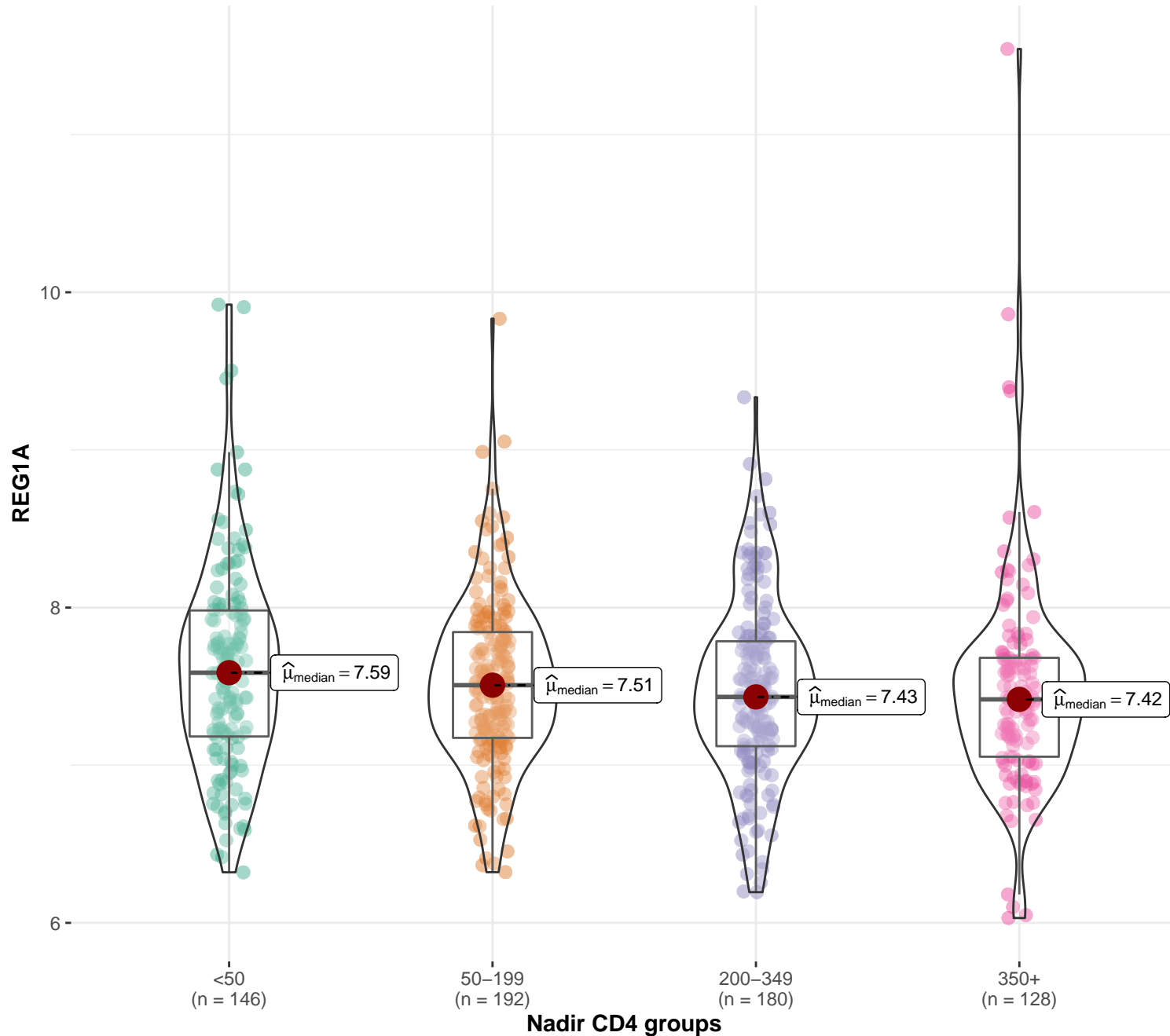
Distribution of REG1A across different CD4 groups

Distribution of REG1A across nadir CD4 groups

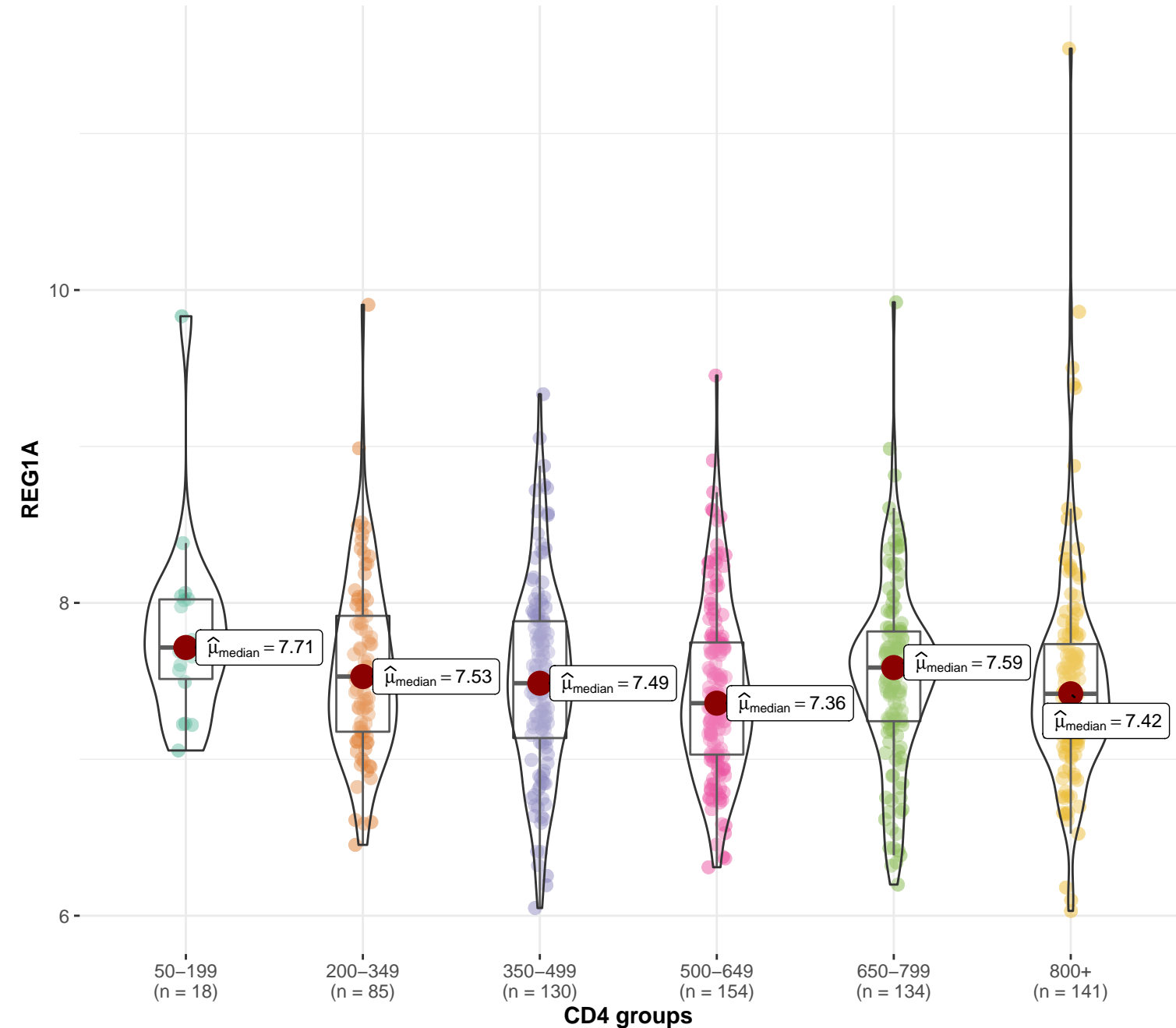
$\chi^2_{\text{Kruskal-Wallis}}(3) = 5.88, p = 0.118, \hat{\epsilon}_{\text{ordinal}}^2 = 9.12\text{e-}03, \text{CI}_{95\%} [3.72\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of REG1A across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 10.57, p = 0.061, \hat{\epsilon}_{\text{ordinal}}^2 = 0.02, \text{CI}_{95\%} [9.16\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

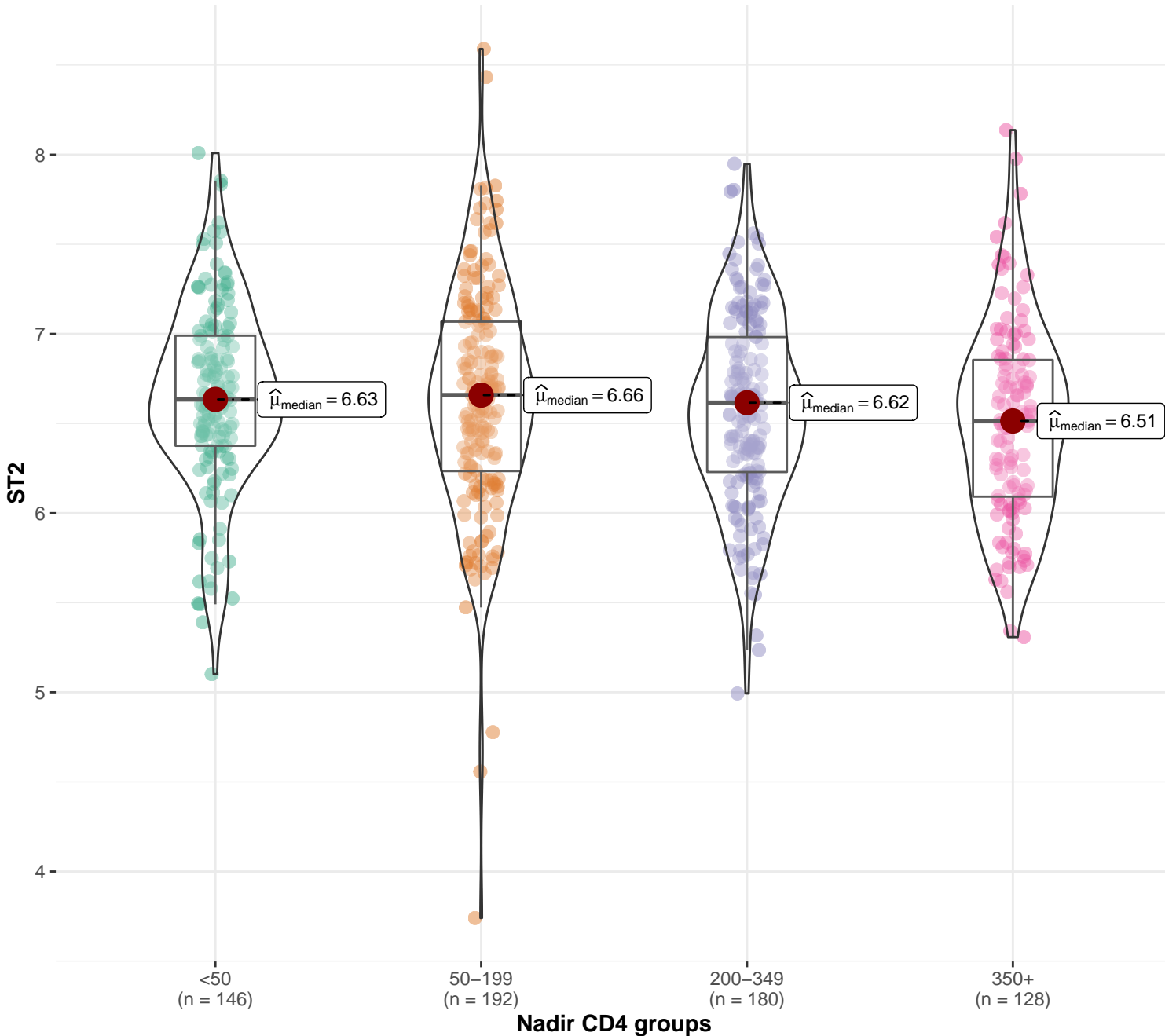


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of ST2 across different CD4 groups

Distribution of ST2 across nadir CD4 groups

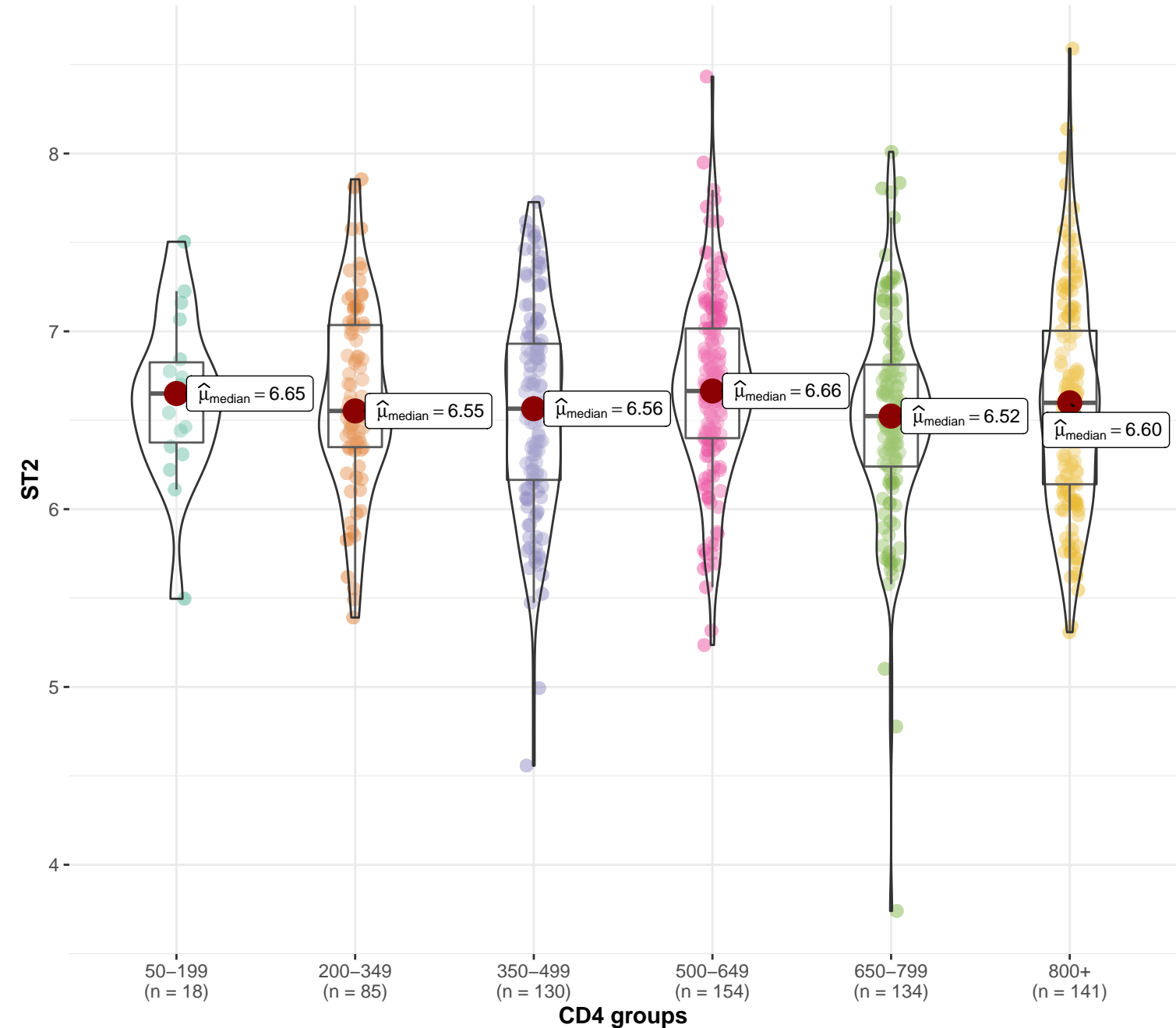
$\chi^2_{\text{Kruskal-Wallis}}(3) = 7.51, p = 0.057, \hat{\epsilon}^2_{\text{ordinal}} = 0.01, \text{CI}_{95\%} [3.36\text{e-}03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of ST2 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 7.60, p = 0.179, \hat{\epsilon}^2_{\text{ordinal}} = 0.01, \text{CI}_{95\%} [4.87\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

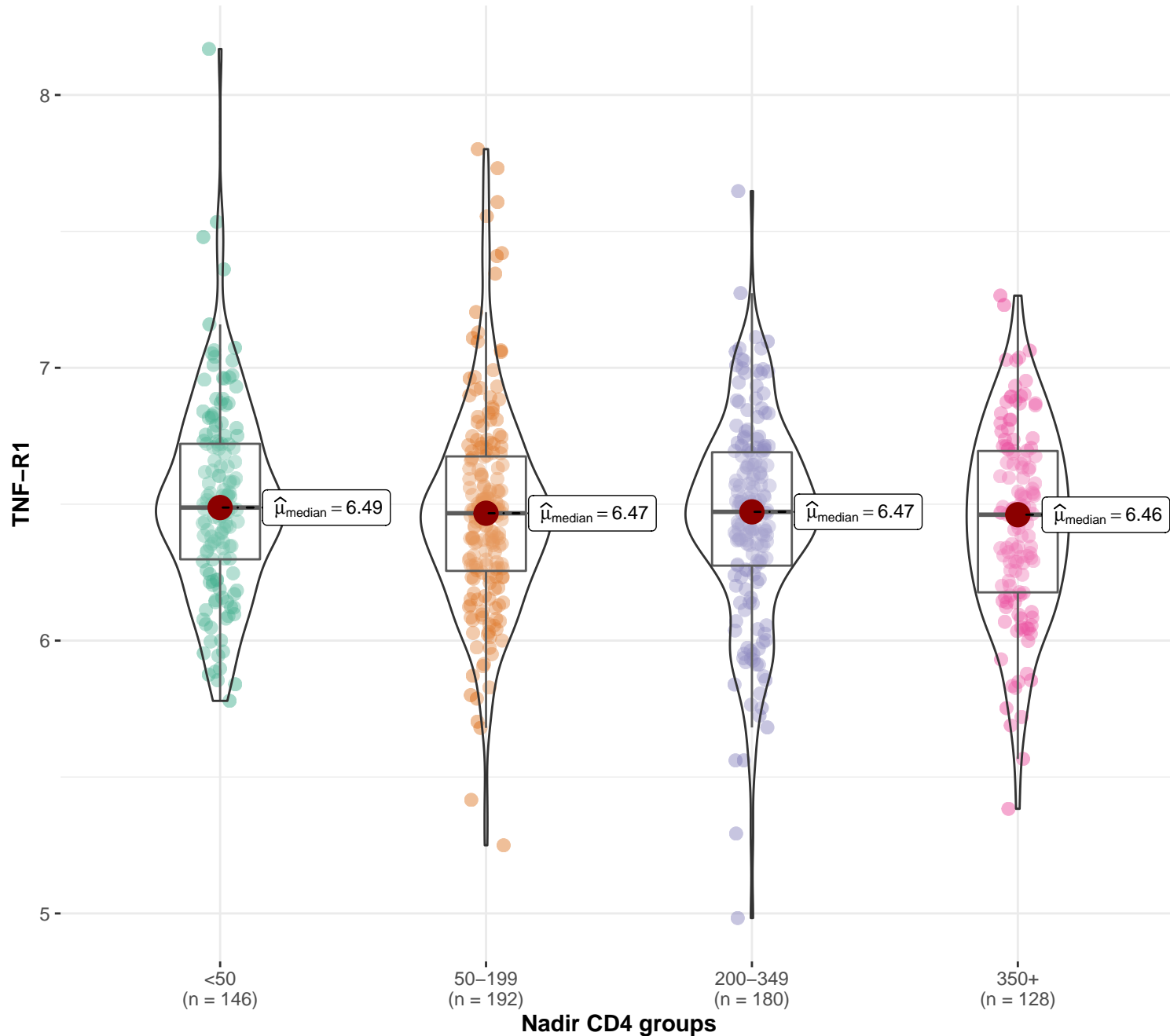
Distribution of TNF-R1 across different CD4 groups

Distribution of TNF-R1 across nadir CD4 groups

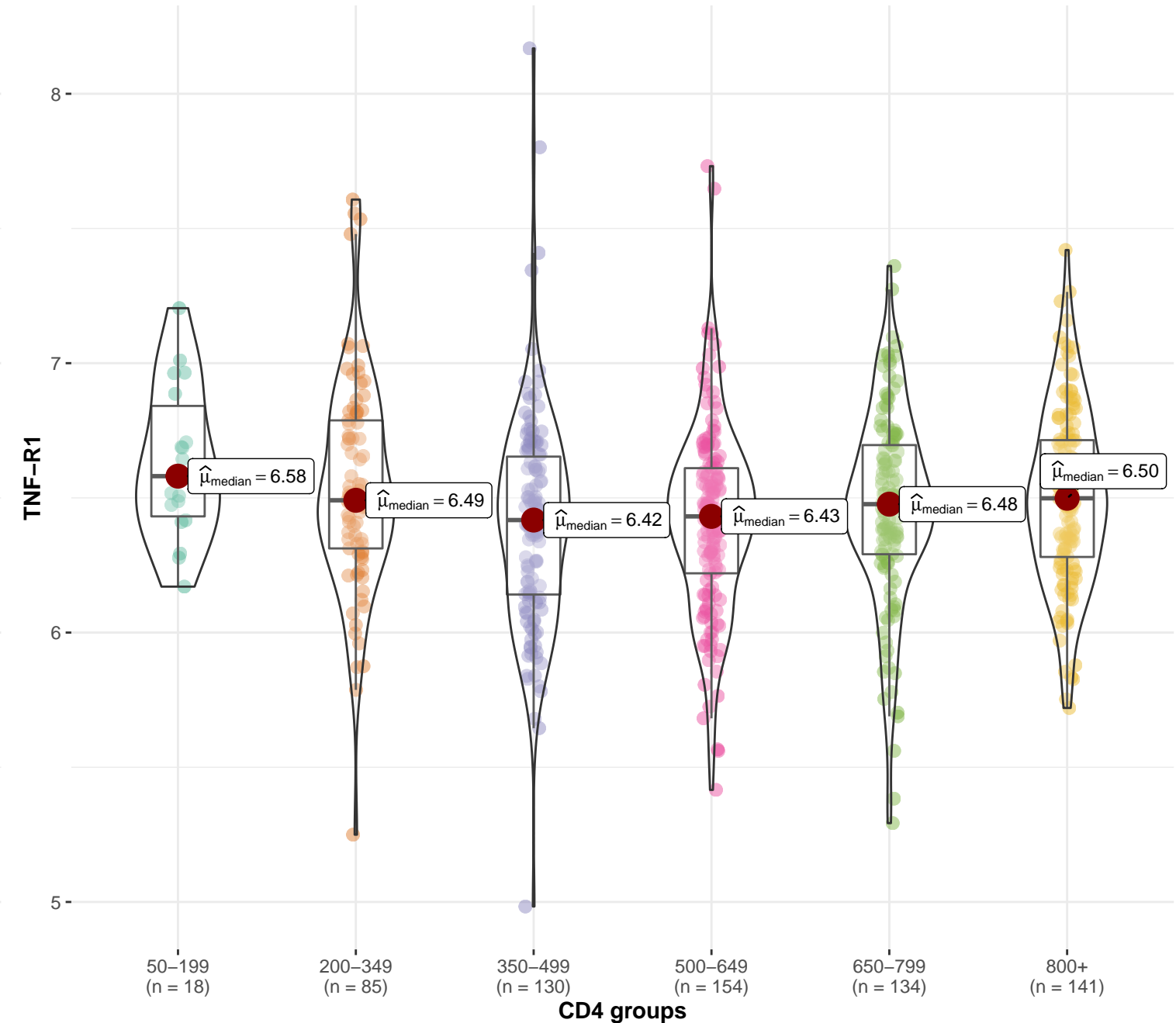
$\chi^2_{\text{Kruskal-Wallis}}(3) = 2.49, p = 0.476, \hat{\epsilon}^2_{\text{ordinal}} = 3.87\text{e-}03, \text{CI}_{95\%} [6.80\text{e-}04, 1.00], n_{\text{obs}} = 646$

Distribution of TNF-R1 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 16.01, p = 0.007, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, \text{CI}_{95\%} [0.01, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

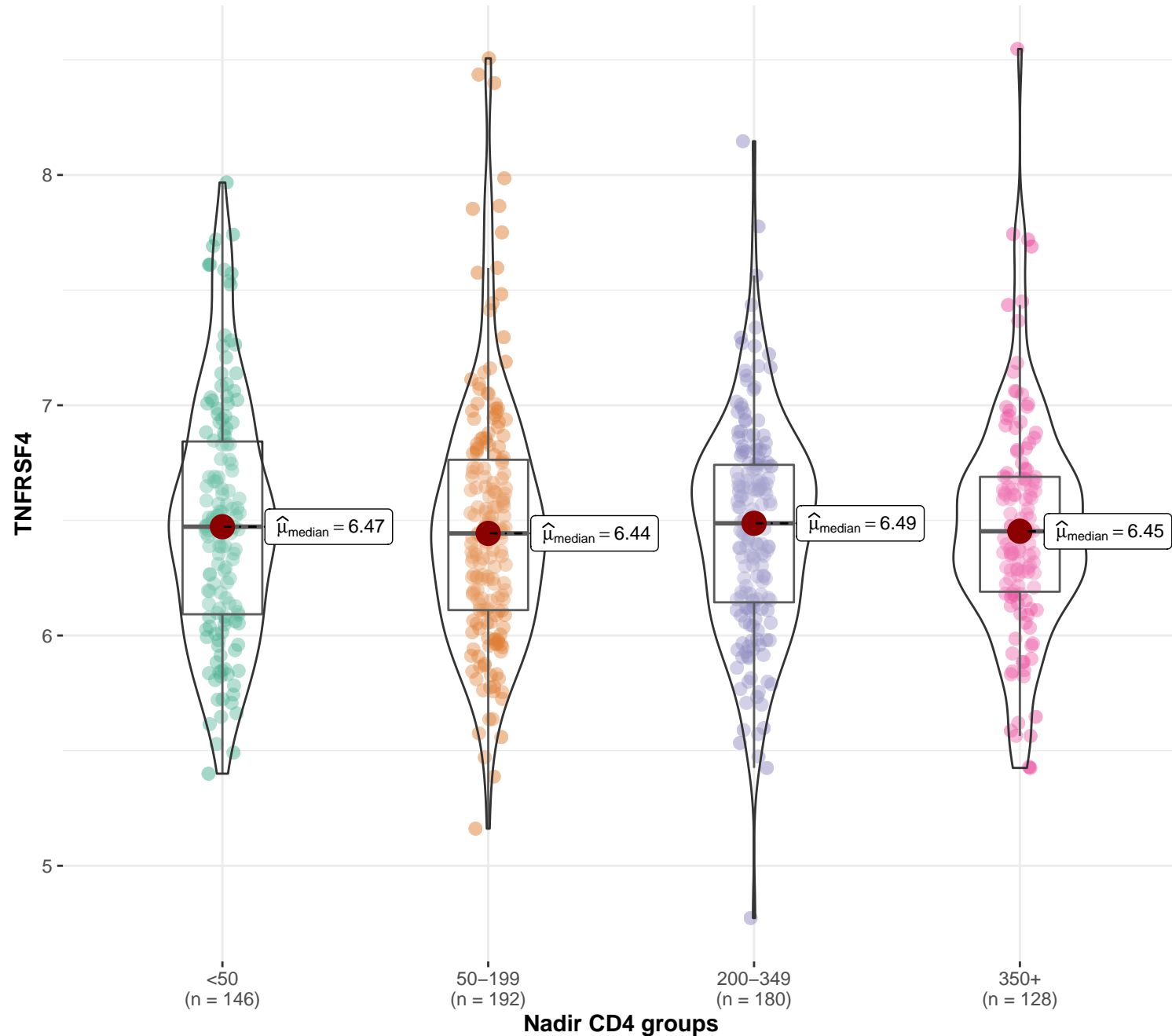
Distribution of TNFRSF4 across different CD4 groups

Distribution of TNFRSF4 across nadir CD4 groups

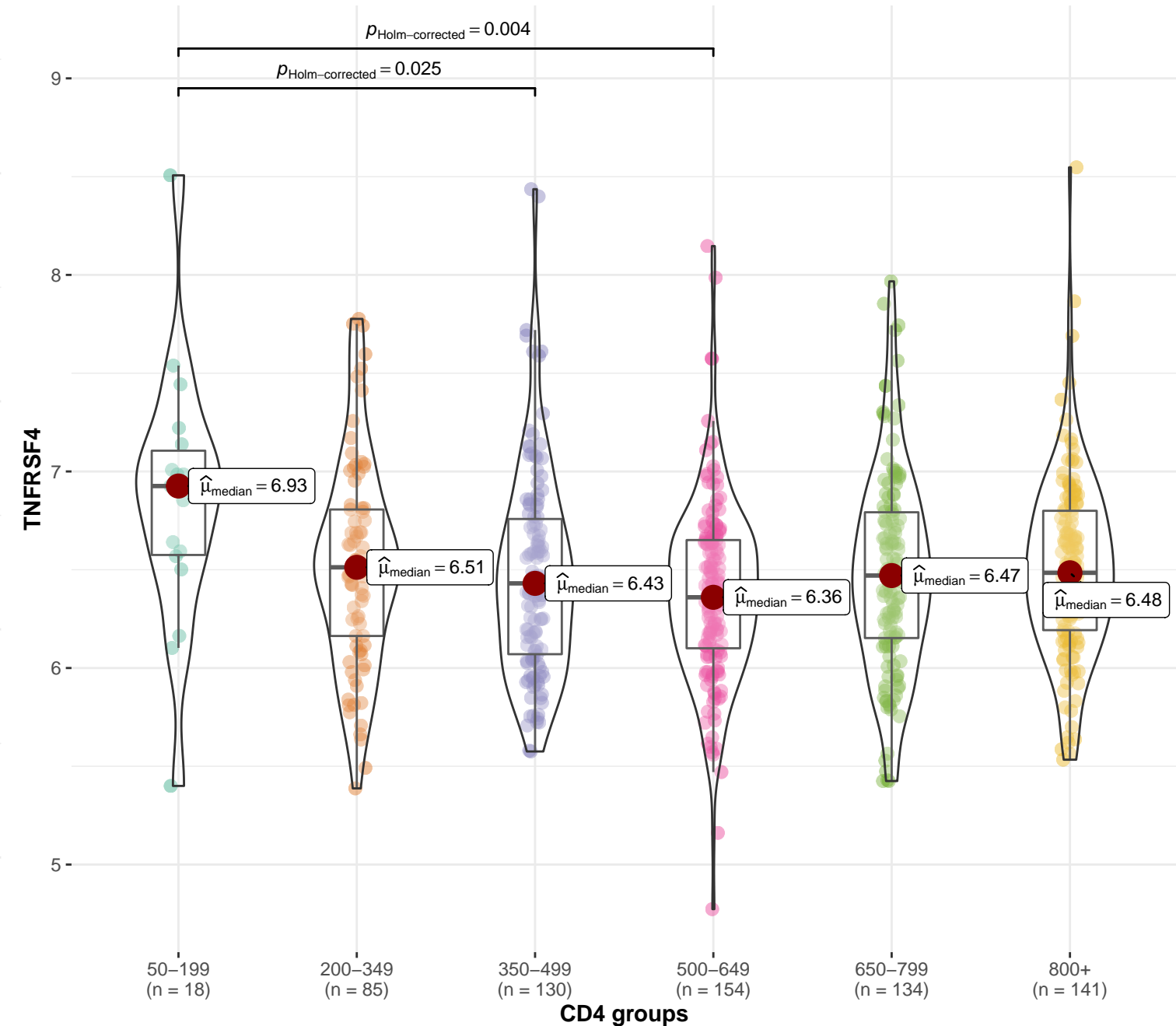
$\chi^2_{\text{Kruskal-Wallis}}(3) = 0.39, p = 0.941, \hat{\epsilon}^2_{\text{ordinal}} = 6.12\text{e-}04, \text{CI}_{95\%} [7.91\text{e-}04, 1.00], n_{\text{obs}} = 646$

Distribution of TNFRSF4 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 16.31, p = 0.006, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, \text{CI}_{95\%} [0.01, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

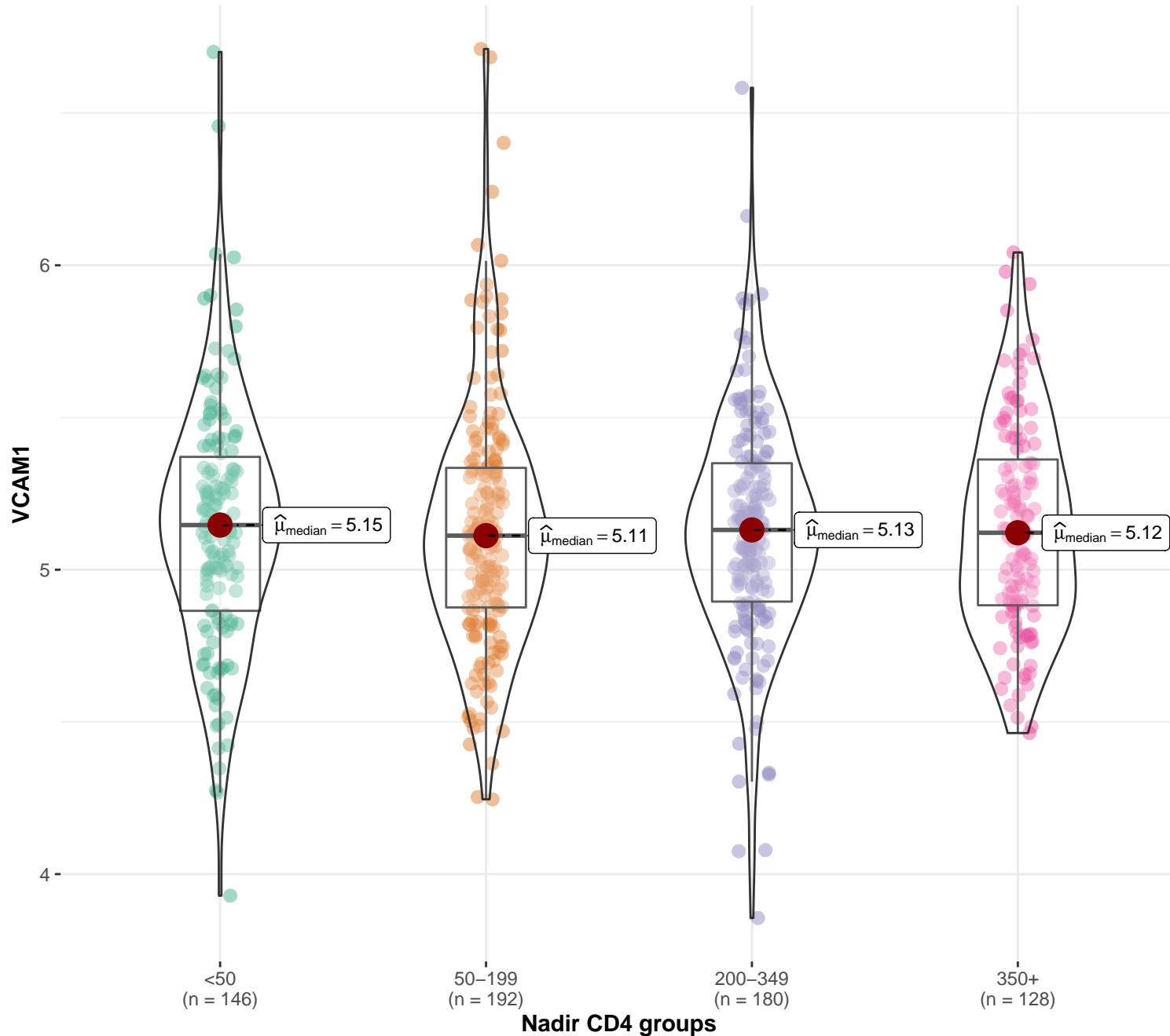


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of VCAM1 across different CD4 groups

Distribution of VCAM1 across nadir CD4 groups

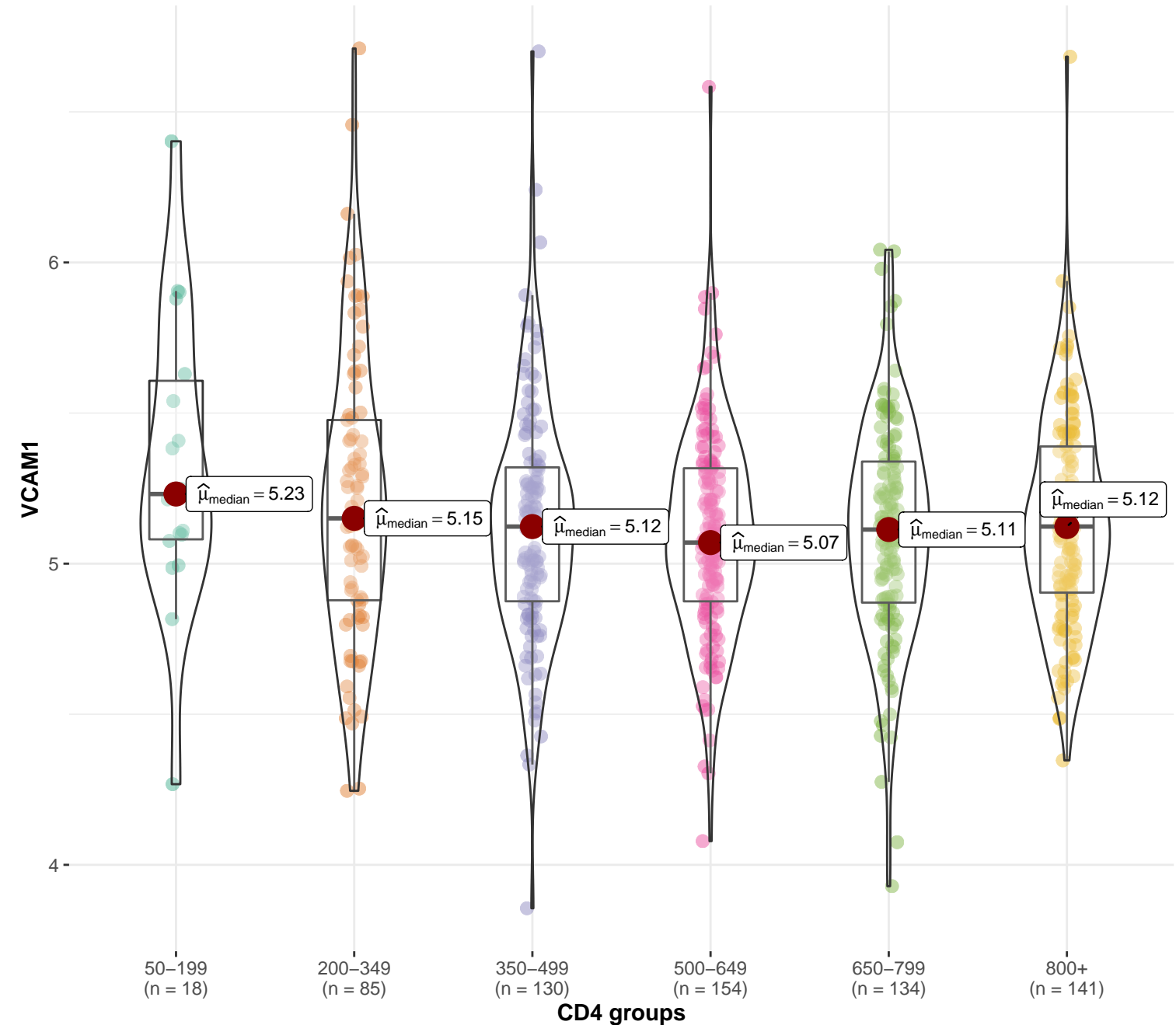
$\chi^2_{\text{Kruskal-Wallis}}(3) = 0.47, p = 0.924, \hat{\epsilon}^2_{\text{ordinal}} = 7.36\text{e-}04, \text{CI}_{95\%} [4.49\text{e-}04, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of VCAM1 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 6.35, p = 0.274, \hat{\epsilon}^2_{\text{ordinal}} = 9.60\text{e-}03, \text{CI}_{95\%} [6.50\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

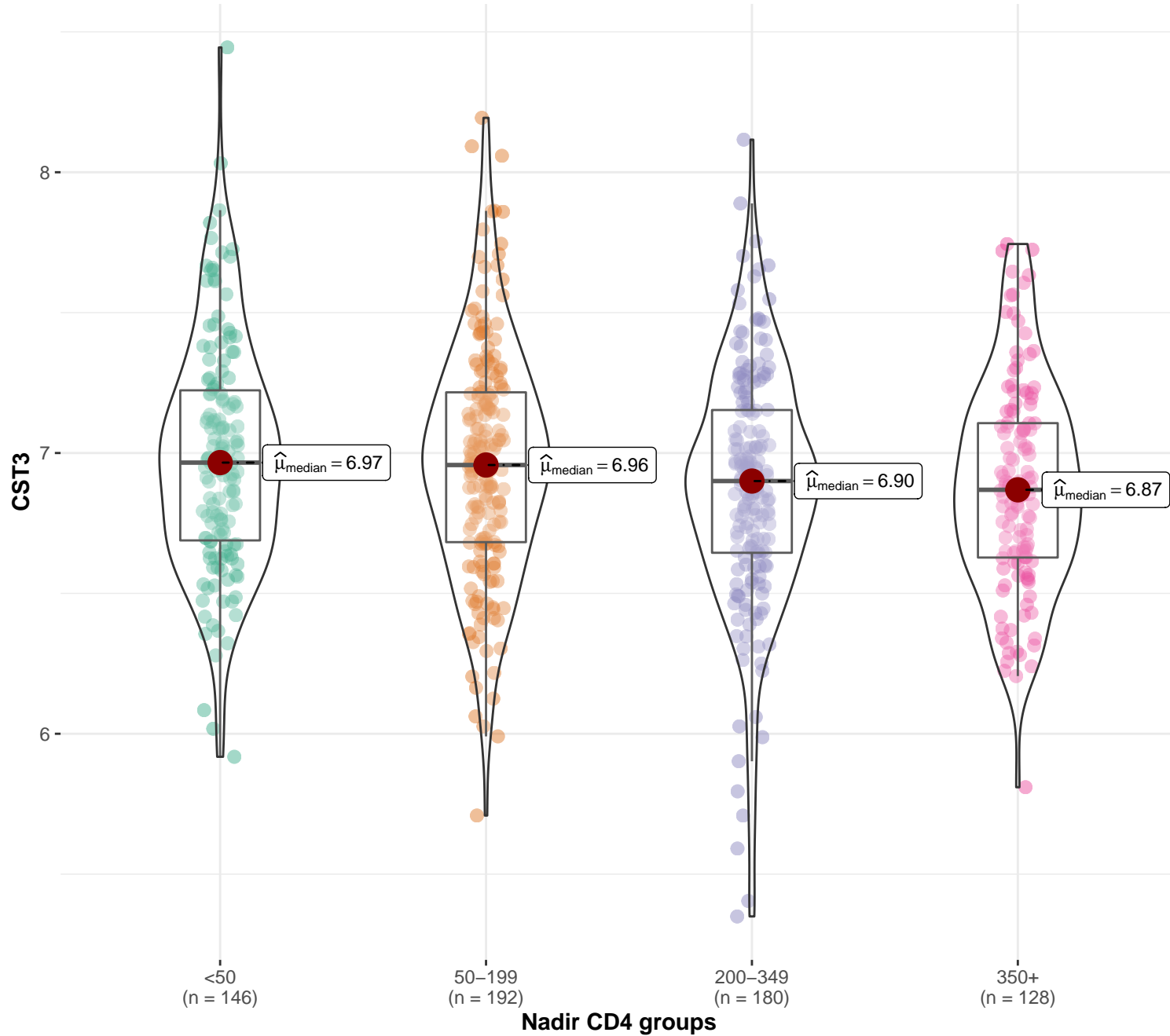
Distribution of CST3 across different CD4 groups

Distribution of CST3 across nadir CD4 groups

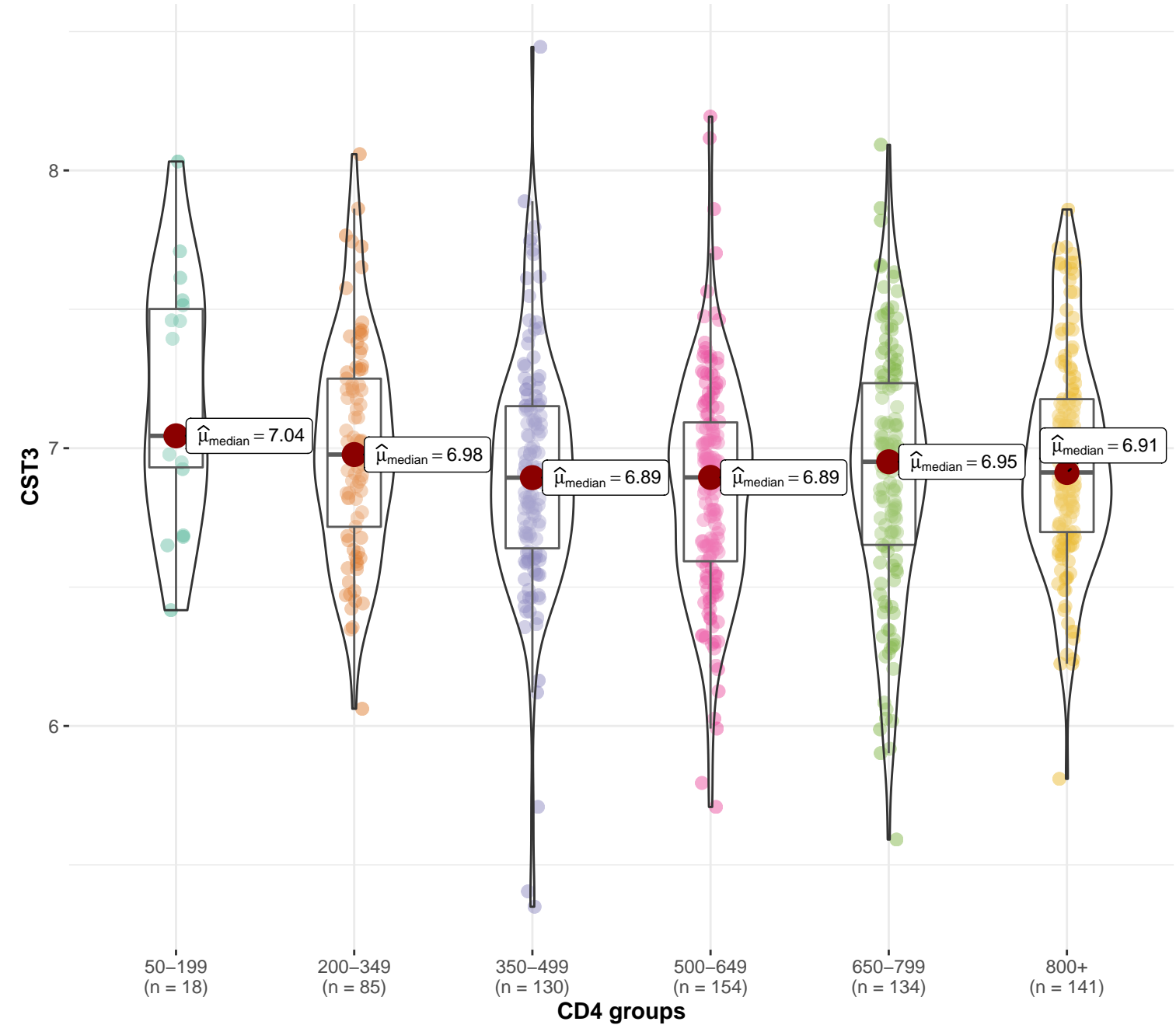
$\chi^2_{\text{Kruskal-Wallis}}(3) = 7.31, p = 0.063, \hat{\epsilon}^2_{\text{ordinal}} = 0.01, \text{CI}_{95\%} [3.29\text{e-}03, 1.00], n_{\text{obs}} = 646$

Distribution of CST3 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 13.22, p = 0.021, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, \text{CI}_{95\%} [0.01, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

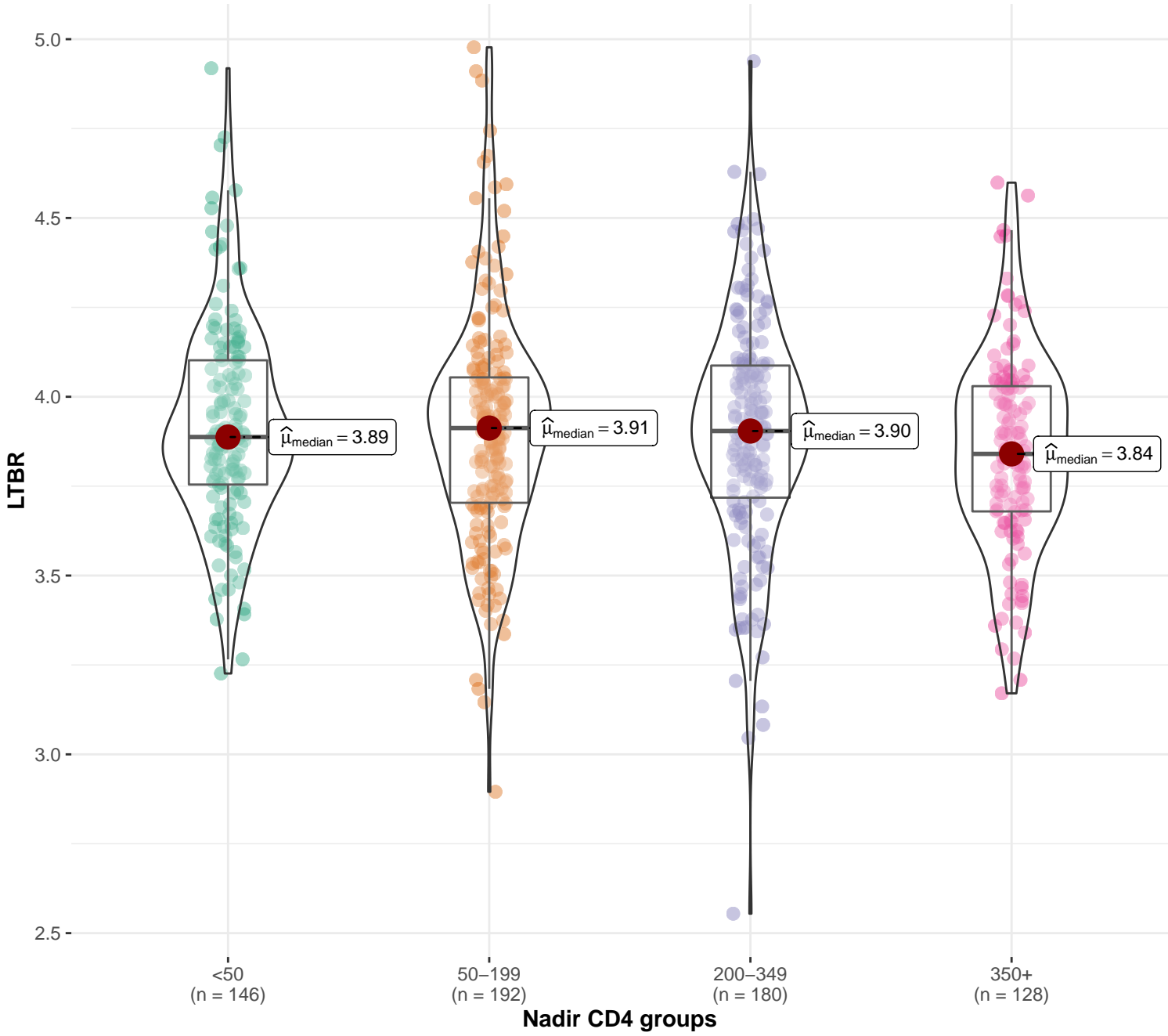


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of LTBR across different CD4 groups

Distribution of LTBR across nadir CD4 groups

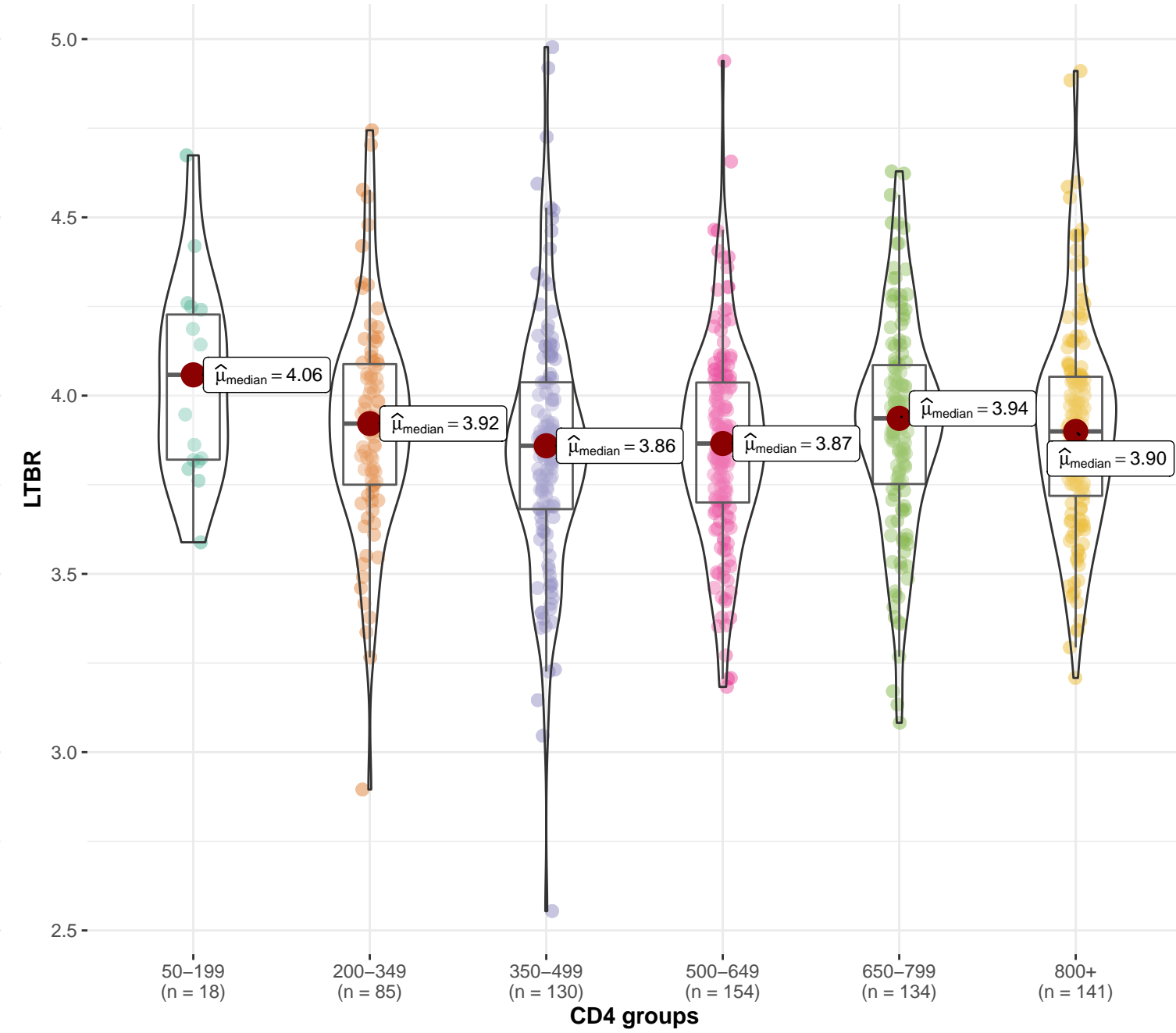
$\chi^2_{\text{Kruskal-Wallis}}(3) = 4.17, p = 0.244, \hat{\epsilon}^2_{\text{ordinal}} = 6.46\text{e-}03, \text{CI}_{95\%} [1.24\text{e-}03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of LTBR across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 10.78, p = 0.056, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, \text{CI}_{95\%} [8.21\text{e-}03, 1.00], n_{\text{obs}} = 662$

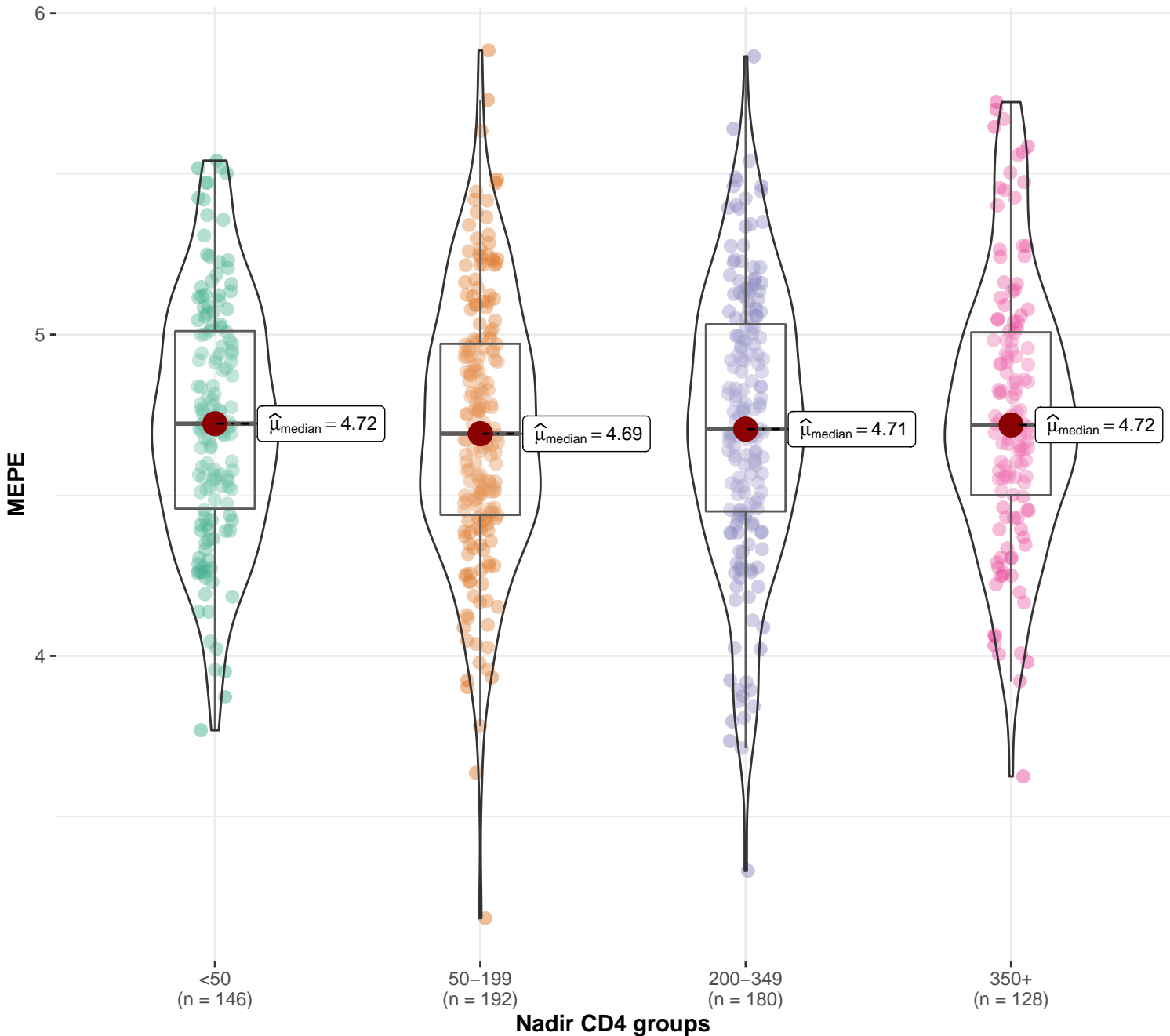


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of MEPE across different CD4 groups

Distribution of MEPE across nadir CD4 groups

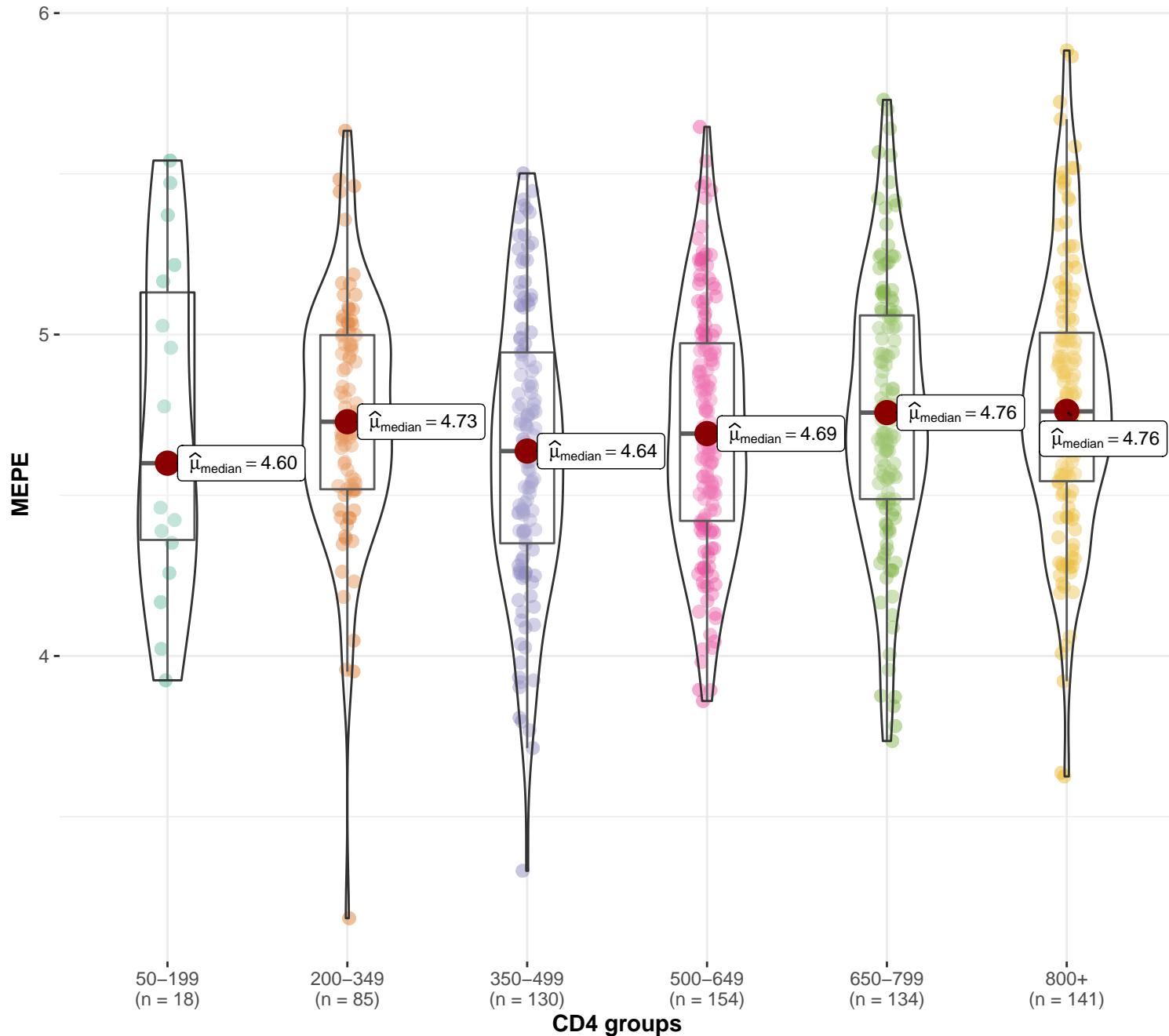
$\chi^2_{\text{Kruskal-Wallis}}(3) = 0.81, p = 0.846, \hat{\epsilon}^2_{\text{ordinal}} = 1.26\text{e-}03, \text{CI}_{95\%} [2.94\text{e-}04, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of MEPE across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 9.63, p = 0.086, \hat{\epsilon}^2_{\text{ordinal}} = 0.01, \text{CI}_{95\%} [6.29\text{e-}03, 1.00], n_{\text{obs}} = 662$

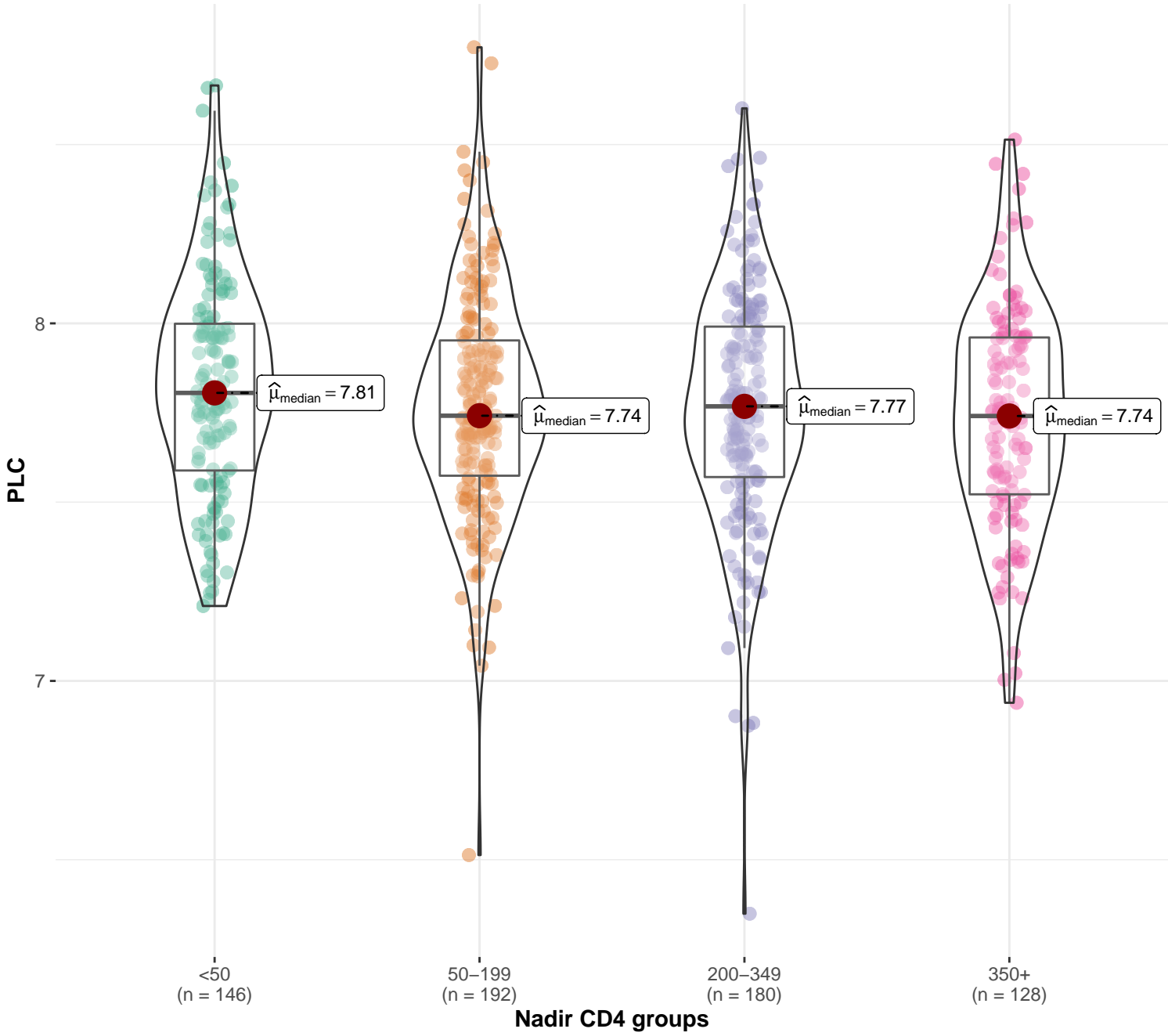


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of PLC across different CD4 groups

Distribution of PLC across nadir CD4 groups

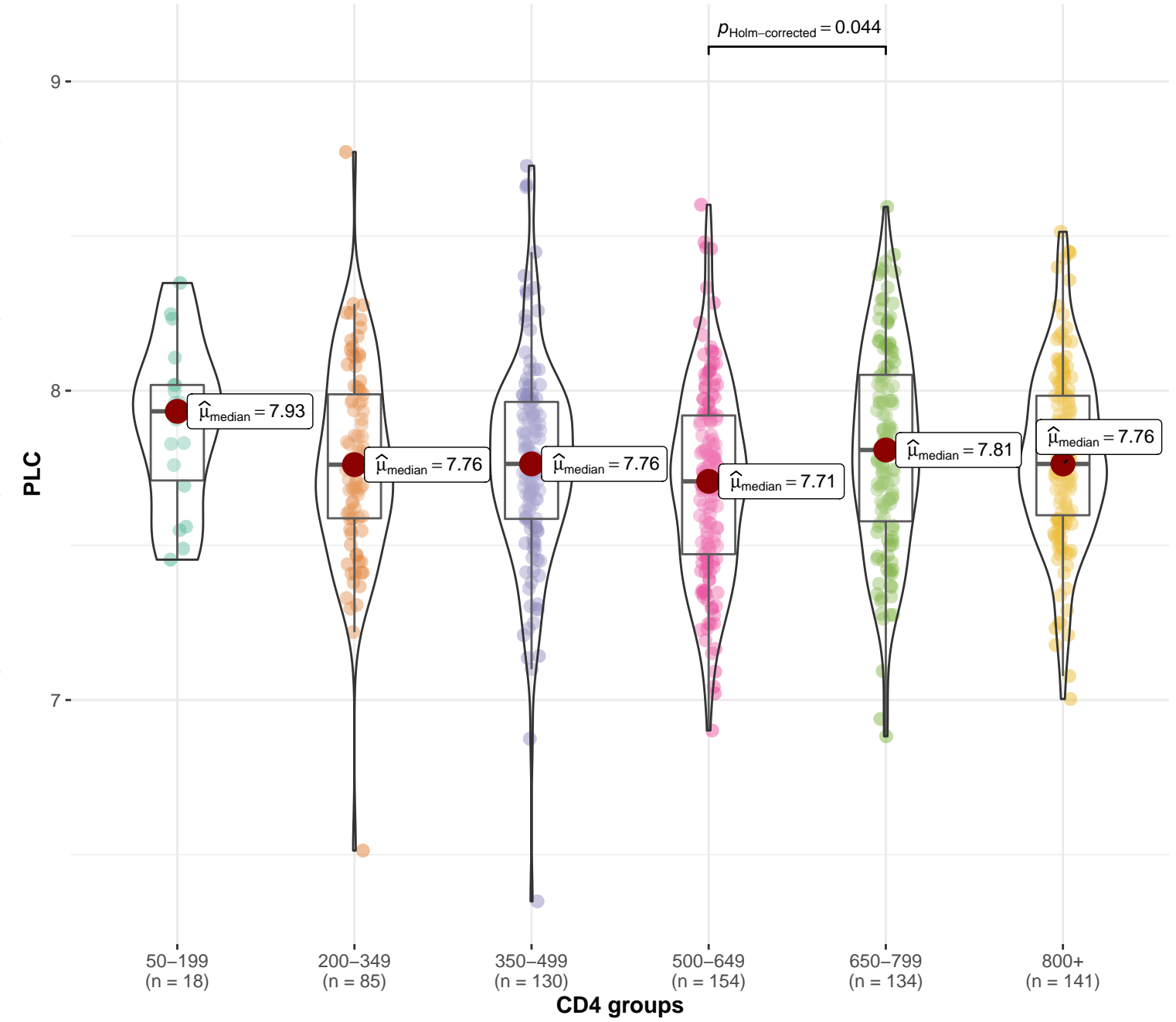
$\chi^2_{\text{Kruskal-Wallis}}(3) = 4.55, p = 0.208, \hat{\epsilon}^2_{\text{ordinal}} = 7.06\text{e-}03, CI_{95\%} [2.53\text{e-}03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of PLC across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 13.02, p = 0.023, \hat{\epsilon}^2_{\text{ordinal}} = 0.02, CI_{95\%} [0.01, 1.00], n_{\text{obs}} = 662$

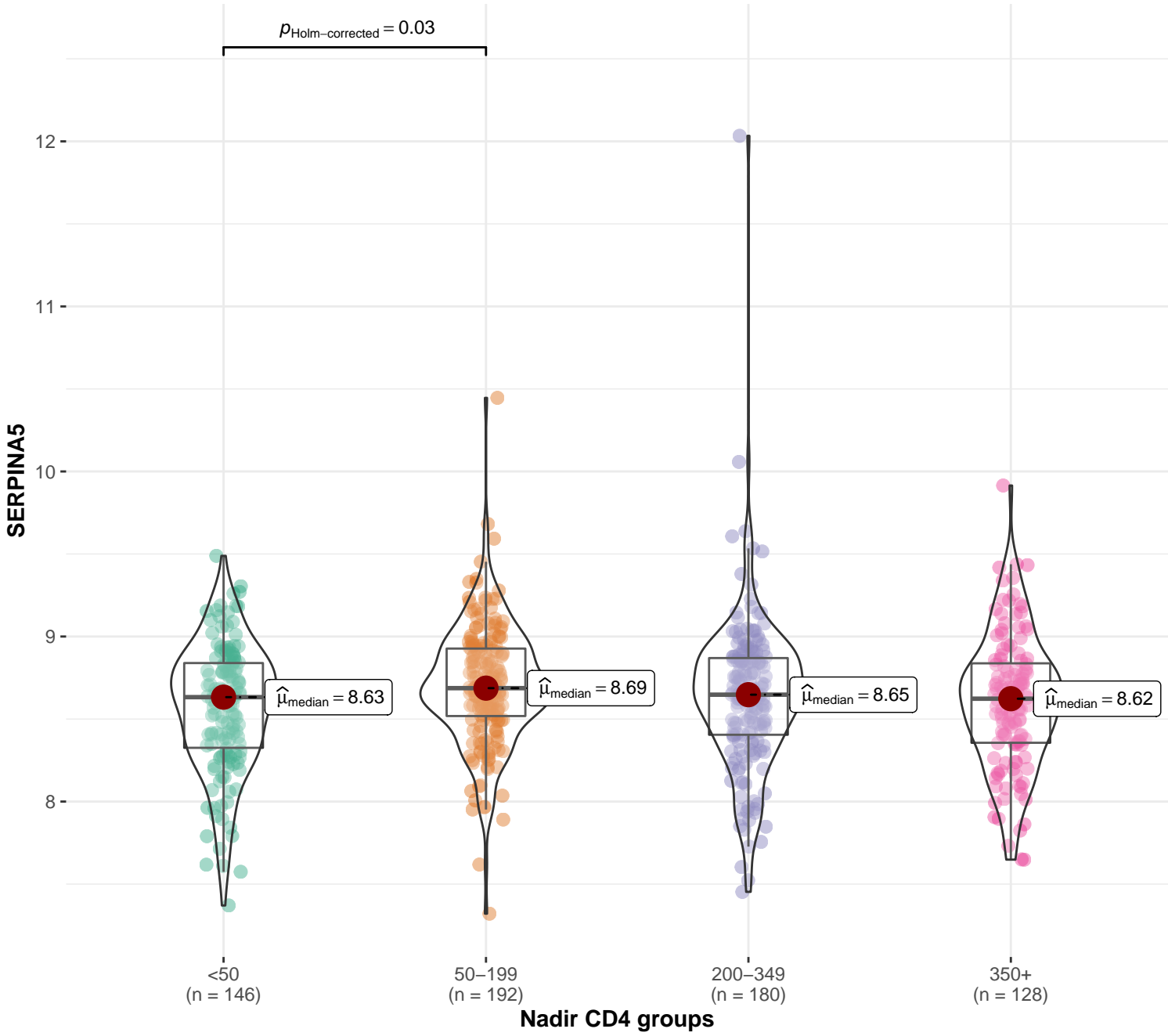


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of SERPINA5 across different CD4 groups

Distribution of SERPINA5 across nadir CD4 groups

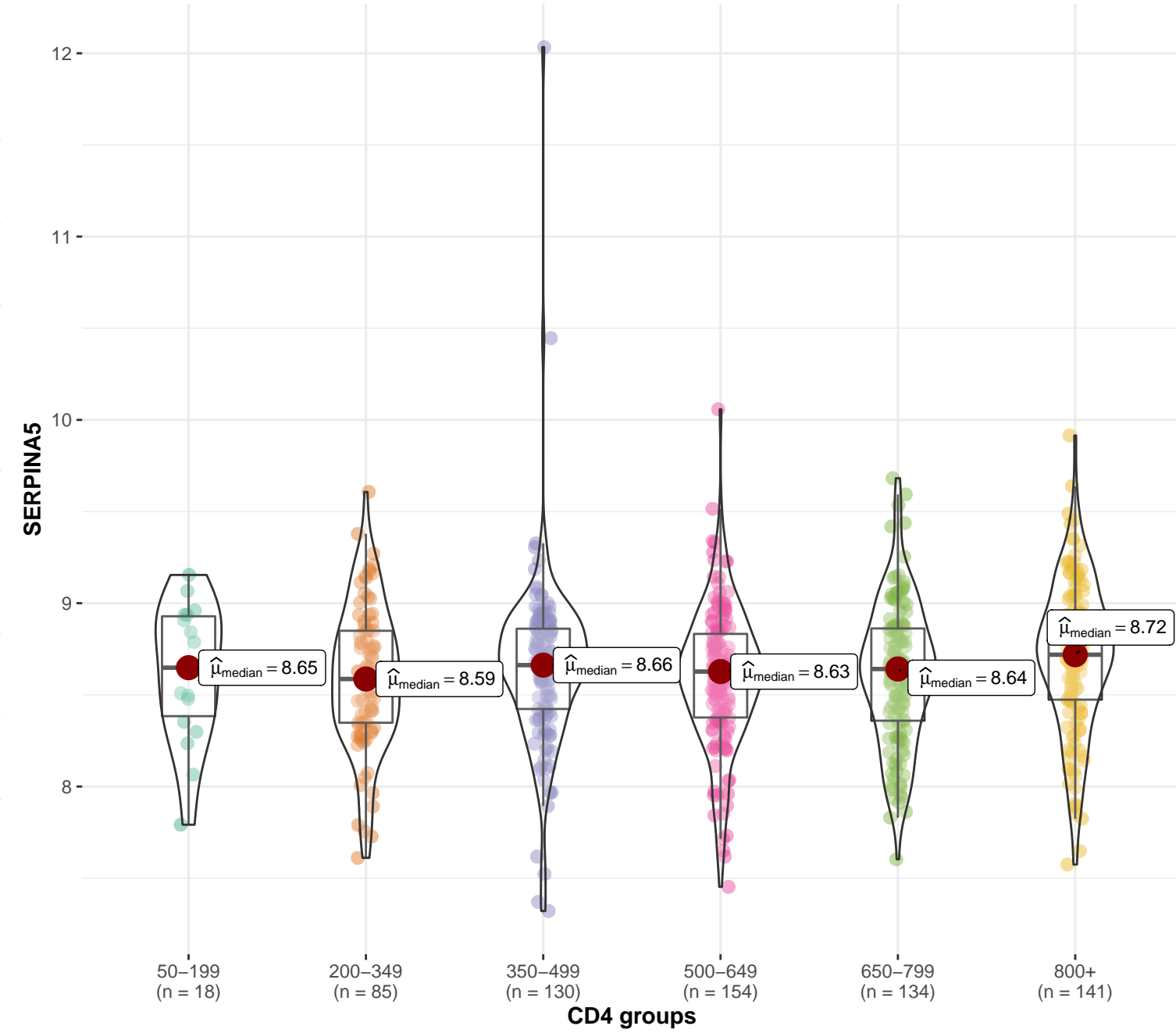
$\chi^2_{\text{Kruskal-Wallis}}(3) = 9.56, p = 0.023, \hat{\epsilon}_{\text{ordinal}}^2 = 0.01, \text{CI}_{95\%} [4.69\text{e-}03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of SERPINA5 across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 10.45, p = 0.063, \hat{\epsilon}_{\text{ordinal}}^2 = 0.02, \text{CI}_{95\%} [7.63\text{e-}03, 1.00], n_{\text{obs}} = 662$

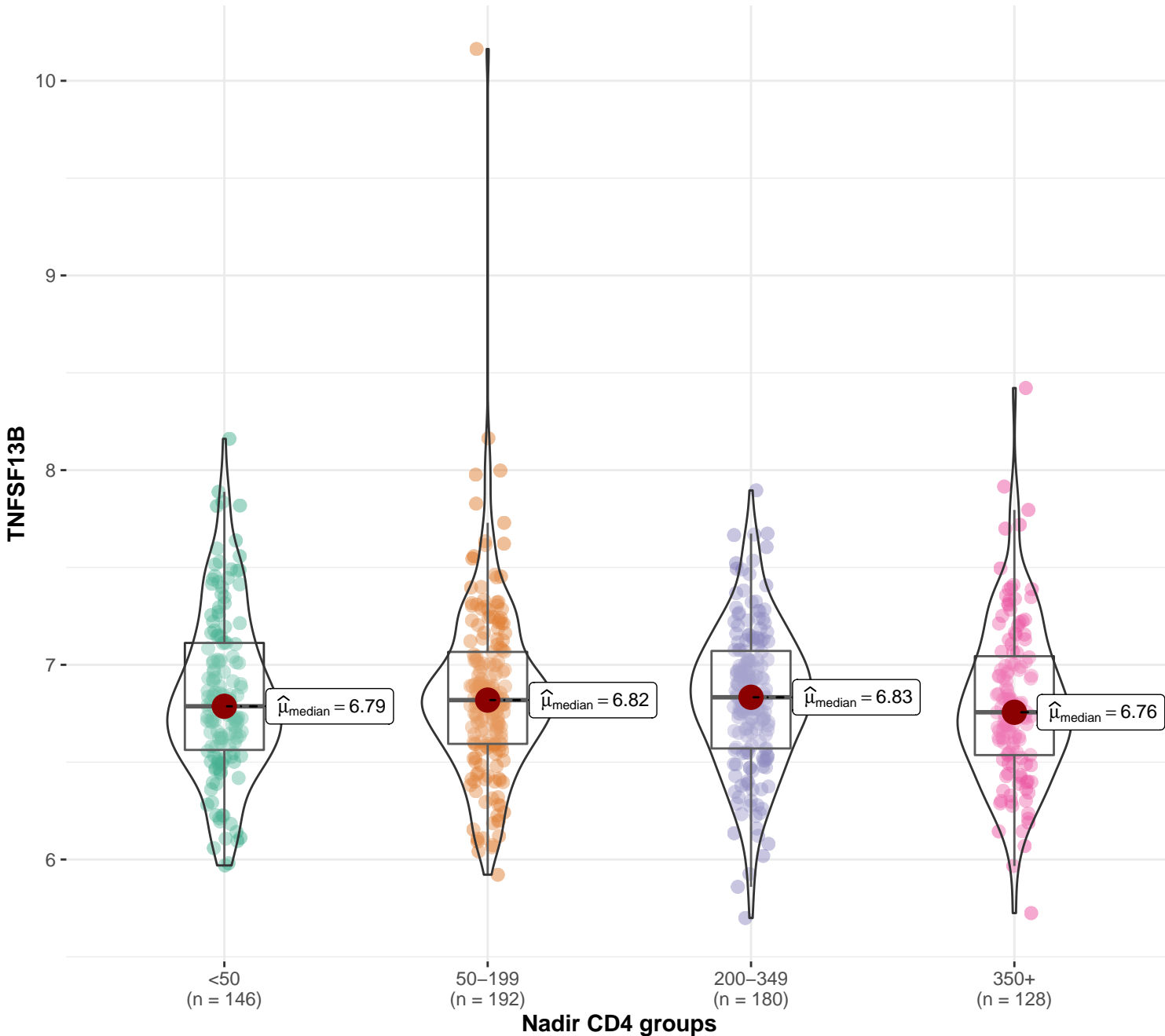


Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of TNFSF13B across different CD4 groups

Distribution of TNFSF13B across nadir CD4 groups

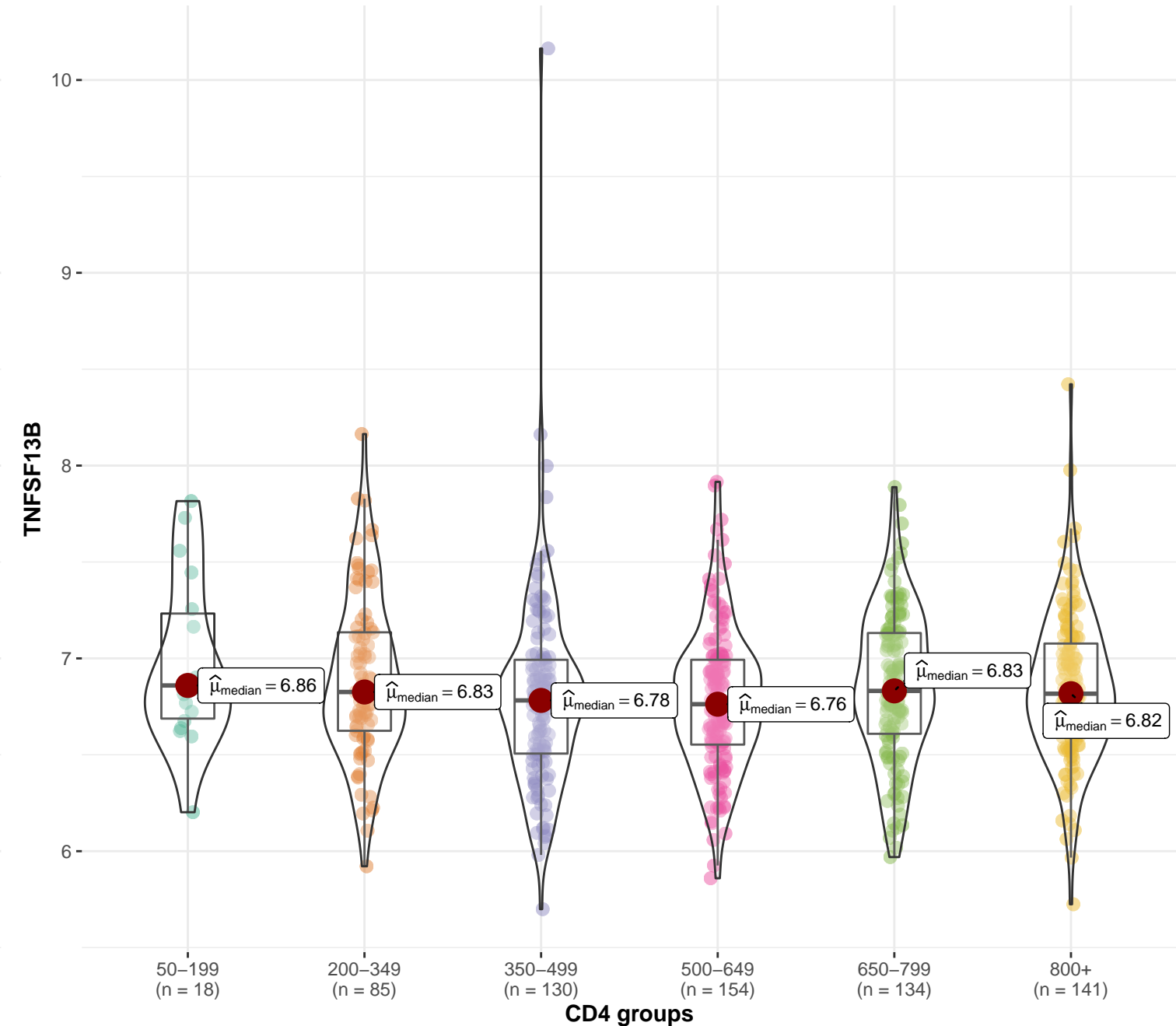
$\chi^2_{\text{Kruskal-Wallis}}(3) = 1.25, p = 0.740, \hat{\epsilon}_{\text{ordinal}}^2 = 1.94\text{e-}03, \text{CI}_{95\%} [1.12\text{e-}03, 1.00], n_{\text{obs}} = 646$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

Distribution of TNFSF13B across CD4 groups

$\chi^2_{\text{Kruskal-Wallis}}(5) = 8.27, p = 0.142, \hat{\epsilon}_{\text{ordinal}}^2 = 0.01, \text{CI}_{95\%} [6.03\text{e-}03, 1.00], n_{\text{obs}} = 662$



Pairwise test: **Dunn test**; Comparisons shown: **only significant**

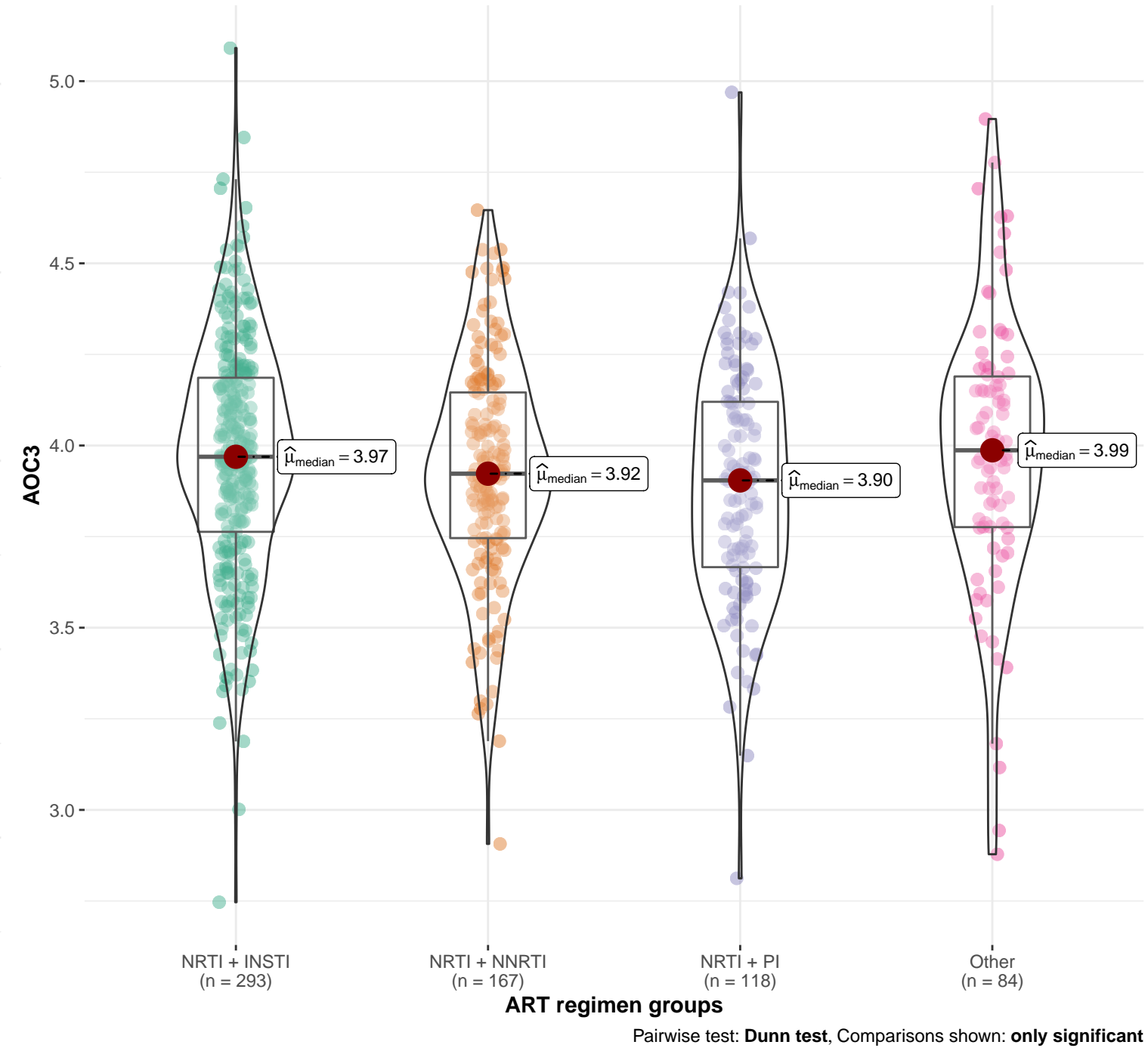
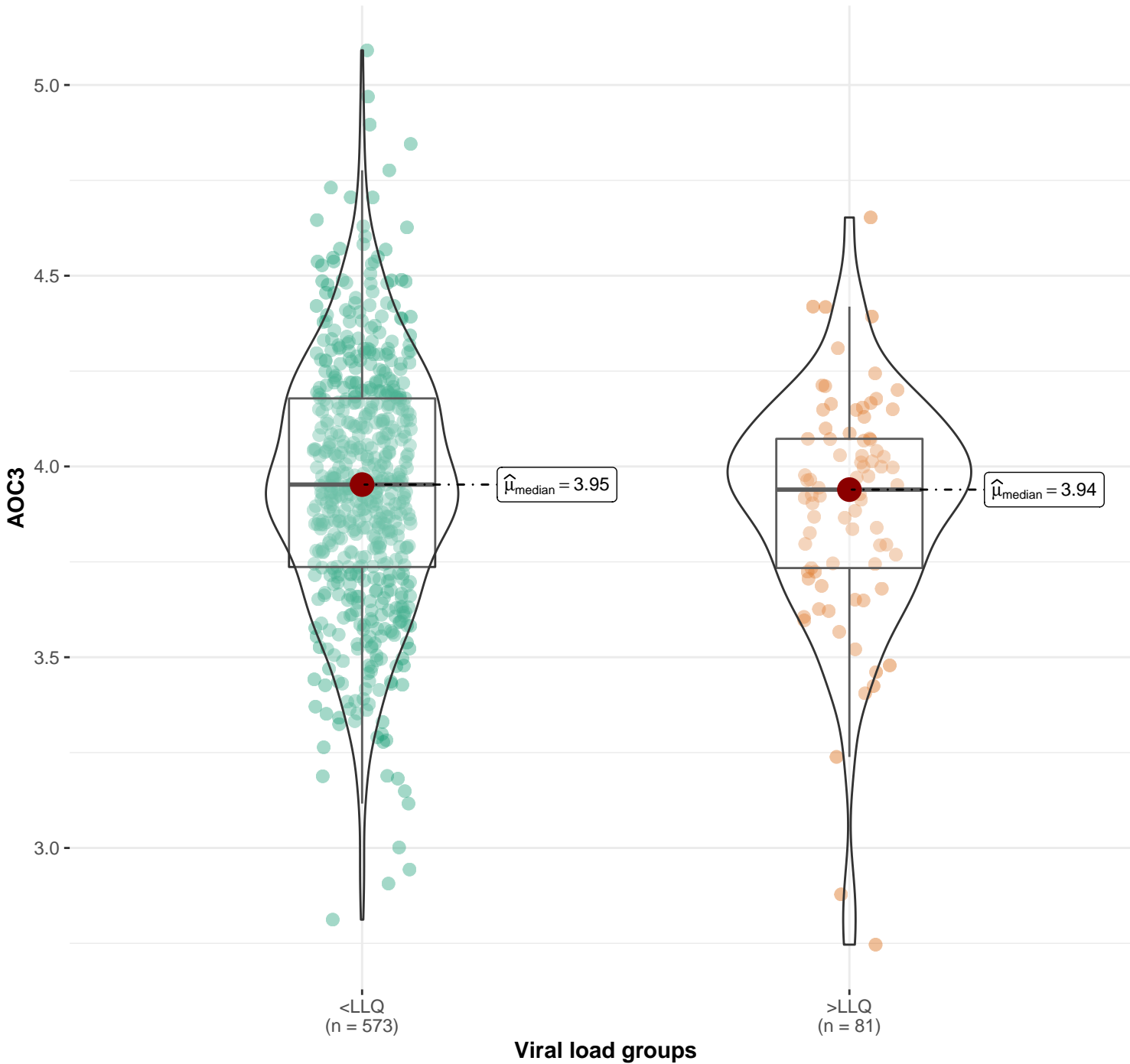
Distribution of AOC3 across different viral loads and ART regimens

Distribution of AOC3 across viral load groups

$W_{\text{Mann-Whitney}} = 25043.00$, $p = 0.25$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.08$, $CI_{95\%} [-0.06, 0.21]$, $n_{\text{obs}} = 654$

Distribution of AOC3 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 6.70$, $p = 0.08$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.01$, $CI_{95\%} [3.08e-03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

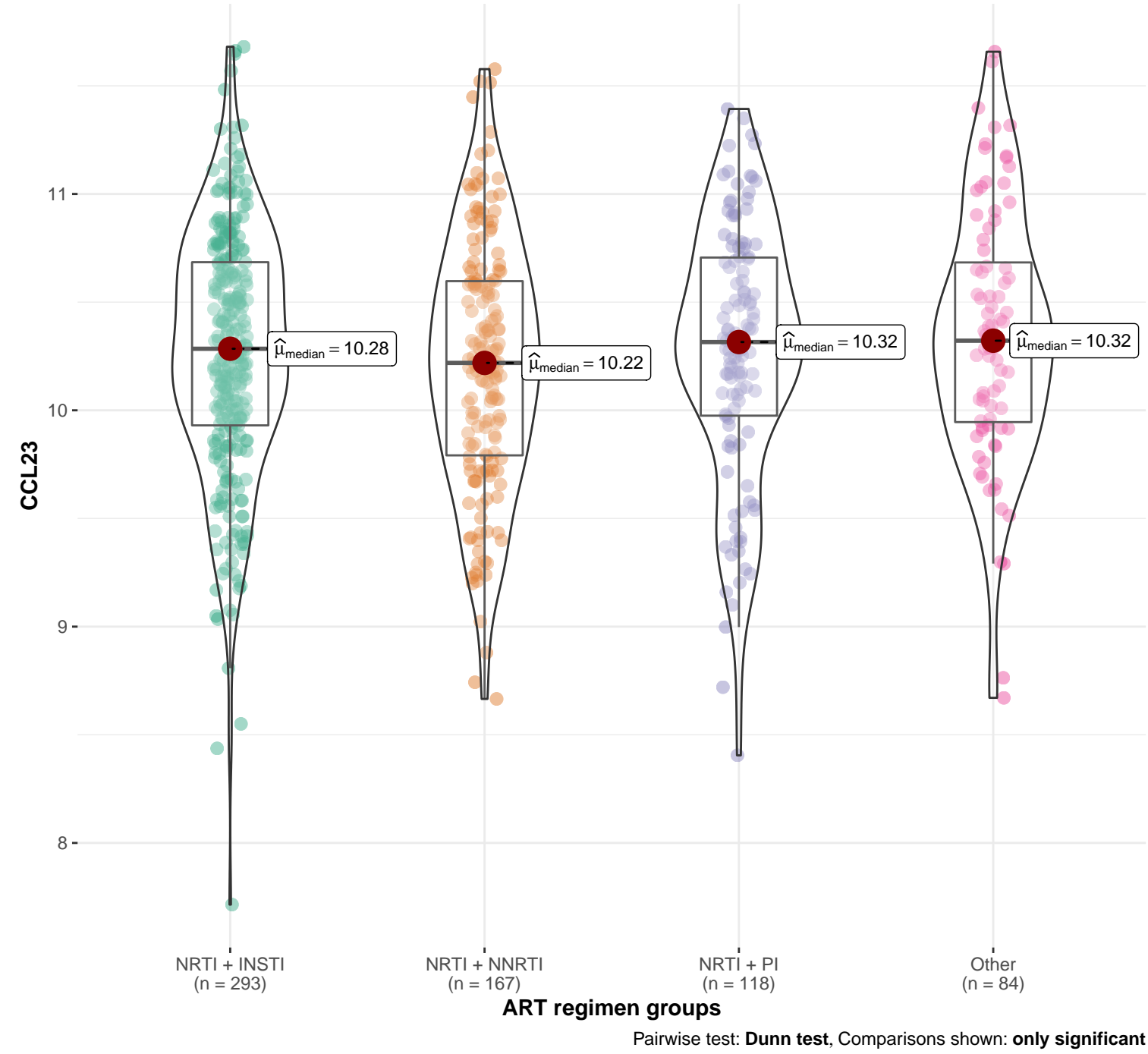
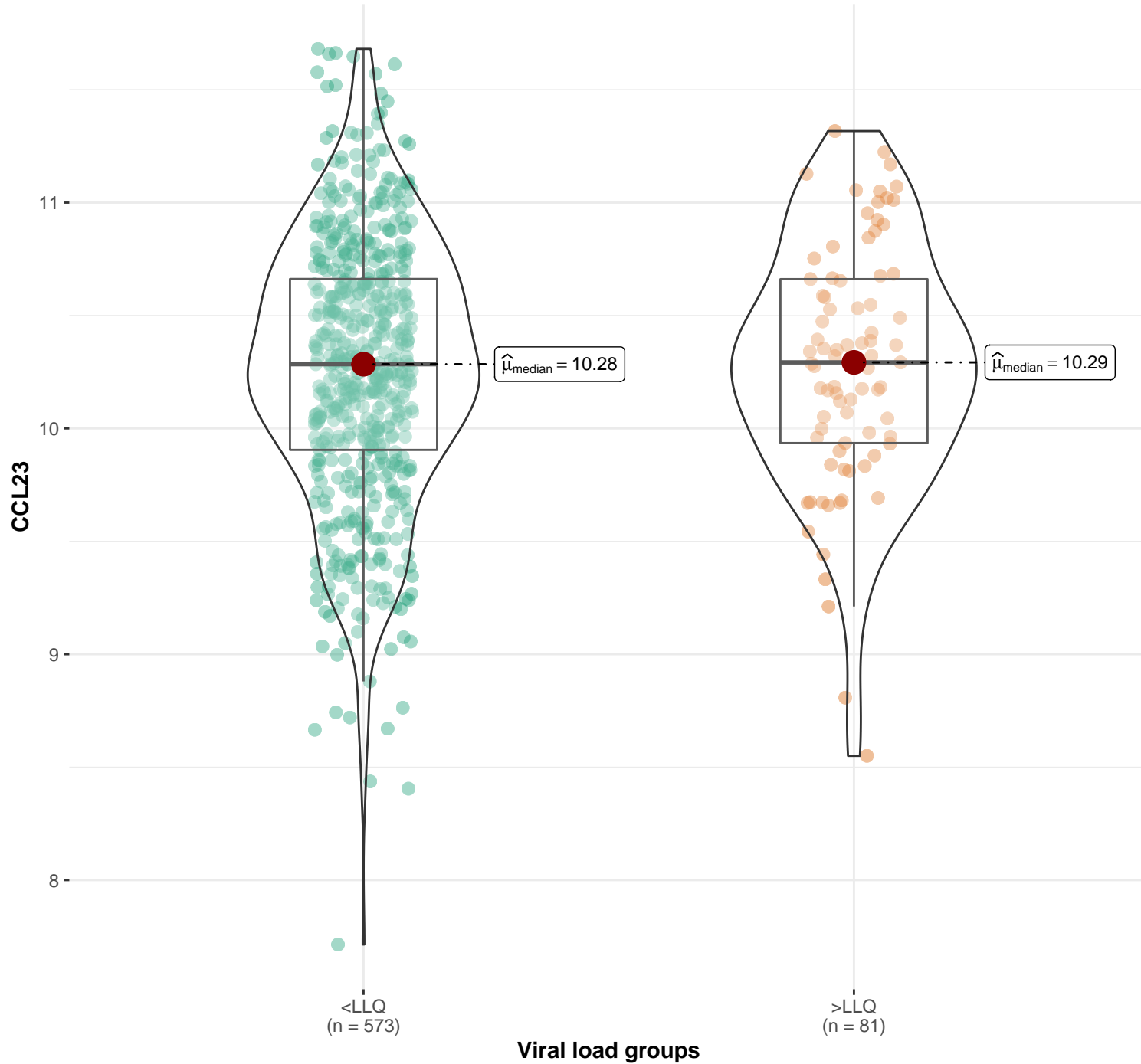
Distribution of CCL23 across different viral loads and ART regimens

Distribution of CCL23 across viral load groups

$W_{\text{Mann-Whitney}} = 22832.00$, $p = 0.81$, $\hat{\rho}_{\text{biserial}}^{\text{rank}} = -0.02$, $CI_{95\%} [-0.15, 0.12]$, $n_{\text{obs}} = 654$

Distribution of CCL23 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 3.11$, $p = 0.37$, $\hat{\epsilon}_{\text{ordinal}}^2 = 4.71e-03$, $CI_{95\%} [1.23e-03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

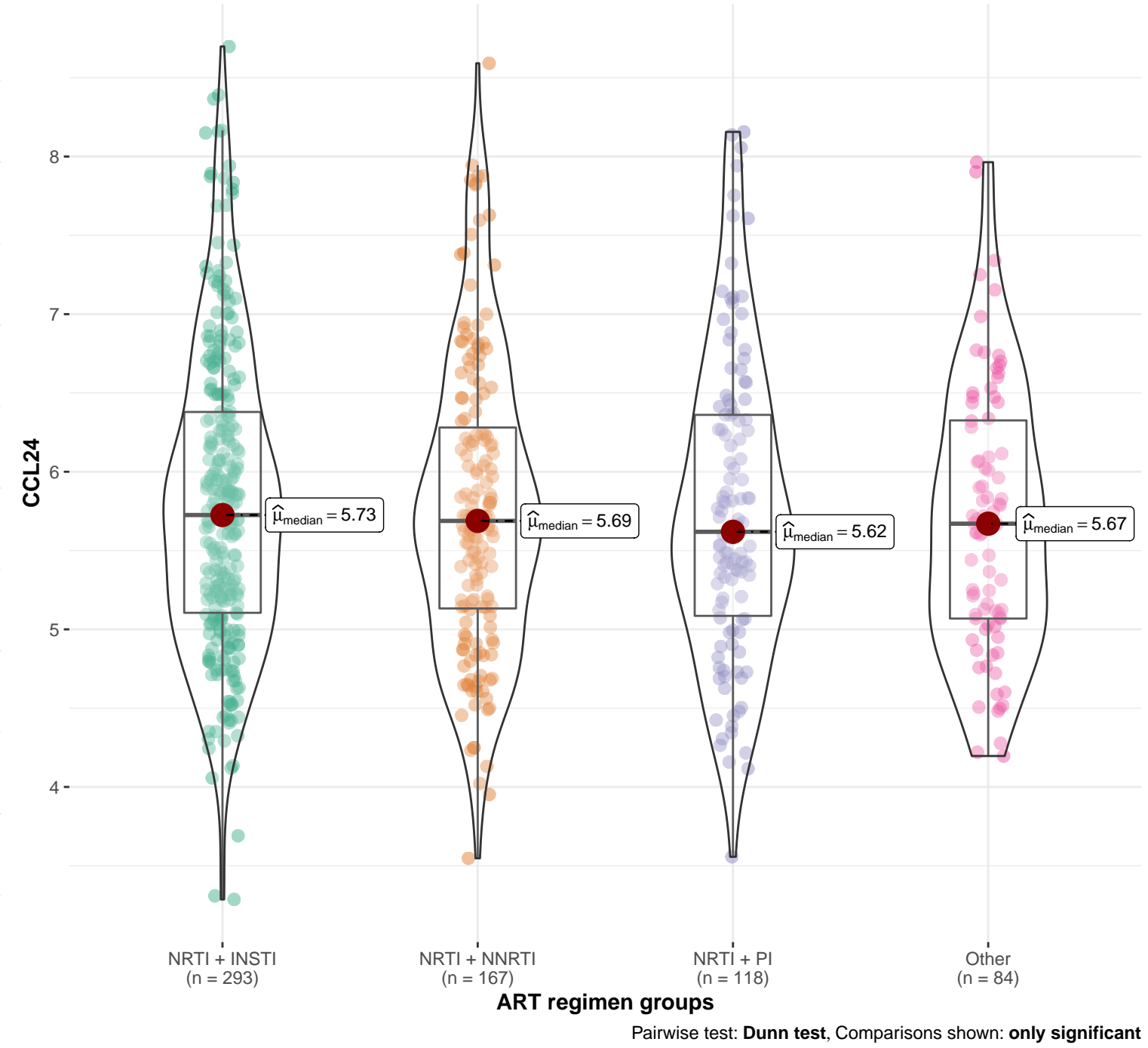
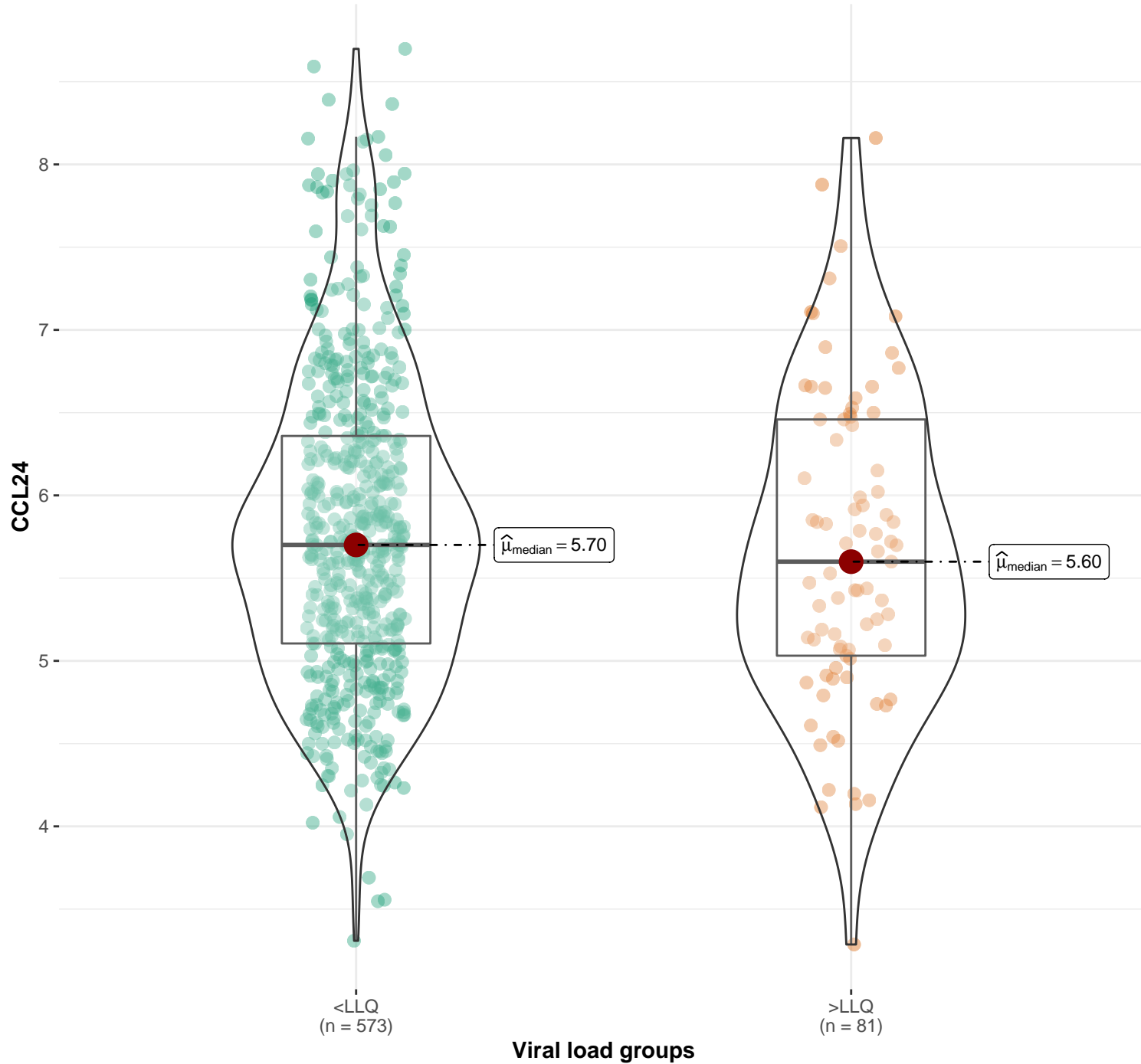
Distribution of CCL24 across different viral loads and ART regimens

Distribution of CCL24 across viral load groups

$W_{\text{Mann-Whitney}} = 24812.50$, $p = 0.31$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.07$, $CI_{95\%} [-0.07, 0.20]$, $n_{\text{obs}} = 654$

Distribution of CCL24 across ART regimens

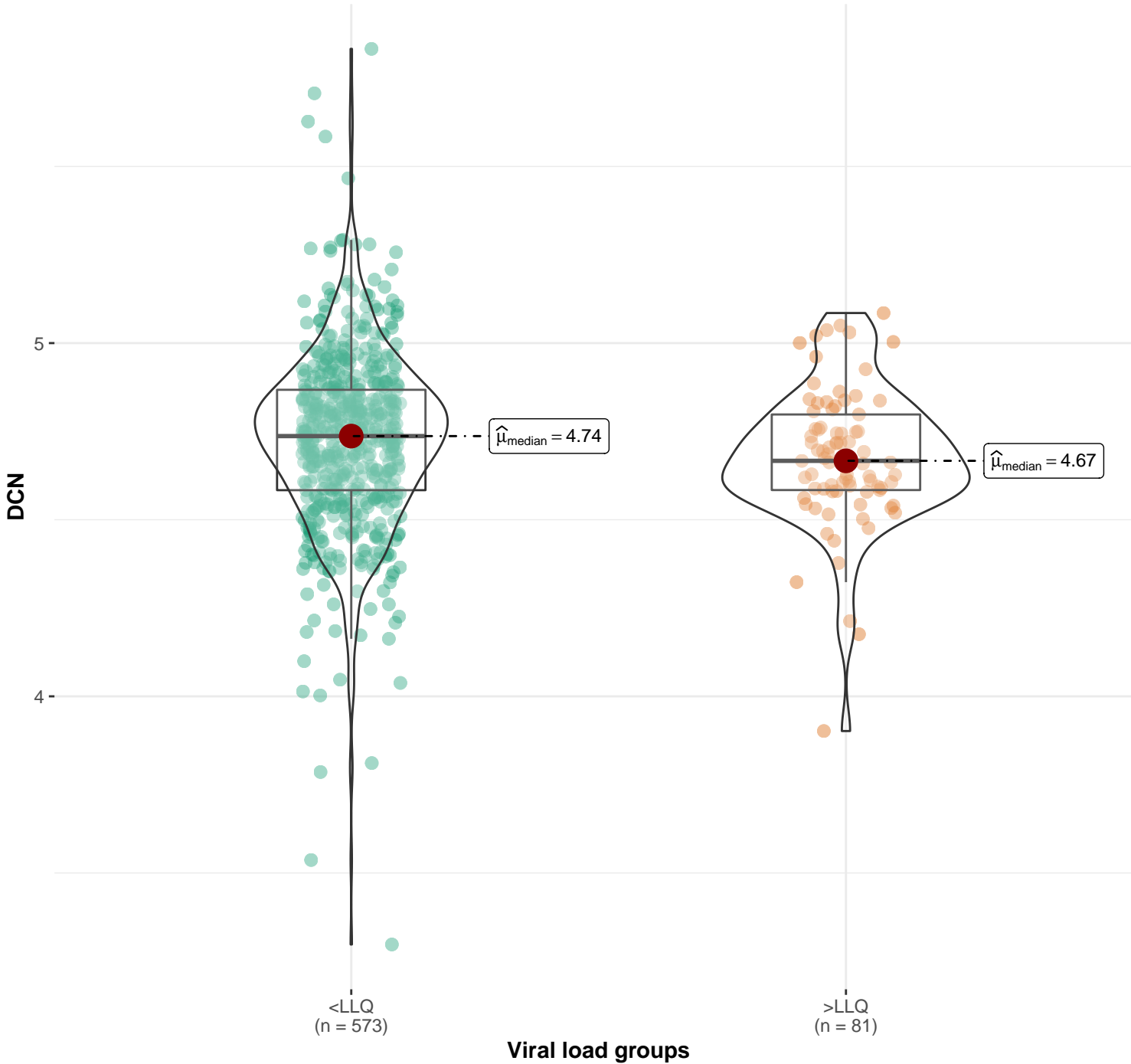
$\chi^2_{\text{Kruskal-Wallis}}(3) = 1.04$, $p = 0.79$, $\hat{\epsilon}_{\text{ordinal}}^2 = 1.57e-03$, $CI_{95\%} [4.36e-04, 1.00]$, $n_{\text{obs}} = 662$



Distribution of DCN across different viral loads and ART regimens

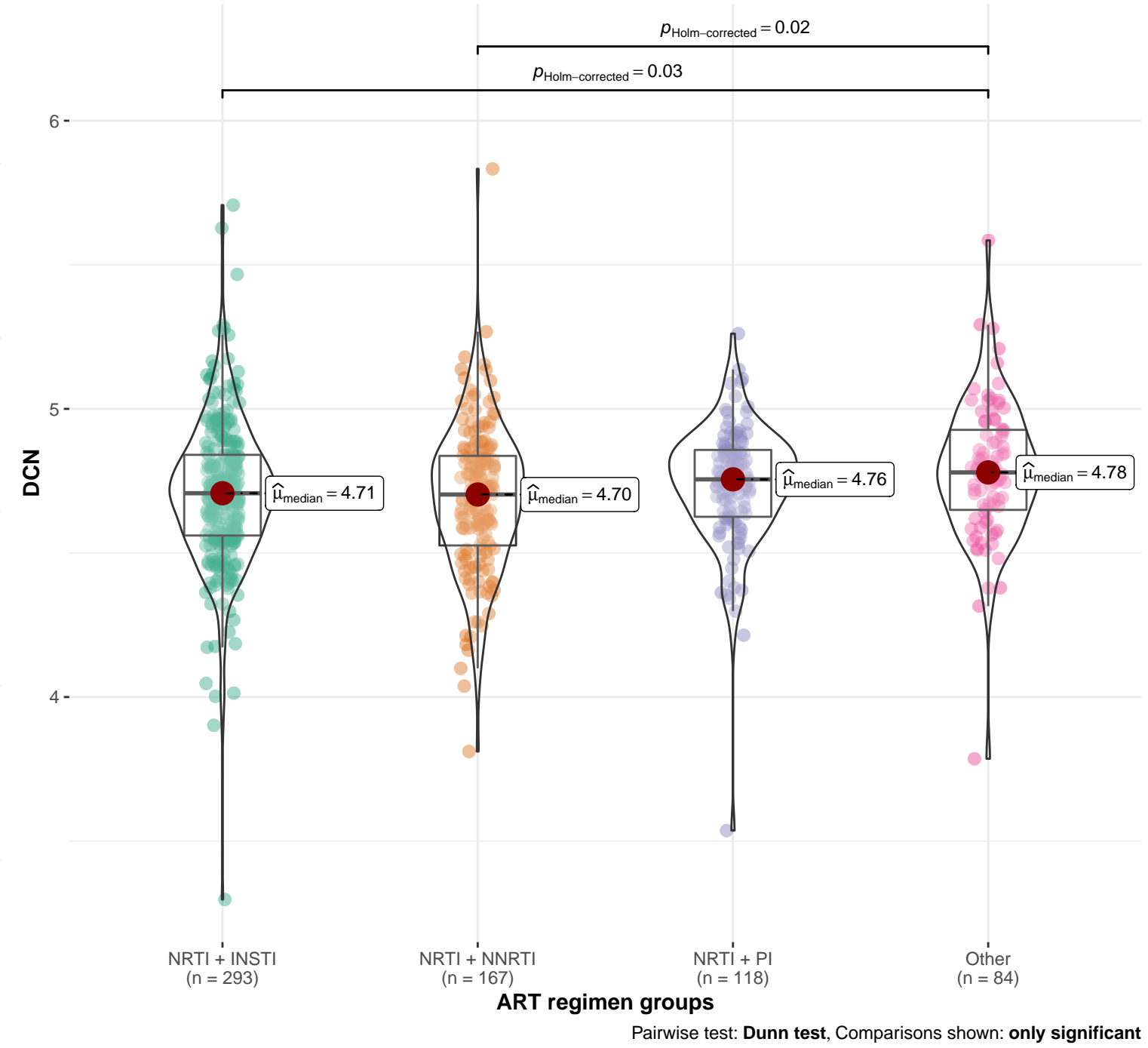
Distribution of DCN across viral load groups

$W_{\text{Mann-Whitney}} = 26593.00$, $p = 0.03$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.15$, $CI_{95\%} [0.01, 0.27]$, $n_{\text{obs}} = 654$



Distribution of DCN across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 11.69$, $p = 8.50e-03$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.02$, $CI_{95\%} [8.21e-03, 1.00]$, $n_{\text{obs}} = 662$

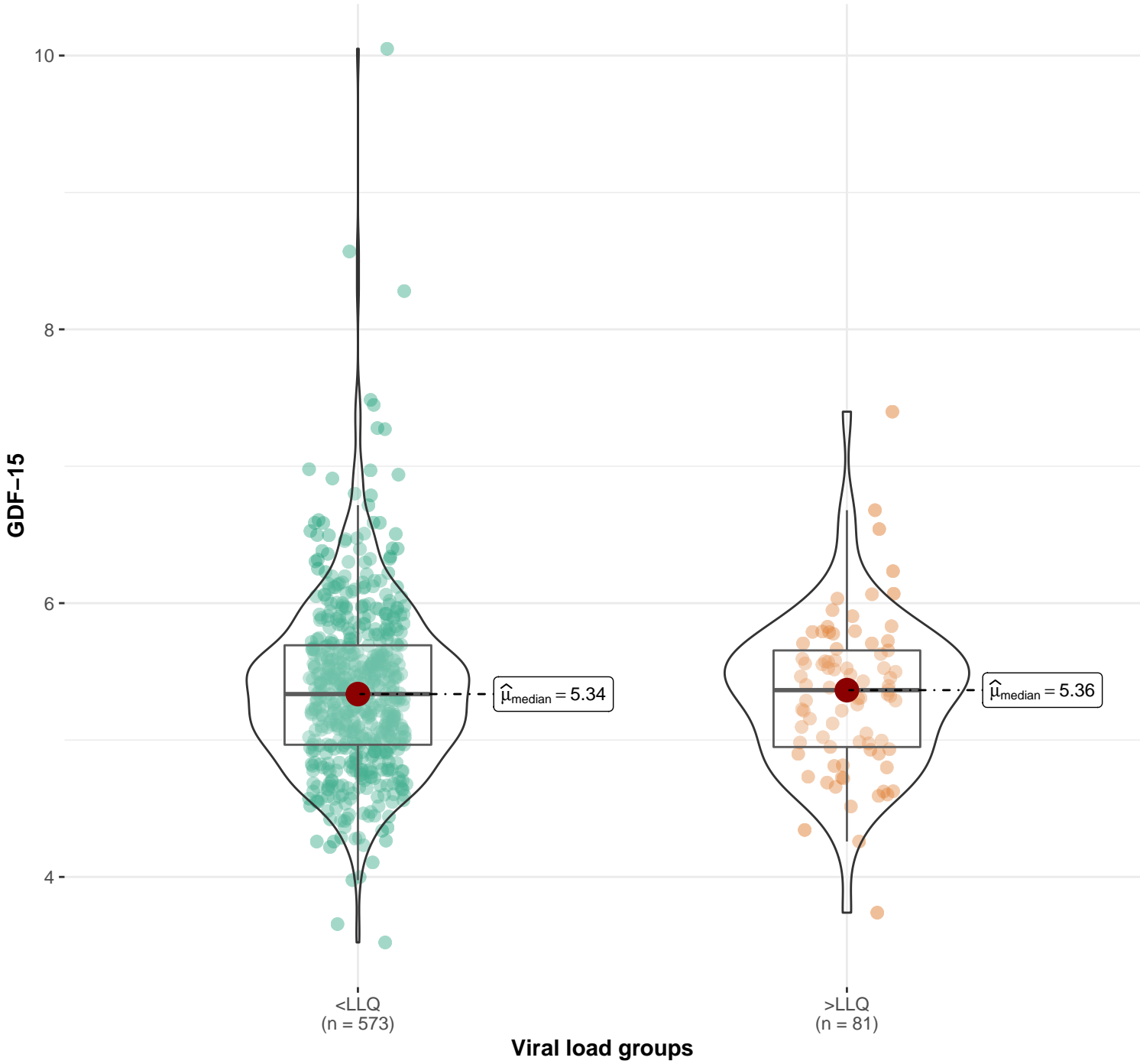


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of GDF-15 across different viral loads and ART regimens

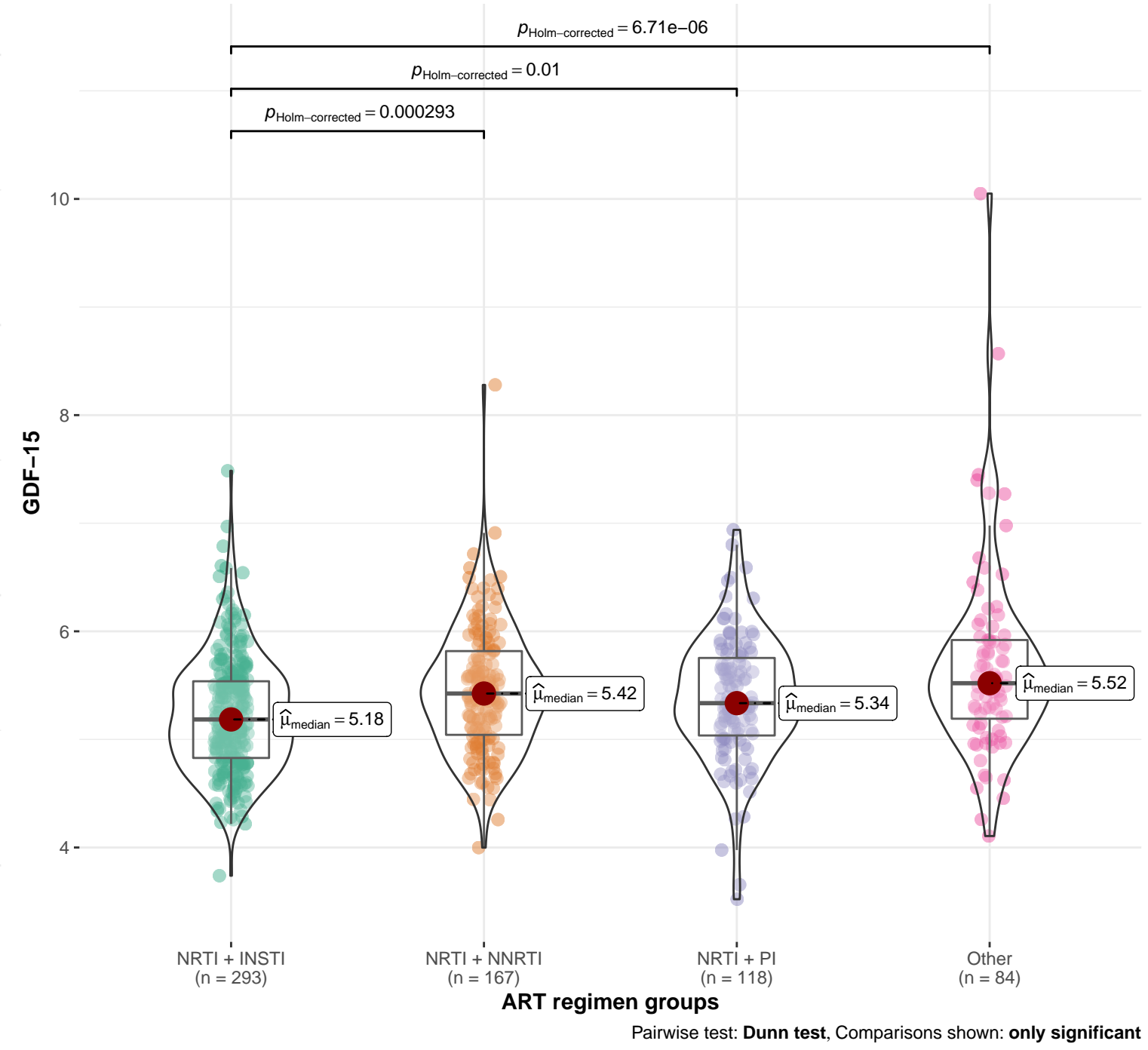
Distribution of GDF-15 across viral load groups

$W_{\text{Mann-Whitney}} = 23553.50$, $p = 0.83$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.01$, $CI_{95\%} [-0.12, 0.15]$, $n_{\text{obs}} = 654$



Distribution of GDF-15 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 32.34$, $p = 4.45e-07$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.05$, $CI_{95\%} [0.03, 1.00]$, $n_{\text{obs}} = 662$

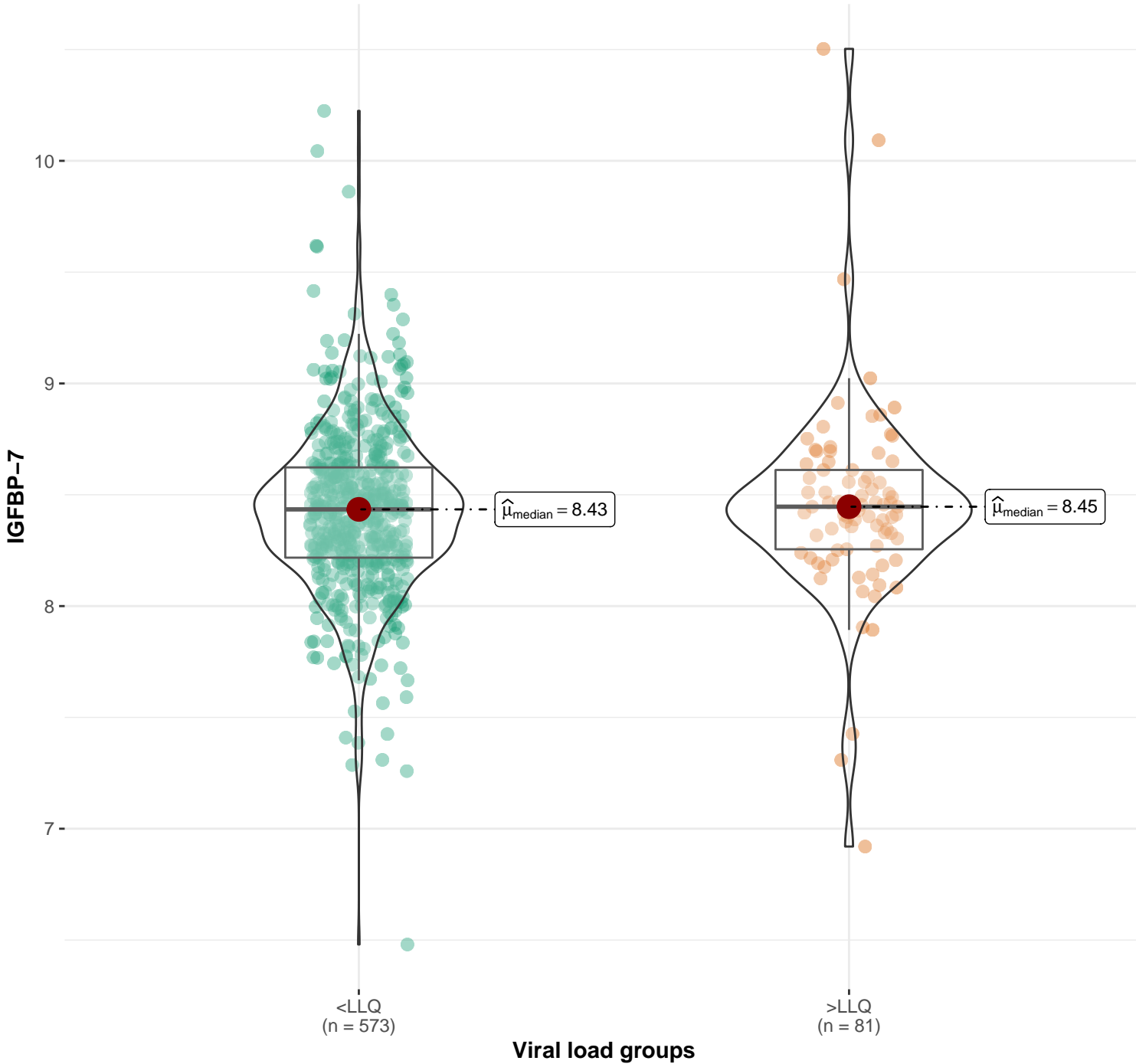


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of IGFBP-7 across different viral loads and ART regimens

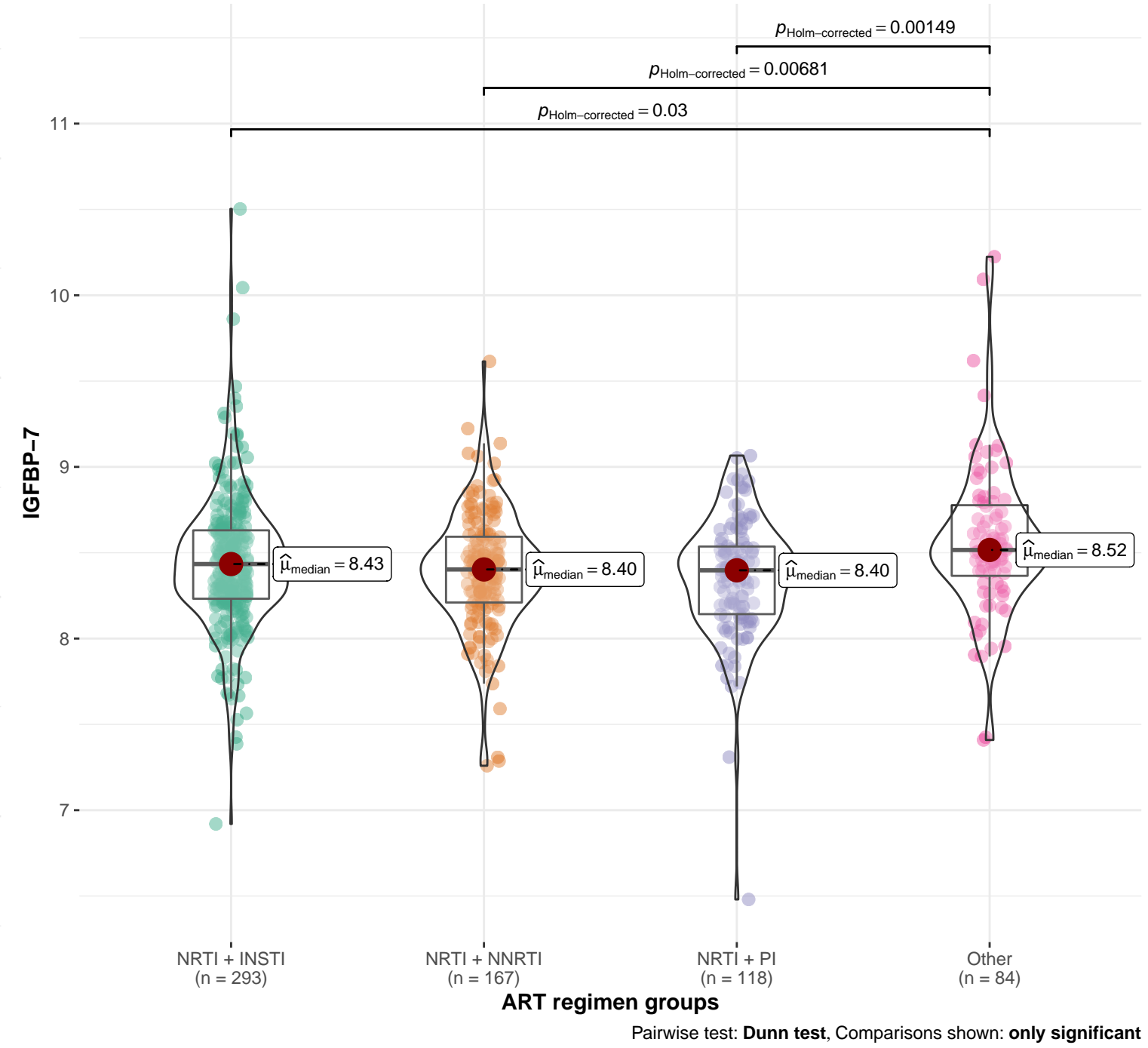
Distribution of IGFBP-7 across viral load groups

$W_{\text{Mann-Whitney}} = 22312.00$, $p = 0.57$, $\hat{\rho}_{\text{biserial}}^{\text{rank}} = -0.04$, $CI_{95\%} [-0.17, 0.10]$, $n_{\text{obs}} = 654$



Distribution of IGFBP-7 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 15.00$, $p = 1.81e-03$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.02$, $CI_{95\%} [0.01, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

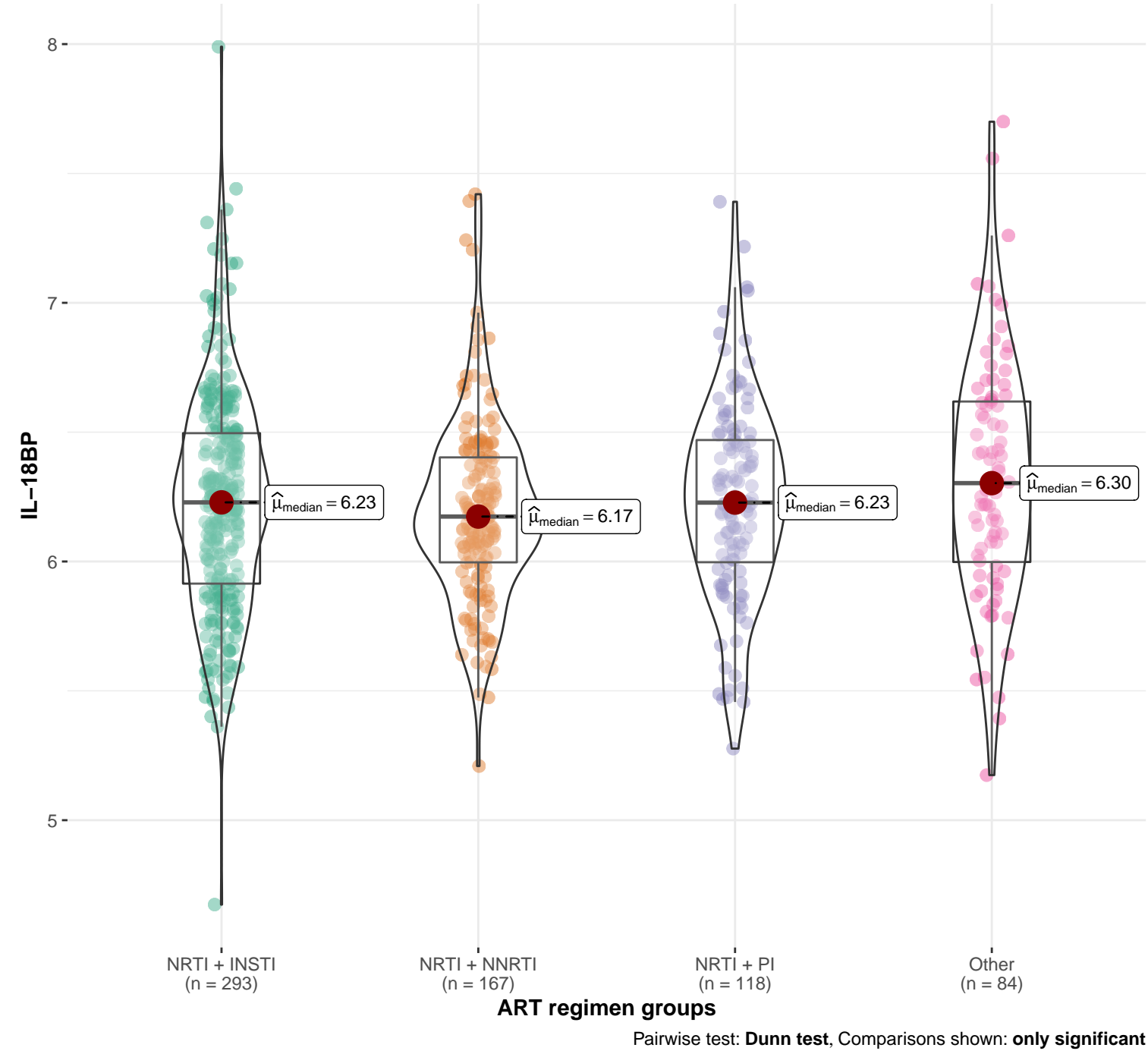
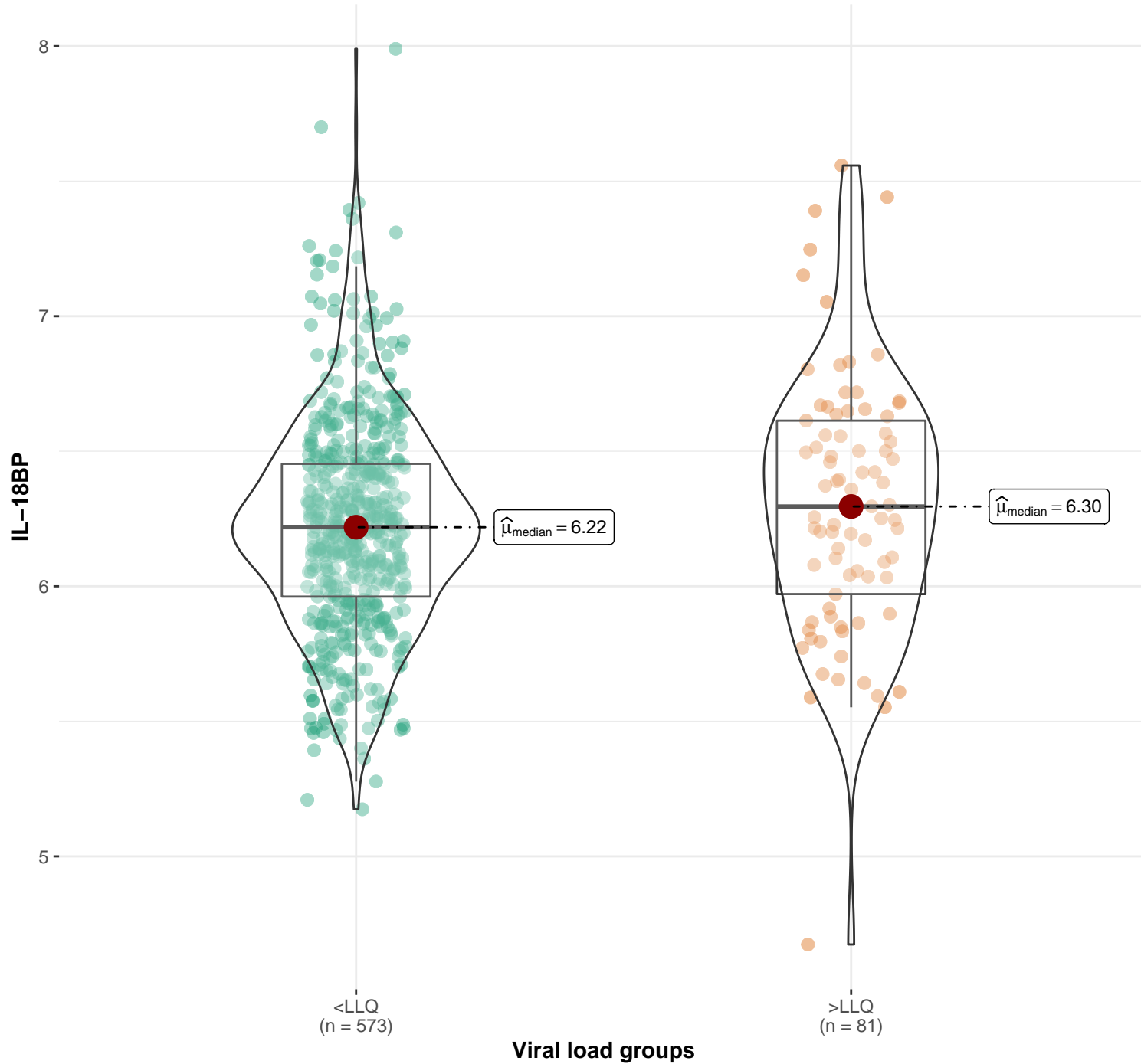
Distribution of IL-18BP across different viral loads and ART regimens

Distribution of IL-18BP across viral load groups

$W_{\text{Mann-Whitney}} = 20641.00$, $p = 0.11$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.11$, $CI_{95\%} [-0.24, 0.02]$, $n_{\text{obs}} = 654$

Distribution of IL-18BP across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 5.43$, $p = 0.14$, $\hat{\epsilon}_{\text{ordinal}}^2 = 8.21e-03$, $CI_{95\%} [2.87e-03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

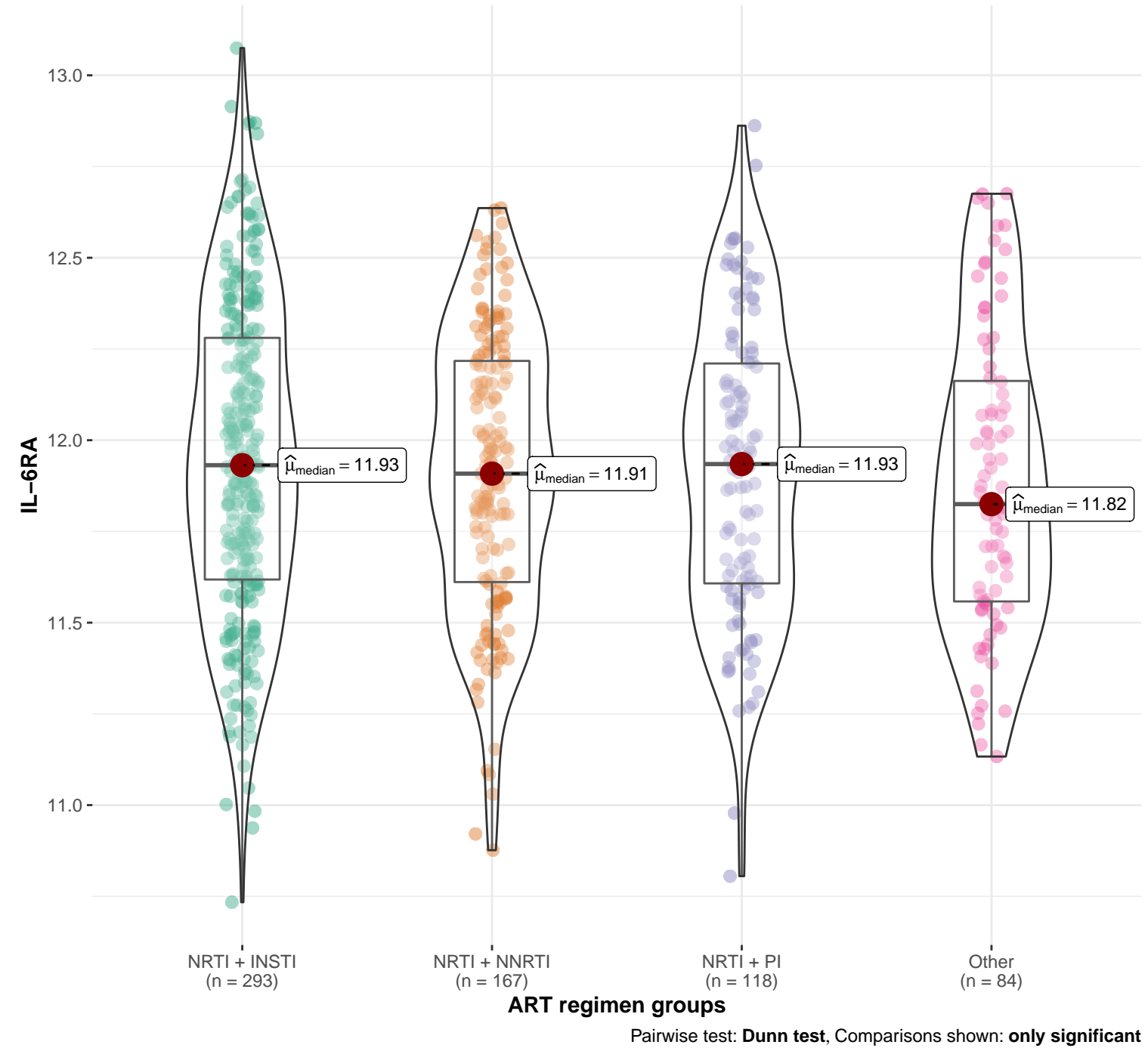
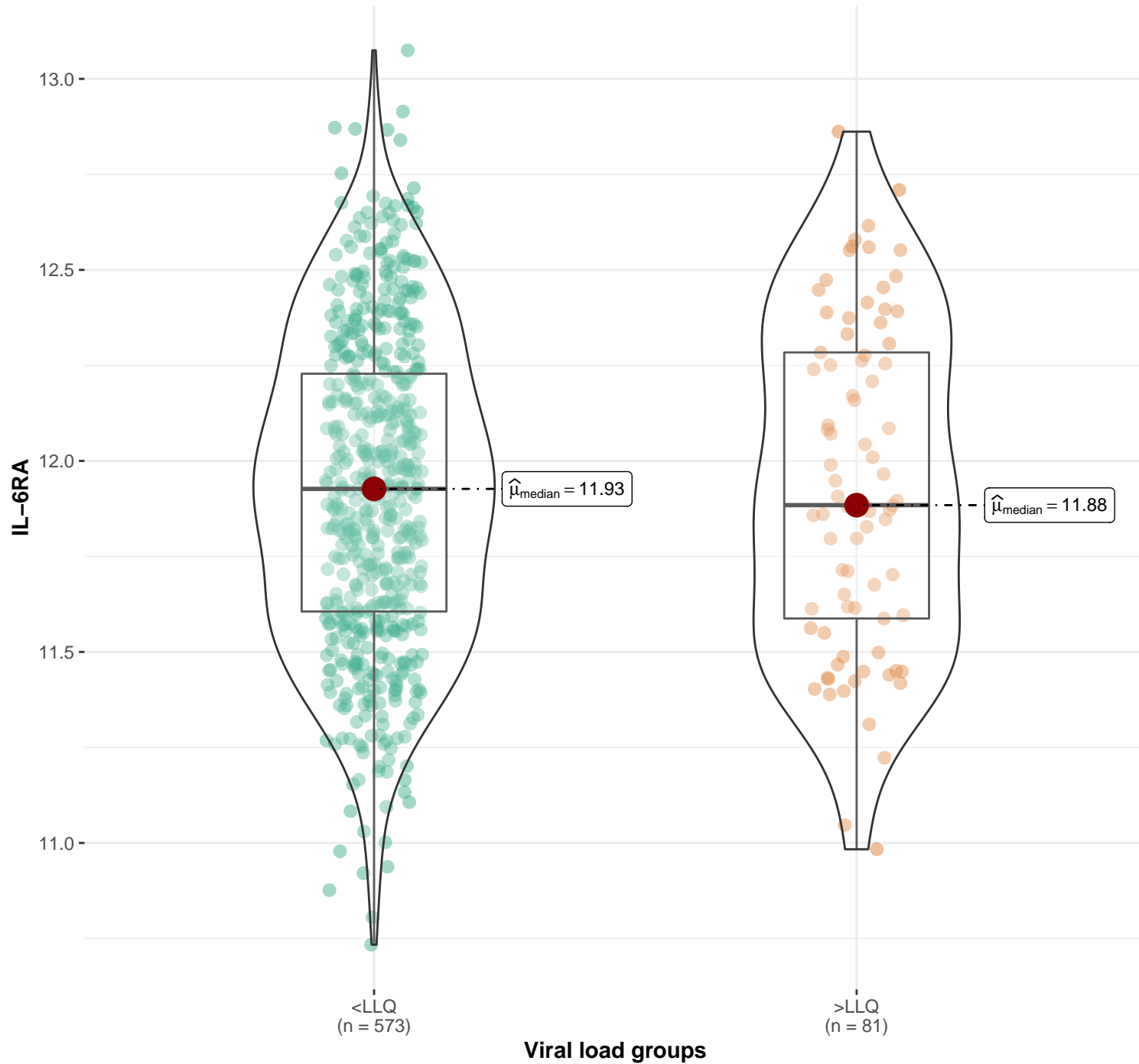
Distribution of IL-6RA across different viral loads and ART regimens

Distribution of IL-6RA across viral load groups

$W_{\text{Mann-Whitney}} = 22857.00$, $p = 0.83$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.02$, $CI_{95\%} [-0.15, 0.12]$, $n_{\text{obs}} = 654$

Distribution of IL-6RA across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 1.60$, $p = 0.66$, $\hat{\epsilon}_{\text{ordinal}}^2 = 2.42e-03$, $CI_{95\%} [6.85e-04, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

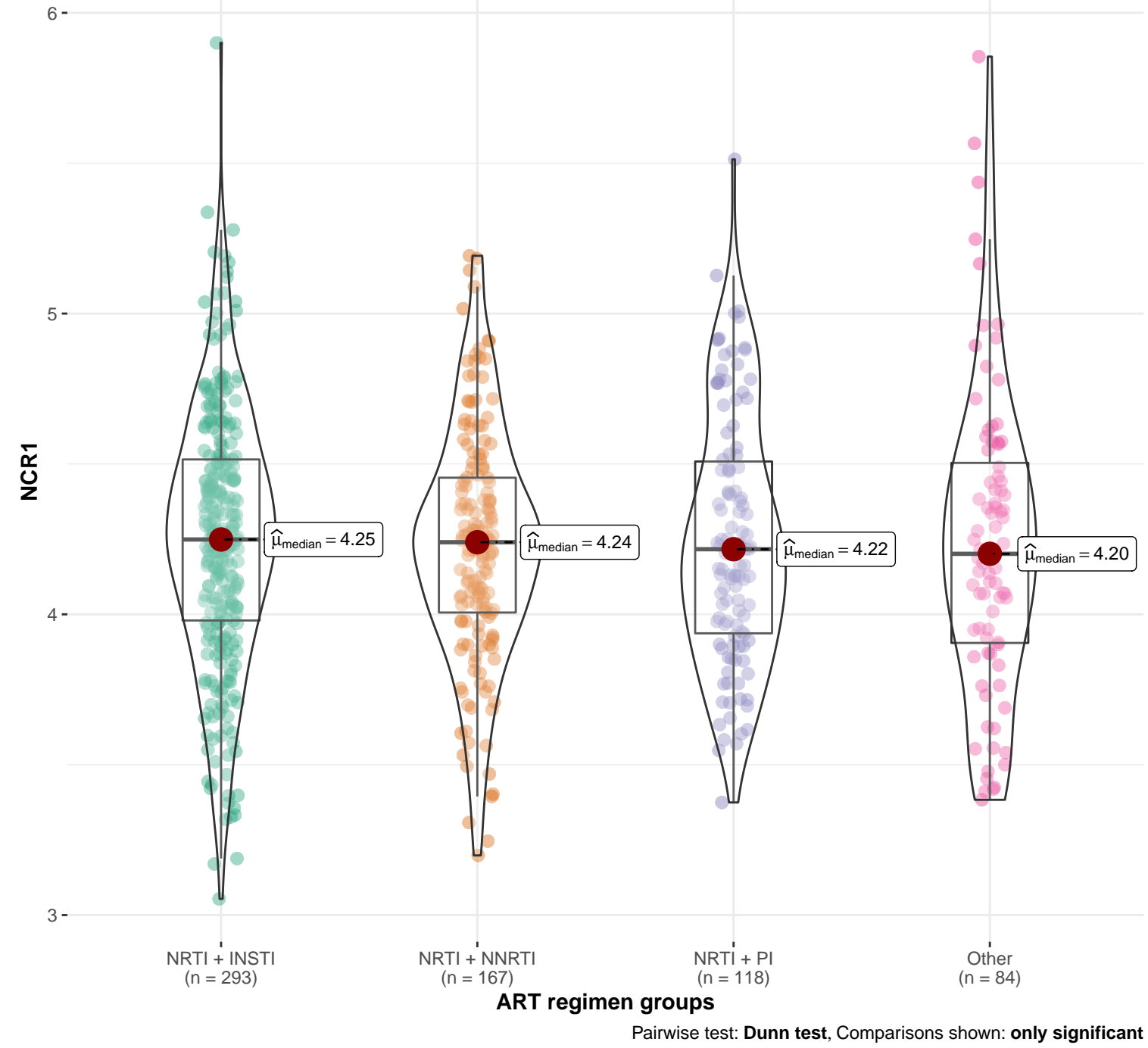
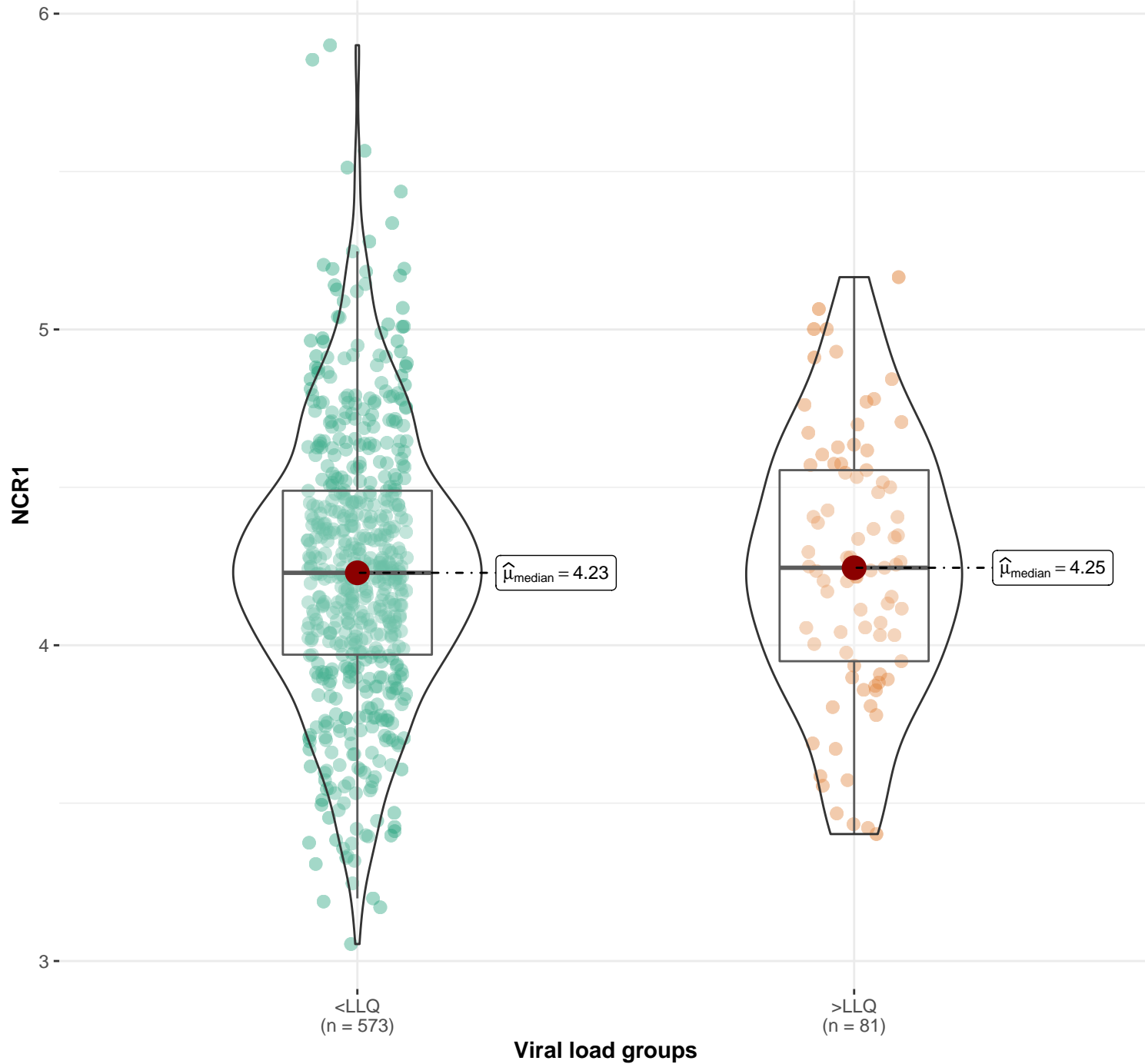
Distribution of NCR1 across different viral loads and ART regimens

Distribution of NCR1 across viral load groups

$W_{\text{Mann-Whitney}} = 22841.00$, $p = 0.82$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.02$, $CI_{95\%} [-0.15, 0.12]$, $n_{\text{obs}} = 654$

Distribution of NCR1 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 0.96$, $p = 0.81$, $\hat{\epsilon}_{\text{ordinal}}^2 = 1.46e-03$, $CI_{95\%} [9.65e-04, 1.00]$, $n_{\text{obs}} = 662$

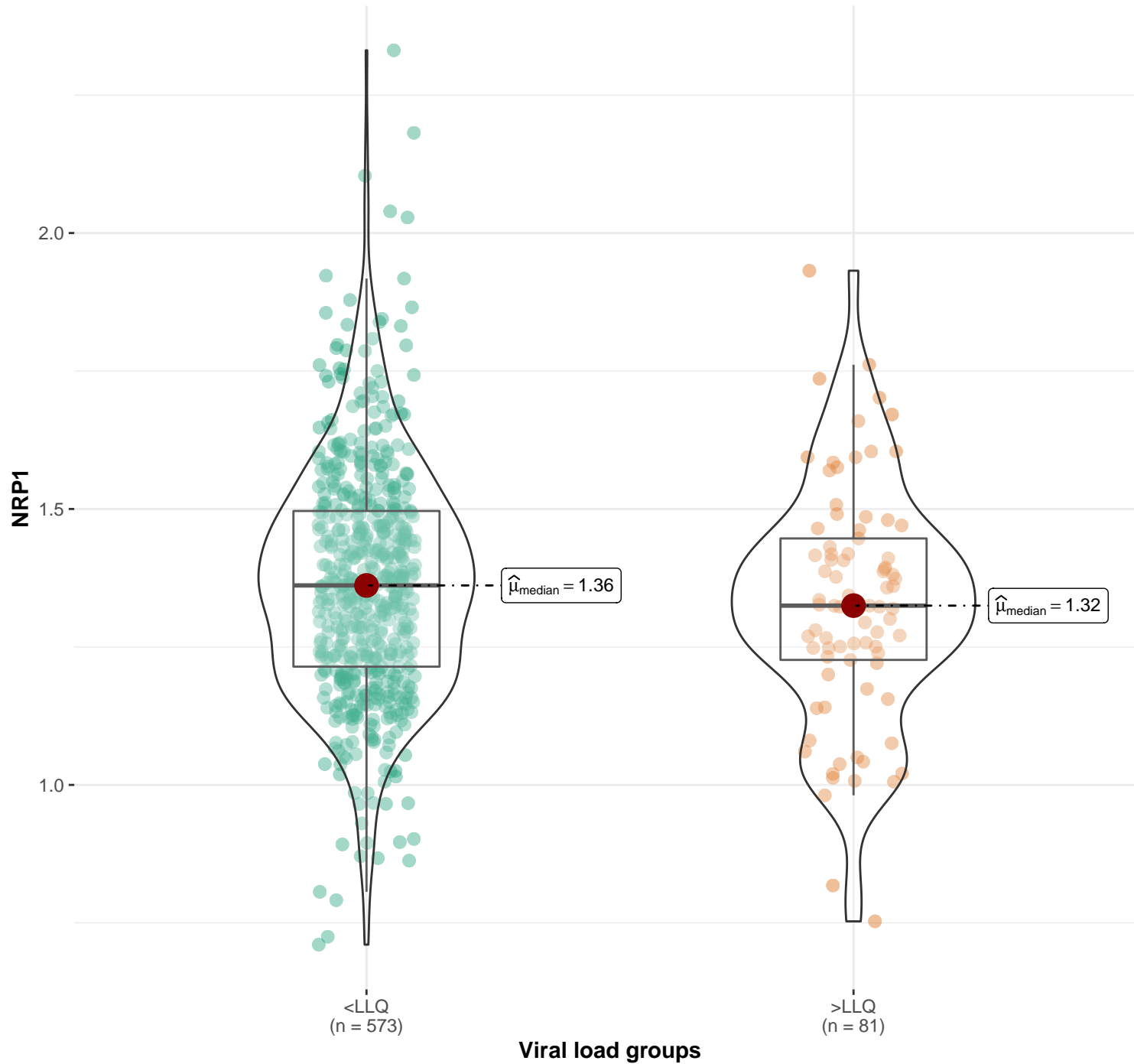


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of NRP1 across different viral loads and ART regimens

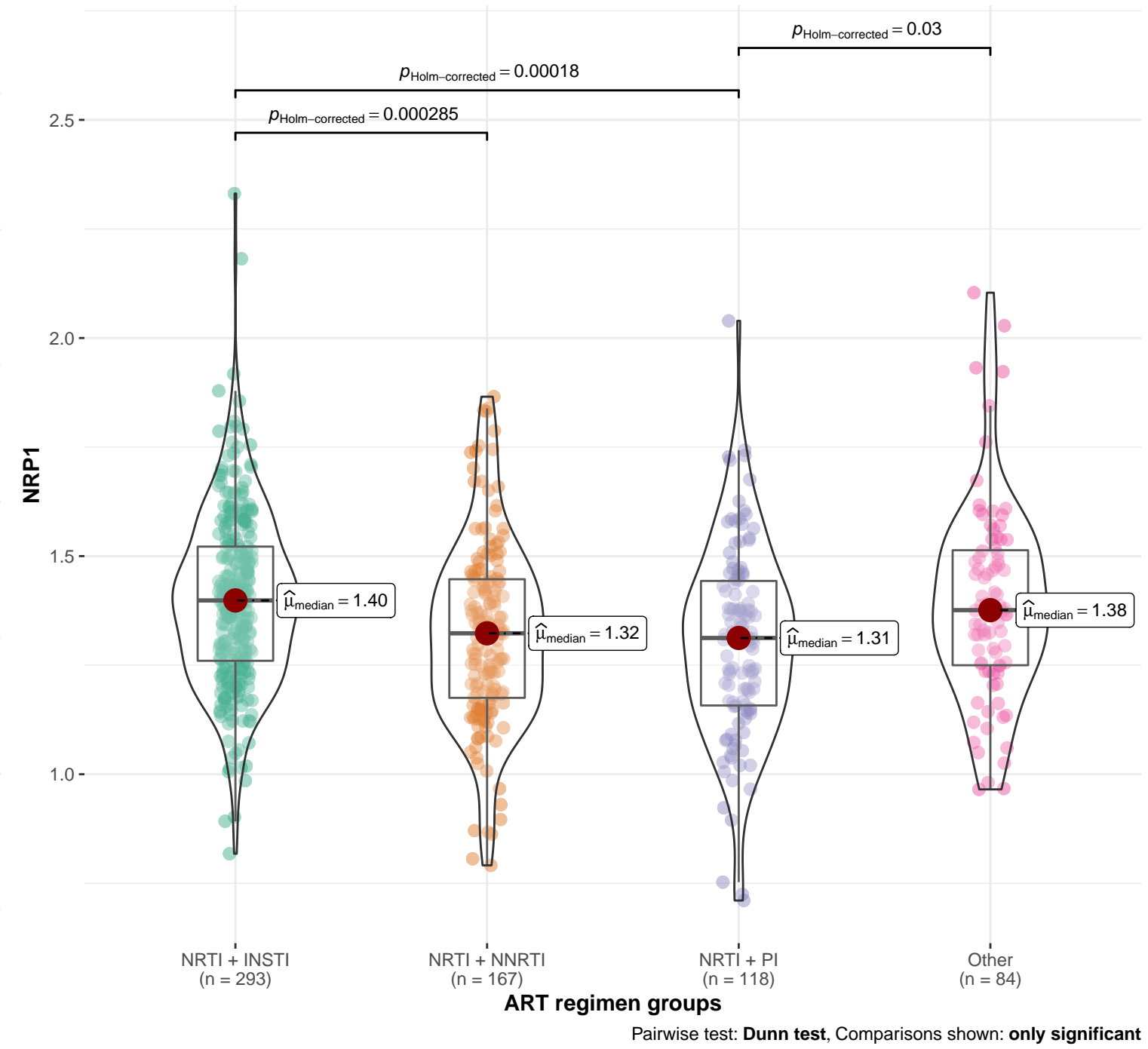
Distribution of NRP1 across viral load groups

$W_{\text{Mann-Whitney}} = 25348.50$, $p = 0.18$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.09$, $CI_{95\%} [-0.04, 0.22]$, $n_{\text{obs}} = 654$



Distribution of NRP1 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 26.73$, $p = 6.70e-06$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.04$, $CI_{95\%} [0.02, 1.00]$, $n_{\text{obs}} = 662$

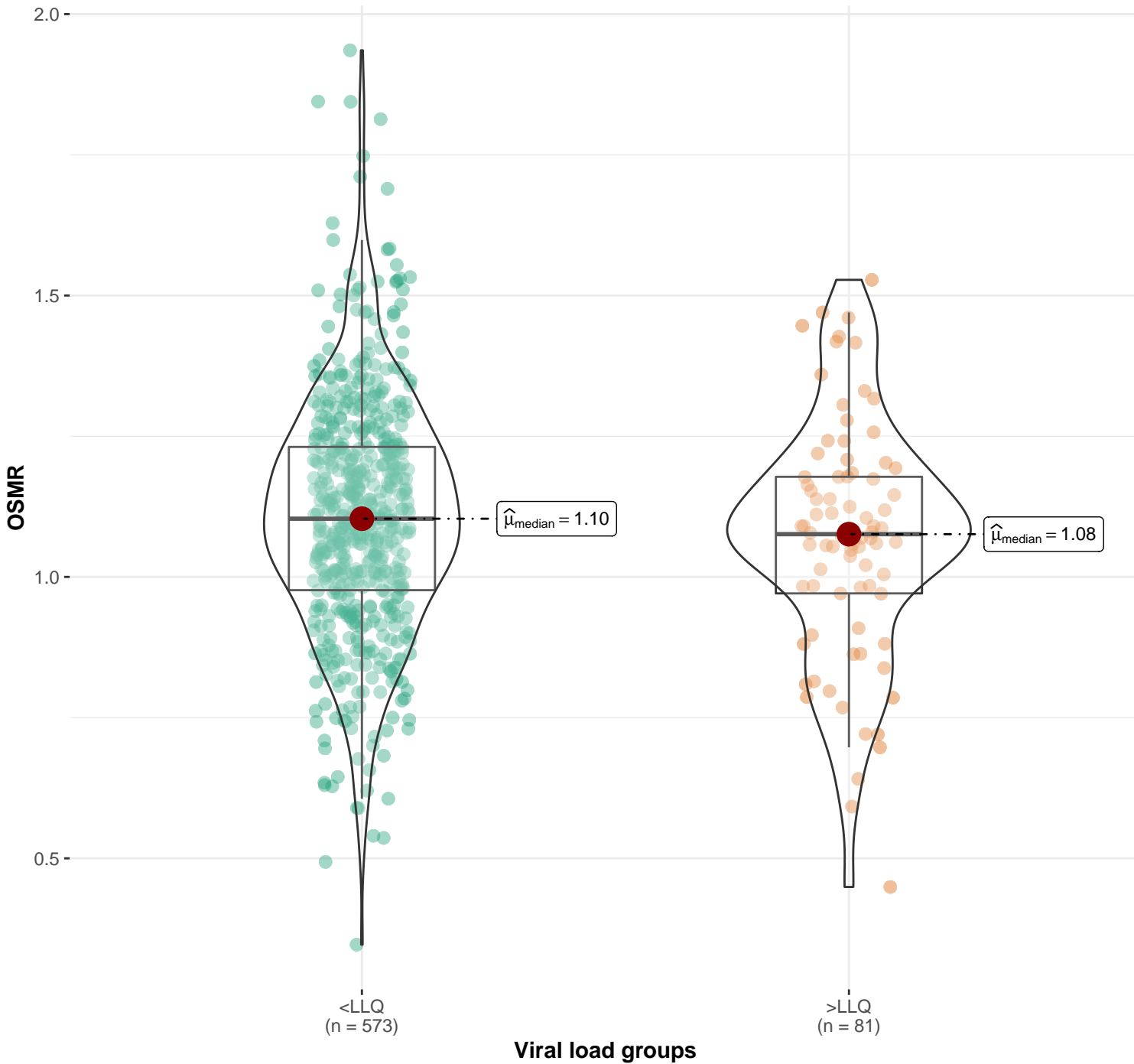


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of OSMR across different viral loads and ART regimens

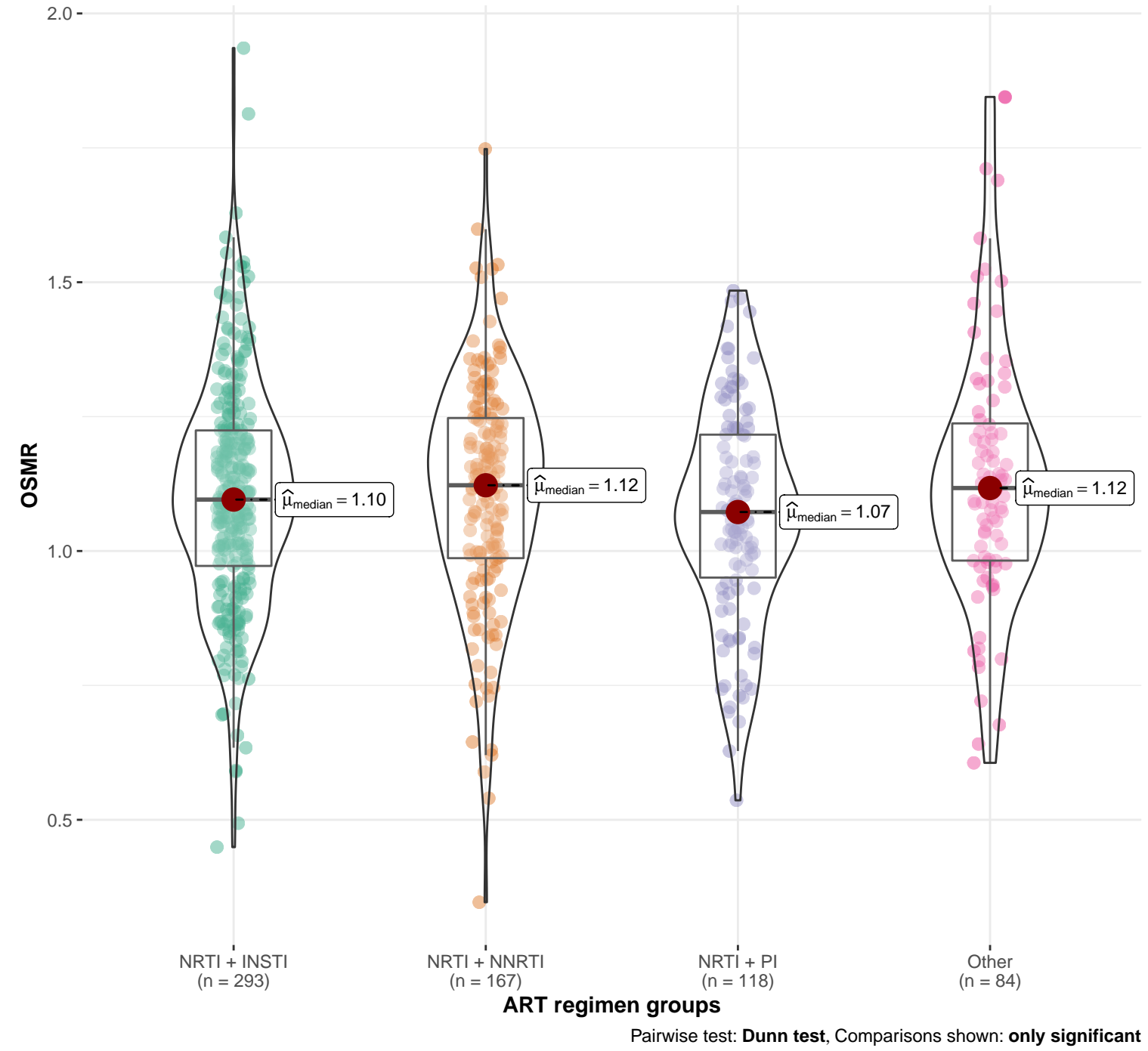
Distribution of OSMR across viral load groups

$W_{\text{Mann-Whitney}} = 25357.00$, $p = 0.18$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.09$, $CI_{95\%} [-0.04, 0.22]$, $n_{\text{obs}} = 654$



Distribution of OSMR across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 3.72$, $p = 0.29$, $\hat{\epsilon}_{\text{ordinal}}^2 = 5.63e-03$, $CI_{95\%} [1.25e-03, 1.00]$, $n_{\text{obs}} = 662$

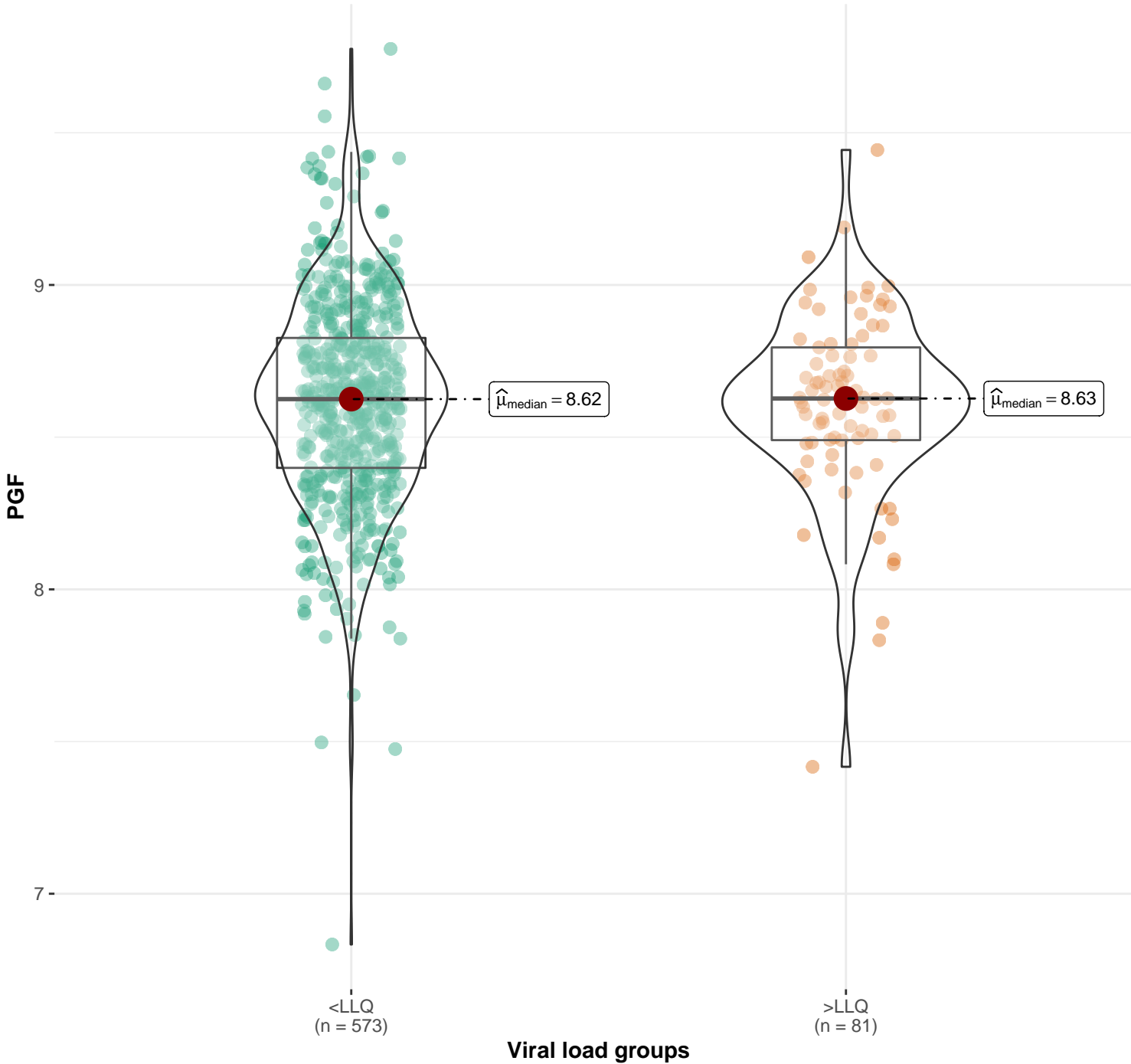


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of PGF across different viral loads and ART regimens

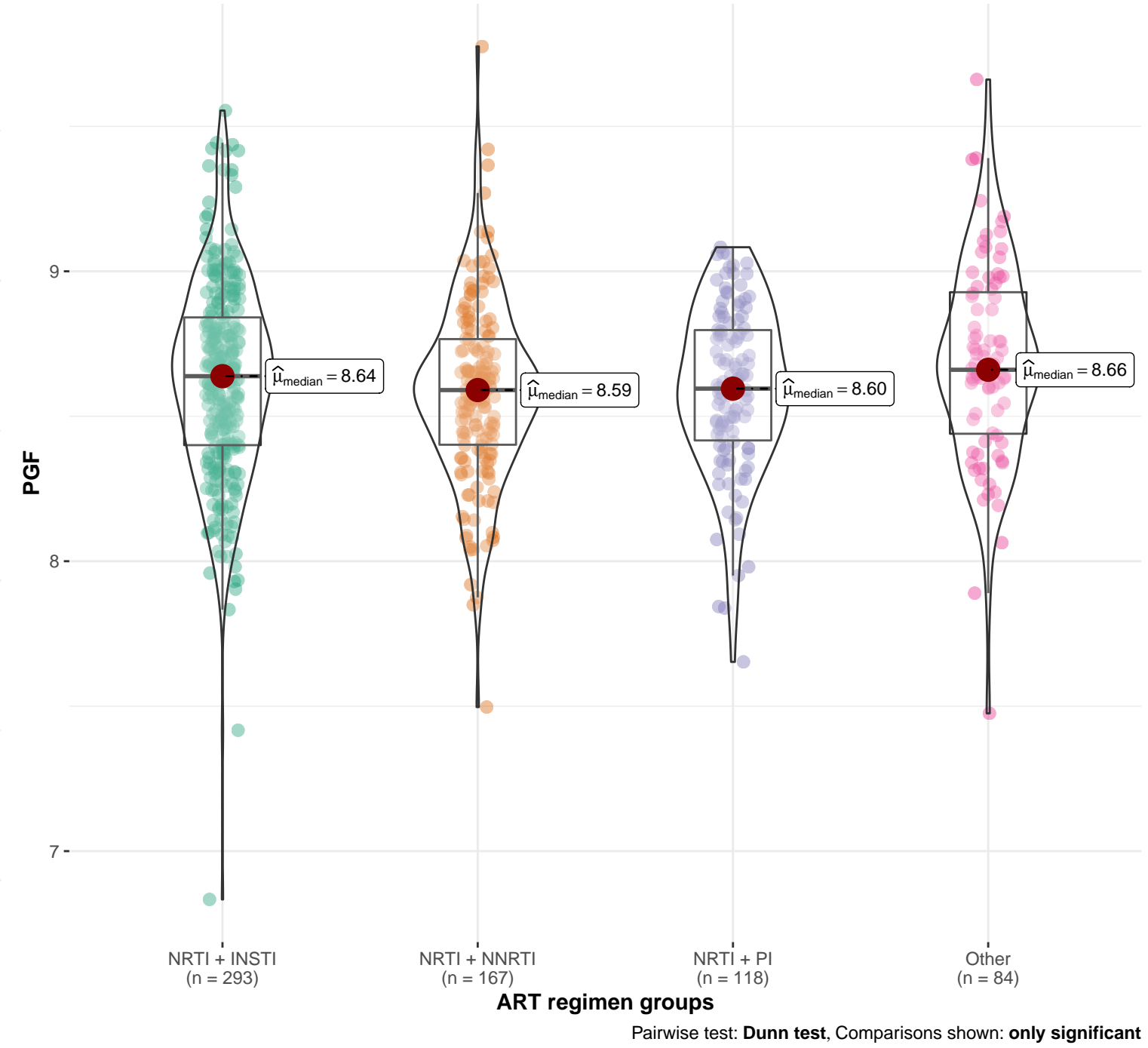
Distribution of PGF across viral load groups

$W_{\text{Mann-Whitney}} = 23107.50$, $p = 0.95$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -4.27\text{e-}03$, $\text{CI}_{95\%} [-0.14, 0.13]$, $n_{\text{obs}} = 654$



Distribution of PGF across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 6.77$, $p = 0.08$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.01$, $\text{CI}_{95\%} [3.45\text{e-}03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

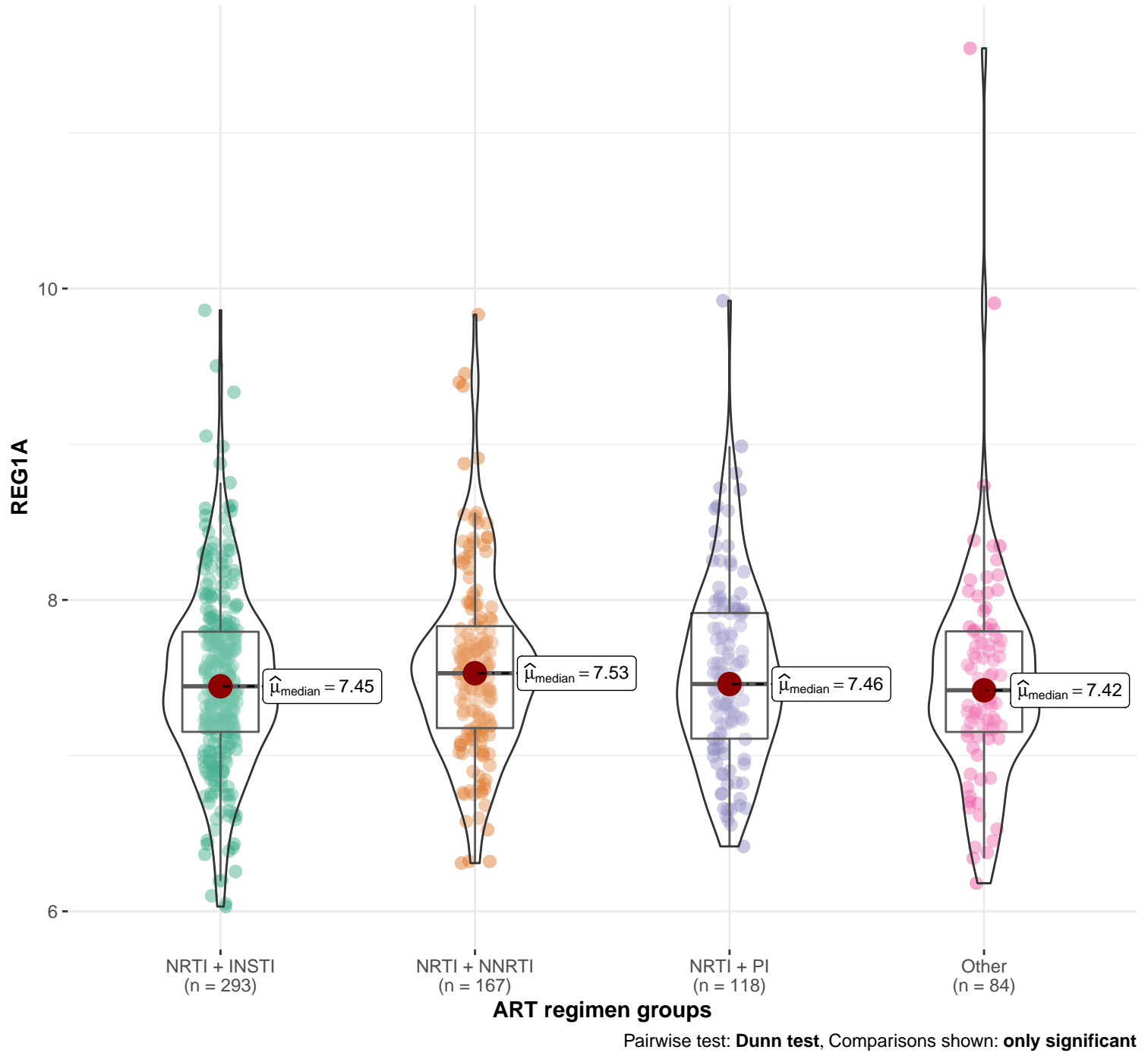
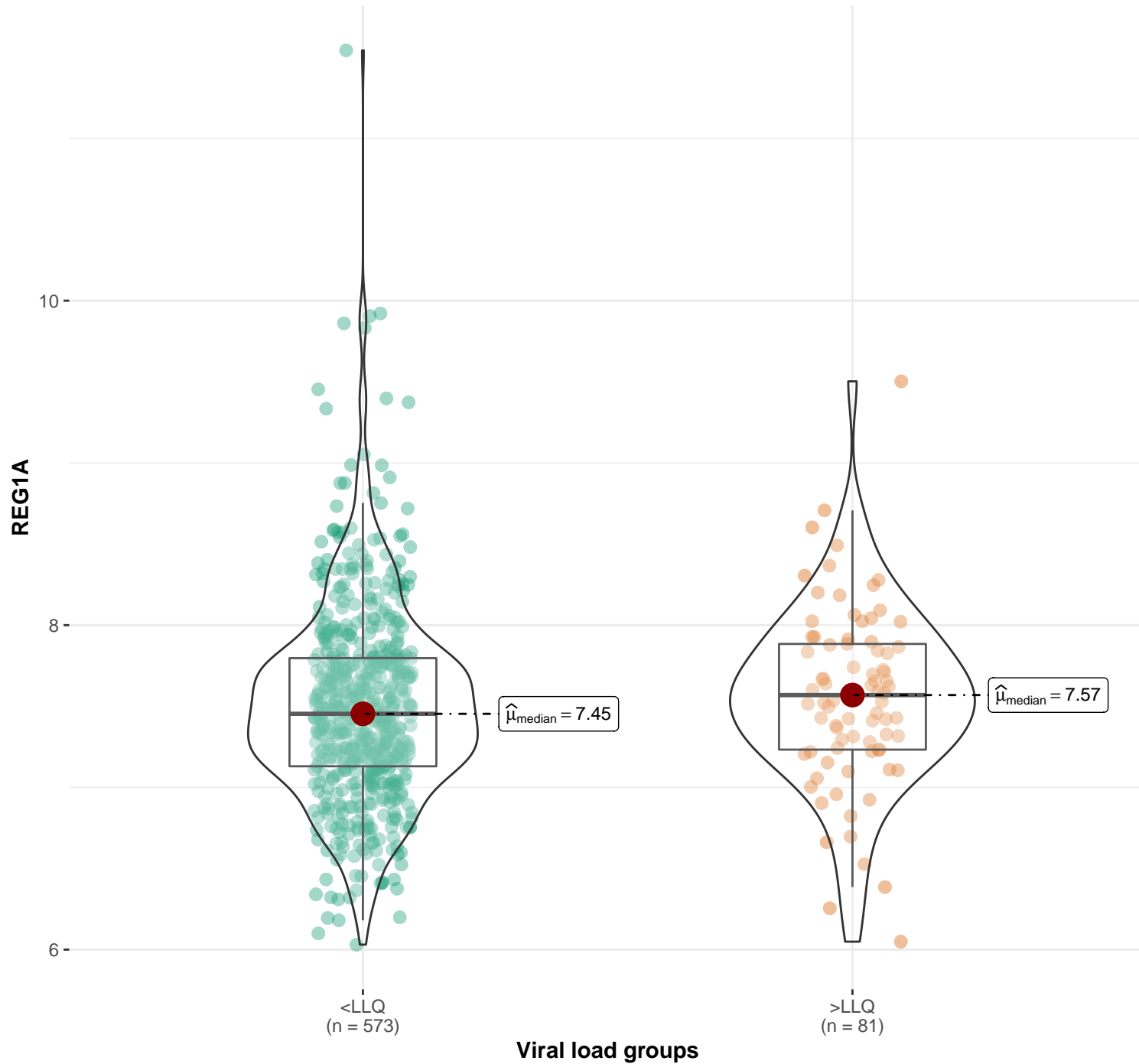
Distribution of REG1A across different viral loads and ART regimens

Distribution of REG1A across viral load groups

$W_{\text{Mann-Whitney}} = 21087.00$, $p = 0.18$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.09$, $CI_{95\%} [-0.22, 0.04]$, $n_{\text{obs}} = 654$

Distribution of REG1A across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 1.93$, $p = 0.59$, $\hat{\epsilon}_{\text{ordinal}}^2 = 2.92e-03$, $CI_{95\%} [1.43e-03, 1.00]$, $n_{\text{obs}} = 662$

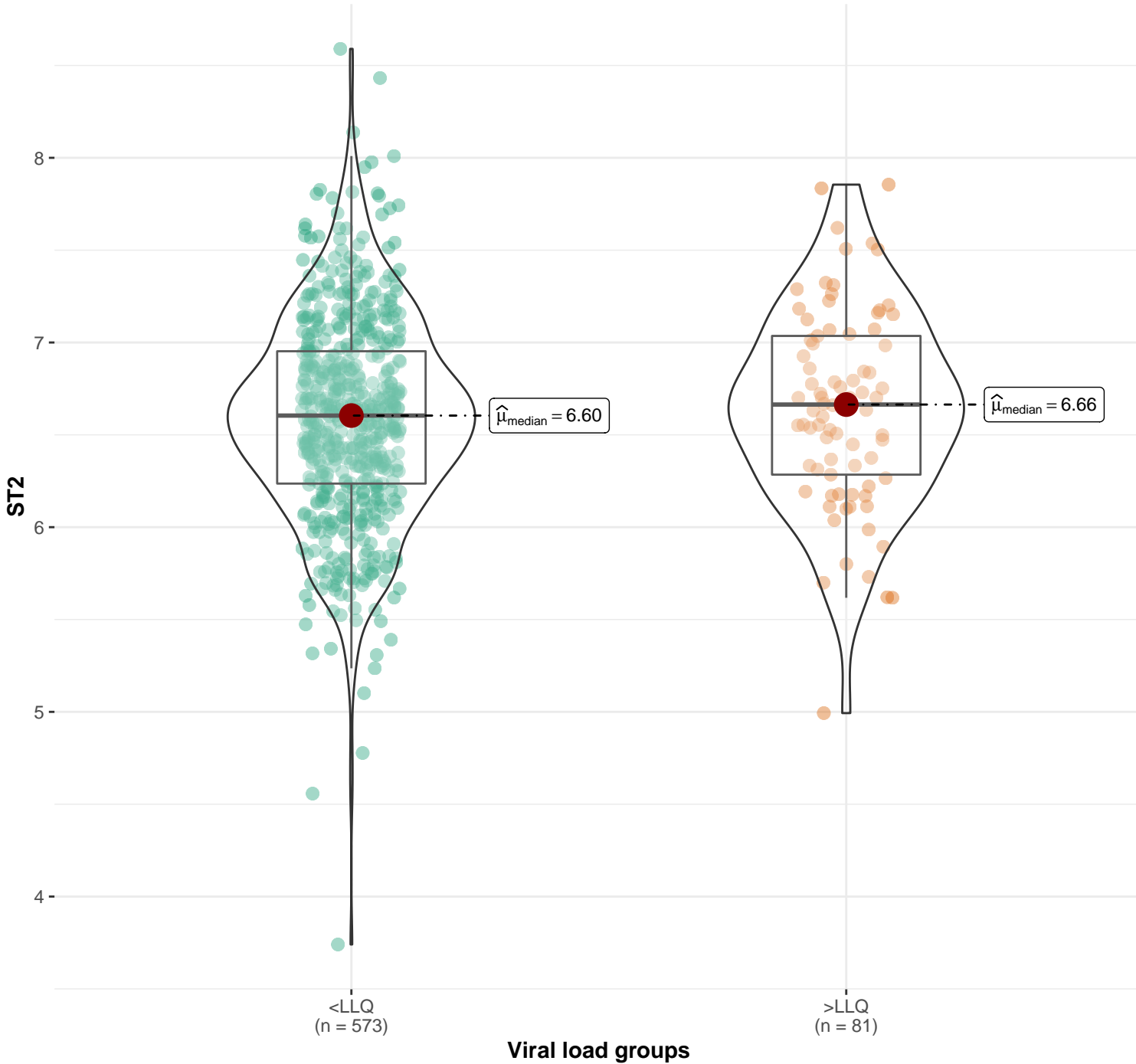


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of ST2 across different viral loads and ART regimens

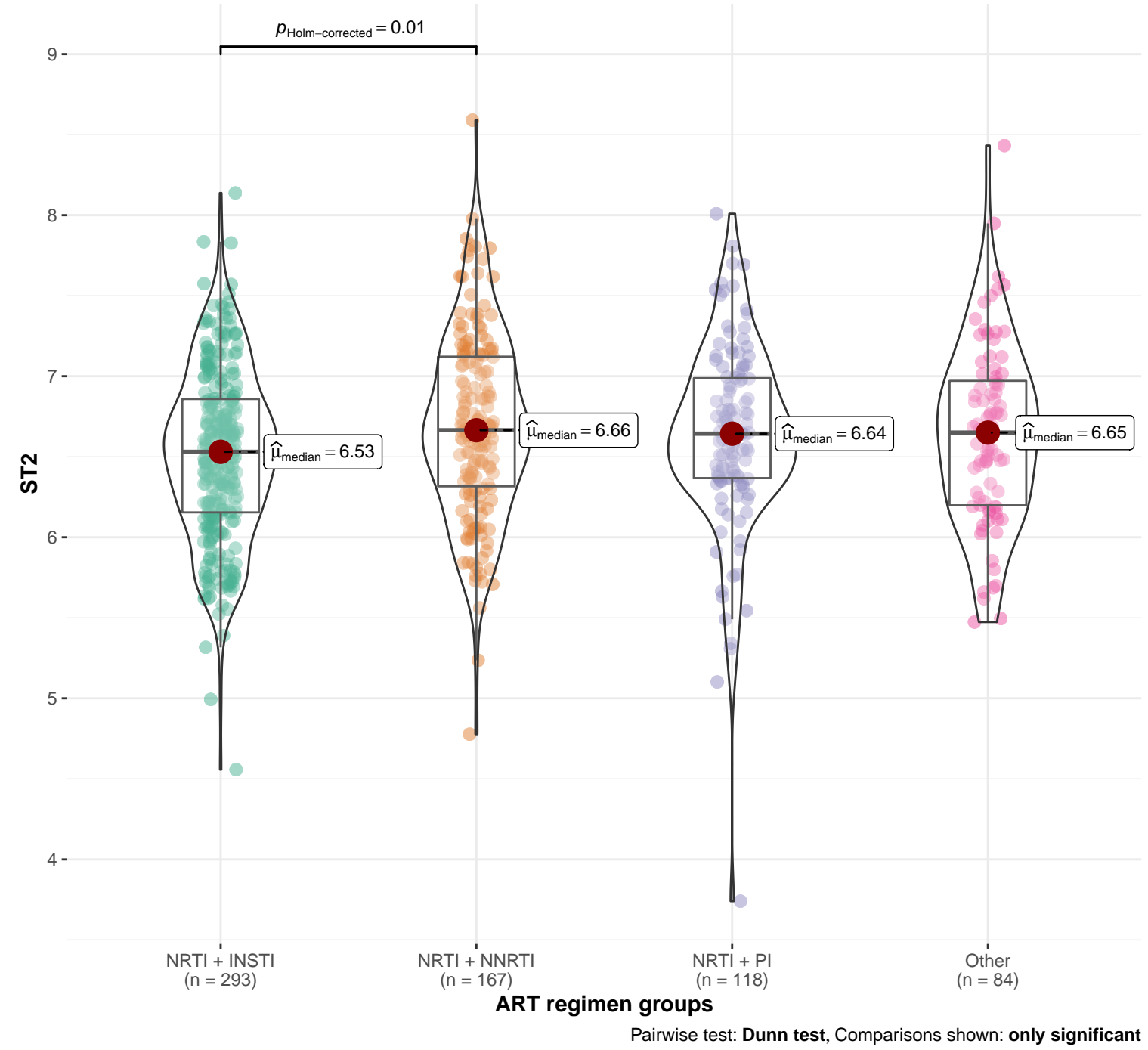
Distribution of ST2 across viral load groups

$W_{\text{Mann-Whitney}} = 21739.00$, $p = 0.36$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.06$, $CI_{95\%} [-0.20, 0.07]$, $n_{\text{obs}} = 654$



Distribution of ST2 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 11.22$, $p = 0.01$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.02$, $CI_{95\%} [7.69e-03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

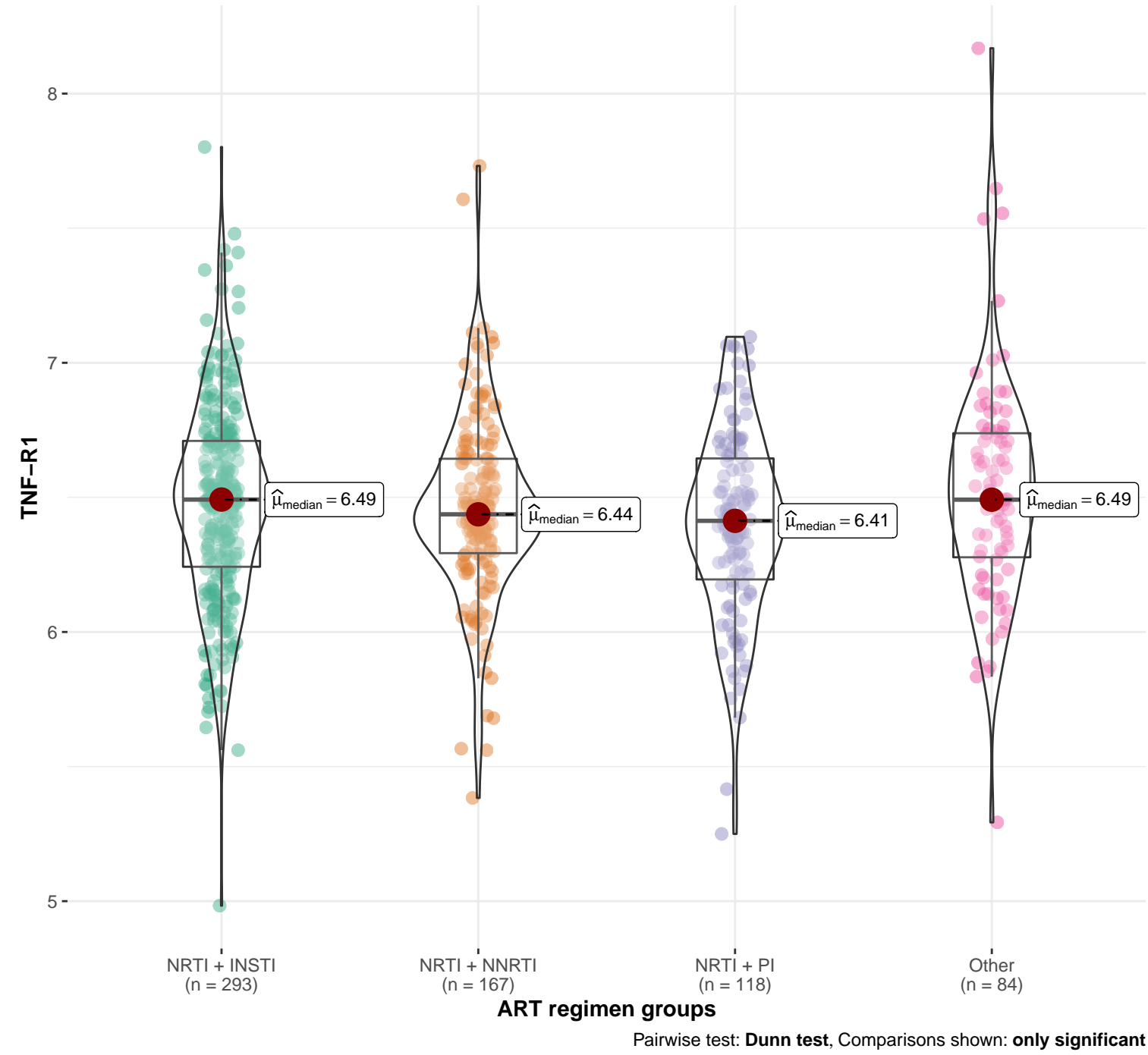
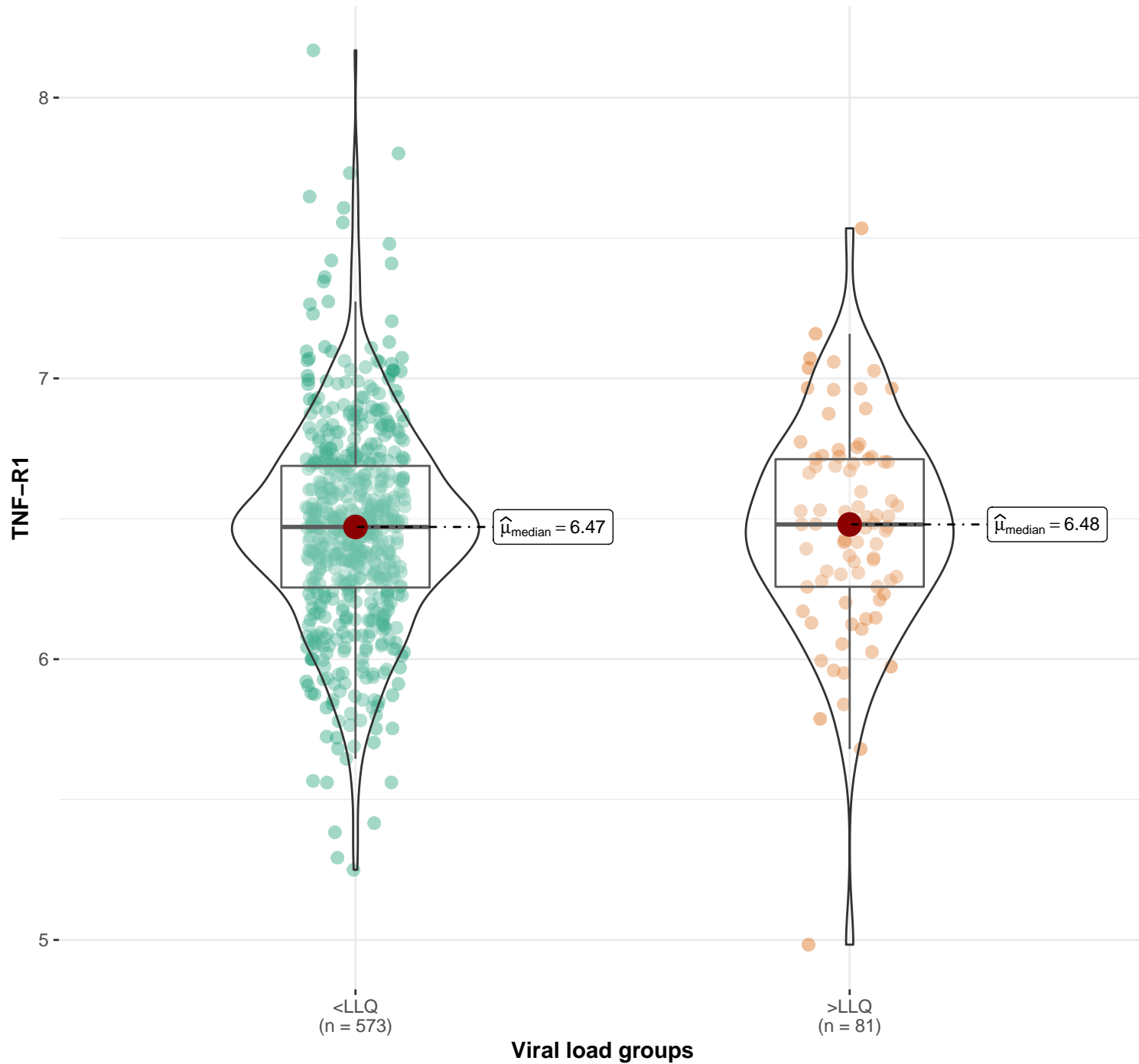
Distribution of TNF-R1 across different viral loads and ART regimens

Distribution of TNF-R1 across viral load groups

$W_{\text{Mann-Whitney}} = 22621.00$, $p = 0.71$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.03$, $CI_{95\%} [-0.16, 0.11]$, $n_{\text{obs}} = 654$

Distribution of TNF-R1 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 5.21$, $p = 0.16$, $\hat{\epsilon}_{\text{ordinal}}^2 = 7.89e-03$, $CI_{95\%} [1.74e-03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

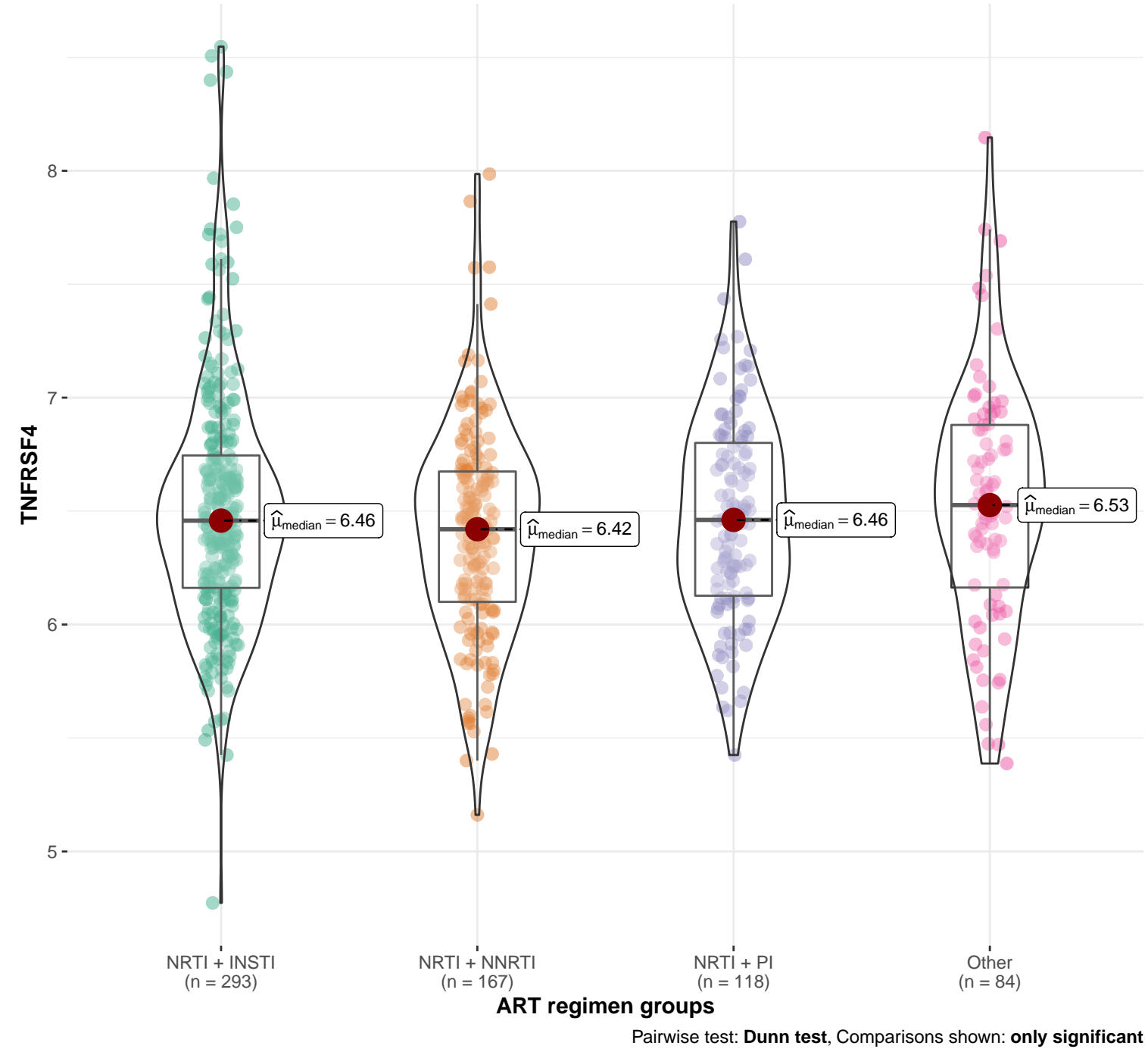
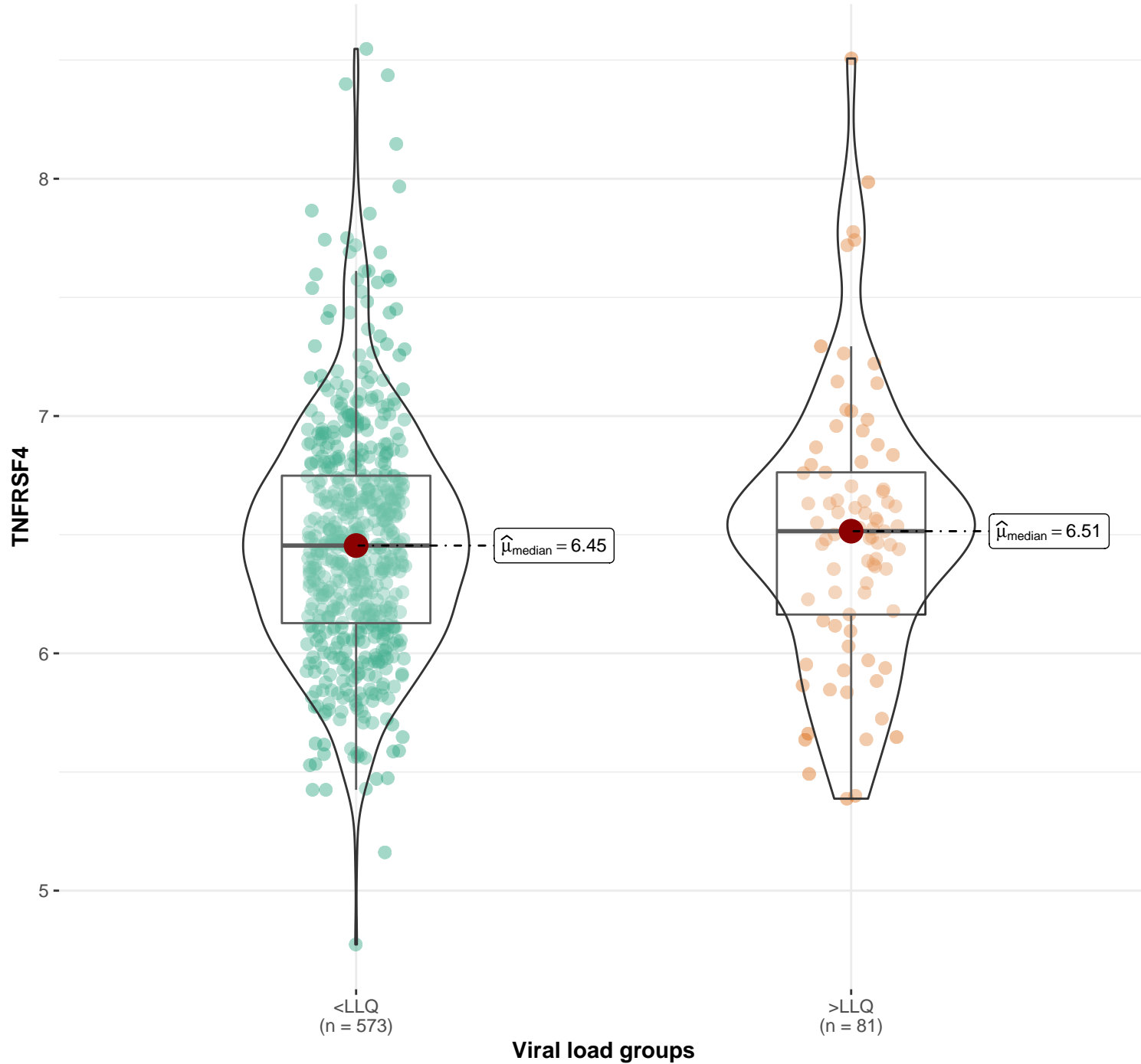
Distribution of TNFRSF4 across different viral loads and ART regimens

Distribution of TNFRSF4 across viral load groups

$W_{\text{Mann-Whitney}} = 22216.00$, $p = 0.53$, $\hat{\tau}_{\text{biserial}}^{\text{rank}} = -0.04$, $CI_{95\%} [-0.18, 0.09]$, $n_{\text{obs}} = 654$

Distribution of TNFRSF4 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 4.64$, $p = 0.20$, $\hat{\epsilon}_{\text{ordinal}}^2 = 7.03e-03$, $CI_{95\%} [1.16e-03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

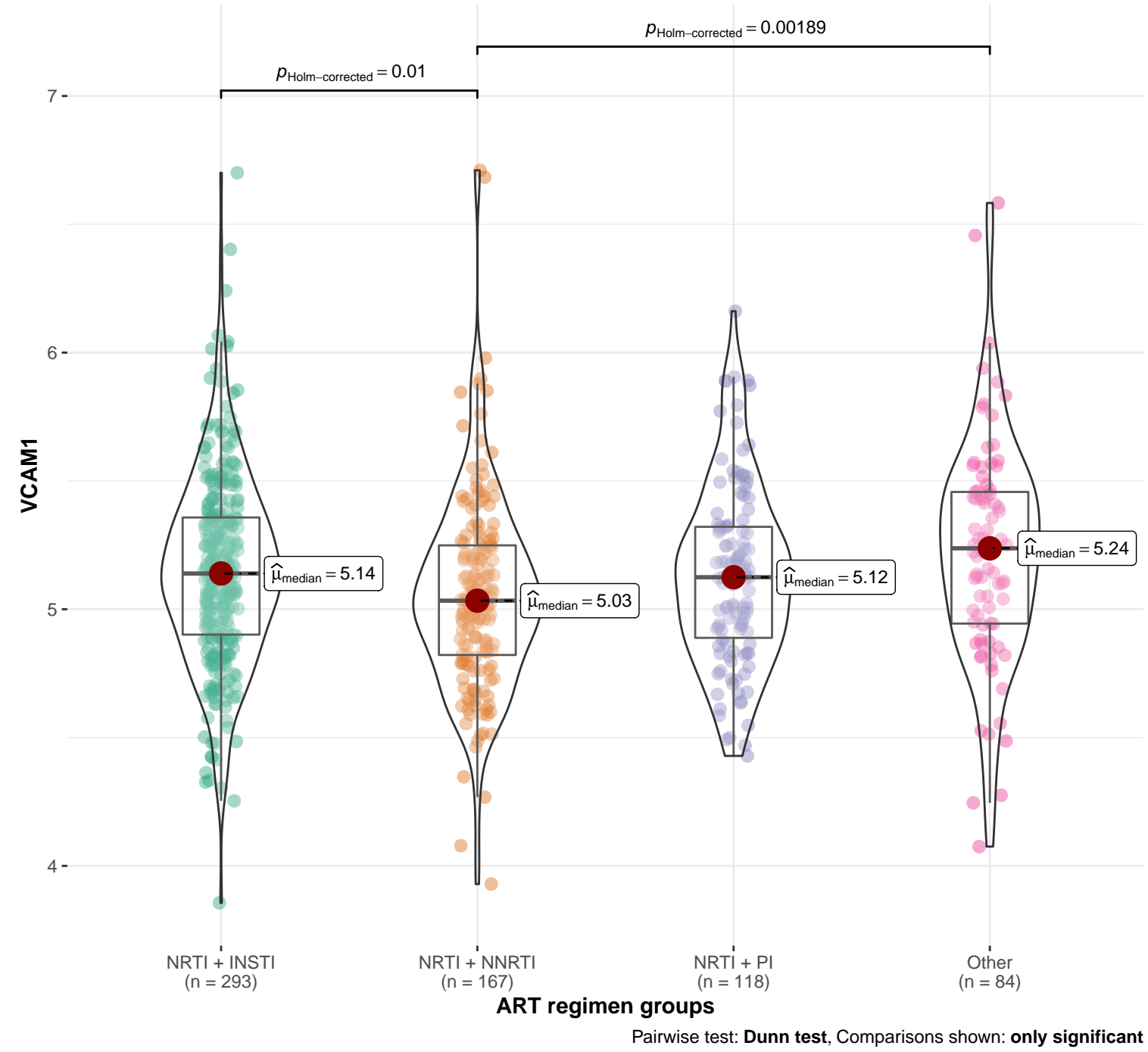
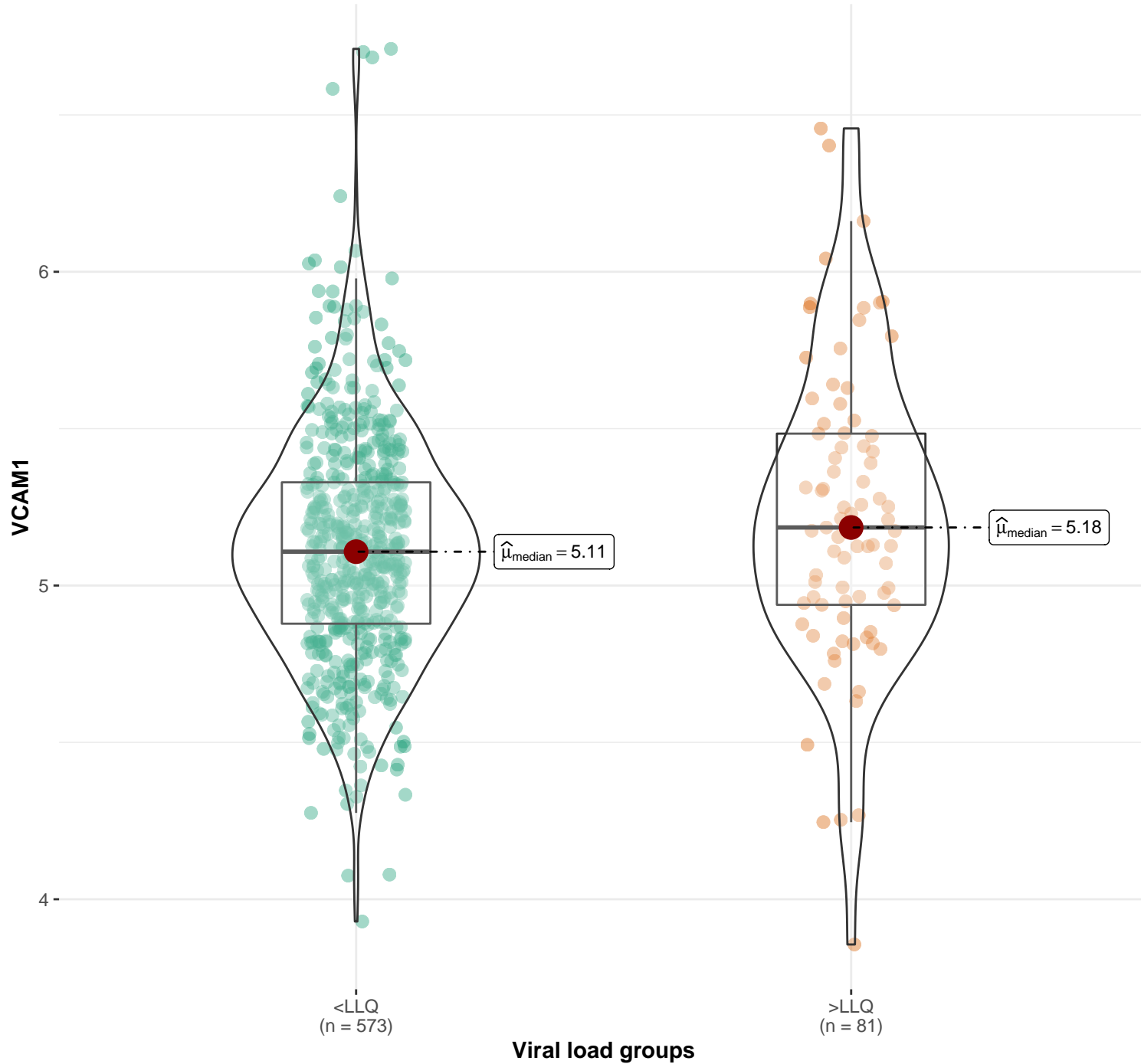
Distribution of VCAM1 across different viral loads and ART regimens

Distribution of VCAM1 across viral load groups

$W_{\text{Mann-Whitney}} = 20077.00$, $p = 0.05$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.13$, $CI_{95\%} [-0.26, -1.25e-03]$, $n_{\text{obs}} = 654$

Distribution of VCAM1 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 15.32$, $p = 1.56e-03$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.02$, $CI_{95\%} [0.01, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

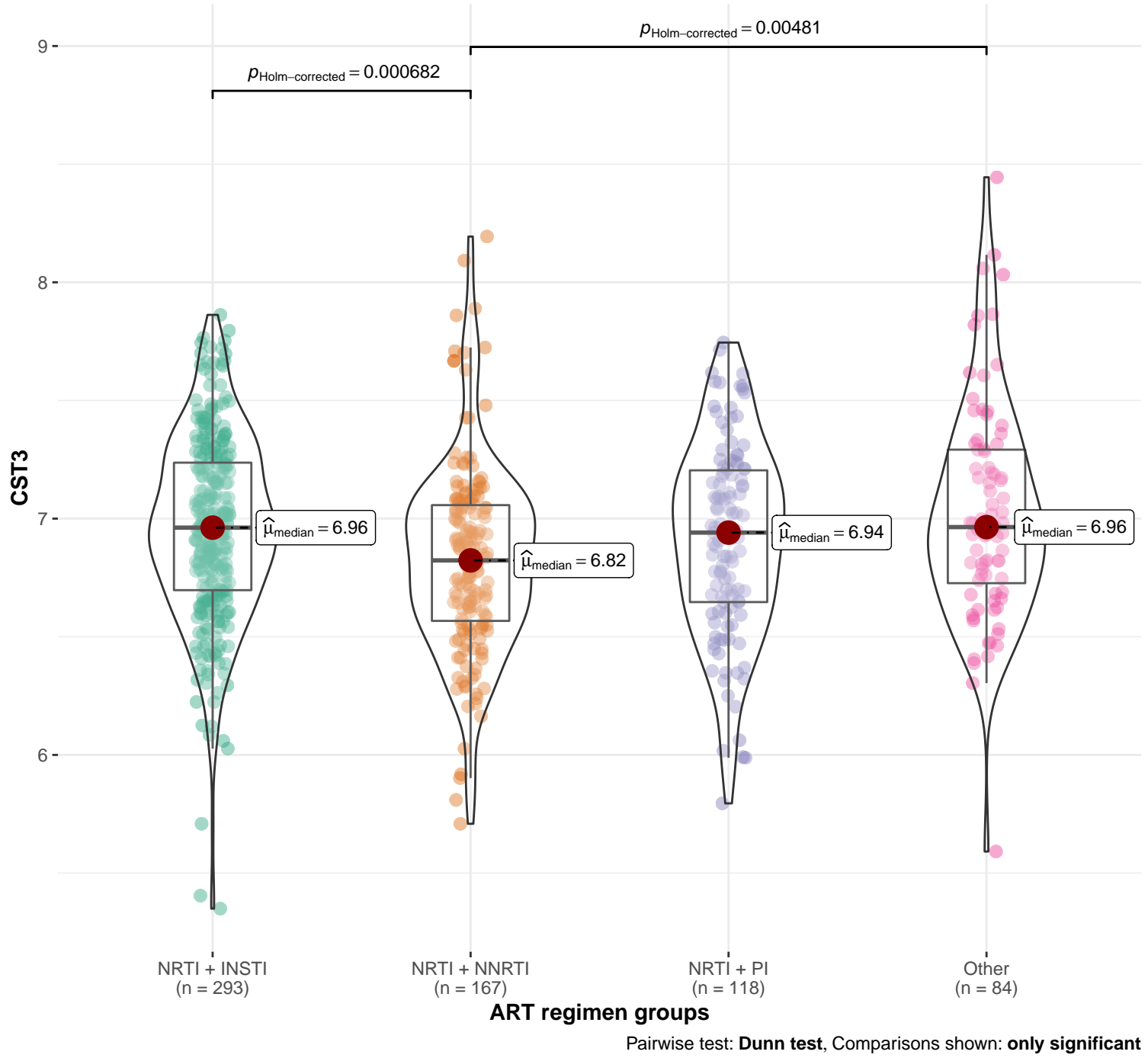
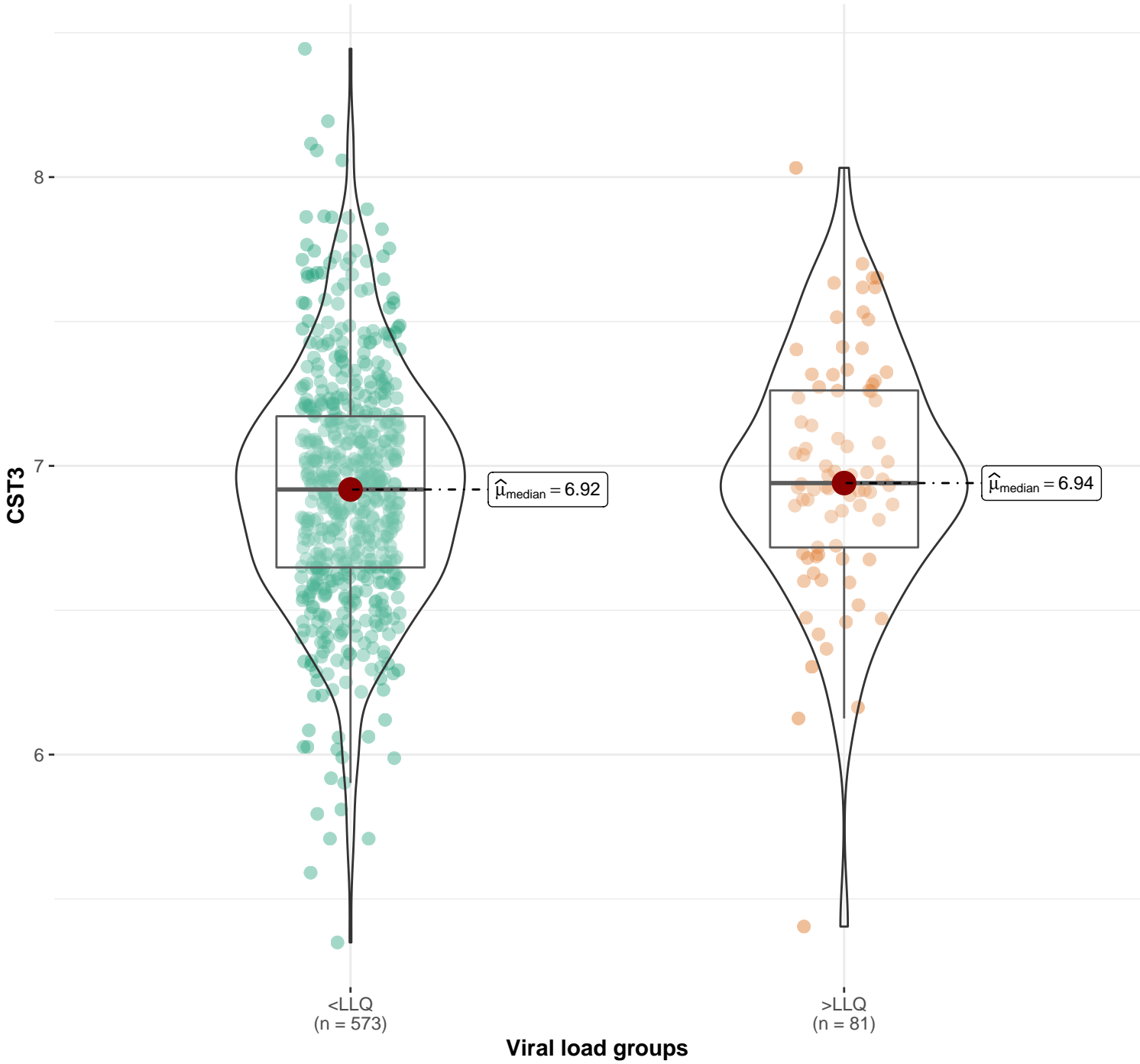
Distribution of CST3 across different viral loads and ART regimens

Distribution of CST3 across viral load groups

$W_{\text{Mann-Whitney}} = 20866.00$, $p = 0.14$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.10$, $CI_{95\%} [-0.23, 0.03]$, $n_{\text{obs}} = 654$

Distribution of CST3 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 17.83$, $p = 4.76e-04$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.03$, $CI_{95\%} [0.02, 1.00]$, $n_{\text{obs}} = 662$

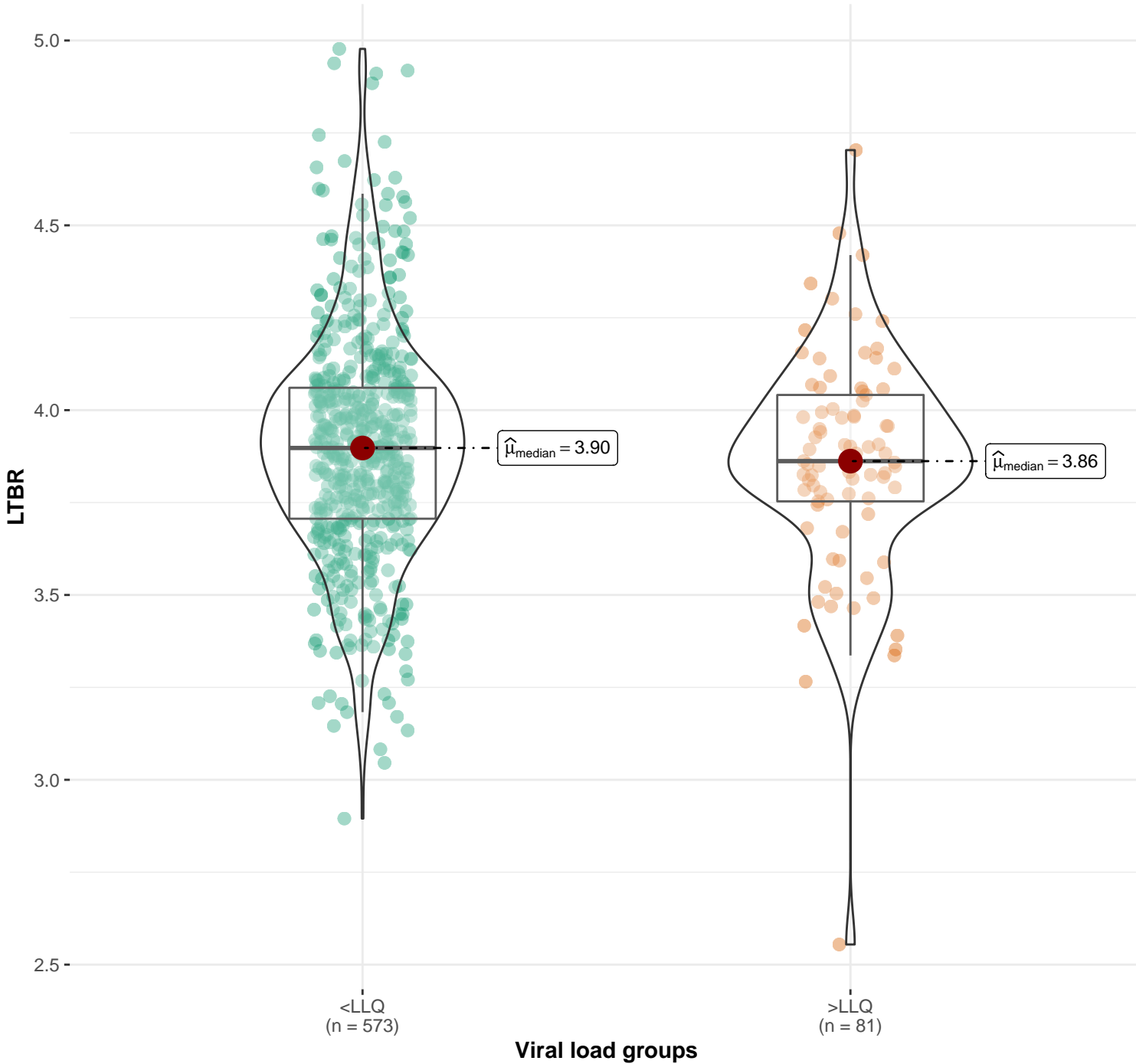


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of LTBR across different viral loads and ART regimens

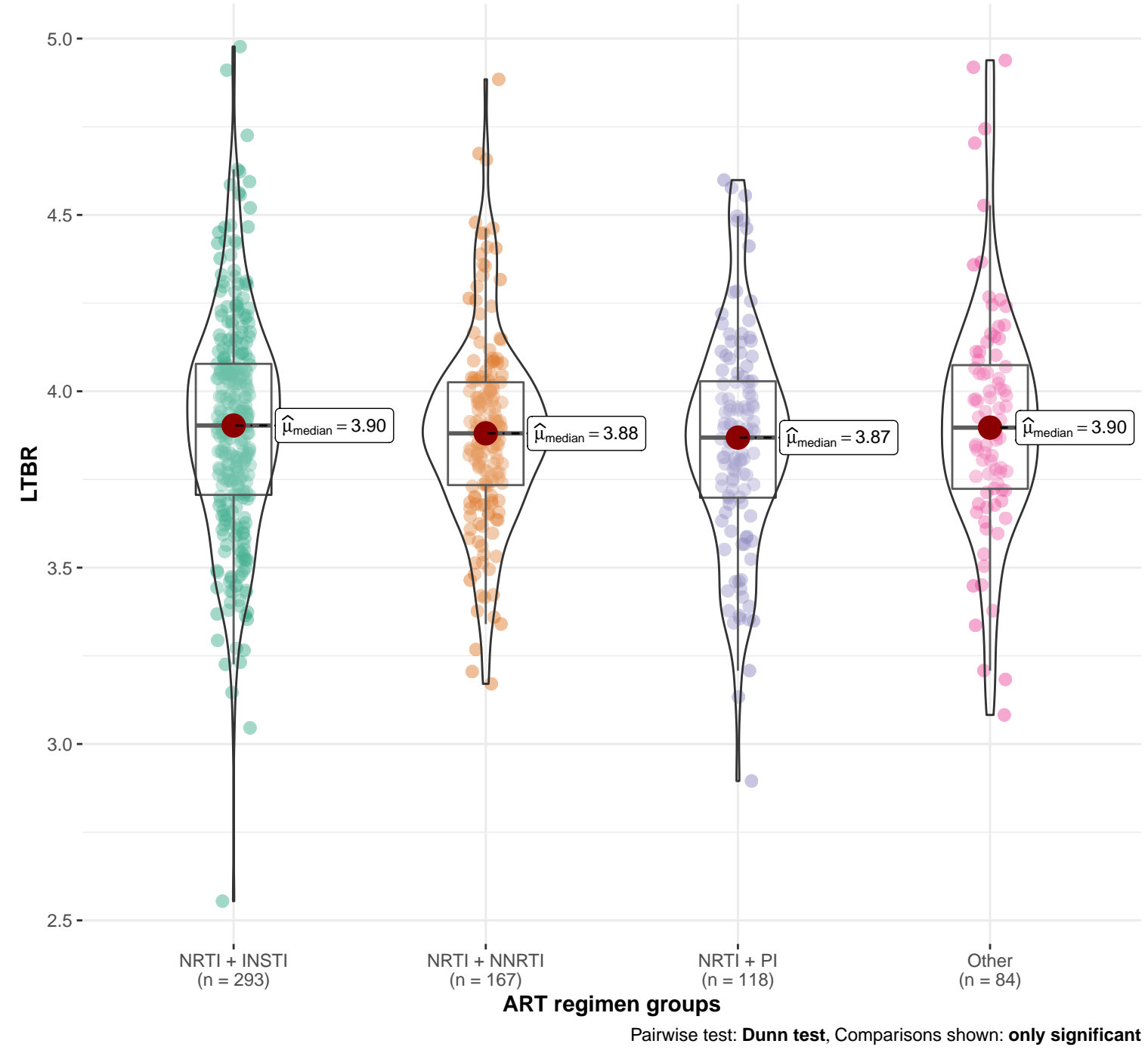
Distribution of LTBR across viral load groups

$W_{\text{Mann-Whitney}} = 24198.00$, $p = 0.53$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.04$, $CI_{95\%} [-0.09, 0.18]$, $n_{\text{obs}} = 654$



Distribution of LTBR across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 2.31$, $p = 0.51$, $\hat{\epsilon}_{\text{ordinal}}^2 = 3.50e-03$, $CI_{95\%} [7.20e-04, 1.00]$, $n_{\text{obs}} = 662$

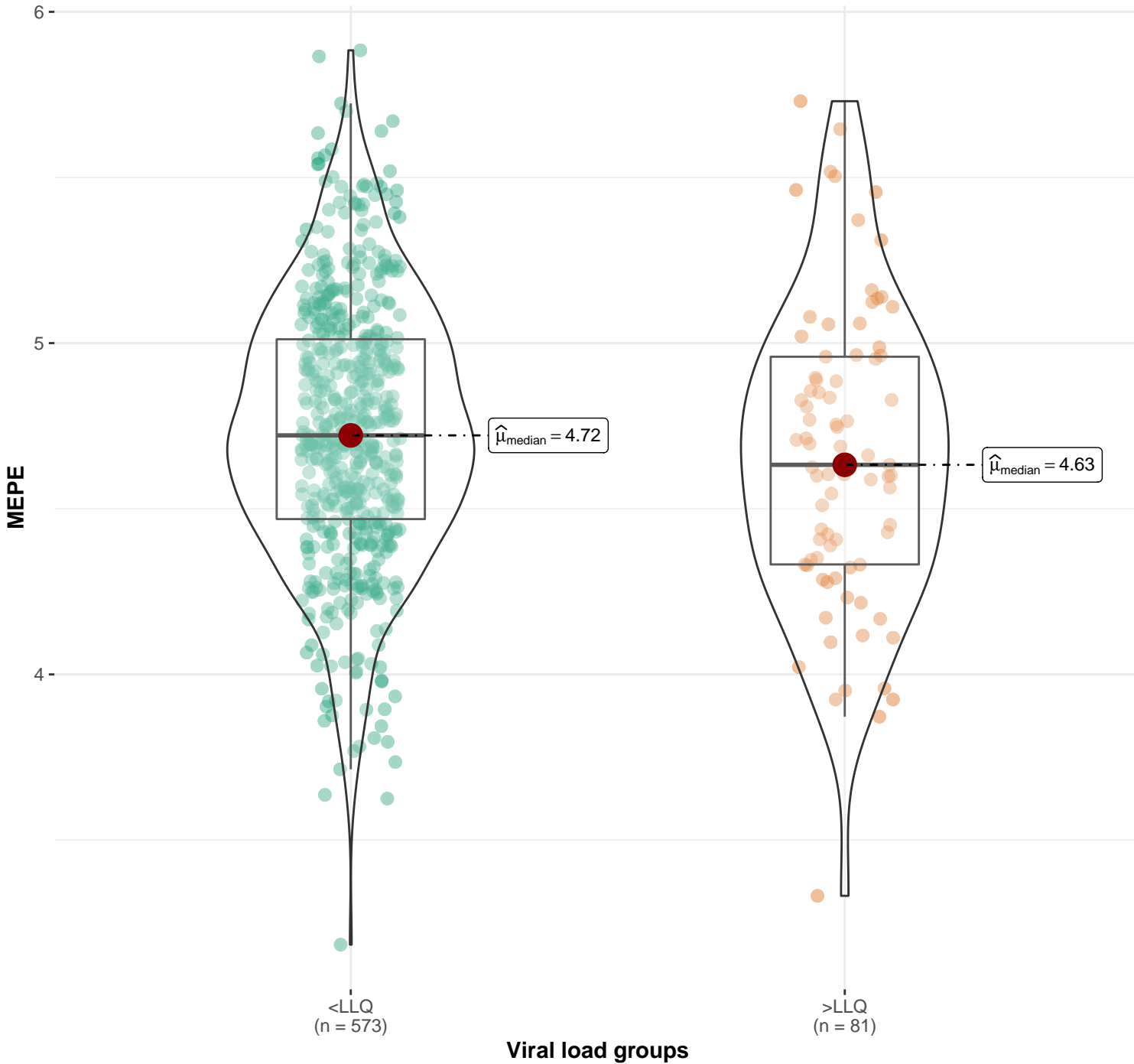


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of MEPE across different viral loads and ART regimens

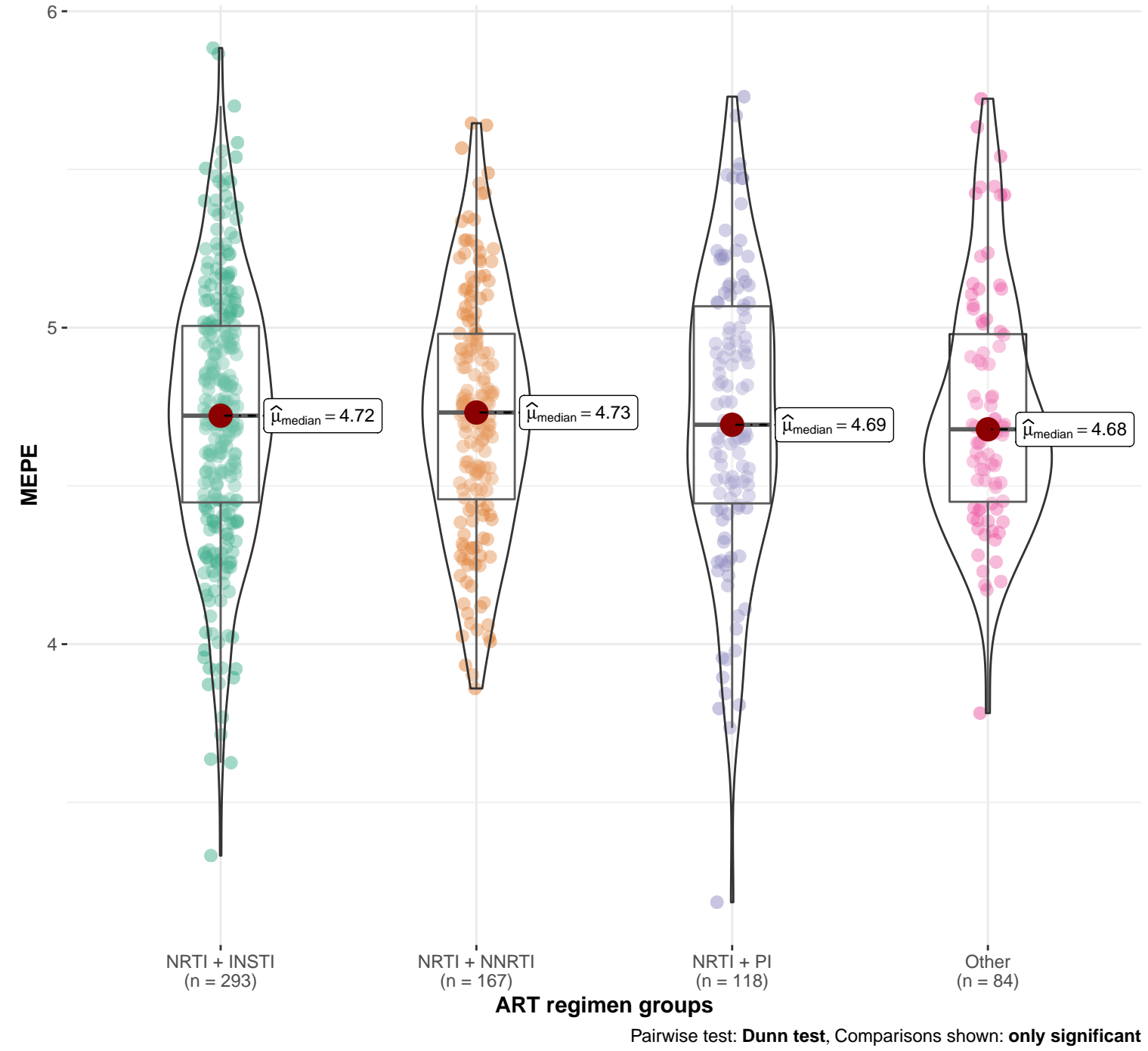
Distribution of MEPE across viral load groups

$W_{\text{Mann-Whitney}} = 25786.00$, $p = 0.11$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.11$, $CI_{95\%} [-0.02, 0.24]$, $n_{\text{obs}} = 654$



Distribution of MEPE across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 0.16$, $p = 0.98$, $\hat{\epsilon}_{\text{ordinal}}^2 = 2.36e-04$, $CI_{95\%} [4.51e-04, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

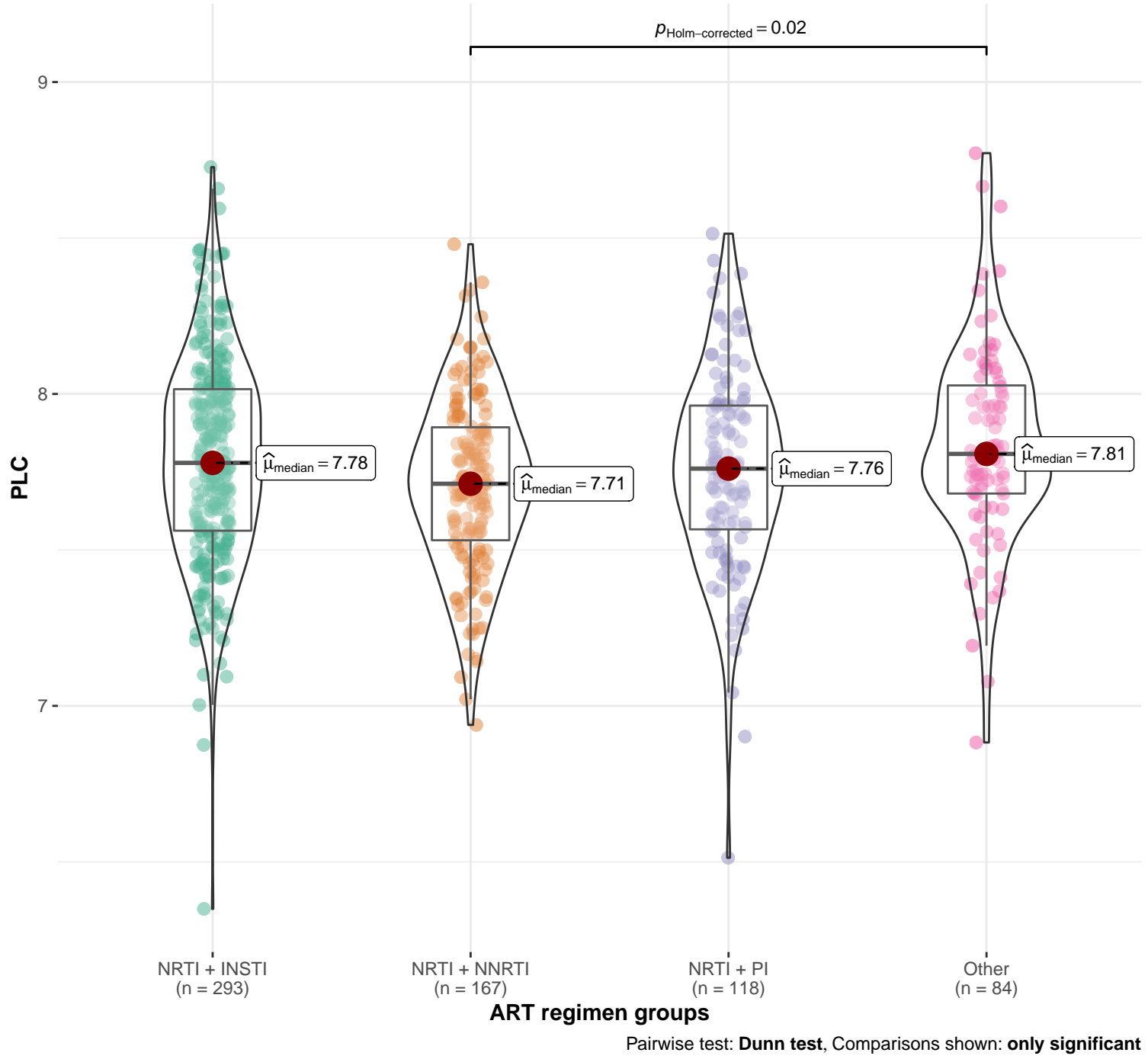
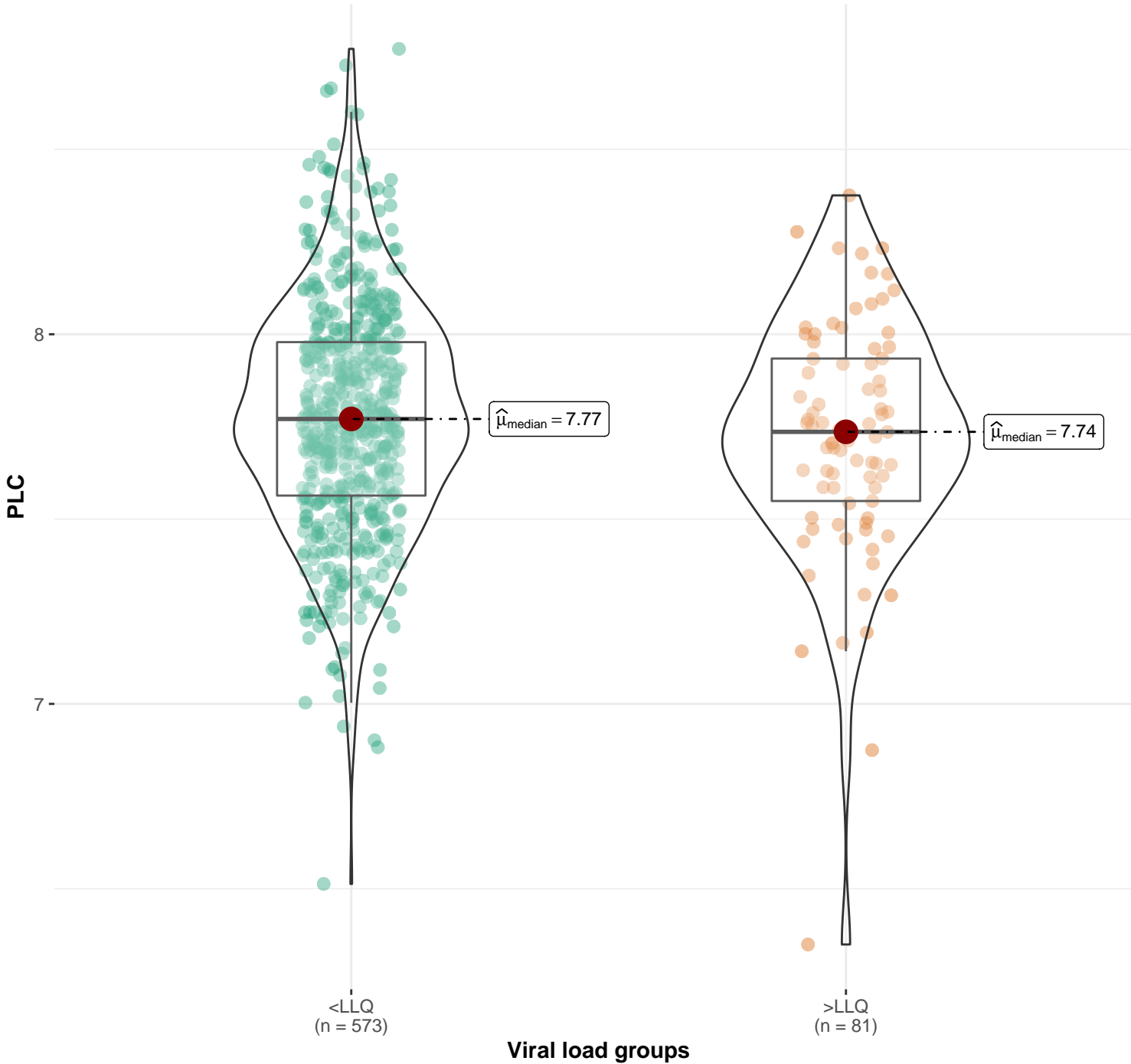
Distribution of PLC across different viral loads and ART regimens

Distribution of PLC across viral load groups

$W_{\text{Mann-Whitney}} = 24943.50$, $p = 0.28$, $\hat{r}_{\text{biserial}}^{\text{rank}} = 0.07$, $CI_{95\%} [-0.06, 0.21]$, $n_{\text{obs}} = 654$

Distribution of PLC across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 10.61$, $p = 0.01$, $\hat{\epsilon}_{\text{ordinal}}^2 = 0.02$, $CI_{95\%} [6.18e-03, 1.00]$, $n_{\text{obs}} = 662$

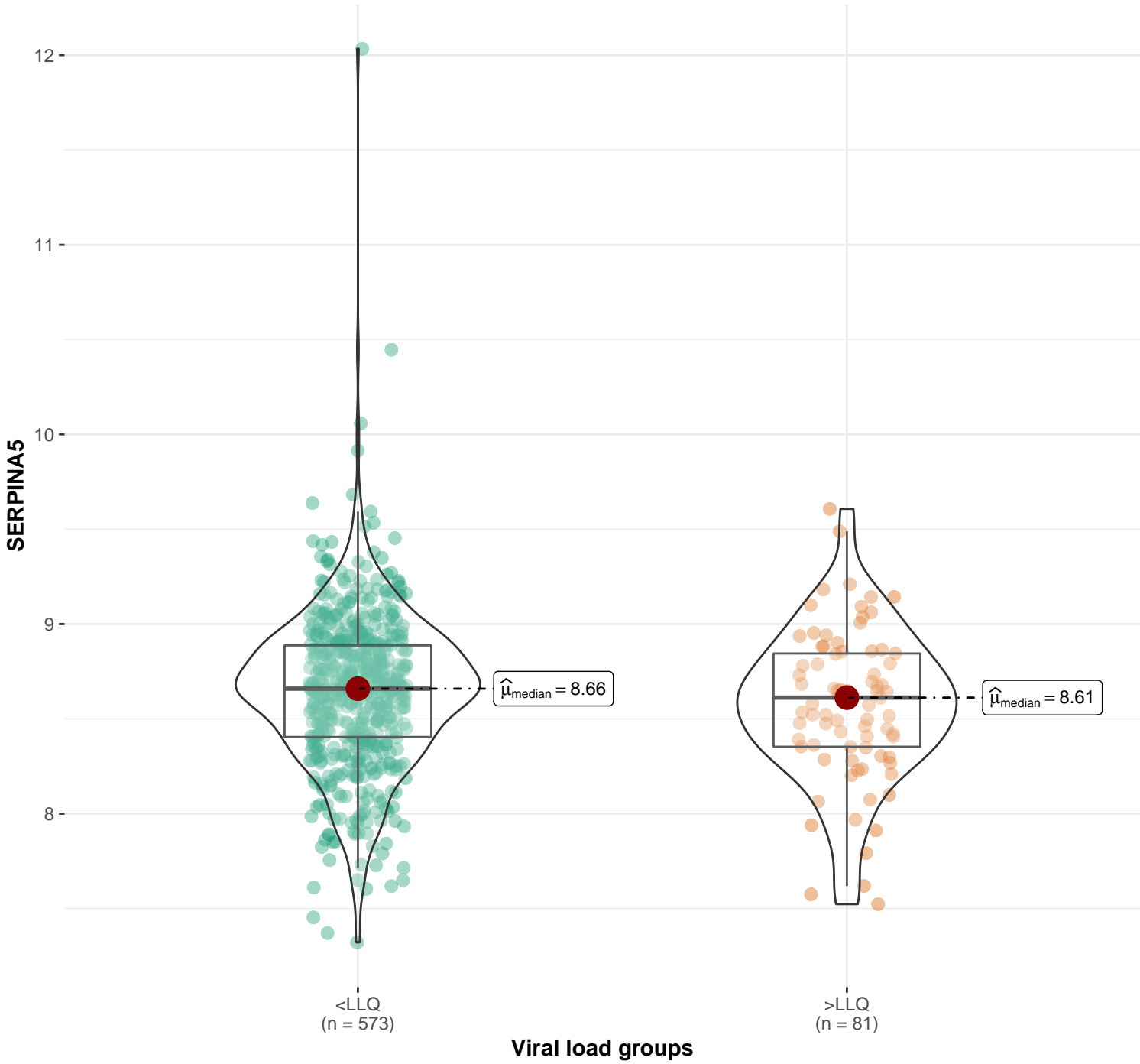


Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Distribution of SERPINA5 across different viral loads and ART regimens

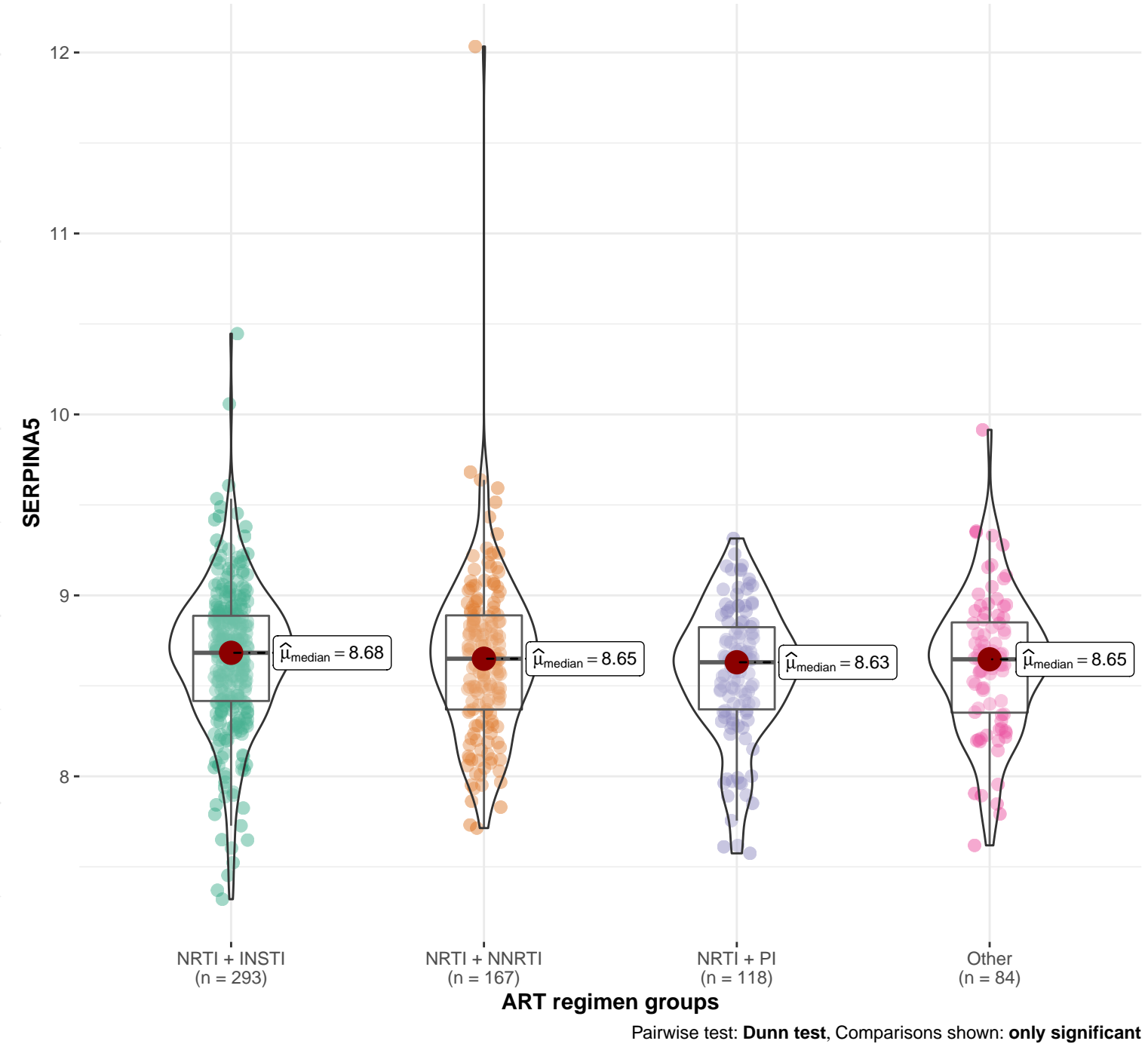
Distribution of SERPINA5 across viral load groups

$W_{\text{Mann-Whitney}} = 25594.50$, $p = 0.13$, $\hat{\rho}_{\text{biserial}}^{\text{rank}} = 0.10$, $CI_{95\%} [-0.03, 0.23]$, $n_{\text{obs}} = 654$



Distribution of SERPINA5 across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 2.89$, $p = 0.41$, $\hat{\epsilon}_{\text{ordinal}}^2 = 4.38e-03$, $CI_{95\%} [1.67e-03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

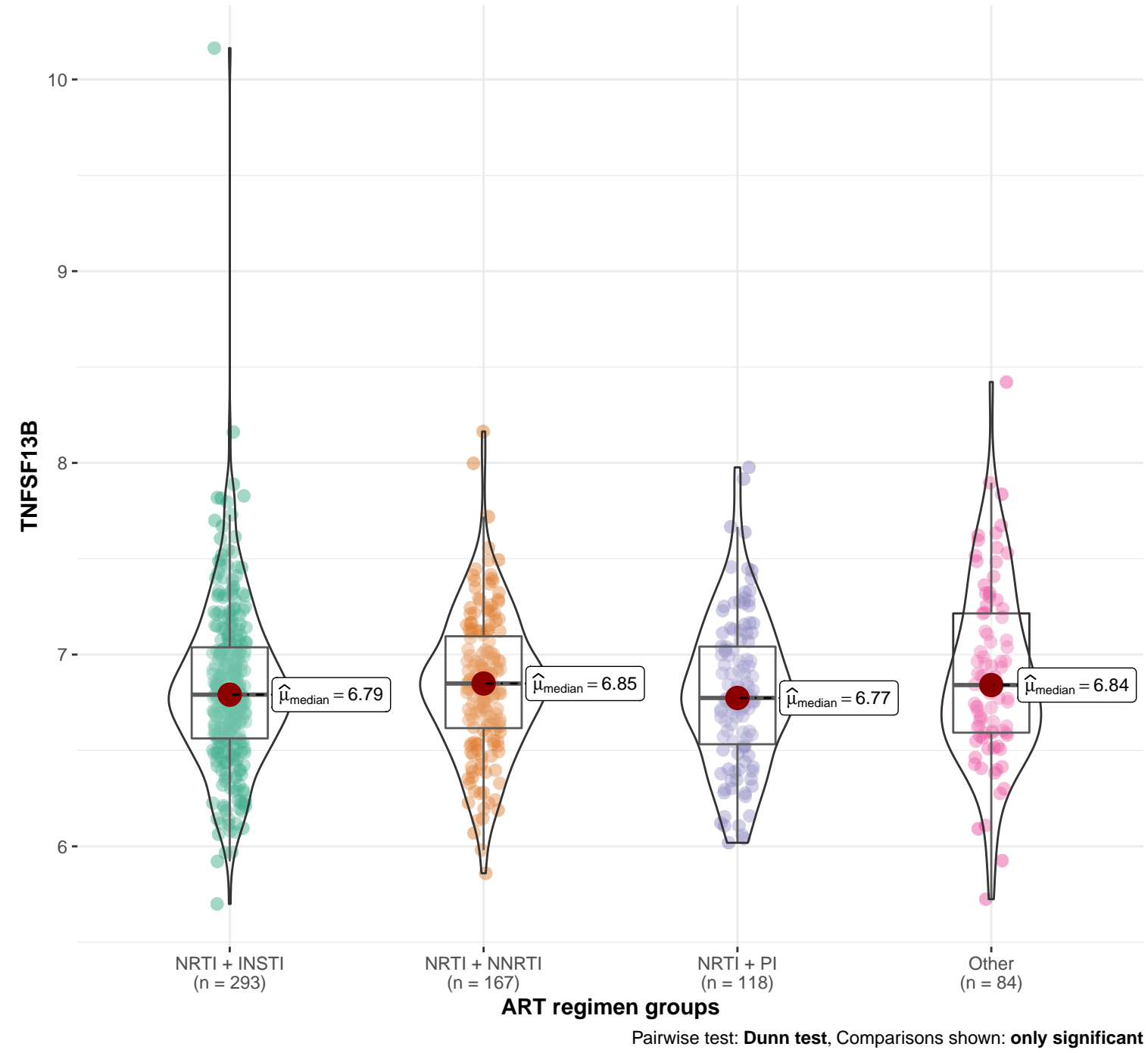
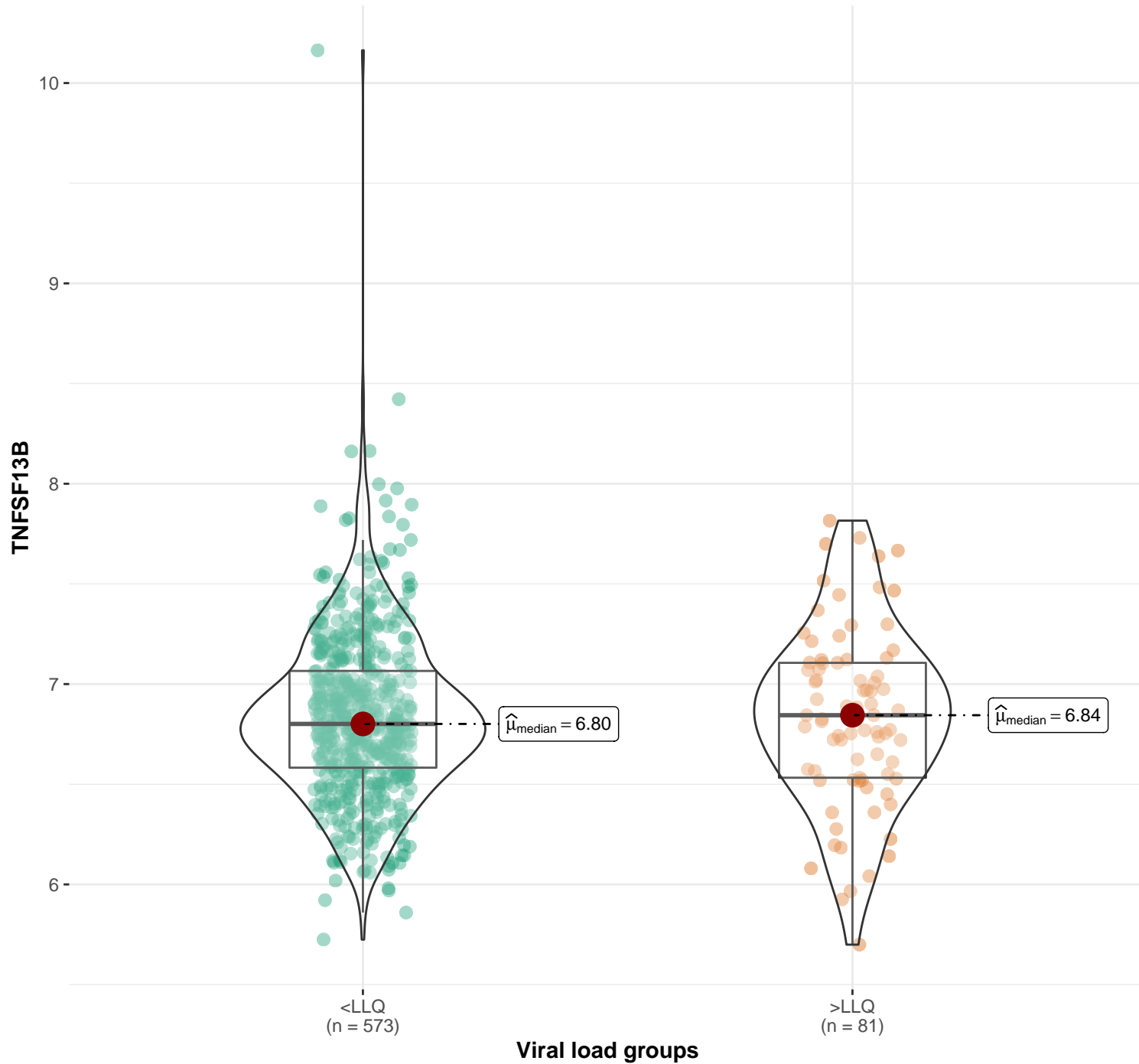
Distribution of TNFSF13B across different viral loads and ART regimens

Distribution of TNFSF13B across viral load groups

$W_{\text{Mann-Whitney}} = 22708.00$, $p = 0.75$, $\hat{r}_{\text{biserial}}^{\text{rank}} = -0.02$, $CI_{95\%} [-0.15, 0.11]$, $n_{\text{obs}} = 654$

Distribution of TNFSF13B across ART regimens

$\chi^2_{\text{Kruskal-Wallis}}(3) = 2.22$, $p = 0.53$, $\hat{\epsilon}_{\text{ordinal}}^2 = 3.35e-03$, $CI_{95\%} [1.40e-03, 1.00]$, $n_{\text{obs}} = 662$



Pairwise test: **Dunn test**, Comparisons shown: **only significant**

Supplementary table 1. Excluded proteins from analysis.

Assay	OlinkID	UniProt	Summary
IL33	OID00788	O95760	Interleukin-33; Cytokine that binds to and signals through the IL1RL1/ST2 receptor which in turn activates NF-kappa-B and MAPK signaling pathways in target cells. Involved in the maturation of Th2 cells inducing the secretion of T-helper type 2-associated cytokines. Also involved in activation of mast cells, basophils, eosinophils and natural killer cells. Acts as a chemoattractant for Th2 cells, and may function as an "alarmin", that amplifies immune responses during tissue injury; Interleukins
SOD1	OID01222	P00441	Superoxide dismutase, cu-zn family; Superoxide dismutase [Cu-Zn]; Destroys radicals which are normally produced within the cells and which are toxic to biological systems
IL-1 ALPHA	OID00757	P01583	Interleukin-1 alpha; Produced by activated macrophages, IL-1 stimulates thymocyte proliferation by inducing IL-2 release, B-cell maturation and proliferation, and fibroblast growth factor activity. IL-1 proteins are involved in the inflammatory response, being identified as endogenous pyrogens, and are reported to stimulate the release of prostaglandin and collagenase from synovial cells
ARG1	OID00815	P05089	Arginase-1; Key element of the urea cycle converting L-arginine to urea and L-ornithine, which is further metabolized into metabolites proline and polyamides that drive collagen synthesis and bioenergetic pathways critical for cell proliferation, respectively; the urea cycle takes place primarily in the liver and, to a lesser extent, in the kidneys
IL4	OID00833	P05112	Interleukin-4; Participates in at least several B-cell activation processes as well as of other cell types. It is a costimulator of DNA-synthesis. It induces the expression of class II MHC molecules on resting B-cells. It enhances both secretion and cell surface expression of IgE and IgG1. It also regulates the expression of the low affinity Fc receptor for IgE (CD23) on both lymphocytes and monocytes. Positively regulates IL31RA expression in macrophages (By similarity); Interleukins
IL5	OID00802	P05113	Interleukin-5; Factor that induces terminal differentiation of late- developing B-cells to immunoglobulin secreting cells; Belongs to the IL-5 family
UMOD	OID01237	P07911	Uromodulin; Uromodulin; Functions in biogenesis and organization of the apical membrane of epithelial cells of the thick ascending limb of Henle's loop (TALH), where it promotes formation of complex filamentous gel-like structure that may play a role in the water barrier permeability (Probable). May serve as a receptor for binding and endocytosis of cytokines (IL-1, IL-2) and TNF. Facilitates neutrophil migration across renal epithelia
FGF2	OID00770	P09038	Fibroblast growth factor 2; Plays an important role in the regulation of cell survival, cell division, angiogenesis, cell differentiation and cell migration. Functions as potent mitogen in vitro. Can induce angiogenesis; Belongs to the heparin-binding growth factors family
CD28	OID00793	P10747	T-cell-specific surface glycoprotein CD28; Involved in T-cell activation, the induction of cell proliferation and cytokine production and promotion of T-cell survival. Enhances the production of IL4 and IL10 in T-cells in conjunction with TCR/CD3 ligation and CD40L costimulation. Isoform 3 enhances CD40L-mediated activation of NF-kappa-B and kinases MAPK8 and PAK2 in T-cells
ITGAM	OID01242	P11215	Integrin alpha-M; Integrin ITGAM/ITGB2 is implicated in various adhesive interactions of monocytes, macrophages and granulocytes as well as in mediating the uptake of complement-coated particles. It is identical with CR-3, the receptor for the iC3b fragment of the third complement component. It probably recognizes the R-G-D peptide in C3b. Integrin ITGAM/ITGB2 is also a receptor for fibrinogen, factor X and ICAM1. It recognizes P1 and P2 peptides of fibrinogen gamma chain. Regulates neutrophil migration
CD59	OID01248	P13987	CD59 glycoprotein; Potent inhibitor of the complement membrane attack complex (MAC) action. Acts by binding to the C8 and/or C9 complements of the assembling MAC, thereby preventing incorporation of the multiple copies of C9 required for complete formation of the osmolytic pore. This inhibitor appears to be species-specific. Involved in signal transduction for T-cell activation complexed to a protein tyrosine kinase; Blood group antigens
PTN	OID00823	P21246	Pleiotrophin; Secreted growth factor that induces neurite outgrowth and which is mitogenic for fibroblasts, epithelial, and endothelial cells. Binds anaplastic lymphoma kinase (ALK) which induces MAPK pathway activation, an important step in the anti-apoptotic signaling of PTN and regulation of cell proliferation. Binds to cell-surface target proteins via their chondroitin sulfate groups. Down-regulates PTPRZ1 activity; Belongs to the pleiotrophin family

GNLY	OID01262	P22749	Granulysin; Antimicrobial protein that kills intracellular pathogens. Active against a broad range of microbes, including Gram-positive and Gram-negative bacteria, fungi, and parasites. Kills <i>Mycobacterium tuberculosis</i>
IL13	OID00836	P35225	Interleukin-13; Cytokine. Inhibits inflammatory cytokine production. Synergizes with IL2 in regulating interferon-gamma synthesis. May be critical in regulating inflammatory and immune responses. Positively regulates IL31RA expression in macrophages (By similarity); Interleukins.
PRCP	OID01272	P42785	Lysosomal Pro-X carboxypeptidase; Cleaves C-terminal amino acids linked to proline in peptides such as angiotensin II, III and des-Arg9-bradykinin. This cleavage occurs at acidic pH, but enzymatic activity is retained with some substrates at neutral pH; M14 carboxypeptidases
KIR3DL1	OID05550	P43629	Killer cell immunoglobulin-like receptor 3DL1; Receptor on natural killer (NK) cells for HLA Bw4 allele. Inhibits the activity of NK cells thus preventing cell lysis; CD molecules
CXCL12	OID00824	P48061	Stromal cell-derived factor 1; Chemoattractant active on T-lymphocytes, monocytes, but not neutrophils. Activates the C-X-C chemokine receptor CXCR4 to induce a rapid and transient rise in the level of intracellular calcium ions and chemotaxis. Also binds to atypical chemokine receptor ACKR3, which activates the beta-arrestin pathway and acts as a scavenger receptor for SDF-1. SDF-1-beta(3-72) and SDF-1- alpha(3-67) show a reduced chemotactic activity. Binding to cell surface proteoglycans seems to inhibit formation of SDF-1-alpha(3- 67) and thus to preserve activity on local sites.
DEFA1	OID01277	P59665	Defensin, alpha 1B; Defensin 1 and defensin 2 have antibacterial, fungicide and antiviral activities. Has antimicrobial activity against Gram- negative and Gram-positive bacteria. Defensins are thought to kill microbes by permeabilizing their plasma membrane; Defensins, alpha
IL2	OID00778	P60568	Interleukin-2; Produced by T-cells in response to antigenic or mitogenic stimulation, this protein is required for T-cell proliferation and other activities crucial to regulation of the immune response. Can stimulate B-cells, monocytes, lymphokine- activated killer cells, natural killer cells, and glioma cells; Interleukins
MCP-3	OID00755	P80098	C-C motif chemokine 7; Chemotactic factor that attracts monocytes and eosinophils, but not neutrophils. Augments monocyte anti-tumor activity. Also induces the release of gelatinase B. This protein can bind heparin. Binds to CCR1, CCR2 and CCR3; Chemokine ligands.
LCN2	OID01278	P80188	Neutrophil gelatinase-associated lipocalin; Iron-trafficking protein involved in multiple processes such as apoptosis, innate immunity and renal development. Binds iron through association with 2,5-dihydroxybenzoic acid (2,5- DHBA), a siderophore that shares structural similarities with bacterial enterobactin, and delivers or removes iron from the cell, depending on the context. Iron-bound form (holo-24p3) is internalized following binding to the SLC22A17 (24p3R) receptor, leading to release of iron and subsequent increase of intracellular iron concentration.
REG3A	OID01280	Q06141	Regenerating islet-derived protein 3-alpha; Bactericidal C-type lectin which acts exclusively against Gram-positive bacteria and mediates bacterial killing by binding to surface-exposed carbohydrate moieties of peptidoglycan. Regulates keratinocyte proliferation and differentiation after skin injury via activation of EXTL3-PI3K-AKT signaling pathway
FAP	OID01282	Q12884	Fibroblast activation protein, alpha; Prolyl endopeptidase FAP; Cell surface glycoprotein serine protease that participates in extracellular matrix degradation and involved in many cellular processes including tissue remodeling, fibrosis, wound healing, inflammation and tumor growth. Both plasma membrane and soluble forms exhibit post-proline cleaving endopeptidase activity, with a marked preference for Ala/Ser-Gly-Pro-Ser/Asn/Ala consensus sequences, on substrate such as alpha-2-antiplasmin SERPINF2 and SPRY2.
PLA2G7	OID01283	Q13093	Platelet-activating factor acetylhydrolase; Modulates the action of platelet-activating factor (PAF) by hydrolyzing the sn-2 ester bond to yield the biologically inactive lyso-PAF. Has a specificity for substrates with a short residue at the sn-2 position. It is inactive against long-chain phospholipids; Phospholipases
LTBP2	OID01288	Q14767	Latent-transforming growth factor beta-binding protein 2; May play an integral structural role in elastic-fiber architectural organization and/or assembly; Latent transforming growth factor beta binding proteins
QPCT	OID01293	Q16769	Glutaminyl-peptide cyclotransferase; Responsible for the biosynthesis of pyroglutamyl peptides. Has a bias against acidic and tryptophan residues adjacent to the N-terminal glutaminyl residue and a lack of importance of chain length after the second residue. Also catalyzes N-terminal pyroglutamate formation. In vitro, catalyzes pyroglutamate formation of N-terminally truncated form of APP amyloid-beta peptides [Glu-3]-amyloid-beta. May be involved in the N-terminal pyroglutamate formation of several amyloid-related plaque-forming peptides

SPON1	OID00599	Q9HCB6	Spondin-1; Cell adhesion protein that promotes the attachment of spinal cord and sensory neuron cells and the outgrowth of neurites in vitro. May contribute to the growth and guidance of axons in both the spinal cord and the PNS (By similarity). Major factor for vascular smooth muscle cell
ADGRG1	OID00764	Q9Y653	Adhesion G-protein coupled receptor G1; Receptor involved in cell adhesion and probably in cell- cell interactions. Mediates cell matrix adhesion in developing neurons and hematopoietic stem cells. Receptor for collagen III/COL3A1 in the developing brain and involved in regulation of cortical development, specifically in maintenance of the pial basement membrane integrity and in cortical lamination (By similarity). Binding to the COL3A1 ligand inhibits neuronal migration and activates the RhoA pathway by coupling to GNA13 and possibly GNA12.
NT-PROBNP	OID00131	P16860	Brain natriuretic peptide 32; Cardiac hormone that plays a key role in mediating cardio-renal homeostasis

Supplementary table 2. Atherosclerosis cardiovascular disease risk score corrected logistic regression results for each included protein.

Assay	UniProt ID	Presence of coronary calcium				Presence of coronary plaque				Presence of vulnerable plaque				Summary
		OR	CI	p value	Adjusted p value	OR	CI	p value	Adjusted p value	OR	CI	p value	Adjusted p value	
ADA	P00813	1.17	[0.88; 1.57]	0.2856	0.6408	1.01	[0.77; 1.34]	0.9242	0.9842	1.14	[0.82; 1.59]	0.4212	0.8761	Adenosine deaminase; Catalyzes the hydrolytic deamination of adenosine and 2- deoxyadenosine. Plays an important role in purine metabolism and in adenosine homeostasis. Modulates signaling by extracellular adenosine, and so contributes indirectly to cellular signaling events. Acts as a positive regulator of T-cell coactivation, by binding DPP4. Its interaction with DPP4 regulates lymphocyte- epithelial cell adhesion. Enhances dendritic cell immunogenicity by affecting dendritic cell costimulatory molecule expression and cytokines and chemokines secretion (By similarity).
ALCAM	Q13740	1.12	[0.69; 1.83]	0.6390	0.8231	1.38	[0.87; 2.23]	0.1774	0.4278	1.29	[0.74; 2.23]	0.3647	0.8622	CD166 antigen; Cell adhesion molecule that mediates both heterotypic cell-cell contacts via its interaction with CD6, as well as homotypic cell-cell contacts. Promotes T-cell activation and proliferation via its interactions with CD6. Contributes to the formation and maturation of the immunological synapse via its interactions with CD6. Mediates homotypic interactions with cells that express ALCAM. Required for normal hematopoietic stem cell engraftment in the bone marrow. Mediates attachment of dendritic cells onto endothelial cells via homotypic interaction.
ANG	P03950	0.86	[0.62; 1.18]	0.3494	0.6765	0.91	[0.67; 1.23]	0.5502	0.7778	0.98	[0.68; 1.39]	0.9109	0.9730	Angiogenin; Binds to actin on the surface of endothelial cells; once bound, angiogenin is endocytosed and translocated to the nucleus. Stimulates ribosomal RNA synthesis including that containing the initiation site sequences of 45S rRNA. Cleaves tRNA within anticodon loops to produce tRNA-derived stress-induced fragments (tiRNAs) which inhibit protein synthesis and triggers the assembly of stress granules (SGs). Angiogenin induces vascularization of normal and malignant tissues. Angiogenic activity is regulated by interaction with RNH1 in vivo; Ribonuclease A family
ANGPT1	Q15389	0.95	[0.82; 1.11]	0.5393	0.7638	0.94	[0.81; 1.09]	0.4407	0.7037	1.04	[0.88; 1.25]	0.6272	0.9630	Angiopoietin-1; Binds and activates TEK/TIE2 receptor by inducing its dimerization and tyrosine phosphorylation. Plays an important role in the regulation of angiogenesis, endothelial cell survival, proliferation, migration, adhesion and cell spreading, reorganization of the actin cytoskeleton, but also maintenance of vascular quiescence. Required for normal angiogenesis and heart development during embryogenesis. After birth, activates or inhibits angiogenesis, depending on the context.

ANGPT2	O15123	1.13	[0.79; 1.62]	0.5139	0.7584	1.34	[0.95; 1.89]	0.0997	0.3375	1.36	[0.9; 2.05]	0.1432	0.8512	Angiopoietin-2; Binds to TEK/TIE2, competing for the ANGPT1 binding site, and modulating ANGPT1 signaling. Can induce tyrosine phosphorylation of TEK/TIE2 in the absence of ANGPT1. In the absence of angiogenic inducers, such as VEGF, ANGPT2-mediated loosening of cell-matrix contacts may induce endothelial cell apoptosis with consequent vascular regression. In concert with VEGF, it may facilitate endothelial cell migration and proliferation, thus serving as a permissive angiogenic signal; Fibrinogen C domain containing
ANGPTL3	Q9Y5C1	1.56	[1.05; 2.32]	0.0271	0.2090	1.56	[1.07; 2.28]	0.0219	0.1541	1.02	[0.65; 1.58]	0.9309	0.9730	Angiopoietin-related protein 3; Acts in part as a hepatokine that is involved in regulation of lipid and glucose metabolism. Proposed to play a role in the trafficking of energy substrates to either storage or oxidative tissues in response to food intake (By similarity). Has a stimulatory effect on plasma triglycerides (TG), which is achieved by suppressing plasma TG clearance via inhibition of LPL activity.
AOC3	Q16853	2.46	[1.47; 4.18]	0.0007	0.0346	2.29	[1.4; 3.77]	0.0010	0.0418	2.23	[1.24; 4.06]	0.0079	0.6498	Amine oxidase, copper containing 3; Membrane primary amine oxidase; Cell adhesion protein that participates in lymphocyte extravasation and recirculation by mediating the binding of lymphocytes to peripheral lymph node vascular endothelial cells in an L-selectin-independent fashion. Has semicarbazide-sensitive (SSAO) monoamine oxidase activity. May play a role in adipogenesis
AP-N	P15144	1.08	[0.64; 1.83]	0.7738	0.8854	1.23	[0.75; 2.03]	0.4131	0.6774	1.23	[0.67; 2.25]	0.5029	0.9589	Alanyl aminopeptidase, membrane; Aminopeptidase N; Broad specificity aminopeptidase which plays a role in the final digestion of peptides generated from hydrolysis of proteins by gastric and pancreatic proteases. Also involved in the processing of various peptides including peptide hormones, such as angiotensin III and IV, neuropeptides, and chemokines. May also be involved the cleavage of peptides bound to major histocompatibility complex class II molecules of antigen presenting cells. May have a role in angiogenesis and promote cholesterol crystallization; Aminopeptidases
APOM	O95445	1.34	[0.87; 2.08]	0.1856	0.4856	1.07	[0.71; 1.63]	0.7385	0.8776	1.45	[0.88; 2.39]	0.1442	0.8512	Apolipoprotein M; Probably involved in lipid transport. Can bind sphingosine-1-phosphate, myristic acid, palmitic acid and stearic acid, retinol, all-trans-retinoic acid and 9-cis-retinoic acid; Apolipoproteins

AXL	P30530	1.44	[0.93; 2.23]	0.1003	0.3379	1.36	[0.9; 2.07]	0.1410	0.3875	0.78	[0.47; 1.27]	0.3134	0.8512	Tyrosine-protein kinase receptor UFO; Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding growth factor GAS6 and which is thus regulating many physiological processes including cell survival, cell proliferation, migration and differentiation. Ligand binding at the cell surface induces dimerization and autophosphorylation of AXL. Following activation by ligand, ALX binds and induces tyrosine phosphorylation of PI3- kinase subunits PIK3R1, PIK3R2 and PIK3R3; but also GRB2, PLCG1, LCK and PTPN11. Other downstream substrate candidate [...]
AZU1	P20160	0.95	[0.76; 1.19]	0.6744	0.8349	0.96	[0.78; 1.19]	0.7254	0.8776	0.99	[0.76; 1.27]	0.9606	0.9766	Azurocidin; This is a neutrophil granule-derived antibacterial and monocyte- and fibroblast-specific chemotactic glycoprotein. Binds heparin. The cytotoxic action is limited to many species of Gram- negative bacteria; this specificity may be explained by a strong affinity of the very basic N-terminal half for the negatively charged lipopolysaccharides that are unique to the Gram-negative bacterial outer envelope. It may play a role in mediating recruitment of monocytes in the second wave of inflammation.
BLM HYDROLASE	Q13867	1.32	[0.96; 1.8]	0.0841	0.3083	1.30	[0.96; 1.77]	0.0878	0.3225	1.20	[0.84; 1.71]	0.3017	0.8512	Bleomycin hydrolase; The normal physiological role of BLM hydrolase is unknown, but it catalyzes the inactivation of the antitumor drug BLM (a glycopeptide) by hydrolyzing the carboxamide bond of its B- aminoalaninamide moiety thus protecting normal and malignant cells from BLM toxicity
C1QTNF1	Q9BXJ1	0.94	[0.73; 1.19]	0.6237	0.8204	0.94	[0.75; 1.18]	0.6128	0.8018	0.81	[0.58; 1.09]	0.1996	0.8512	Complement C1q tumor necrosis factor-related protein 1; C1q and TNF related 1
C2	P06681	1.46	[0.91; 2.38]	0.1252	0.3889	1.22	[0.78; 1.91]	0.3833	0.6549	1.53	[0.88; 2.73]	0.1372	0.8512	Complement C2; Component C2 which is part of the classical pathway of the complement system is cleaved by activated factor C1 into two fragments: C2b and C2a. C2a, a serine protease, then combines with complement factor C4b to generate the C3 or C5 convertase; Belongs to the peptidase S1 family
CA1	P00915	0.97	[0.8; 1.17]	0.7587	0.8722	1.03	[0.86; 1.23]	0.7362	0.8776	1.12	[0.9; 1.38]	0.3003	0.8512	Carbonic anhydrase 1; Reversible hydration of carbon dioxide. Can hydrates cyanamide to urea; Carbonic anhydrases
CA3	P07451	0.96	[0.67; 1.33]	0.7931	0.8991	0.85	[0.6; 1.17]	0.3288	0.6083	0.98	[0.65; 1.41]	0.9033	0.9730	Carbonic anhydrase 3; Reversible hydration of carbon dioxide; Carbonic anhydrases
CA4	P22748	0.85	[0.5; 1.29]	0.4988	0.7584	0.89	[0.57; 1.31]	0.5588	0.7856	1.31	[0.85; 2.07]	0.2059	0.8512	Carbonic anhydrase 4; Reversible hydration of carbon dioxide. May stimulate the sodium/bicarbonate transporter activity of SLC4A4 that acts in pH homeostasis. It is essential for acid overload removal from the retina and retina epithelium, and acid release in the choriocapillaris in the choroid; Belongs to the alpha-carbonic anhydrase family

CAIX	Q16790	1.40	[1.04; 1.9]	0.0279	0.2090	1.26	[0.94; 1.69]	0.1177	0.3711	1.29	[0.92; 1.8]	0.1406	0.8512	Carbonic anhydrase 9; Reversible hydration of carbon dioxide. Participates in pH regulation. May be involved in the control of cell proliferation and transformation. Appears to be a novel specific biomarker for a cervical neoplasia; Belongs to the alpha-carbonic anhydrase family
CASP-3	P42574	0.99	[0.91; 1.09]	0.9114	0.9603	0.99	[0.91; 1.09]	0.8922	0.9621	0.95	[0.86; 1.06]	0.3474	0.8622	Caspase-3; Involved in the activation cascade of caspases responsible for apoptosis execution. At the onset of apoptosis it proteolytically cleaves poly(ADP-ribose) polymerase (PARP) at a '216-Asp- -Gly-217' bond. Cleaves and activates sterol regulatory element binding proteins (SREBPs) between the basic helix-loop- helix leucine zipper domain and the membrane attachment domain. Cleaves and activates caspase-6, -7 and -9. Involved in the cleavage of huntingtin. Triggers cell adhesion in sympathetic neurons through RET cleavage
CASP-8	Q14790	1.07	[0.89; 1.28]	0.5001	0.7584	1.00	[0.83; 1.19]	0.9587	0.9854	1.02	[0.82; 1.26]	0.8607	0.9730	Caspase-8; Most upstream protease of the activation cascade of caspases responsible for the TNFRSF6/FAS mediated and TNFRSF1A induced cell death. Binding to the adapter molecule FADD recruits it to either receptor. The resulting aggregate called death- inducing signaling complex (DISC) performs CASP8 proteolytic activation. The active dimeric enzyme is then liberated from the DISC and free to activate downstream apoptotic proteases. Proteolytic fragments of the N-terminal propeptide (termed CAP3, CAP5 and CAP6) are likely retained in the DISC.
CCL14	Q16627	1.07	[0.72; 1.58]	0.7467	0.8722	0.94	[0.65; 1.36]	0.7478	0.8820	0.77	[0.49; 1.2]	0.2511	0.8512	C-C motif chemokine ligand 14
CCL15	Q16663	1.09	[0.83; 1.42]	0.5518	0.7673	0.90	[0.69; 1.16]	0.4078	0.6733	0.84	[0.61; 1.15]	0.2935	0.8512	C-C motif chemokine 15; Chemotactic factor that attracts T-cells and monocytes, but not neutrophils, eosinophils, or B-cells. Acts mainly via CC chemokine receptor CCR1. Also binds to CCR3. CCL15(22-92), CCL15(25-92) and CCL15(29-92) are more potent chemoattractants than the small-inducible cytokine A15; Belongs to the intercrine beta (chemokine CC) family
CCL16	O15467	0.88	[0.72; 1.06]	0.1805	0.4800	0.89	[0.74; 1.07]	0.2083	0.4795	0.98	[0.79; 1.23]	0.8656	0.9730	C-C motif chemokine 16; Shows chemotactic activity for lymphocytes and monocytes but not neutrophils. Also shows potent myelosuppressive activity, suppresses proliferation of myeloid progenitor cells. Recombinant SCYA16 shows chemotactic activity for monocytes and THP-1 monocytes, but not for resting lymphocytes and neutrophils. Induces a calcium flux in THP-1 cells that were desensitized by prior expression to RANTES; Belongs to the intercrine beta (chemokine CC) family
CCL17	Q92583	1.01	[0.89; 1.15]	0.8201	0.9171	0.98	[0.87; 1.11]	0.7903	0.9051	1.01	[0.87; 1.16]	0.9309	0.9730	C-C motif chemokine 17; Chemotactic factor for T-lymphocytes but not monocytes or granulocytes. May play a role in T-cell development in thymus and in trafficking and activation of mature T-cells. Binds to CCR4; Belongs to the intercrine beta (chemokine CC) family

CCL18	P55774	0.90	[0.7; 1.15]	0.4050	0.7041	1.04	[0.83; 1.32]	0.7273	0.8776	0.90	[0.67; 1.18]	0.4594	0.9264	C-C motif chemokine 18; Chemotactic factor that attracts lymphocytes but not monocytes or granulocytes. May be involved in B-cell migration into B-cell follicles in lymph nodes. Attracts naive T-lymphocytes toward dendritic cells and activated macrophages in lymph nodes, has chemotactic activity for naive T-cells, CD4+ and CD8+ T-cells and thus may play a role in both humoral and cell-mediated immunity responses; Chemokine ligands
CCL19	Q99731	0.91	[0.74; 1.11]	0.3728	0.6880	0.90	[0.74; 1.09]	0.2943	0.5746	0.85	[0.67; 1.07]	0.1806	0.8512	C-C motif chemokine 19; May play a role not only in inflammatory and immunological responses but also in normal lymphocyte recirculation and homing. May play an important role in trafficking of T-cells in thymus, and T-cell and B-cell migration to secondary lymphoid organs. Binds to chemokine receptor CCR7. Recombinant CCL19 shows potent chemotactic activity for T-cells and B-cells but not for granulocytes and monocytes. Binds to atypical chemokine receptor ACKR4 and mediates the recruitment of beta-arrestin (ARRB1/2) to ACKR4; Belongs to the intercrine beta (chemokine CC) family
CCL20	P78556	1.04	[0.9; 1.2]	0.6020	0.8061	0.98	[0.85; 1.13]	0.8064	0.9100	0.93	[0.77; 1.1]	0.3806	0.8761	C-C motif chemokine 20; Acts as a ligand for C-C chemokine receptor CCR6. Signals through binding and activation of CCR6 and induces a strong chemotactic response and mobilization of intracellular calcium ions. The ligand-receptor pair CCL20-CCR6 is responsible for the chemotaxis of dendritic cells (DC), effector/memory T-cells and B-cells and plays an important role at skin and mucosal surfaces under homeostatic and inflammatory conditions, as well as in pathology, including cancer and various autoimmune diseases.
CCL23	P55773	1.63	[1.22; 2.18]	0.0009	0.0346	1.63	[1.24; 2.15]	0.0005	0.0418	1.41	[1.02; 1.96]	0.0380	0.8308	C-C motif chemokine ligand 23
CCL24	O00175	1.36	[1.14; 1.63]	0.0006	0.0346	1.27	[1.07; 1.51]	0.0059	0.0920	1.04	[0.85; 1.27]	0.6767	0.9630	C-C motif chemokine 24; Chemotactic for resting T-lymphocytes, and eosinophils. Has lower chemotactic activity for neutrophils but none for monocytes and activated lymphocytes. Is a strong suppressor of colony formation by a multipotential hematopoietic progenitor cell line. Binds to CCR3; Belongs to the intercrine beta (chemokine CC) family
CCL3	P10147	0.96	[0.8; 1.13]	0.6358	0.8231	0.98	[0.83; 1.15]	0.8053	0.9100	0.89	[0.71; 1.09]	0.3032	0.8512	C-C motif chemokine 3; Monokine with inflammatory and chemokinetic properties. Binds to CCR1, CCR4 and CCR5. One of the major HIV-suppressive factors produced by CD8+ T-cells. Recombinant MIP-1-alpha induces a dose-dependent inhibition of different strains of HIV-1, HIV-2, and simian immunodeficiency virus (SIV); Belongs to the intercrine beta (chemokine CC) family

CCL4	P13236	1.36	[1.07; 1.75]	0.0128	0.1575	1.21	[0.96; 1.54]	0.1119	0.3592	0.99	[0.75; 1.3]	0.9567	0.9766	C-C motif chemokine 4; Monokine with inflammatory and chemokinetic properties. Binds to CCR5. One of the major HIV-suppressive factors produced by CD8+ T-cells. Recombinant MIP-1-beta induces a dose-dependent inhibition of different strains of HIV-1, HIV-2, and simian immunodeficiency virus (SIV). The processed form MIP-1-beta(3-69) retains the abilities to induce down-modulation of surface expression of the chemokine receptor CCR5 and to inhibit the CCR5-mediated entry of HIV-1 in T-cells. MIP-1-beta(3-69) is also a ligand for CCR1 and CCR2 isoform B;
CCL5	P13501	0.97	[0.89; 1.06]	0.5402	0.7638	0.97	[0.9; 1.06]	0.5311	0.7737	0.95	[0.86; 1.05]	0.3147	0.8512	C-C motif chemokine 5; Chemoattractant for blood monocytes, memory T-helper cells and eosinophils. Causes the release of histamine from basophils and activates eosinophils. May activate several chemokine receptors including CCR1, CCR3, CCR4 and CCR5. One of the major HIV-suppressive factors produced by CD8+ T-cells. Recombinant RANTES protein induces a dose-dependent inhibition of different strains of HIV-1, HIV-2, and simian immunodeficiency virus (SIV). The processed form RANTES(3-68) acts as a natural chemotaxis inhibitor and is a more potent inhibitor of HIV-1 infection.
CD163	Q86VB7	1.26	[0.94; 1.7]	0.1265	0.3889	1.24	[0.93; 1.65]	0.1368	0.3875	0.95	[0.67; 1.33]	0.7510	0.9723	Scavenger receptor cysteine-rich type 1 protein M130; Acute phase-regulated receptor involved in clearance and endocytosis of hemoglobin/haptoglobin complexes by macrophages and may thereby protect tissues from free hemoglobin-mediated oxidative damage. May play a role in the uptake and recycling of iron, via endocytosis of hemoglobin/haptoglobin and subsequent breakdown of heme. Binds hemoglobin/haptoglobin complexes in a calcium-dependent and pH-dependent manner.
CD244	Q9BZW8	1.02	[0.79; 1.32]	0.8607	0.9494	1.07	[0.83; 1.37]	0.6021	0.7920	1.10	[0.82; 1.47]	0.5148	0.9589	Natural killer cell receptor 2B4; Heterophilic receptor of the signaling lymphocytic activation molecule (SLAM) family; its ligand is CD48. SLAM receptors triggered by homo- or heterotypic cell-cell interactions are modulating the activation and differentiation of a wide variety of immune cells and thus are involved in the regulation and interconnection of both innate and adaptive immune response. Activities are controlled by presence or absence of small cytoplasmic adapter proteins, SH2D1A/SAP and/or SH2D1B/EAT-2. Acts as activating natural killer (NK) cell receptor
CD27	P26842	1.01	[0.69; 1.48]	0.9611	0.9690	0.96	[0.66; 1.38]	0.8170	0.9153	0.90	[0.58; 1.39]	0.6347	0.9630	Tumor necrosis factor receptor superfamily member 7; CD27 antigen; Receptor for CD70/CD27L. May play a role in survival of activated T-cells. May play a role in apoptosis through association with SIVA1

CD4	P01730	0.97	[0.62; 1.5]	0.8919	0.9603	1.14	[0.75; 1.73]	0.5410	0.7737	0.94	[0.57; 1.54]	0.8016	0.9730	T-cell surface glycoprotein CD4; Integral membrane glycoprotein that plays an essential role in the immune response and serves multiple functions in responses against both external and internal offenses. In T-cells, functions primarily as a coreceptor for MHC class II molecule:peptide complex. The antigens presented by class II peptides are derived from extracellular proteins while class I peptides are derived from cytosolic proteins. Interacts simultaneously with the T-cell receptor (TCR) and the MHC class II presented by antigen presenting cells (APCs).
CD40	P25942	1.05	[0.82; 1.33]	0.7103	0.8523	1.05	[0.83; 1.32]	0.6879	0.8634	0.98	[0.75; 1.28]	0.8811	0.9730	Tumor necrosis factor receptor superfamily member 5; Receptor for TNFSF5/CD40LG. Transduces TRAF6- and MAP3K8-mediated signals that activate ERK in macrophages and B cells, leading to induction of immunoglobulin secretion
CD40-L	P29965	0.97	[0.89; 1.06]	0.5069	0.7584	0.96	[0.88; 1.04]	0.3422	0.6101	0.95	[0.86; 1.05]	0.3301	0.8622	CD40 ligand; Cytokine that binds to CD40/TNFRSF5. Costimulates T-cell proliferation and cytokine production. Its cross-linking on T-cells generates a costimulatory signal which enhances the production of IL4 and IL10 in conjunction with the TCR/CD3 ligation and CD28 costimulation. Induces the activation of NF-kappa-B and kinases MAPK8 and PAK2 in T- cells. Induces tyrosine phosphorylation of isoform 3 of CD28. Mediates B-cell proliferation in the absence of costimulus as well as IgE production in the presence of IL4. Involved in immunoglobulin class switching (By similarity);
CD46	P15529	0.97	[0.83; 1.13]	0.6822	0.8349	0.97	[0.84; 1.12]	0.6502	0.8289	0.95	[0.79; 1.12]	0.5380	0.9589	Membrane cofactor protein; Acts as a cofactor for complement factor I, a serine protease which protects autologous cells against complement- mediated injury by cleaving C3b and C4b deposited on host tissue. May be involved in the fusion of the spermatozoa with the oocyte during fertilization. Also acts as a costimulatory factor for T- cells which induces the differentiation of CD4+ into T-regulatory 1 cells. T-regulatory 1 cells suppress immune responses by secreting interleukin-10, and therefore are thought to prevent autoimmunity
CD5	P06127	0.82	[0.55; 1.21]	0.3289	0.6688	0.89	[0.61; 1.29]	0.5464	0.7770	0.89	[0.57; 1.38]	0.6081	0.9630	T-cell surface glycoprotein CD5; May act as a receptor in regulating T-cell proliferation; CD molecules
CD70	P32970	1.13	[0.78; 1.62]	0.5203	0.7584	0.97	[0.68; 1.37]	0.8435	0.9347	1.09	[0.72; 1.64]	0.6837	0.9630	CD70 antigen; Cytokine that binds to CD27. Plays a role in T-cell activation. Induces the proliferation of costimulated T-cells and enhances the generation of cytolytic T-cells; Belongs to the tumor necrosis factor family
CD83	Q01151	1.35	[0.92; 1.99]	0.1214	0.3828	1.65	[1.13; 2.43]	0.0100	0.1025	1.57	[1.02; 2.41]	0.0385	0.8308	CD83 antigen; May play a significant role in antigen presentation or the cellular interactions that follow lymphocyte activation; CD molecules

CD8A	P01732	1.26	[1.02; 1.57]	0.0336	0.2177	1.26	[1.03; 1.55]	0.0286	0.1675	0.93	[0.73; 1.18]	0.5449	0.9589	T-cell surface glycoprotein CD8 alpha chain; Integral membrane glycoprotein that plays an essential role in the immune response and serves multiple functions in responses against both external and internal offenses. In T-cells, functions primarily as a coreceptor for MHC class I molecule:peptide complex. The antigens presented by class I peptides are derived from cytosolic proteins while class II derived from extracellular proteins. Interacts simultaneously with the T-cell receptor (TCR) and the MHC class I proteins presented by antigen presenting cells (APCs).
CD93	Q9NPY3	1.37	[0.88; 2.15]	0.1639	0.4635	1.60	[1.05; 2.47]	0.0315	0.1729	1.09	[0.66; 1.8]	0.7396	0.9678	Complement component C1q receptor; Receptor (or element of a larger receptor complex) for C1q, mannose-binding lectin (MBL2) and pulmonary surfactant protein A (SPA). May mediate the enhancement of phagocytosis in monocytes and macrophages upon interaction with soluble defense collagens. May play a role in intercellular adhesion; C-type lectin domain containing
CDH1	P12830	1.09	[0.72; 1.63]	0.6786	0.8349	1.33	[0.9; 1.97]	0.1537	0.4053	1.02	[0.64; 1.61]	0.9217	0.9730	Cadherin-1; Cadherins are calcium-dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. CDH1 is involved in mechanisms regulating cell-cell adhesions, mobility and proliferation of epithelial cells. Has a potent invasive suppressor role. It is a ligand for integrin alpha-E/beta-7
CDH5	P33151	1.13	[0.72; 1.78]	0.6004	0.8061	1.17	[0.76; 1.82]	0.4777	0.7302	0.90	[0.53; 1.5]	0.6778	0.9630	Cadherin-5; Cadherins are calcium-dependent cell adhesion proteins. They preferentially interact with themselves in a homophilic manner in connecting cells; cadherins may thus contribute to the sorting of heterogeneous cell types. This cadherin may play a important role in endothelial cell biology through control of the cohesion and organization of the intercellular junctions. It associates with alpha-catenin forming a link to the cytoskeleton. Acts in concert with KRIT1 to establish and maintain correct endothelial cell polarity and vascular lumen.
CES1	P23141	1.15	[0.92; 1.45]	0.2260	0.5615	1.04	[0.83; 1.3]	0.7348	0.8776	0.95	[0.73; 1.24]	0.7229	0.9665	Liver carboxylesterase 1; Involved in the detoxification of xenobiotics and in the activation of ester and amide prodrugs. Hydrolyzes aromatic and aliphatic esters, but has no catalytic activity toward amides or a fatty acyl-CoA ester. Hydrolyzes the methyl ester group of cocaine to form benzoylecgonine. Catalyzes the transesterification of cocaine to form cocaethylene. Displays fatty acid ethyl ester synthase activity, catalyzing the ethyl esterification of oleic acid to ethyloleate; Carboxylesterases
CFHR5	Q9BXR6	0.85	[0.61; 1.18]	0.3400	0.6736	1.01	[0.73; 1.39]	0.9653	0.9854	1.17	[0.81; 1.71]	0.3987	0.8761	Complement factor H-related protein 5; Involved in complement regulation. The dimerized forms have avidity for tissue-bound complement fragments and efficiently compete with the physiological complement inhibitor CFH

CHI3L1	P36222	1.19	[1.03; 1.37]	0.0193	0.1878	1.20	[1.05; 1.38]	0.0098	0.1025	1.10	[0.94; 1.29]	0.2417	0.8512	Chitinase-3-like protein 1; Carbohydrate-binding lectin with a preference for chitin. Has no chitinase activity. May play a role in tissue remodeling and in the capacity of cells to respond to and cope with changes in their environment. Plays a role in T-helper cell type 2 (Th2) inflammatory response and IL-13-induced inflammation, regulating allergen sensitization, inflammatory cell apoptosis, dendritic cell accumulation and M2 macrophage differentiation. Facilitates invasion of pathogenic enteric bacteria into colonic mucosa and lymphoid organs.
CHIT1	Q13231	1.01	[0.9; 1.14]	0.8255	0.9189	1.03	[0.92; 1.15]	0.6409	0.8255	1.05	[0.93; 1.2]	0.4238	0.8761	Chitotriosidase-1; Degrades chitin, chitotriose and chitobiose. May participate in the defense against nematodes and other pathogens. Isoform 3 has no enzymatic activity; Belongs to the glycosyl hydrolase 18 family. Chitinase class II subfamily
CHL1	O00533	1.57	[0.9; 2.76]	0.1166	0.3753	1.49	[0.88; 2.54]	0.1430	0.3875	1.45	[0.77; 2.76]	0.2501	0.8512	Neural cell adhesion molecule L1-like protein; Extracellular matrix and cell adhesion protein that plays a role in nervous system development and in synaptic plasticity. Both soluble and membranous forms promote neurite outgrowth of cerebellar and hippocampal neurons and suppress neuronal cell death. Plays a role in neuronal positioning of pyramidal neurons and in regulation of both the number of interneurons and the efficacy of GABAergic synapses. May play a role in regulating cell migration in nerve regeneration and cortical development
CNDP1	Q96KN2	1.02	[0.81; 1.29]	0.8769	0.9603	1.13	[0.9; 1.41]	0.2996	0.5804	1.31	[1; 1.77]	0.0608	0.8308	Beta-ala-his dipeptidase; Carnosine dipeptidase 1; Belongs to the peptidase M20A family
CNTN1	Q12860	1.20	[0.72; 2.04]	0.4900	0.7584	1.14	[0.7; 1.88]	0.5931	0.7886	0.76	[0.42; 1.38]	0.3680	0.8622	Contactin-1; Contactins mediate cell surface interactions during nervous system development. Involved in the formation of paranodal axo-glia junctions in myelinated peripheral nerves and in the signaling between axons and myelinating glial cells via its association with CNTNAP1. Participates in oligodendrocytes generation by acting as a ligand of NOTCH1. Its association with NOTCH1 promotes NOTCH1 activation through the released notch intracellular domain (NICD) and subsequent translocation to the nucleus
COL18A1	P39060	1.55	[0.96; 2.52]	0.0740	0.3083	1.74	[1.1; 2.79]	0.0199	0.1534	1.18	[0.68; 2.03]	0.5425	0.9589	Collagen alpha-1(XVIII) chain; Probably plays a major role in determining the retinal structure as well as in the closure of the neural tube; Belongs to the multiplexin collagen family
COL1A1	P02452	1.05	[0.7; 1.58]	0.7981	0.9006	1.13	[0.77; 1.66]	0.5379	0.7737	1.31	[0.82; 2.09]	0.2571	0.8512	Collagen alpha-1(I) chain; Type I collagen is a member of group I collagen (fibrillar forming collagen); Collagens

COMP	P49747	1.50	[1.04; 2.17]	0.0306	0.2090	1.59	[1.12; 2.28]	0.0095	0.1025	1.23	[0.82; 1.87]	0.3149	0.8512	Cartilage oligomeric matrix protein; May play a role in the structural integrity of cartilage via its interaction with other extracellular matrix proteins such as the collagens and fibronectin. Can mediate the interaction of chondrocytes with the cartilage extracellular matrix through interaction with cell surface integrin receptors. Could play a role in the pathogenesis of osteoarthritis. Potent suppressor of apoptosis in both primary chondrocytes and transformed cells
CPA1	P15085	1.24	[0.99; 1.55]	0.0596	0.2854	1.17	[0.95; 1.46]	0.1419	0.3875	0.92	[0.72; 1.19]	0.5359	0.9589	Carboxypeptidase A1; Carboxypeptidase that catalyzes the release of a C- terminal amino acid, but has little or no action with -Asp, -Glu, -Arg, -Lys or -Pro; Belongs to the peptidase M14 family
CPB1	P15086	1.26	[1; 1.59]	0.0465	0.2551	1.18	[0.95; 1.47]	0.1383	0.3875	0.86	[0.66; 1.11]	0.2535	0.8512	Carboxypeptidase b1; M14 carboxypeptidases; Belongs to the peptidase M14 family
CR2	P20023	1.27	[0.93; 1.73]	0.1350	0.4100	1.17	[0.87; 1.57]	0.3078	0.5903	1.18	[0.83; 1.68]	0.3627	0.8622	Complement receptor type 2; Receptor for complement C3Dd, for the Epstein-Barr virus on human B-cells and T-cells and for HNRNPU. Participates in B lymphocytes activation; CD molecules
CRTAC1	Q9NQ79	1.15	[0.8; 1.65]	0.4378	0.7256	1.01	[0.72; 1.43]	0.9417	0.9854	1.20	[0.79; 1.8]	0.3891	0.8761	Cartilage acidic protein 1
CRTAM	O95727	1.12	[0.88; 1.42]	0.3409	0.6736	1.07	[0.85; 1.34]	0.5703	0.7860	1.10	[0.84; 1.43]	0.5055	0.9589	Cytotoxic and regulatory T-cell molecule; Interaction with CADM1 promotes natural killer (NK) cell cytotoxicity and interferon-gamma (IFN-gamma) secretion by CD8+ cells in vitro as well as NK cell-mediated rejection of tumors expressing CADM3 in vivo; Belongs to the nectin family
CSF-1	P09603	2.12	[1.12; 4.11]	0.0229	0.1878	1.96	[1.06; 3.64]	0.0324	0.1730	1.76	[0.86; 3.72]	0.1293	0.8512	Macrophage colony-stimulating factor 1; Cytokine that plays an essential role in the regulation of survival, proliferation and differentiation of hematopoietic precursor cells, especially mononuclear phagocytes, such as macrophages and monocytes. Promotes the release of proinflammatory chemokines, and thereby plays an important role in innate immunity and in inflammatory processes. Plays an important role in the regulation of osteoclast proliferation and differentiation, the regulation of bone resorption, and is required for normal bone development
CST3	P01034	1.63	[1.08; 2.46]	0.0194	0.1878	1.71	[1.16; 2.53]	0.0072	0.0979	1.15	[0.73; 1.83]	0.5472	0.9589	Cystatin-C; As an inhibitor of cysteine proteinases, this protein is thought to serve an important physiological role as a local regulator of this enzyme activity; Belongs to the cystatin family
CSTB	P04080	1.02	[0.76; 1.35]	0.8889	0.9603	1.17	[0.89; 1.55]	0.2513	0.5285	1.20	[0.87; 1.64]	0.2533	0.8512	Cystatin-a/b; Cystatin-B; This is an intracellular thiol proteinase inhibitor. Tightly binding reversible inhibitor of cathepsins L, H and B; Belongs to the cystatin family
CTSD	P07339	1.32	[0.97; 1.79]	0.0756	0.3083	1.15	[0.85; 1.54]	0.3630	0.6333	1.08	[0.76; 1.53]	0.6524	0.9630	Cathepsin D; Acid protease active in intracellular protein breakdown. Plays a role in APP processing following cleavage and activation by ADAM30 which leads to APP degradation. Involved in the pathogenesis of several diseases such as breast cancer and possibly Alzheimer disease; Cathepsins

CTSZ	Q9UBR2	1.25	[0.82; 1.9]	0.2947	0.6416	1.36	[0.91; 2.03]	0.1341	0.3875	1.13	[0.7; 1.81]	0.6217	0.9630	Cathepsin Z; Exhibits carboxy-monopeptidase as well as carboxy- dipeptidase activity; Cathepsins
CX3CL1	P78423	1.24	[0.79; 1.95]	0.3459	0.6754	1.15	[0.75; 1.76]	0.5346	0.7737	1.30	[0.78; 2.18]	0.3099	0.8512	C-X3-C motif chemokine ligand 1; Fractalkine; Acts as a ligand for both CX3CR1 and integrins. Binds to CX3CR1. Binds to integrins ITGAV:ITGB3 and ITGA4:ITGB1. Can activate integrins in both a CX3CR1-dependent and CX3CR1-independent manner. In the presence of CX3CR1, activates integrins by binding to the classical ligand-binding site (site 1) in integrins. In the absence of CX3CR1, binds to a second site (site 2) in integrins which is distinct from site 1 and enhances the binding of other integrin ligands to site 1.
CXCL1	P09341	1.00	[0.89; 1.12]	0.9398	0.9603	0.99	[0.89; 1.11]	0.8617	0.9506	1.01	[0.89; 1.16]	0.8612	0.9730	Growth-regulated alpha protein; Has chemotactic activity for neutrophils. May play a role in inflammation and exerts its effects on endothelial cells in an autocrine fashion. In vitro, the processed forms GRO- alpha(4-73), GRO-alpha(5-73) and GRO-alpha(6-73) show a 30-fold higher chemotactic activity; Chemokine ligands
CXCL10	P02778	1.04	[0.87; 1.24]	0.6509	0.8321	0.97	[0.82; 1.15]	0.7020	0.8658	0.83	[0.67; 1.02]	0.0782	0.8367	C-X-C motif chemokine 10; Chemotactic for monocytes and T-lymphocytes. Binds to CXCR3; Belongs to the intercrine alpha (chemokine CxC) family
CXCL11	O14625	0.95	[0.82; 1.11]	0.5267	0.7584	0.88	[0.76; 1.02]	0.0878	0.3225	0.89	[0.75; 1.05]	0.1836	0.8512	C-X-C motif chemokine 11; Chemotactic for interleukin-activated T-cells but not unstimulated T-cells, neutrophils or monocytes. Induces calcium release in activated T-cells. Binds to CXCR3. May play an important role in CNS diseases which involve T-cell recruitment. May play a role in skin immune responses; Belongs to the intercrine alpha (chemokine CxC) family
CXCL13	O43927	1.08	[0.9; 1.3]	0.3979	0.7041	0.97	[0.81; 1.15]	0.6973	0.8658	0.95	[0.76; 1.17]	0.6647	0.9630	C-X-C motif chemokine 13; Chemotactic for B-lymphocytes but not for T-lymphocytes, monocytes and neutrophils. Does not induce calcium release in B-lymphocytes. Binds to BLR1/CXCR5; Chemokine ligands
CXCL16	Q9H2A7	0.84	[0.5; 1.4]	0.4962	0.7584	0.99	[0.61; 1.61]	0.9616	0.9854	0.94	[0.53; 1.69]	0.8365	0.9730	C-X-C motif chemokine 16; Acts as a scavenger receptor on macrophages, which specifically binds to OxLDL (oxidized low density lipoprotein), suggesting that it may be involved in pathophysiology such as atherogenesis (By similarity). Induces a strong chemotactic response. Induces calcium mobilization. Binds to CXCR6/Bonzo; Belongs to the intercrine alpha (chemokine CxC) family
CXCL5	P42830	0.96	[0.88; 1.05]	0.3977	0.7041	0.95	[0.88; 1.04]	0.2666	0.5489	0.98	[0.89; 1.08]	0.7018	0.9630	C-X-C motif chemokine 5; Involved in neutrophil activation. In vitro, ENA-78(8-78) and ENA-78(9-78) show a threefold higher chemotactic activity for neutrophil granulocytes; Chemokine ligands
CXCL9	Q07325	1.18	[0.99; 1.42]	0.0705	0.3083	1.07	[0.9; 1.27]	0.4664	0.7215	1.00	[0.81; 1.23]	0.9948	0.9948	C-X-C motif chemokine 9; Cytokine that affects the growth, movement, or activation state of cells that participate in immune and inflammatory response. Chemotactic for activated T-cells. Binds to CXCR3; Belongs to the intercrine alpha (chemokine CxC) family

DCN	P07585	2.74	[1.39; 5.52]	0.0042	0.0640	2.25	[1.18; 4.36]	0.0141	0.1243	1.98	[0.92; 4.32]	0.0820	0.8367	Decorin; May affect the rate of fibrils formation; Small leucine rich repeat proteoglycans
DLK-1	P80370	1.25	[0.98; 1.6]	0.0764	0.3083	1.36	[1.07; 1.73]	0.0127	0.1157	1.05	[0.8; 1.39]	0.7152	0.9665	Delta like non-canonical notch ligand 1; Protein delta homolog 1; May have a role in neuroendocrine differentiation
DPP4	P27487	1.33	[0.85; 2.08]	0.2203	0.5529	1.24	[0.81; 1.9]	0.3289	0.6083	1.54	[0.92; 2.59]	0.0987	0.8449	Dipeptidyl peptidase 4; Cell surface glycoprotein receptor involved in the costimulatory signal essential for T-cell receptor (TCR)-mediated T-cell activation. Acts as a positive regulator of T-cell coactivation, by binding at least ADA, CAV1, IGF2R, and PTPRC. Its binding to CAV1 and CARD11 induces T-cell proliferation and NF- kappa-B activation in a T-cell receptor/CD3-dependent manner. Its interaction with ADA also regulates lymphocyte-epithelial cell adhesion. In association with FAP is involved in the pericellular proteolysis of the extracellular matrix (ECM)
EFEMP1	Q12805	1.60	[1.03; 2.49]	0.0352	0.2218	1.41	[0.93; 2.15]	0.1073	0.3520	0.96	[0.58; 1.58]	0.8736	0.9730	EGF-containing fibulin-like extracellular matrix protein 1; Binds EGFR, the EGF receptor, inducing EGFR autophosphorylation and the activation of downstream signaling pathways. May play a role in cell adhesion and migration. May function as a negative regulator of chondrocyte differentiation. In the olfactory epithelium, it may regulate glial cell migration, differentiation and the ability of glial cells to support neuronal neurite outgrowth; Belongs to the fibulin family
EGF	P01133	0.97	[0.89; 1.06]	0.5037	0.7584	0.95	[0.88; 1.03]	0.2332	0.4989	0.96	[0.87; 1.05]	0.3560	0.8622	Pro-epidermal growth factor; EGF stimulates the growth of various epidermal and epithelial tissues in vivo and in vitro and of some fibroblasts in cell culture. Magnesiotropic hormone that stimulates magnesium reabsorption in the renal distal convoluted tubule via engagement of EGFR and activation of the magnesium channel TRPM6. Can induce neurite outgrowth in motoneurons of the pond snail <i>Lymnaea stagnalis</i> in vitro
EGFR	P00533	1.77	[0.77; 4.13]	0.1796	0.4800	1.97	[0.9; 4.39]	0.0918	0.3274	1.79	[0.69; 4.76]	0.2337	0.8512	Epidermal growth factor receptor; Receptor tyrosine kinase binding ligands of the EGF family and activating several signaling cascades to convert extracellular cues into appropriate cellular responses. Known ligands include EGF, TGFA/TGF-alpha, amphiregulin, epigen/EPGN, BTC/betacellulin, epiregulin/EREG and HBEGF/heparin-binding EGF. Ligand binding triggers receptor homo- and/or heterodimerization and autophosphorylation on key cytoplasmic residues. The phosphorylated receptor recruits adapter proteins like GRB2 which in turn activates complex downstream signaling cascades.

ENG	P17813	1.22	[0.78; 1.91]	0.3712	0.6880	1.15	[0.75; 1.78]	0.5180	0.7682	1.08	[0.63; 1.78]	0.7569	0.9730	Endoglin; Vascular endothelium glycoprotein that plays an important role in the regulation of angiogenesis. Required for normal structure and integrity of adult vasculature. Regulates the migration of vascular endothelial cells. Required for normal extraembryonic angiogenesis and for embryonic heart development (By similarity). May play a critical role in the binding of endothelial cells to integrins and/or other RGD receptors. Acts as TGF-beta coreceptor and is involved in the TGF-beta/BMP signaling cascade that ultimately leads to the activation of SMAD transcription factors.
EP-CAM	P16422	1.01	[0.83; 1.23]	0.9190	0.9603	1.07	[0.89; 1.29]	0.4434	0.7037	1.12	[0.89; 1.39]	0.3347	0.8622	Epithelial cell adhesion molecule; May act as a physical homophilic interaction molecule between intestinal epithelial cells (IECs) and intraepithelial lymphocytes (IELs) at the mucosal epithelium for providing immunological barrier as a first line of defense against mucosal infection. Plays a role in embryonic stem cells proliferation and differentiation. Up-regulates the expression of FABP5, MYC and cyclins A and E; CD molecules
EPHB4	P54760	1.20	[0.69; 2.1]	0.5218	0.7584	1.51	[0.89; 2.57]	0.1295	0.3875	0.90	[0.48; 1.69]	0.7378	0.9678	Ephrin type-B receptor 4; Receptor tyrosine kinase which binds promiscuously transmembrane ephrin-B family ligands residing on adjacent cells, leading to contact-dependent bidirectional signaling into neighboring cells. The signaling pathway downstream of the receptor is referred to as forward signaling while the signaling pathway downstream of the ephrin ligand is referred to as reverse signaling. Together with its cognate ligand/functional ligand EFNB2 plays a central role in heart morphogenesis and angiogenesis through regulation of cell adhesion and cell migration
F11	P03951	1.58	[1; 2.51]	0.0505	0.2702	1.80	[1.16; 2.84]	0.0098	0.1025	1.57	[0.94; 2.63]	0.0850	0.8367	Coagulation factor XI; Factor XI triggers the middle phase of the intrinsic pathway of blood coagulation by activating factor IX
F7	P08709	1.63	[0.95; 2.83]	0.0799	0.3083	1.79	[1.07; 3.03]	0.0277	0.1675	1.97	[1.05; 3.72]	0.0356	0.8308	Coagulation factor VII; Initiates the extrinsic pathway of blood coagulation. Serine protease that circulates in the blood in a zymogen form. Factor VII is converted to factor VIIa by factor Xa, factor XIIIa, factor IXa, or thrombin by minor proteolysis. In the presence of tissue factor and calcium ions, factor VIIa then converts factor X to factor Xa by limited proteolysis. Factor VIIa will also convert factor IX to factor IXa in the presence of tissue factor and calcium; Gla domain containing
FABP4	P15090	0.97	[0.77; 1.21]	0.7583	0.8722	0.98	[0.8; 1.22]	0.8834	0.9621	1.00	[0.77; 1.29]	0.9767	0.9888	Fatty acid-binding protein, adipocyte; Lipid transport protein in adipocytes. Binds both long chain fatty acids and retinoic acid. Delivers long-chain fatty acids and retinoic acid to their cognate receptors in the nucleus (By similarity); Belongs to the calycin superfamily. Fatty-acid binding protein (FABP) family

FAS	P25445	1.26	[0.86; 1.86]	0.2326	0.5721	1.58	[1.07; 2.39]	0.0257	0.1621	1.43	[0.95; 2.19]	0.0850	0.8367	Tumor necrosis factor receptor superfamily member 6; Receptor for TNFSF6/FASLG. The adapter molecule FADD recruits caspase-8 to the activated receptor. The resulting death- inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. FAS-mediated apoptosis may have a role in the induction of peripheral tolerance, in the antigen-stimulated suicide of mature T-cells, or both. The secreted isoforms 2 to 6 block apoptosis (in vitro); CD molecules
FASLG	P48023	1.17	[0.81; 1.7]	0.4031	0.7041	0.95	[0.66; 1.35]	0.7604	0.8866	0.76	[0.5; 1.16]	0.2106	0.8512	Tumor necrosis factor ligand superfamily member 6; Cytokine that binds to TNFRSF6/FAS, a receptor that transduces the apoptotic signal into cells. Involved in cytotoxic T-cell-mediated apoptosis, natural killer cell-mediated apoptosis and in T-cell development. Initiates fratricidal/suicidal activation-induced cell death (AICD) in antigen-activated T-cells contributing to the termination of immune responses (By similarity). TNFRSF6/FAS-mediated apoptosis has also a role in the induction of peripheral tolerance (By similarity)
FCGR2A	P12318	0.88	[0.69; 1.12]	0.3076	0.6468	0.82	[0.65; 1.04]	0.0982	0.3375	0.85	[0.65; 1.13]	0.2636	0.8512	Low affinity immunoglobulin gamma Fc region receptor II-a; Binds to the Fc region of immunoglobulins gamma. Low affinity receptor. By binding to IgG it initiates cellular responses against pathogens and soluble antigens. Promotes phagocytosis of opsonized antigens; CD molecules
FCGR3B	O75015	1.00	[0.75; 1.35]	0.9757	0.9797	1.11	[0.84; 1.48]	0.4620	0.7193	1.32	[0.94; 1.86]	0.1089	0.8512	Low affinity immunoglobulin gamma Fc region receptor III-B; Receptor for the Fc region of immunoglobulins gamma. Low affinity receptor. Binds complexed or aggregated IgG and also monomeric IgG. Contrary to III-A, is not capable to mediate antibody-dependent cytotoxicity and phagocytosis. May serve as a trap for immune complexes in the peripheral circulation which does not activate neutrophils; CD molecules
FCN2	Q15485	1.27	[1; 1.63]	0.0536	0.2787	1.24	[0.98; 1.56]	0.0704	0.2887	1.14	[0.87; 1.51]	0.3574	0.8622	Ficolin-2; May function in innate immunity through activation of the lectin complement pathway. Calcium-dependent and GlcNAc- binding lectin. Enhances phagocytosis of S.typhimurium by neutrophils, suggesting an opsonic effect via the collagen region; Fibrinogen C domain containing
FETUB	Q9UGM5	0.95	[0.69; 1.32]	0.7545	0.8722	0.99	[0.73; 1.35]	0.9572	0.9854	0.98	[0.68; 1.43]	0.9104	0.9730	Fetuin-B; Protease inhibitor required for egg fertilization. Required to prevent premature zona pellucida hardening before fertilization, probably by inhibiting the protease activity of ASTL, a protease that mediates the cleavage of ZP2 and triggers zona pellucida hardening (By similarity); Belongs to the fetuin family

GAL-1	P09382	1.30	[0.74; 2.3]	0.3681	0.6880	1.35	[0.78; 2.33]	0.2779	0.5513	1.46	[0.76; 2.83]	0.2571	0.8512	Galectin-1; Lectin that binds beta-galactoside and a wide array of complex carbohydrates. Plays a role in regulating apoptosis, cell proliferation and cell differentiation. Inhibits CD45 protein phosphatase activity and therefore the dephosphorylation of Lyn kinase. Strong inducer of T-cell apoptosis; Endogenous ligands
GAL-3	P17931	1.11	[0.72; 1.7]	0.6322	0.8231	1.07	[0.71; 1.6]	0.7493	0.8820	0.86	[0.52; 1.4]	0.5451	0.9589	Galectin-3; Galactose-specific lectin which binds IgE. May mediate with the alpha-3, beta-1 integrin the stimulation by CSPG4 of endothelial cells migration. Together with DMBT1, required for terminal differentiation of columnar epithelial cells during early embryogenesis (By similarity). In the nucleus: acts as a pre-mRNA splicing factor. Involved in acute inflammatory responses including neutrophil activation and adhesion, chemoattraction of monocytes macrophages, opsonization of apoptotic neutrophils, and activation of mast cells; Endogenous ligands
GAL-4	P56470	1.09	[0.84; 1.4]	0.5178	0.7584	0.96	[0.75; 1.22]	0.7322	0.8776	0.82	[0.61; 1.1]	0.1935	0.8512	Galectin-4; Galectin that binds lactose and a related range of sugars. May be involved in the assembly of adherens junctions; Galectins
GAL-9	O00182	1.49	[0.99; 2.27]	0.0591	0.2854	1.47	[0.99; 2.2]	0.0585	0.2615	1.22	[0.76; 1.95]	0.4098	0.8761	Galectin-9; Binds galactosides. Has high affinity for the Forssman pentasaccharide. Ligand for HAVCR2/TIM3. Binding to HAVCR2 induces T-helper type 1 lymphocyte (Th1) death. Also stimulates bactericidal activity in infected macrophages by causing macrophage activation and IL1B secretion which restricts intracellular bacterial growth (By similarity). Ligand for P4HB; the interaction retains P4HB at the cell surface of Th2 T-helper cells, increasing disulfide reductase activity at the plasma membrane, altering the plasma membrane redox state and enhancing cell migration.
GAS6	Q14393	1.82	[1.13; 2.94]	0.0136	0.1597	1.69	[1.08; 2.67]	0.0231	0.1541	1.32	[0.77; 2.27]	0.3052	0.8512	Growth arrest-specific protein 6; Ligand for tyrosine-protein kinase receptors AXL, TYRO3 and MER whose signaling is implicated in cell growth and survival, cell adhesion and cell migration. GAS6/AXL signaling plays a role in various processes such as endothelial cell survival during acidification by preventing apoptosis, optimal cytokine signaling during human natural killer cell development, hepatic regeneration, gonadotropin-releasing hormone neuron survival and migration, platelet activation, or regulation of thrombotic responses; Gla domain containing
GDF-15	Q99988	1.59	[1.21; 2.1]	0.0009	0.0346	1.46	[1.13; 1.92]	0.0051	0.0920	1.22	[0.9; 1.64]	0.1903	0.8512	Growth differentiation factor 15; Belongs to the TGF-beta family
GP1BA	P07359	0.94	[0.83; 1.06]	0.3015	0.6424	0.94	[0.84; 1.06]	0.3120	0.5903	0.90	[0.78; 1.04]	0.1562	0.8512	Platelet glycoprotein Ib alpha chain; GP-Ib, a surface membrane protein of platelets, participates in the formation of platelet plugs by binding to the A1 domain of vWF, which is already bound to the subendothelium; CD molecules

GP6	Q9HCN6	1.03	[0.87; 1.21]	0.7437	0.8722	1.00	[0.85; 1.17]	0.9964	0.9964	0.95	[0.79; 1.15]	0.5921	0.9630	Platelet glycoprotein VI; Collagen receptor involved in collagen-induced platelet adhesion and activation. Plays a key role in platelet procoagulant activity and subsequent thrombin and fibrin formation. This procoagulant function may contribute to arterial and venous thrombus formation. The signaling pathway involves the FcR gamma-chain, the Src kinases (likely FYN or LYN) and SYK, the adapter protein LAT and leads to the activation of PLCG2; Ig-like cell adhesion molecule family
GRN	P28799	1.58	[0.96; 2.62]	0.0728	0.3083	1.41	[0.88; 2.27]	0.1612	0.4088	1.20	[0.68; 2.11]	0.5211	0.9589	Granulin precursor; Granulins; Granulins have possible cytokine-like activity. They may play a role in inflammation, wound repair, and tissue remodeling
GZMA	P12544	0.92	[0.72; 1.17]	0.5012	0.7584	0.94	[0.75; 1.19]	0.6177	0.8040	0.94	[0.7; 1.23]	0.6521	0.9630	Granzyme A; Abundant protease in the cytosolic granules of cytotoxic T-cells and NK-cells which activates caspase-independent cell death with morphological features of apoptosis when delivered into the target cell through the immunological synapse. It cleaves after Lys or Arg. Cleaves APEX1 after 'Lys-31' and destroys its oxidative repair activity. Cleaves the nucleosome assembly protein SET after 'Lys-189', which disrupts its nucleosome assembly activity and allows the SET complex to translocate into the nucleus to nick and degrade the DNA; Belongs to the peptidase S1 family
GZMB	P10144	0.94	[0.8; 1.1]	0.4592	0.7481	0.96	[0.82; 1.12]	0.6267	0.8114	1.04	[0.87; 1.24]	0.6496	0.9630	Granzyme B; This enzyme is necessary for target cell lysis in cell-mediated immune responses. It cleaves after Asp. Seems to be linked to an activation cascade of caspases (aspartate-specific cysteine proteases) responsible for apoptosis execution. Cleaves caspase-3, -7, -9 and 10 to give rise to active enzymes mediating apoptosis; Belongs to the peptidase S1 family. Granzyme subfamily
GZMH	P20718	0.94	[0.81; 1.09]	0.4230	0.7128	0.95	[0.82; 1.09]	0.4500	0.7097	0.99	[0.83; 1.17]	0.9409	0.9730	Granzyme h (cathepsin g-like 2); Granzyme H; Cytotoxic chymotrypsin-like serine protease with preference for bulky and aromatic residues at the P1 position and acidic residues at the P3' and P4' sites. Probably necessary for target cell lysis in cell-mediated immune responses. Participates in the antiviral response via direct cleavage of several proteins essential for viral replication
HGF	P14210	1.23	[0.86; 1.74]	0.2540	0.6066	1.23	[0.88; 1.73]	0.2171	0.4795	1.23	[0.83; 1.82]	0.3002	0.8512	Hepatocyte growth factor; Potent mitogen for mature parenchymal hepatocyte cells, seems to be a hepatotropic factor, and acts as a growth factor for a broad spectrum of tissues and cell types. Activating ligand for the receptor tyrosine kinase MET by binding to it and promoting its dimerization; Deafness associated genes

HO-1	P09601	1.56	[1.08; 2.26]	0.0180	0.1878	1.25	[0.88; 1.77]	0.2140	0.4795	1.21	[0.8; 1.83]	0.3664	0.8622	Heme oxygenase 1; Heme oxygenase cleaves the heme ring at the alpha methene bridge to form biliverdin. Biliverdin is subsequently converted to bilirubin by biliverdin reductase. Under physiological conditions, the activity of heme oxygenase is highest in the spleen, where senescent erythrocytes are sequestered and destroyed. Exhibits cytoprotective effects since excess of free heme sensitizes cells to undergo apoptosis
ICAM-2	P13598	1.02	[0.66; 1.6]	0.9213	0.9603	0.94	[0.62; 1.44]	0.7750	0.8993	0.66	[0.4; 1.09]	0.0996	0.8449	Intercellular adhesion molecule 2; ICAM proteins are ligands for the leukocyte adhesion protein LFA-1 (integrin alpha-L/beta-2). ICAM2 may play a role in lymphocyte recirculation by blocking LFA-1-dependent cell adhesion. It mediates adhesive interactions important for antigen- specific immune response, NK-cell mediated clearance, lymphocyte recirculation, and other cellular interactions important for immune response and surveillance; CD molecules
ICAM1	P05362	1.39	[0.9; 2.15]	0.1436	0.4255	1.50	[0.99; 2.29]	0.0600	0.2636	1.15	[0.7; 1.89]	0.5841	0.9630	Intercellular adhesion molecule 1; ICAM proteins are ligands for the leukocyte adhesion protein LFA-1 (integrin alpha-L/beta-2). During leukocyte trans-endothelial migration, ICAM1 engagement promotes the assembly of endothelial apical cups through ARHGEF26/SGEF and RHOG activation; CD molecules
ICAM3	P32942	0.79	[0.49; 1.22]	0.3029	0.6424	0.70	[0.45; 1.07]	0.1124	0.3592	0.89	[0.52; 1.44]	0.6559	0.9630	Intercellular adhesion molecule 3; ICAM proteins are ligands for the leukocyte adhesion protein LFA-1 (integrin alpha-L/beta-2). ICAM3 is also a ligand for integrin alpha-D/beta-2. In association with integrin alpha-L/beta-2, contributes to apoptotic neutrophil phagocytosis by macrophages; CD molecules
ICOSLG	O75144	1.03	[0.52; 2.03]	0.9242	0.9603	1.45	[0.76; 2.77]	0.2594	0.5408	1.38	[0.64; 3]	0.4103	0.8761	Inducible T-cell co-stimulator ligand; Ligand for the T-cell-specific cell surface receptor ICOS. Acts as a costimulatory signal for T-cell proliferation and cytokine secretion; induces also B-cell proliferation and differentiation into plasma cells. Could play an important role in mediating local tissue responses to inflammatory conditions, as well as in modulating the secondary immune response by co- stimulating memory T-cell function (By similarity); Belongs to the immunoglobulin superfamily. BTN/MOG family
IFN-GAMMA	P01579	1.10	[0.96; 1.26]	0.1692	0.4712	1.05	[0.92; 1.2]	0.4836	0.7302	1.05	[0.9; 1.22]	0.5394	0.9589	Interferon gamma; Produced by lymphocytes activated by specific antigens or mitogens. IFN-gamma, in addition to having antiviral activity, has important immunoregulatory functions. It is a potent activator of macrophages, it has antiproliferative effects on transformed cells and it can potentiate the antiviral and antitumor effects of the type I interferons; Belongs to the type II (or gamma) interferon family

IGFBP-1	P08833	1.20	[1.03; 1.39]	0.0199	0.1878	1.15	[1; 1.33]	0.0495	0.2296	1.11	[0.93; 1.31]	0.2470	0.8512	Insulin-like growth factor-binding protein 1; IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors. Promotes cell migration
IGFBP-2	P18065	1.15	[0.94; 1.41]	0.1814	0.4800	1.06	[0.88; 1.29]	0.5312	0.7737	1.01	[0.8; 1.27]	0.9414	0.9730	Insulin-like growth factor-binding protein 2; Inhibits IGF-mediated growth and developmental rates. IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors
IGFBP-7	Q16270	1.96	[1.26; 3.1]	0.0033	0.0598	1.98	[1.29; 3.09]	0.0021	0.0567	1.25	[0.76; 2.04]	0.3863	0.8761	Insulin-like growth factor-binding protein 7; Binds IGF-I and IGF-II with a relatively low affinity. Stimulates prostacyclin (PGI2) production. Stimulates cell adhesion; I-set domain containing
IGFBP3	P17936	1.25	[0.89; 1.77]	0.1956	0.4996	1.28	[0.92; 1.77]	0.1433	0.3875	1.51	[1.02; 2.26]	0.0447	0.8308	Insulin-like growth factor-binding protein 3; IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors. Also exhibits IGF-independent antiproliferative and apoptotic effects mediated by its receptor TMEM219/IGFBP-3R
IGFBP6	P24592	1.49	[0.94; 2.37]	0.0950	0.3293	1.69	[1.09; 2.65]	0.0205	0.1534	1.16	[0.69; 1.97]	0.5805	0.9630	Insulin-like growth factor-binding protein 6; IGF-binding proteins prolong the half-life of the IGFs and have been shown to either inhibit or stimulate the growth promoting effects of the IGFs on cell culture. They alter the interaction of IGFs with their cell surface receptors
IGLC2	P0DOY2	1.10	[0.83; 1.45]	0.5160	0.7584	1.02	[0.78; 1.33]	0.8897	0.9621	0.78	[0.56; 1.07]	0.1299	0.8512	Ig lambda-2 chain C regions; Constant region of immunoglobulin light chains. Immunoglobulins, also known as antibodies, are membrane-bound or secreted glycoproteins produced by B lymphocytes. In the recognition phase of humoral immunity, the membrane-bound immunoglobulins serve as receptors which, upon binding of a specific antigen, trigger the clonal expansion and differentiation of B lymphocytes into immunoglobulins-secreting plasma cells. Secreted immunoglobulins mediate the effector phase of humoral immunity, which results in the elimination of bound antigens
IL-17RA	Q96F46	1.11	[0.84; 1.46]	0.4625	0.7485	0.95	[0.73; 1.24]	0.7039	0.8658	1.08	[0.79; 1.48]	0.6266	0.9630	Interleukin-17 receptor A; Receptor for IL17A. Receptor for IL17F. Binds to IL17A with higher affinity than to IL17F. Binds IL17A and IL17F homodimers as part of a heterodimeric complex with IL17RC. Also binds heterodimers formed by IL17A and IL17F as part of a heterodimeric complex with IL17RC. Receptor for IL17C as part of a heterodimeric complex with IL17RE. Activation of IL17RA leads to induction of expression of inflammatory chemokines and cytokines such as CXCL1, CXCL8/IL8 and IL6; CD molecules

IL-18BP	O95998	1.87	[1.24; 2.83]	0.0029	0.0598	1.88	[1.27; 2.82]	0.0018	0.0557	1.05	[0.66; 1.66]	0.8319	0.9730	Interleukin-18-binding protein; Isoform A binds to IL-18 and inhibits its activity. Functions as an inhibitor of the early TH1 cytokine response; Immunoglobulin like domain containing
IL-1RT1	P14778	1.54	[0.87; 2.74]	0.1408	0.4223	1.32	[0.77; 2.27]	0.3102	0.5903	0.55	[0.29; 1.05]	0.0709	0.8367	Interleukin-1 receptor type 1; Receptor for IL1A, IL1B and IL1RN. After binding to interleukin-1 associates with the coreceptor IL1RAP to form the high affinity interleukin-1 receptor complex which mediates interleukin-1-dependent activation of NF-kappa-B, MAPK and other pathways. Signaling involves the recruitment of adapter molecules such as TOLLIP, MYD88, and IRAK1 or IRAK2 via the respective TIR domains of the receptor/coreceptor subunits. Binds ligands with comparable affinity and binding of antagonist IL1RN prevents association with IL1RAP to form a signaling complex
IL-1RT2	P27930	0.87	[0.55; 1.36]	0.5388	0.7638	1.00	[0.65; 1.55]	0.9862	0.9943	0.96	[0.57; 1.61]	0.8802	0.9730	Interleukin-1 receptor type 2; Non-signaling receptor for IL1A, IL1B and IL1RN. Reduces IL1B activities. Serves as a decoy receptor by competitive binding to IL1B and preventing its binding to IL1R1. Also modulates cellular response through non-signaling association with IL1RAP after binding to IL1B. IL1R2 (membrane and secreted forms) preferentially binds IL1B and poorly IL1A and IL1RN. The secreted IL1R2 recruits secreted IL1RAP with high affinity; this complex formation may be the dominant mechanism for neutralization of IL1B by secreted/soluble receptors; CD molecules
IL-6RA	P08887	1.84	[1.23; 2.78]	0.0034	0.0598	1.60	[1.09; 2.35]	0.0176	0.1495	1.58	[1; 2.51]	0.0517	0.8308	Interleukin-6 receptor subunit alpha; Part of the receptor for interleukin 6. Binds to IL6 with low affinity, but does not transduce a signal. Signal activation necessitate an association with IL6ST. Activation may lead to the regulation of the immune response, acute-phase reactions and hematopoiesis; CD molecules
IL10	P22301	1.26	[1; 1.58]	0.0467	0.2551	1.11	[0.89; 1.39]	0.3372	0.6101	1.08	[0.82; 1.38]	0.5820	0.9630	Interleukin-10; Inhibits the synthesis of a number of cytokines, including IFN-gamma, IL-2, IL-3, TNF and GM-CSF produced by activated macrophages and by helper T-cells; Belongs to the IL-10 family
IL12	P29459	1.26	[1.01; 1.57]	0.0407	0.2382	1.24	[1; 1.53]	0.0481	0.2296	1.00	[0.78; 1.28]	0.9886	0.9926	Interleukin-12 subunit alpha; Cytokine that can act as a growth factor for activated T and NK cells, enhance the lytic activity of NK/lymphokine- activated Killer cells, and stimulate the production of IFN-gamma by resting PBMC; Interleukins
IL12RB1	P42701	0.99	[0.65; 1.46]	0.9415	0.9603	1.18	[0.81; 1.74]	0.3814	0.6549	1.03	[0.65; 1.6]	0.8930	0.9730	Interleukin-12 receptor subunit beta-1; Functions as an interleukin receptor which binds interleukin-12 with low affinity and is involved in IL12 transduction. Associated with IL12RB2 it forms a functional, high affinity receptor for IL12. Associates also with IL23R to form the interleukin-23 receptor which functions in IL23 signal transduction probably through activation of the Jak-Stat signaling cascade; CD molecules

IL15	P40933	1.43	[0.88; 2.32]	0.1511	0.4339	1.51	[0.95; 2.42]	0.0814	0.3157	1.56	[0.9; 2.72]	0.1152	0.8512	Interleukin-15; Cytokine that stimulates the proliferation of T- lymphocytes. Stimulation by IL-15 requires interaction of IL-15 with components of IL-2R, including IL-2R beta and probably IL-2R gamma but not IL-2R alpha; Belongs to the IL-15/IL-21 family
IL18	Q14116	1.25	[0.98; 1.61]	0.0715	0.3083	1.27	[1; 1.62]	0.0488	0.2296	1.28	[0.97; 1.69]	0.0794	0.8367	Interleukin-18; Augments natural killer cell activity in spleen cells and stimulates interferon gamma production in T-helper type I cells; Belongs to the IL-1 family
IL2-RA	P01589	1.02	[0.71; 1.44]	0.9294	0.9603	1.10	[0.79; 1.54]	0.5661	0.7860	0.93	[0.61; 1.38]	0.7064	0.9630	Interleukin-2 receptor subunit alpha; Receptor for interleukin-2. The receptor is involved in the regulation of immune tolerance by controlling regulatory T cells (TREGs) activity. TREGs suppress the activation and expansion of autoreactive T-cells; CD molecules
IL6	P05231	1.20	[0.96; 1.49]	0.1099	0.3604	1.20	[0.97; 1.49]	0.1036	0.3444	1.28	[1; 1.64]	0.0431	0.8308	Interleukin-6; Cytokine with a wide variety of biological functions. It is a potent inducer of the acute phase response. Plays an essential role in the final differentiation of B-cells into Ig- secreting cells Involved in lymphocyte and monocyte differentiation. Acts on B-cells, T-cells, hepatocytes, hematopoietic progenitor cells and cells of the CNS. Required for the generation of T(H)17 cells. Also acts as a myokine. It is discharged into the bloodstream after muscle contraction and acts to increase the breakdown of fats and to improve insulin resistance.
IL7	P13232	1.09	[0.93; 1.27]	0.2823	0.6408	1.02	[0.88; 1.18]	0.7910	0.9051	1.10	[0.93; 1.31]	0.2766	0.8512	Interleukin-7; Hematopoietic growth factor capable of stimulating the proliferation of lymphoid progenitors. It is important for proliferation during certain stages of B-cell maturation; Belongs to the IL-7/IL-9 family
IL7R	P16871	0.82	[0.55; 1.22]	0.3279	0.6688	0.78	[0.54; 1.13]	0.1936	0.4546	0.76	[0.49; 1.19]	0.2392	0.8512	Interleukin-7 receptor subunit alpha; Receptor for interleukin-7. Also acts as a receptor for thymic stromal lymphopoietin (TSLP); Belongs to the type I cytokine receptor family. Type 4 subfamily
IL8	P10145	1.33	[1.07; 1.66]	0.0101	0.1379	1.27	[1.03; 1.58]	0.0294	0.1684	1.30	[1.02; 1.65]	0.0337	0.8308	Interleukin-8; IL-8 is a chemotactic factor that attracts neutrophils, basophils, and T-cells, but not monocytes. It is also involved in neutrophil activation. It is released from several cell types in response to an inflammatory stimulus. IL-8(6-77) has a 5-10-fold higher activity on neutrophil activation, IL-8(5-77) has increased activity on neutrophil activation and IL-8(7-77) has a higher affinity to receptors CXCR1 and CXCR2 as compared to IL-8(1-77), respectively; Chemokine ligands
ITGB2	P05107	0.97	[0.64; 1.47]	0.8959	0.9603	0.83	[0.56; 1.24]	0.3609	0.6333	0.91	[0.56; 1.46]	0.6842	0.9630	Integrin beta-2; Integrin ITGAL/ITGB2 is a receptor for ICAM1, ICAM2, ICAM3 and ICAM4. Integrins ITGAM/ITGB2 and ITGAX/ITGB2 are receptors for the iC3b fragment of the third complement component and for fibrinogen. Integrin ITGAX/ITGB2 recognizes the sequence G-P-R in fibrinogen alpha-chain. Integrin ITGAM/ITGB2 recognizes P1 and P2 peptides of fibrinogen gamma chain. Integrin ITGAM/ITGB2 is also a receptor for factor X. Integrin ITGAD/ITGB2 is a receptor for ICAM3 and VCAM1. Contributes to natural killer cell cytotoxicity.

JAM-A	Q9Y624	1.03	[0.9; 1.17]	0.6780	0.8349	1.03	[0.92; 1.17]	0.5790	0.7860	0.98	[0.85; 1.13]	0.8032	0.9730	Junctional adhesion molecule A; Seems to play a role in epithelial tight junction formation. Appears early in primordial forms of cell junctions and recruits PARD3. The association of the PARD6- PARD3 complex may prevent the interaction of PARD3 with JAM1, thereby preventing tight junction assembly (By similarity). Plays a role in regulating monocyte transmigration involved in integrity of epithelial barrier (By similarity). Ligand for integrin alpha- L/beta-2 involved in memory T-cell and neutrophil transmigration. Involved in platelet activation; Belongs to the immunoglobulin superfamily
KIT	P10721	0.99	[0.63; 1.58]	0.9804	0.9804	0.98	[0.63; 1.53]	0.9341	0.9854	0.97	[0.57; 1.65]	0.9077	0.9730	Mast/stem cell growth factor receptor Kit; Tyrosine-protein kinase that acts as cell-surface receptor for the cytokine KITLG/SCF and plays an essential role in the regulation of cell survival and proliferation, hematopoiesis, stem cell maintenance, gametogenesis, mast cell development, migration and function, and in melanogenesis. In response to KITLG/SCF binding, KIT can activate several signaling pathways. Phosphorylates PIK3R1, PLCG1, SH2B2/APS and CBL. Activates the AKT1 signaling pathway by phosphorylation of PIK3R1, the regulatory subunit of phosphatidylinositol 3-kinase.
KLK6	Q92876	1.28	[0.81; 2.01]	0.2911	0.6408	1.61	[1.04; 2.5]	0.0335	0.1753	1.05	[0.63; 1.76]	0.8467	0.9730	Kallikrein-6; Serine protease which exhibits a preference for Arg over Lys in the substrate P1 position and for Ser or Pro in the P2 position. Shows activity against amyloid precursor protein, myelin basic protein, gelatin, casein and extracellular matrix proteins such as fibronectin, laminin, vitronectin and collagen. Degrades alpha-synuclein and prevents its polymerization, indicating that it may be involved in the pathogenesis of Parkinson disease and other synucleinopathies. May be involved in regulation of axon outgrowth following spinal cord injury.
KLRD1	Q13241	0.99	[0.78; 1.26]	0.9447	0.9603	0.99	[0.79; 1.25]	0.9517	0.9854	0.93	[0.71; 1.22]	0.5975	0.9630	Natural killer cells antigen CD94; Plays a role as a receptor for the recognition of MHC class I HLA-E molecules by NK cells and some cytotoxic T-cells; C-type lectin domain containing
LAG3	P18627	1.31	[1.01; 1.71]	0.0437	0.2498	1.24	[0.96; 1.6]	0.1002	0.3375	1.04	[0.76; 1.4]	0.8148	0.9730	Lymphocyte activation gene 3 protein; Involved in lymphocyte activation. Binds to HLA class-II antigens; CD molecules
LAMP3	Q9UQV4	1.10	[0.88; 1.36]	0.4064	0.7041	1.14	[0.93; 1.41]	0.2182	0.4795	0.97	[0.75; 1.24]	0.7968	0.9730	Lysosome-associated membrane glycoprotein 3; May play a role in dendritic cell function and in adaptive immunity; CD molecules
LAP TGF-BETA-1	P01137	1.04	[0.83; 1.3]	0.7293	0.8667	1.02	[0.82; 1.26]	0.8864	0.9621	1.06	[0.82; 1.36]	0.6395	0.9630	Transforming growth factor beta-1; Multifunctional protein that controls proliferation, differentiation and other functions in many cell types. Many cells synthesize TGFBI and have specific receptors for it. It positively and negatively regulates many other growth factors. It plays an important role in bone remodeling as it is a potent stimulator of osteoblastic bone formation, causing chemotaxis, proliferation and differentiation in committed osteoblasts (By similarity).

LDL RECEPTOR	P01130	0.89	[0.68; 1.17]	0.4166	0.7117	1.17	[0.91; 1.52]	0.2225	0.4843	1.02	[0.75; 1.38]	0.9243	0.9730	Low-density lipoprotein receptor; Binds LDL, the major cholesterol-carrying lipoprotein of plasma, and transports it into cells by endocytosis. In order to be internalized, the receptor-ligand complexes must first cluster into clathrin-coated pits; Belongs to the LDLR family
LILRB1	Q8NHL6	1.18	[0.78; 1.79]	0.4395	0.7256	0.82	[0.55; 1.23]	0.3411	0.6101	0.89	[0.54; 1.43]	0.6344	0.9630	Leukocyte immunoglobulin-like receptor subfamily B member 1; Receptor for class I MHC antigens. Recognizes a broad spectrum of HLA-A, HLA-B, HLA-C and HLA-G alleles. Receptor for H301/UL18, a human cytomegalovirus class I MHC homolog. Ligand binding results in inhibitory signals and down-regulation of the immune response. Engagement of LILRB1 present on natural killer cells or T-cells by class I MHC molecules protects the target cells from lysis. Interaction with HLA-B or HLA-E leads to inhibition of the signal triggered by FCER1A and inhibits serotonin release.
LILRB2	Q8N423	1.51	[1.06; 2.25]	0.0306	0.2090	1.29	[0.92; 1.86]	0.1545	0.4053	1.07	[0.71; 1.54]	0.7391	0.9678	Leukocyte immunoglobulin-like receptor subfamily B member 2; Receptor for class I MHC antigens. Recognizes a broad spectrum of HLA-A, HLA-B, HLA-C and HLA-G alleles. Involved in the down-regulation of the immune response and the development of tolerance. Competes with CD8A for binding to class I MHC antigens. Inhibits FCGR1A-mediated phosphorylation of cellular proteins and mobilization of intracellular calcium ions
LILRB5	O75023	1.11	[0.86; 1.43]	0.4217	0.7128	1.07	[0.85; 1.36]	0.5635	0.7860	1.08	[0.82; 1.45]	0.5919	0.9630	Leukocyte immunoglobulin-like receptor subfamily B member 5; May act as receptor for class I MHC antigens; CD molecules
LTBR	P36941	1.96	[1.15; 3.39]	0.0146	0.1627	2.34	[1.4; 3.98]	0.0014	0.0493	1.46	[0.79; 2.69]	0.2276	0.8512	Tumor necrosis factor receptor superfamily member 3; Receptor for the heterotrimeric lymphotoxin containing LTA and LTβ, and for TNFS14/LIGHT. Promotes apoptosis via TRAF3 and TRAF5. May play a role in the development of lymphoid organs; Tumor necrosis factor receptor superfamily
LYVE1	Q9Y5Y7	1.46	[0.95; 2.25]	0.0831	0.3083	1.12	[0.74; 1.68]	0.5972	0.7898	1.10	[0.68; 1.78]	0.7082	0.9630	Lymphatic vessel endothelial hyaluronic acid receptor 1; Ligand-specific transporter trafficking between intracellular organelles (TGN) and the plasma membrane. Plays a role in autocrine regulation of cell growth mediated by growth regulators containing cell surface retention sequence binding (CRS). May act as a hyaluronan (HA) transporter, either mediating its uptake for catabolism within lymphatic endothelial cells themselves, or its transport into the lumen of afferent lymphatic vessels for subsequent re-uptake and degradation in lymph nodes
MB	P02144	1.08	[0.82; 1.42]	0.5785	0.7950	1.07	[0.83; 1.4]	0.5879	0.7860	1.04	[0.77; 1.41]	0.7906	0.9730	Myoglobin; Serves as a reserve supply of oxygen and facilitates the movement of oxygen within muscles

MBL2	P11226	1.11	[0.98; 1.25]	0.1071	0.3559	1.10	[0.98; 1.24]	0.0984	0.3375	1.03	[0.89; 1.18]	0.7192	0.9665	Mannose-binding protein C; Calcium-dependent lectin involved in innate immune defense. Binds mannose, fucose and N-acetylglucosamine on different microorganisms and activates the lectin complement pathway. Binds to late apoptotic cells, as well as to apoptotic blebs and to necrotic cells, but not to early apoptotic cells, facilitating their uptake by macrophages. May bind DNA; Collectins
MCP-1	P13500	1.56	[1.03; 2.38]	0.0369	0.2271	1.73	[1.16; 2.61]	0.0079	0.1025	1.38	[0.86; 2.21]	0.1774	0.8512	C-C motif chemokine 2; Chemotactic factor that attracts monocytes and basophils but not neutrophils or eosinophils. Augments monocyte anti-tumor activity. Has been implicated in the pathogenesis of diseases characterized by monocytic infiltrates, like psoriasis, rheumatoid arthritis or atherosclerosis. May be involved in the recruitment of monocytes into the arterial wall during the disease process of atherosclerosis; Belongs to the intercrine beta (chemokine CC) family
MCP-2	P80075	0.97	[0.77; 1.21]	0.7582	0.8722	0.89	[0.72; 1.1]	0.2759	0.5513	0.96	[0.74; 1.24]	0.7664	0.9730	C-C motif chemokine 8; Chemotactic factor that attracts monocytes, lymphocytes, basophils and eosinophils. May play a role in neoplasia and inflammatory host responses. This protein can bind heparin. The processed form MCP-2(6-76) does not show monocyte chemotactic activity, but inhibits the chemotactic effect most predominantly of CCL7, and also of CCL2 and CCL5 and CCL8; Belongs to the intercrine beta (chemokine CC) family
MCP-4	Q99616	0.96	[0.8; 1.16]	0.6734	0.8349	0.95	[0.79; 1.13]	0.5401	0.7737	0.94	[0.76; 1.16]	0.5736	0.9630	C-C motif chemokine 13; Chemotactic factor that attracts monocytes, lymphocytes, basophils and eosinophils, but not neutrophils. Signals through CCR2B and CCR3 receptors. Plays a role in the accumulation of leukocytes at both sides of allergic and non-allergic inflammation. May be involved in the recruitment of monocytes into the arterial wall during the disease process of atherosclerosis. May play a role in the monocyte attraction in tissues chronically exposed to exogenous pathogens; Chemokine ligands
MEGF9	Q9H1U4	1.60	[0.94; 2.76]	0.0865	0.3083	1.37	[0.82; 2.29]	0.2304	0.4973	1.30	[0.71; 2.36]	0.3919	0.8761	Multiple epidermal growth factor-like domains protein 9; Multiple EGF like domains 9
MEPE	Q9NQ76	1.43	[0.95; 2.16]	0.0848	0.3083	2.04	[1.38; 3.04]	0.0004	0.0418	1.91	[1.19; 3.08]	0.0079	0.6498	Matrix extracellular phosphoglycoprotein; Promotes renal phosphate excretion and modulates mineralization; SIBLING family
MET	P08581	1.45	[0.7; 3.04]	0.3251	0.6688	1.17	[0.59; 2.36]	0.6530	0.8289	1.20	[0.52; 2.78]	0.6751	0.9630	Hepatocyte growth factor receptor; Receptor tyrosine kinase that transduces signals from the extracellular matrix into the cytoplasm by binding to hepatocyte growth factor/HGF ligand. Regulates many physiological processes including proliferation, scattering, morphogenesis and survival. Ligand binding at the cell surface induces autophosphorylation of MET on its intracellular domain that provides docking sites for downstream signaling molecules. Following activation by ligand, interacts with the PI3-kinase subunit PIK3R1, PLCG1, SRC, GRB2, STAT3 or the adapter GAB1.

MFAP5	Q13361	1.03	[0.55; 1.93]	0.9263	0.9603	1.27	[0.7; 2.32]	0.4255	0.6856	1.40	[0.68; 2.86]	0.3606	0.8622	Microfibrillar-associated protein 5; May play a role in hematopoiesis. In the cardiovascular system, could regulate growth factors or participate in cell signaling in maintaining large vessel integrity (By similarity). Component of the elastin-associated microfibrils
MIC-A/B	Q29983	1.04	[0.94; 1.15]	0.4699	0.7541	1.11	[1.01; 1.22]	0.0389	0.1913	1.10	[0.98; 1.24]	0.1297	0.8512	MHC class I polypeptide-related sequence A; Seems to have no role in antigen presentation. Acts as a stress-induced self-antigen that is recognized by gamma delta T- cells. Ligand for the KLRK1/NKG2D receptor. Binding to KLRK1 leads to cell lysis; Belongs to the MHC class I family. MIC subfamily
MMP-2	P08253	1.24	[0.77; 2.01]	0.3778	0.6880	1.37	[0.87; 2.18]	0.1709	0.4163	0.87	[0.5; 1.49]	0.6040	0.9630	Matrix metalloproteinase-2 (gelatinase a); 72 kDa type IV collagenase; Ubiquitous metalloproteinase that is involved in diverse functions such as remodeling of the vasculature, angiogenesis, tissue repair, tumor invasion, inflammation, and atherosclerotic plaque rupture. As well as degrading extracellular matrix proteins, can also act on several nonmatrix proteins such as big endothelial 1 and beta-type CGRP promoting vasoconstriction. Also cleaves KISS at a Gly- -Leu bond. Appears to have a role in myocardial cell death pathways.
MMP-3	P08254	1.12	[0.86; 1.46]	0.4017	0.7041	1.24	[0.97; 1.61]	0.0898	0.3248	1.13	[0.83; 1.53]	0.4488	0.9124	Matrix metalloproteinase-3 (stromelysin 1, progelatinase); Stromelysin-1; Can degrade fibronectin, laminin, gelatins of type I, III, IV, and V; collagens III, IV, X, and IX, and cartilage proteoglycans. Activates procollagenase; Belongs to the peptidase M10A family
MMP-9	P14780	0.95	[0.76; 1.17]	0.6092	0.8101	0.95	[0.78; 1.17]	0.6537	0.8289	1.14	[0.9; 1.45]	0.2841	0.8512	Matrix metalloproteinase-9; May play an essential role in local proteolysis of the extracellular matrix and in leukocyte migration. Could play a role in bone osteoclastic resorption. Cleaves KISS1 at a Gly- -Leu bond. Cleaves type IV and type V collagen into large C-terminal three quarter fragments and shorter N-terminal one quarter fragments. Degrades fibronectin but not laminin or Pz-peptide; M10 matrix metallopeptidases
MMP12	P39900	1.13	[0.9; 1.41]	0.2808	0.6408	1.08	[0.87; 1.35]	0.4597	0.7193	1.03	[0.79; 1.31]	0.8470	0.9730	Matrix metalloproteinase-12 (macrophage elastase); Macrophage metalloelastase; May be involved in tissue injury and remodeling. Has significant elastolytic activity. Can accept large and small amino acids at the P1' site, but has a preference for leucine. Aromatic or hydrophobic residues are preferred at the P1 site, with small hydrophobic residues (preferably alanine) occupying P3; Belongs to the peptidase M10A family
MMP7	P09237	1.17	[0.93; 1.48]	0.1748	0.4777	1.18	[0.95; 1.47]	0.1353	0.3875	0.99	[0.76; 1.28]	0.9174	0.9730	Matrix metalloproteinase-7 (matrilysin, uterine); Matrilysin; Degrades casein, gelatins of types I, III, IV, and V, and fibronectin. Activates procollagenase; M10 matrix metallopeptidases

MPO	P05164	0.85	[0.57; 1.25]	0.4158	0.7117	0.81	[0.55; 1.17]	0.2677	0.5489	0.97	[0.61; 1.51]	0.8784	0.9730	Myeloperoxidase; Part of the host defense system of polymorphonuclear leukocytes. It is responsible for microbicidal activity against a wide range of organisms. In the stimulated PMN, MPO catalyzes the production of hypohalous acids, primarily hypochlorous acid in physiologic situations, and other toxic intermediates that greatly enhance PMN microbicidal activity; Belongs to the peroxidase family. XPO subfamily
MUC-16	Q8WXI7	1.22	[0.98; 1.51]	0.0769	0.3083	1.22	[0.99; 1.51]	0.0634	0.2644	1.11	[0.87; 1.42]	0.4010	0.8761	Mucin-16; Thought to provide a protective, lubricating barrier against particles and infectious agents at mucosal surfaces; Mucins
NCAM1	P13591	1.59	[0.94; 2.7]	0.0861	0.3083	1.40	[0.85; 2.31]	0.1897	0.4530	1.40	[0.77; 2.56]	0.2698	0.8512	Neural cell adhesion molecule 1; This protein is a cell adhesion molecule involved in neuron-neuron adhesion, neurite fasciculation, outgrowth of neurites, etc; CD molecules
NCR1	O76036	1.93	[1.31; 2.86]	0.0010	0.0346	1.71	[1.18; 2.51]	0.0050	0.0920	1.02	[0.66; 1.57]	0.9356	0.9730	Natural cytotoxicity triggering receptor 1; Cytotoxicity-activating receptor that may contribute to the increased efficiency of activated natural killer (NK) cells to mediate tumor cell lysis
NID1	P14543	0.96	[0.79; 1.16]	0.6923	0.8389	0.93	[0.77; 1.11]	0.4254	0.6856	0.99	[0.79; 1.22]	0.9205	0.9730	Nidogen (entactin); Nidogen-1; Sulfated glycoprotein widely distributed in basement membranes and tightly associated with laminin. Also binds to collagen IV and perlecan. It probably has a role in cell-extracellular matrix interactions
NOS3	P29474	0.91	[0.68; 1.23]	0.5521	0.7673	0.96	[0.72; 1.27]	0.7569	0.8866	0.71	[0.5; 1]	0.0563	0.8308	Nitric-oxide synthase, endothelial; Nitric oxide synthase, endothelial; Produces nitric oxide (NO) which is implicated in vascular smooth muscle relaxation through a cGMP-mediated signal transduction pathway. NO mediates vascular endothelial growth factor (VEGF)-induced angiogenesis in coronary vessels and promotes blood clotting through the activation of platelets
NOTCH3	Q9UM47	0.89	[0.58; 1.36]	0.5895	0.8046	0.80	[0.53; 1.19]	0.2702	0.5493	0.68	[0.42; 1.11]	0.1256	0.8512	Neurogenic locus notch homolog protein 3; Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBPJ/RBPSUH and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs (By similarity)
NOTCH1	P46531	2.12	[0.98; 4.64]	0.0572	0.2854	1.58	[0.77; 3.28]	0.2153	0.4795	1.31	[0.55; 3.16]	0.5466	0.9589	Neurogenic locus notch homolog protein 1; Functions as a receptor for membrane-bound ligands Jagged1, Jagged2 and Delta1 to regulate cell-fate determination. Upon ligand activation through the released notch intracellular domain (NICD) it forms a transcriptional activator complex with RBPJ/RBPSUH and activates genes of the enhancer of split locus. Affects the implementation of differentiation, proliferation and apoptotic programs. Involved in angiogenesis; negatively regulates endothelial cell proliferation and migration and angiogenic sprouting.

NRP1	O14786	5.10	[2.32; 11.44]	0.0001	0.0151	2.87	[1.36; 6.12]	0.0059	0.0920	3.29	[1.38; 7.94]	0.0075	0.6498	Neuropilin-1; The membrane-bound isoform 1 is a receptor involved in the development of the cardiovascular system, in angiogenesis, in the formation of certain neuronal circuits and in organogenesis outside the nervous system. It mediates the chemorepulsant activity of semaphorins. It binds to semaphorin 3A, The PLGF-2 isoform of PGF, The VEGF165 isoform of VEGFA and VEGFB. Coexpression with KDR results in increased VEGF165 binding to KDR as well as increased chemotaxis. Regulate VEGF-induced angiogenesis.
OPG	O00300	1.66	[1.08; 2.57]	0.0223	0.1878	1.61	[1.06; 2.47]	0.0257	0.1621	1.06	[0.64; 1.72]	0.8304	0.9730	Tumor necrosis factor receptor superfamily member 11B; Acts as decoy receptor for TNFSF11/RANKL and thereby neutralizes its function in osteoclastogenesis. Inhibits the activation of osteoclasts and promotes osteoclast apoptosis in vitro. Bone homeostasis seems to depend on the local ratio between TNFSF11 and TNFRSF11B. May also play a role in preventing arterial calcification. May act as decoy receptor for TNFSF10/TRAIL and protect against apoptosis. TNFSF10/TRAIL binding blocks the inhibition of osteoclastogenesis; Tumor necrosis factor receptor superfamily
OPN	P10451	1.28	[0.97; 1.71]	0.0834	0.3083	1.23	[0.94; 1.62]	0.1331	0.3875	1.39	[1.01; 1.92]	0.0414	0.8308	Secreted phosphoprotein 1; Osteopontin; Binds tightly to hydroxyapatite. Appears to form an integral part of the mineralized matrix. Probably important to cell-matrix interaction; Endogenous ligands
OSMR	Q99650	3.71	[1.7; 8.24]	0.0011	0.0346	2.69	[1.28; 5.73]	0.0093	0.1025	1.53	[0.64; 3.67]	0.3412	0.8622	Oncostatin-M-specific receptor subunit beta; Associates with IL31RA to form the IL31 receptor. Binds IL31 to activate STAT3 and possibly STAT1 and STAT5. Capable of transducing OSM-specific signaling events; Fibronectin type III domain containing
PAI	P05121	1.06	[0.9; 1.26]	0.4790	0.7584	1.16	[0.98; 1.36]	0.0821	0.3157	1.22	[1.01; 1.48]	0.0446	0.8308	Plasminogen activator inhibitor 1; Serine protease inhibitor. This inhibitor acts as 'bait' for tissue plasminogen activator, urokinase, protein C and matriptase-3/TMPRSS7. Its rapid interaction with PLAT may function as a major control point in the regulation of fibrinolysis; Serpin peptidase inhibitors
PAM	P19021	1.14	[0.64; 2.02]	0.6528	0.8321	1.30	[0.76; 2.24]	0.3415	0.6101	1.11	[0.57; 2.13]	0.7498	0.9723	Peptidylglycine monooxygenase / peptidylamidoglycolate lyase; Peptidyl-glycine alpha-amidating monooxygenase; Bifunctional enzyme that catalyzes 2 sequential steps in C-terminal alpha-amidation of peptides. The monooxygenase part produces an unstable peptidyl(2-hydroxyglycine) intermediate that is dismutated to glyoxylate and the corresponding desglycine peptide amide by the lyase part. C-terminal amidation of peptides such as neuropeptides is essential for full biological activity
PCOLCE	Q15113	1.23	[0.83; 1.81]	0.3029	0.6424	1.48	[1.02; 2.16]	0.0379	0.1904	1.46	[0.94; 2.28]	0.0940	0.8449	Procollagen C-endopeptidase enhancer 1; Binds to the C-terminal propeptide of type I procollagen and enhances procollagen C-proteinase activity

PCSK9	Q8NBP7	0.98	[0.59; 1.63]	0.9405	0.9603	1.14	[0.71; 1.85]	0.5856	0.7860	0.84	[0.47; 1.51]	0.5637	0.9630	Proprotein convertase subtilisin/kexin type 9; Crucial player in the regulation of plasma cholesterol homeostasis. Binds to low-density lipoprotein receptor family members: low density lipoprotein receptor (LDLR), very low density lipoprotein receptor (VLDLR), apolipoprotein E receptor (LRP1/APOER) and apolipoprotein receptor 2 (LRP8/APOER2), and promotes their degradation in intracellular acidic compartments. Acts via a non-proteolytic mechanism to enhance the degradation of the hepatic LDLR through a clathrin LDLRAP1/ARH-mediated pathway
PD-L1	Q9NZQ7	1.23	[0.9; 1.69]	0.1970	0.4996	1.15	[0.85; 1.56]	0.3624	0.6333	1.10	[0.77; 1.57]	0.6003	0.9630	Programmed cell death 1 ligand 1; Involved in the costimulatory signal, essential for T- cell proliferation and production of IL10 and IFNG, in an IL2- dependent and a PDCD1-independent manner. Interaction with PDCD1 inhibits T-cell proliferation and cytokine production; Belongs to the immunoglobulin superfamily. BTN/MOG family
PD-L2	Q9BQ51	0.98	[0.65; 1.48]	0.9379	0.9603	1.14	[0.77; 1.68]	0.5081	0.7621	0.82	[0.5; 1.32]	0.4258	0.8761	Programmed cell death 1 ligand 2; Involved in the costimulatory signal, essential for T- cell proliferation and IFNG production in a PDCD1-independent manner. Interaction with PDCD1 inhibits T-cell proliferation by blocking cell cycle progression and cytokine production (By similarity); Belongs to the immunoglobulin superfamily. BTN/MOG family
PDCD1	Q15116	0.97	[0.74; 1.28]	0.8537	0.9460	1.00	[0.77; 1.3]	0.9938	0.9964	1.04	[0.76; 1.42]	0.8008	0.9730	Programmed cell death protein 1; Inhibitory cell surface receptor involved in the regulation of T-cell function during immunity and tolerance. Upon ligand binding, inhibits T-cell effector functions in an antigen- specific manner. Possible cell death inducer, in association with other factors; CD molecules
PDGF SUBUNIT A	P04085	1.03	[0.87; 1.22]	0.7246	0.8653	0.99	[0.84; 1.16]	0.8925	0.9621	1.04	[0.85; 1.26]	0.7070	0.9630	Platelet-derived growth factor subunit A; Growth factor that plays an essential role in the regulation of embryonic development, cell proliferation, cell migration, survival and chemotaxis. Potent mitogen for cells of mesenchymal origin. Required for normal lung alveolar septum formation during embryogenesis, normal development of the gastrointestinal tract, normal development of Leydig cells and spermatogenesis. Required for normal oligodendrocyte development and normal myelination in the spinal cord and cerebellum. Plays an important role in wound healing.
PDGF SUBUNIT B	P01127	0.97	[0.82; 1.14]	0.6898	0.8389	0.93	[0.8; 1.09]	0.3989	0.6722	1.00	[0.84; 1.22]	0.9608	0.9766	Platelet-derived growth factor subunit B; Growth factor that plays an essential role in the regulation of embryonic development, cell proliferation, cell migration, survival and chemotaxis. Potent mitogen for cells of mesenchymal origin. Required for normal proliferation and recruitment of pericytes and vascular smooth muscle cells in the central nervous system, skin, lung, heart and placenta. Required for normal blood vessel development, and for normal development of kidney glomeruli. Plays an important role in wound healing.

PECAM-1	P16284	1.05	[0.87; 1.27]	0.5920	0.8046	1.05	[0.88; 1.26]	0.5846	0.7860	0.97	[0.78; 1.2]	0.7866	0.9730	Platelet endothelial cell adhesion molecule; Cell adhesion molecule which is required for leukocyte transendothelial migration (TEM) under most inflammatory conditions. Tyr-690 plays a critical role in TEM and is required for efficient trafficking of PECAM1 to and from the lateral border recycling compartment (LBRC) and is also essential for the LBRC membrane to be targeted around migrating leukocytes. Heterophilic interaction with CD177 plays a role in transendothelial migration of neutrophils.
PGF	P49763	2.28	[1.36; 3.85]	0.0018	0.0504	2.81	[1.72; 4.68]	0.0001	0.0125	2.16	[1.2; 3.92]	0.0108	0.6662	Placental growth factor; Placenta growth factor; Growth factor active in angiogenesis and endothelial cell growth, stimulating their proliferation and migration. It binds to the receptor FLT1/VEGFR-1. Isoform PIGF-2 binds NRP1/neuropilin-1 and NRP2/neuropilin-2 in a heparin-dependent manner. Also promotes cell tumor growth
PGLYRP1	O75594	1.14	[0.82; 1.58]	0.4350	0.7256	1.15	[0.84; 1.57]	0.3865	0.6558	1.03	[0.71; 1.5]	0.8638	0.9730	Peptidoglycan recognition protein 1; Pattern receptor that binds to murein peptidoglycans (PGN) of Gram-positive bacteria. Has bactericidal activity towards Gram-positive bacteria. May kill Gram-positive bacteria by interfering with peptidoglycan biosynthesis. Binds also to Gram-negative bacteria, and has bacteriostatic activity towards Gram-negative bacteria. Plays a role in innate immunity; Peptidoglycan recognition proteins
PI3	P19957	0.95	[0.72; 1.27]	0.7449	0.8722	1.03	[0.79; 1.35]	0.8186	0.9153	0.92	[0.66; 1.27]	0.5953	0.9630	Elafin; Neutrophil and pancreatic elastase-specific inhibitor of skin. It may prevent elastase-mediated tissue proteolysis; WAP four-disulfide core domain containing
PLC	P98160	1.81	[1.07; 3.09]	0.0294	0.2090	2.07	[1.25; 3.46]	0.0053	0.0920	1.14	[0.63; 2.08]	0.6651	0.9630	Basement membrane-specific heparan sulfate proteoglycan core protein; Integral component of basement membranes. Component of the glomerular basement membrane (GBM), responsible for the fixed negative electrostatic membrane charge, and which provides a barrier which is both size- and charge-selective. It serves as an attachment substrate for cells. Plays essential roles in vascularization. Critical for normal heart development and for regulating the vascular response to injury. Also required for avascular cartilage development; I-set domain containing
PLTP	P55058	1.63	[0.84; 3.16]	0.1474	0.4317	1.36	[0.73; 2.57]	0.3339	0.6101	1.53	[0.72; 3.24]	0.2635	0.8512	Phospholipid transfer protein; Facilitates the transfer of a spectrum of different lipid molecules, including diacylglycerol, phosphatidic acid, sphingomyelin, phosphatidylcholine, phosphatidylglycerol, cerebroside and phosphatidyl ethanolamine. Essential for the transfer of excess surface lipids from triglyceride-rich lipoproteins to HDL, thereby facilitating the formation of smaller lipoprotein remnants, contributing to the formation of LDL, and assisting in the maturation of HDL particles.

PLXNB2	O15031	1.21	[0.71; 2]	0.4721	0.7541	0.99	[0.6; 1.63]	0.9805	0.9926	0.97	[0.51; 1.73]	0.9153	0.9730	Plexin-B2; Cell surface receptor for SEMA4C, SEMA4D and SEMA4G that plays an important role in cell-cell signaling. Binding to class 4 semaphorins promotes downstream activation of RHOA and phosphorylation of ERBB2 at 'Tyr-1248'. Required for normal differentiation and migration of neuronal cells during brain corticogenesis and for normal embryonic brain development. Regulates the migration of cerebellar granule cells in the developing brain. Plays a role in RHOA activation and subsequent changes of the actin cytoskeleton.
PON3	Q15166	1.32	[1.05; 1.67]	0.0206	0.1878	1.23	[0.99; 1.54]	0.0583	0.2615	1.15	[0.89; 1.5]	0.2909	0.8512	Serum paraoxonase/lactonase 3; Has low activity towards the organophosphate paraxon and aromatic carboxylic acid esters. Rapidly hydrolyzes lactones such as statin prodrugs (e.g. lovastatin). Hydrolyzes aromatic lactones and 5- or 6-member ring lactones with aliphatic substituents but not simple lactones or those with polar substituents; Belongs to the paraoxonase family
PROC	P04070	1.25	[0.79; 1.99]	0.3423	0.6736	1.40	[0.91; 2.19]	0.1301	0.3875	1.40	[0.83; 2.39]	0.2124	0.8512	Vitamin K-dependent protein C; Protein C is a vitamin K-dependent serine protease that regulates blood coagulation by inactivating factors Va and VIIIa in the presence of calcium ions and phospholipids. Exerts a protective effect on the endothelial cell barrier function; Belongs to the peptidase S1 family
PRSS2	P07478	1.16	[0.83; 1.62]	0.3804	0.6880	1.07	[0.77; 1.47]	0.6953	0.8658	0.95	[0.65; 1.38]	0.7907	0.9730	Trypsin-2; In the ileum, may be involved in defensin processing, including DEFA5; Belongs to the peptidase S1 family
PRTN3	P24158	1.17	[0.85; 1.61]	0.3358	0.6736	1.02	[0.75; 1.38]	0.8956	0.9621	0.91	[0.63; 1.32]	0.6389	0.9630	Myeloblastin; Serine protease that degrades elastin, fibronectin, laminin, vitronectin, and collagen types I, III, and IV (in vitro). By cleaving and activating receptor F2RL1/PAR-2, enhances endothelial cell barrier function and thus vascular integrity during neutrophil transendothelial migration. May play a role in neutrophil transendothelial migration, probably when associated with CD177; Belongs to the peptidase S1 family. Elastase subfamily
PSP-D	P35247	1.26	[0.98; 1.64]	0.0774	0.3083	1.34	[1.04; 1.72]	0.0232	0.1541	1.00	[0.75; 1.34]	0.9859	0.9926	Pulmonary surfactant-associated protein D; Contributes to the lung's defense against inhaled microorganisms, organic antigens and toxins. Interacts with compounds such as bacterial lipopolysaccharides, oligosaccharides and fatty acids and modulates leukocyte action in immune response. May participate in the extracellular reorganization or turnover of pulmonary surfactant. Binds strongly maltose residues and to a lesser extent other alpha-glucosyl moieties; C-type lectin domain containing

PTPRS	Q13332	1.46	[0.72; 2.98]	0.2918	0.6408	1.53	[0.78; 3.05]	0.2183	0.4795	1.27	[0.57; 2.83]	0.5496	0.9589	Receptor-type tyrosine-protein phosphatase S; Cell surface receptor that binds to glycosaminoglycans, including chondroitin sulfate proteoglycans and heparan sulfate proteoglycan. Binding to chondroitin sulfate and heparan sulfate proteoglycans has opposite effects on PTPRS oligomerization and regulation of neurite outgrowth. Contributes to the inhibition of neurite and axonal outgrowth by chondroitin sulfate proteoglycans, also after nerve transection. Plays a role in stimulating neurite outgrowth in response to the heparan sulfate proteoglycan GPC2
RARRES2	Q99969	1.14	[0.74; 1.77]	0.5496	0.7673	1.30	[0.86; 1.96]	0.2136	0.4795	0.94	[0.58; 1.55]	0.8096	0.9730	Retinoic acid receptor responder protein 2; Adipocyte-secreted protein (adipokine) that regulates adipogenesis, metabolism and inflammation through activation of the chemokine-like receptor 1 (CMKLR1). Its other ligands include G protein-coupled receptor 1 (GPR1) and chemokine receptor-like 2 (CCRL2). Positively regulates adipocyte differentiation, modulates the expression of adipocyte genes involved in lipid and glucose metabolism and might play a role in angiogenesis, a process essential for the expansion of white adipose tissue.
REG1A	P05451	1.52	[1.16; 2]	0.0027	0.0598	1.44	[1.11; 1.88]	0.0070	0.0979	1.13	[0.83; 1.54]	0.4273	0.8761	Lithostathine-1-alpha; Might act as an inhibitor of spontaneous calcium carbonate precipitation. May be associated with neuronal sprouting in brain, and with brain and pancreas regeneration; C-type lectin domain containing
RETN	Q9HD89	0.99	[0.74; 1.33]	0.9508	0.9626	0.84	[0.63; 1.12]	0.2377	0.5041	0.81	[0.58; 1.13]	0.2236	0.8512	Resistin; Hormone that seems to suppress insulin ability to stimulate glucose uptake into adipose cells (By similarity). Potentially links obesity to diabetes (By similarity). Promotes chemotaxis in myeloid cells
SAA4	P35542	0.86	[0.67; 1.1]	0.2412	0.5818	0.89	[0.7; 1.12]	0.3200	0.6010	1.04	[0.78; 1.37]	0.8015	0.9730	Serum amyloid A-4 protein; Major acute phase reactant. Apolipoprotein of the HDL complex; Belongs to the SAA family
SCGB3A2	Q96PL1	0.90	[0.72; 1.12]	0.3562	0.6792	0.87	[0.7; 1.07]	0.1940	0.4546	0.99	[0.77; 1.27]	0.9369	0.9730	Secretoglobulin family 3A member 2; Secreted cytokine-like protein. Binds to the scavenger receptor MARCO. Can also bind to pathogens including the Gram-positive bacterium L.monocytogenes, the Gram-negative bacterium P.aeruginosa, and yeast. Strongly inhibits phospholipase A2 (PLA2G1B) activity. Seems to have anti-inflammatory effects in respiratory epithelium (By similarity). Also has anti-fibrotic activity in lung. May play a role in fetal lung development and maturation. Promotes branching morphogenesis during early stages of lung development
SELE	P16581	0.96	[0.73; 1.27]	0.7927	0.8991	0.96	[0.74; 1.25]	0.7824	0.9036	0.88	[0.65; 1.2]	0.4202	0.8761	E-selectin; Cell-surface glycoprotein having a role in immunoadhesion. Mediates in the adhesion of blood neutrophils in cytokine-activated endothelium through interaction with PSGL1/SELP1G. May have a role in capillary morphogenesis; Belongs to the selectin/LECAM family

SELL	P14151	1.24	[0.79; 1.96]	0.3520	0.6765	0.99	[0.65; 1.52]	0.9709	0.9869	1.05	[0.63; 1.76]	0.8563	0.9730	L-selectin; Cell surface adhesion protein. Mediates the adherence of lymphocytes to endothelial cells of high endothelial venules in peripheral lymph nodes. Promotes initial tethering and rolling of leukocytes in endothelia; C-type lectin domain containing
SELP	P16109	1.05	[0.89; 1.24]	0.5272	0.7584	1.06	[0.9; 1.24]	0.4779	0.7302	1.02	[0.85; 1.23]	0.8255	0.9730	P-selectin; Ca(2+)-dependent receptor for myeloid cells that binds to carbohydrates on neutrophils and monocytes. Mediates the interaction of activated endothelial cells or platelets with leukocytes. The ligand recognized is sialyl-Lewis X. Mediates rapid rolling of leukocyte rolling over vascular surfaces during the initial steps in inflammation through interaction with PSGL1; Belongs to the selectin/LECAM family
SERPINA5	P05154	1.44	[0.96; 2.17]	0.0777	0.3083	1.75	[1.18; 2.62]	0.0060	0.0920	1.54	[0.99; 2.45]	0.0595	0.8308	Plasma serine protease inhibitor; Heparin-dependent serine protease inhibitor acting in body fluids and secretions. Inactivates serine proteases by binding irreversibly to their serine activation site. Involved in the regulation of intravascular and extravascular proteolytic activities. Plays hemostatic roles in the blood plasma. Acts as a procoagulant and proinflammatory factor by inhibiting the anticoagulant activated protein C factor as well as the generation of activated protein C factor by the thrombin/thrombomodulin complex.
SERPINA7	P05543	1.15	[0.77; 1.71]	0.4993	0.7584	1.23	[0.85; 1.8]	0.2735	0.5513	1.17	[0.75; 1.86]	0.4943	0.9589	Thyroxine-binding globulin; Major thyroid hormone transport protein in serum; Belongs to the serpin family
SHPS-1	P78324	1.40	[0.92; 2.15]	0.1175	0.3753	1.47	[0.98; 2.21]	0.0623	0.2644	1.18	[0.73; 1.91]	0.4977	0.9589	Tyrosine-protein phosphatase non-receptor type substrate 1; Immunoglobulin-like cell surface receptor for CD47. Acts as docking protein and induces translocation of PTPN6, PTPN11 and other binding partners from the cytosol to the plasma membrane. Supports adhesion of cerebellar neurons, neurite outgrowth and glial cell attachment. May play a key role in intracellular signaling during synaptogenesis and in synaptic function (By similarity). Involved in the negative regulation of receptor tyrosine kinase-coupled cellular responses induced by cell adhesion, growth factors or insulin.
SPARCL1	Q14515	1.05	[0.58; 1.89]	0.8837	0.9603	0.98	[0.56; 1.72]	0.9462	0.9854	1.10	[0.56; 2.17]	0.7899	0.9730	SPARC-like protein 1; SPARC family
ST2	Q01638	1.56	[1.16; 2.11]	0.0039	0.0640	1.40	[1.05; 1.86]	0.0208	0.1534	1.09	[0.78; 1.53]	0.6066	0.9630	Interleukin-1 receptor-like 1; Receptor for interleukin-33 (IL-33); signaling requires association of the coreceptor IL1RAP. Its stimulation recruits MYD88, IRAK1, IRAK4, and TRAF6, followed by phosphorylation of MAPK3/ERK1 and/or MAPK1/ERK2, MAPK14, and MAPK8. Possibly involved in helper T-cell function; I-set domain containing
ST6GAL1	P15907	0.96	[0.78; 1.17]	0.6817	0.8349	0.98	[0.81; 1.18]	0.8040	0.9100	0.98	[0.77; 1.22]	0.8321	0.9730	Beta-galactoside alpha-2,6-sialyltransferase 1; Transfers sialic acid from CMP-sialic acid to galactose-containing acceptor substrates; Sialyltransferases

T-PA	P00750	0.96	[0.79; 1.16]	0.6965	0.8399	1.14	[0.95; 1.36]	0.1683	0.4141	1.04	[0.84; 1.29]	0.6934	0.9630	Plasminogen activator, tissue type; Tissue-type plasminogen activator; Converts the abundant, but inactive, zymogen plasminogen to plasmin by hydrolyzing a single Arg-Val bond in plasminogen. By controlling plasmin-mediated proteolysis, it plays an important role in tissue remodeling and degradation, in cell migration and many other physiopathological events. Plays a direct role in facilitating neuronal migration
TCN2	P20062	0.98	[0.65; 1.45]	0.9123	0.9603	0.76	[0.52; 1.11]	0.1662	0.4130	0.92	[0.57; 1.44]	0.7086	0.9630	Transcobalamin-2; Primary vitamin B12-binding and transport protein. Delivers cobalamin to cells; Belongs to the eukaryotic cobalamin transport proteins family
TFF3	Q07654	1.45	[1.03; 2.05]	0.0336	0.2177	1.33	[0.96; 1.86]	0.0869	0.3225	1.28	[0.86; 1.87]	0.2156	0.8512	Trefoil factor 3; Involved in the maintenance and repair of the intestinal mucosa. Promotes the mobility of epithelial cells in healing processes (motogen)
TFPI	P10646	1.23	[0.78; 1.96]	0.3783	0.6880	1.41	[0.91; 2.2]	0.1242	0.3867	1.29	[0.76; 2.2]	0.3500	0.8622	Tissue factor pathway inhibitor; Inhibits factor X (X(a)) directly and, in a Xa-dependent way, inhibits VIIa/tissue factor activity, presumably by forming a quaternary Xa/LACI/VIIa/TF complex. It possesses an antithrombotic action and also the ability to associate with lipoproteins in plasma
TGFBI	Q15582	1.11	[0.75; 1.66]	0.6029	0.8061	1.11	[0.76; 1.63]	0.5878	0.7860	0.85	[0.53; 1.34]	0.4862	0.9589	Transforming growth factor-beta-induced protein ig-h3; Plays a role in cell adhesion. May play a role in cell-collagen interactions (By similarity)
TGFBR3	Q03167	1.22	[0.73; 2.04]	0.4522	0.7416	1.11	[0.68; 1.8]	0.6751	0.8516	0.73	[0.4; 1.31]	0.2853	0.8512	Transforming growth factor beta receptor type 3; Binds to TGF-beta. Could be involved in capturing and retaining TGF-beta for presentation to the signaling receptors; Proteoglycans
THBS4	P35443	1.06	[0.84; 1.33]	0.6365	0.8231	1.19	[0.95; 1.48]	0.1319	0.3875	1.05	[0.8; 1.36]	0.7288	0.9678	Thrombospondin 2/3/4/5; Thrombospondin-4; Adhesive glycoprotein that mediates cell-to-cell and cell-to-matrix interactions and is involved in various processes including cellular proliferation, migration, adhesion and attachment, inflammatory response to CNS injury, regulation of vascular inflammation and adaptive responses of the heart to pressure overload and in myocardial function and remodeling. Binds to structural extracellular matrix (ECM) proteins and modulates the ECM in response to tissue damage, contributing to cardioprotective and adaptive ECM remodeling.
TIE1	P35590	1.49	[0.77; 2.89]	0.2378	0.5793	1.23	[0.66; 2.31]	0.5184	0.7682	1.16	[0.54; 2.46]	0.7021	0.9630	Tyrosine kinase with immunoglobulin like and egf like domains 1; Tyrosine-protein kinase receptor Tie-1; Transmembrane tyrosine-protein kinase that may modulate TEK/TIE2 activity and contribute to the regulation of angiogenesis

TIE2	Q02763	1.94	[1.07; 3.55]	0.0301	0.2090	1.89	[1.07; 3.34]	0.0282	0.1675	1.61	[0.82; 3.21]	0.1677	0.8512	Angiopoietin-1 receptor; Tyrosine-protein kinase that acts as cell-surface receptor for ANGPT1, ANGPT2 and ANGPT4 and regulates angiogenesis, endothelial cell survival, proliferation, migration, adhesion and cell spreading, reorganization of the actin cytoskeleton, but also maintenance of vascular quiescence. Has anti-inflammatory effects by preventing the leakage of proinflammatory plasma proteins and leukocytes from blood vessels. Required for normal angiogenesis and heart development during embryogenesis. Required for post- natal hematopoiesis.
TIMD4	Q96H15	1.16	[0.84; 1.6]	0.3675	0.6880	1.15	[0.84; 1.56]	0.3794	0.6549	1.24	[0.86; 1.78]	0.2469	0.8512	T-cell immunoglobulin and mucin domain-containing protein 4; Phosphatidylserine receptor that enhances the engulfment of apoptotic cells. Involved in regulating T-cell proliferation and lymphotoxin signaling. Ligand for HAVCR1/TIMD1 (By similarity); Belongs to the immunoglobulin superfamily. TIM family
TIMP1	P01033	1.15	[0.89; 1.47]	0.2871	0.6408	1.09	[0.85; 1.39]	0.4838	0.7302	1.03	[0.76; 1.37]	0.8292	0.9730	Metalloproteinase inhibitor 1; Metalloproteinase inhibitor that functions by forming one to one complexes with target metalloproteinases, such as collagenases, and irreversibly inactivates them by binding to their catalytic zinc cofactor. Acts on MMP1, MMP2, MMP3, MMP7, MMP8, MMP9, MMP10, MMP11, MMP12, MMP13 and MMP16. Does not act on MMP14. Also functions as a growth factor that regulates cell differentiation, migration and cell death and activates cellular signaling cascades via CD63 and ITGB1. Plays a role in integrin signaling.
TIMP4	Q99727	1.02	[0.74; 1.4]	0.9075	0.9603	0.92	[0.68; 1.24]	0.5784	0.7860	0.72	[0.49; 1.03]	0.0785	0.8367	Metalloproteinase inhibitor 4; Complexes with metalloproteinases (such as collagenases) and irreversibly inactivates them by binding to their catalytic zinc cofactor. Known to act on MMP-1, MMP-2, MMP-3, MMP-7 and MMP- 9; Tissue inhibitor of metallopeptidases
TLT-2	Q5T2D2	1.22	[0.87; 1.72]	0.2571	0.6081	1.15	[0.83; 1.6]	0.4047	0.6733	0.96	[0.65; 1.42]	0.8450	0.9730	Trem-like transcript 2 protein; Cell surface receptor that may play a role in the innate and adaptive immune response. Acts as a counter-receptor for CD276 and interaction with CD276 on T-cells enhances T-cell activation; V-set domain containing
TNC	P24821	1.33	[0.99; 1.78]	0.0544	0.2787	1.12	[0.85; 1.48]	0.4077	0.6733	1.08	[0.77; 1.5]	0.6488	0.9630	Tenascin; Extracellular matrix protein implicated in guidance of migrating neurons as well as axons during development, synaptic plasticity as well as neuronal regeneration. Promotes neurite outgrowth from cortical neurons grown on a monolayer of astrocytes. Ligand for integrins alpha-8/beta-1, alpha-9/beta-1, alpha-V/beta-3 and alpha-V/beta-6. In tumors, stimulates angiogenesis by elongation, migration and sprouting of endothelial cells; Belongs to the tenascin family

TNF	P01375	1.13	[0.8; 1.59]	0.4884	0.7584	1.01	[0.72; 1.41]	0.9558	0.9854	0.88	[0.59; 1.3]	0.5300	0.9589	Tumor necrosis factor; Cytokine that binds to TNFRSF1A/TNFR1 and TNFRSF1B/TNFR2. It is mainly secreted by macrophages and can induce cell death of certain tumor cell lines. It is potent pyrogen causing fever by direct action or by stimulation of interleukin-1 secretion and is implicated in the induction of cachexia. Under certain conditions it can stimulate cell proliferation and induce cell differentiation. Impairs regulatory T-cells (Treg) function in individuals with rheumatoid arthritis via FOXP3 dephosphorylation.
TNF-R1	P19438	1.88	[1.19; 3]	0.0069	0.0996	2.12	[1.37; 3.33]	0.0009	0.0418	1.35	[0.81; 2.27]	0.2493	0.8512	Tumor necrosis factor receptor superfamily member 1A; Receptor for TNFSF2/TNF-alpha and homotrimeric TNFSF1/lymphotoxin-alpha. The adapter molecule FADD recruits caspase-8 to the activated receptor. The resulting death-inducing signaling complex (DISC) performs caspase-8 proteolytic activation which initiates the subsequent cascade of caspases (aspartate-specific cysteine proteases) mediating apoptosis. Contributes to the induction of non-cytocidal TNF effects including anti-viral state and activation of the acid sphingomyelinase; CD molecules
TNF-R2	P20333	1.31	[0.89; 1.94]	0.1705	0.4712	1.43	[0.98; 2.09]	0.0624	0.2644	0.99	[0.63; 1.54]	0.9594	0.9766	Tumor necrosis factor receptor superfamily member 1B; Receptor with high affinity for TNFSF2/TNF-alpha and approximately 5-fold lower affinity for homotrimeric TNFSF1/lymphotoxin-alpha. The TRAF1/TRAF2 complex recruits the apoptotic suppressors BIRC2 and BIRC3 to TNFRSF1B/TNFR2. This receptor mediates most of the metabolic effects of TNF-alpha. Isoform 2 blocks TNF-alpha-induced apoptosis, which suggests that it regulates TNF-alpha function by antagonizing its biological activity; CD molecules
TNFRSF10C	O14798	0.79	[0.56; 1.12]	0.1923	0.4979	0.79	[0.57; 1.1]	0.1633	0.4100	0.84	[0.57; 1.25]	0.3955	0.8761	Tumor necrosis factor receptor superfamily member 10C; Receptor for the cytotoxic ligand TRAIL. Lacks a cytoplasmic death domain and hence is not capable of inducing apoptosis. May protect cells against TRAIL mediated apoptosis by competing with TRAIL-R1 and R2 for binding to the ligand; CD molecules
TNFRSF12A	Q9NP84	1.37	[0.95; 1.97]	0.0914	0.3211	1.37	[0.97; 1.95]	0.0743	0.2948	1.19	[0.78; 1.8]	0.4134	0.8761	Tumor necrosis factor receptor superfamily member 12A; Receptor for TNFSF12/TWEAK. Weak inducer of apoptosis in some cell types. Promotes angiogenesis and the proliferation of endothelial cells. May modulate cellular adhesion to matrix proteins; CD molecules
TNFRSF14	Q92956	1.37	[0.94; 2]	0.0986	0.3367	1.61	[1.12; 2.34]	0.0106	0.1041	1.28	[0.83; 1.95]	0.2623	0.8512	Tumor necrosis factor receptor superfamily member 14; Receptor for BTLA. Receptor for TNFSF14/LIGHT and homotrimeric TNFSF1/lymphotoxin-alpha. Involved in lymphocyte activation. Plays an important role in HSV pathogenesis because it enhanced the entry of several wild-type HSV strains of both serotypes into CHO cells, and mediated HSV entry into activated human T-cells; CD molecules

TNFRSF21	O75509	2.37	[1.22; 4.69]	0.0118	0.1524	2.24	[1.19; 4.24]	0.0125	0.1157	1.57	[0.75; 3.36]	0.2395	0.8512	Tumor necrosis factor receptor superfamily member 21; Promotes apoptosis, possibly via a pathway that involves the activation of NF-kappa-B. Can also promote apoptosis mediated by BAX and by the release of cytochrome c from the mitochondria into the cytoplasm. Plays a role in neuronal apoptosis, including apoptosis in response to amyloid peptides derived from APP, and is required for both normal cell body death and axonal pruning
TNFRSF4	P43489	1.63	[1.18; 2.28]	0.0033	0.0598	1.73	[1.25; 2.39]	0.0009	0.0418	1.24	[0.86; 1.78]	0.2420	0.8512	Tumor necrosis factor receptor superfamily member 4; Receptor for TNFSF4/OX40L/GP34. Is a costimulatory molecule implicated in long-term T-cell immunity; CD molecules
TNFRSF9	Q07011	1.33	[0.96; 1.84]	0.0836	0.3083	1.41	[1.03; 1.94]	0.0316	0.1729	1.48	[1.03; 2.12]	0.0325	0.8308	Tumor necrosis factor receptor superfamily member 9; Receptor for TNFSF9/4-1BBL. Possibly active during T cell activation; CD molecules
TNFSF13B	Q9Y275	1.59	[1.07; 2.37]	0.0214	0.1878	1.78	[1.21; 2.64]	0.0036	0.0891	1.18	[0.75; 1.83]	0.4641	0.9282	Tumor necrosis factor ligand superfamily member 13B; Cytokine that binds to TNFRSF13B/TACI and TNFRSF17/BCMA. TNFSF13/APRIL binds to the same 2 receptors. Together, they form a 2 ligands -2 receptors pathway involved in the stimulation of B- and T-cell function and the regulation of humoral immunity. A third B-cell specific BAFF-receptor (BAFFR/BR3) promotes the survival of mature B-cells and the B-cell response; CD molecules
TNFSF14	O43557	0.98	[0.79; 1.2]	0.8134	0.9137	0.96	[0.79; 1.17]	0.7205	0.8776	0.98	[0.77; 1.23]	0.8430	0.9730	Tumor necrosis factor ligand superfamily member 14; Cytokine that binds to TNFRSF3/LTBR. Binding to the decoy receptor TNFRSF6B modulates its effects. Activates NFKB, stimulates the proliferation of T-cells, and inhibits growth of the adenocarcinoma HT-29. Acts as a receptor for Herpes simplex virus; CD molecules
TNXB	P22105	0.84	[0.45; 1.54]	0.5769	0.7950	1.02	[0.57; 1.85]	0.9442	0.9854	1.77	[0.9; 3.42]	0.0924	0.8449	Tenascin-X; Appears to mediate interactions between cells and the extracellular matrix. Substrate-adhesion molecule that appears to inhibit cell migration. Accelerates collagen fibril formation. May play a role in supporting the growth of epithelial tumors; Fibrinogen C domain containing
TR	P02786	0.86	[0.66; 1.13]	0.2876	0.6408	0.90	[0.7; 1.16]	0.4264	0.6856	0.86	[0.63; 1.17]	0.3340	0.8622	Transferrin receptor protein 1; Cellular uptake of iron occurs via receptor-mediated endocytosis of ligand-occupied transferrin receptor into specialized endosomes. Endosomal acidification leads to iron release. The apotransferrin-receptor complex is then recycled to the cell surface with a return to neutral pH and the concomitant loss of affinity of apotransferrin for its receptor. Transferrin receptor is necessary for development of erythrocytes and the nervous system (By similarity).
TR-AP	P13686	0.91	[0.58; 1.42]	0.6714	0.8349	0.96	[0.62; 1.47]	0.8378	0.9326	1.16	[0.69; 1.94]	0.5726	0.9630	Tartrate-resistant acid phosphatase type 5; Involved in osteopontin/bone sialoprotein dephosphorylation. Its expression seems to increase in certain pathological states such as Gaucher and Hodgkin diseases, the hairy cell, the B-cell, and the T-cell leukemias; Belongs to the metallophosphoesterase superfamily. Purple acid phosphatase family

TRAIL	P50591	0.90	[0.54; 1.48]	0.6699	0.8349	1.03	[0.64; 1.66]	0.9108	0.9742	1.31	[0.74; 2.34]	0.3489	0.8622	Tumor necrosis factor ligand superfamily member 10; Cytokine that binds to TNFRSF10A/TRAILR1, TNFRSF10B/TRAILR2, TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and possibly also to TNFRSF11B/OPG. Induces apoptosis. Its activity may be modulated by binding to the decoy receptors TNFRSF10C/TRAILR3, TNFRSF10D/TRAILR4 and TNFRSF11B/OPG that cannot induce apoptosis; CD molecules
TWEAK	O43508	1.24	[0.81; 1.91]	0.3250	0.6688	1.25	[0.83; 1.89]	0.2851	0.5611	1.37	[0.84; 2.24]	0.2026	0.8512	Tumor necrosis factor ligand superfamily member 12; Binds to FN14 and possibly also to TNFRSF12/APO3. Weak inducer of apoptosis in some cell types. Mediates NF-kappa-B activation. Promotes angiogenesis and the proliferation of endothelial cells. Also involved in induction of inflammatory cytokines. Promotes IL8 secretion; Tumor necrosis factor superfamily
U-PAR	Q03405	1.03	[0.68; 1.54]	0.8885	0.9603	1.33	[0.9; 1.97]	0.1565	0.4053	1.38	[0.88; 2.17]	0.1575	0.8512	Urokinase plasminogen activator surface receptor; Acts as a receptor for urokinase plasminogen activator. Plays a role in localizing and promoting plasmin formation. Mediates the proteolysis-independent signal transduction activation effects of U-PA. It is subject to negative-feedback regulation by U-PA which cleaves it into an inactive form; CD molecules
UPA	P00749	1.42	[1; 2.1]	0.0603	0.2854	1.60	[1.1; 2.43]	0.0197	0.1534	1.23	[0.84; 1.79]	0.2682	0.8512	Urokinase-type plasminogen activator; Specifically cleaves the zymogen plasminogen to form the active enzyme plasmin
VASN	Q6EMK4	1.63	[0.84; 3.19]	0.1517	0.4339	2.12	[1.12; 4.04]	0.0212	0.1534	1.57	[0.74; 3.39]	0.2448	0.8512	Vasorin; May act as an inhibitor of TGF-beta signaling
VCAM1	P19320	2.10	[1.36; 3.25]	0.0008	0.0346	1.56	[1.04; 2.36]	0.0346	0.1771	1.18	[0.72; 1.91]	0.5124	0.9589	Vascular cell adhesion protein 1; Important in cell-cell recognition. Appears to function in leukocyte-endothelial cell adhesion. Interacts with integrin alpha-4/beta-1 (ITGA4/ITGB1) on leukocytes, and mediates both adhesion and signal transduction. The VCAM1/ITGA4/ITGB1 interaction may play a pathophysiologic role both in immune responses and in leukocyte emigration to sites of inflammation; C2-set domain containing
VEGFA	P15692	1.51	[1.02; 2.24]	0.0392	0.2352	1.42	[0.97; 2.08]	0.0732	0.2948	1.36	[0.88; 2.1]	0.1628	0.8512	Vascular endothelial growth factor A; Growth factor active in angiogenesis, vasculogenesis and endothelial cell growth. Induces endothelial cell proliferation, promotes cell migration, inhibits apoptosis and induces permeabilization of blood vessels. Binds to the FLT1/VEGFR1 and KDR/VEGFR2 receptors, heparan sulfate and heparin. NRP1/Neuropilin-1 binds isoforms VEGF-165 and VEGF-145. Isoform VEGF165B binds to KDR but does not activate downstream signaling pathways, does not activate angiogenesis and inhibits tumor growth.

VEGFR-2	P35968	1.18	[0.62; 2.26]	0.6172	0.8163	1.56	[0.84; 2.91]	0.1590	0.4075	2.15	[1.02; 4.68]	0.0486	0.8308	Vascular endothelial growth factor receptor 2; Tyrosine-protein kinase that acts as a cell-surface receptor for VEGFA, VEGFC and VEGFD. Plays an essential role in the regulation of angiogenesis, vascular development, vascular permeability, and embryonic hematopoiesis. Promotes proliferation, survival, migration and differentiation of endothelial cells. Promotes reorganization of the actin cytoskeleton. Isoforms lacking a transmembrane domain, such as isoform 2 and isoform 3, may function as decoy receptors for VEGFA, VEGFC and/or VEGFD
VWF	P04275	1.14	[0.9; 1.44]	0.2757	0.6408	1.18	[0.94; 1.47]	0.1561	0.4053	1.25	[0.95; 1.63]	0.1099	0.8512	Von Willebrand factor; Important in the maintenance of hemostasis, it promotes adhesion of platelets to the sites of vascular injury by forming a molecular bridge between sub-endothelial collagen matrix and platelet-surface receptor complex GPIb-IX-V. Also acts as a chaperone for coagulation factor VIII, delivering it to the site of injury, stabilizing its heterodimeric structure and protecting it from premature clearance from plasma; Endogenous ligands

Supplementary table 3. Patient characteristics for total population and individuals fulfilling inclusion and exclusion criteria.

Variable	Patients with available CT data (n=718)	Patients also with proteomic data fulfilling QA/QC requirements (n=662)	p-value
Demographic and behavioral			
Age [y]	50.9 ± 5.8	50.8 ± 5.8	0.79
Natal sex			0.85
Female	121 (17%)	115 (17%)	
Male	597 (83%)	547 (83%)	
Race			0.98
Asian	10 (1.4%)	8 (1.2%)	
Black or African American	249 (35%)	233 (35%)	
White	389 (54%)	354 (53%)	
Other	70 (9.7%)	67 (10%)	
Ethnicity			0.96
Hispanic or Latino	175 (25%)	163 (25%)	
Not Hispanic or Latino	534 (75%)	490 (75%)	
Smoking status			0.95
Current	169 (24%)	158 (24%)	
Former	225 (31%)	211 (32%)	
Never	323 (45%)	292 (44%)	
Substance use			0.99
Current	16 (2.2%)	14 (2.1%)	
Former	351 (49%)	324 (49%)	
Never	349 (49%)	322 (49%)	
Cardiovascular and metabolic			
ASCVD [%]	5.0 ± 3.2	4.9 ± 3.1	0.76
ASCVD risk group			>0.99
0-2.5	169 (24%)	156 (24%)	
2.5-5	237 (33%)	224 (34%)	
5-7.5	169 (24%)	154 (23%)	

7.5-10	99 (14%)	88 (13%)	
>10	44 (6.1%)	40 (6.0%)	
Family history of premature CVD	159 (23%)	145 (23%)	0.98
Hypertension	233 (32%)	213 (32%)	0.96
Diabetes	3 (0.4%)	3 (0.5%)	>0.99
BMI [kg/m ²]	27.3 ± 4.4	27.3 ± 4.3	0.92
Fasting glucose [mg/dL]	93.0 ± 12.5	92.9 ± 12.5	0.82
eGFR [mL/min/1.73m ²]	88.1 ± 16.3	88.4 ± 16.3	0.80
LDL-C [mg/mL]	108.2 ± 30.7	108.3 ± 30.5	0.96
HDL-C [mg/dL]	50.6 ± 18.6	50.9 ± 18.7	0.81
Triglycerides [mg/dL]	134.6 ± 85.4	133.6 ± 85.2	0.83
Prior statin use	57 (7.9%)	53 (8.0%)	>0.99
Prior antihypertensive medication	148 (21%)	133 (20%)	0.86
HIV-related health history			
Total ART use [y]	11.7 ± 6.6	11.6 ± 6.5	0.87
Entry ART regimen			>0.99
NRTI + INSTI	322 (45%)	293 (44%)	
NRTI + NNRTI	184 (26%)	167 (25%)	
NRTI + PI	122 (17%)	118 (18%)	
NRTI-sparing	20 (2.8%)	20 (3.0%)	
Other NRTI-containing	70 (9.7%)	64 (9.7%)	
HIV RNA [copies/mL]			0.97
<LLQ	623 (88%)	573 (88%)	
LLQ - 400	69 (9.7%)	65 (9.9%)	
400+	16 (2.3%)	16 (2.4%)	
CD4 category [cells/mm ³]	624.8 ± 273.9	624.2 ± 275.1	0.97
Nadir CD4 category [cells/mm ³]			>0.99
<50	155 (22%)	146 (23%)	
50-199	206 (30%)	192 (30%)	
200-349	193 (28%)	180 (28%)	
350+	141 (20%)	128 (20%)	

Data are presented as mean \pm standard deviations, or as frequencies and percentages. Continuous variables are compared using the t-test, while categorical parameters are compared using the chi-square test.

Supplementary table 4. Protein-protein interactions scores provided by the STRING database.

Protein 1	Protein 2	Combined score	Homology	Coexpression	Experimentally determined interaction	Database annotated	Automated textmining
AOC3	TNF-R1	0.32	0.00	0.00	0.00	0.00	0.32
AOC3	LTBR	0.23	0.00	0.00	0.00	0.00	0.23
AOC3	ST2	0.32	0.00	0.00	0.00	0.00	0.32
AOC3	NRP1	0.24	0.00	0.00	0.00	0.00	0.24
AOC3	NCR1	0.65	0.00	0.00	0.00	0.00	0.65
AOC3	VCAM1	0.48	0.00	0.07	0.00	0.00	0.47
AOC3	IL-6RA	0.24	0.00	0.00	0.00	0.00	0.24
AOC3	TNFSF13B	0.28	0.00	0.00	0.00	0.00	0.28
AOC3	TNFRSF4	0.40	0.00	0.00	0.00	0.00	0.40
CCL23	TNF-R1	0.18	0.00	0.06	0.00	0.00	0.16
CCL23	VCAM1	0.25	0.00	0.05	0.00	0.00	0.24
CCL23	IL-6RA	0.19	0.00	0.09	0.00	0.00	0.15
CCL23	TNFSF13B	0.19	0.00	0.09	0.00	0.00	0.15
CCL23	IL-18BP	0.17	0.00	0.06	0.00	0.00	0.16
CCL23	CCL24	0.66	0.00	0.11	0.00	0.00	0.64
CCL24	TNF-R1	0.31	0.00	0.06	0.00	0.00	0.29
CCL24	ST2	0.32	0.00	0.06	0.00	0.00	0.31
CCL24	GDF-15	0.21	0.00	0.00	0.00	0.00	0.21
CCL24	VCAM1	0.42	0.00	0.14	0.00	0.00	0.36
CCL24	IL-6RA	0.25	0.00	0.00	0.00	0.00	0.25
CCL24	TNFSF13B	0.23	0.00	0.00	0.00	0.00	0.23
CCL24	TNFRSF4	0.17	0.00	0.08	0.00	0.00	0.14
CCL24	IL-18BP	0.19	0.00	0.05	0.00	0.00	0.18
CCL24	CCL23	0.66	0.00	0.11	0.00	0.00	0.64
CST3	DCN	0.17	0.00	0.06	0.00	0.00	0.15
CST3	TNF-R1	0.24	0.00	0.07	0.00	0.00	0.22
CST3	ST2	0.16	0.00	0.00	0.00	0.00	0.16
CST3	GDF-15	0.57	0.00	0.00	0.00	0.00	0.57
CST3	VCAM1	0.38	0.00	0.06	0.00	0.00	0.37
CST3	IGFBP-7	0.62	0.00	0.10	0.00	0.00	0.60
CST3	PGF	0.24	0.00	0.00	0.00	0.00	0.24
DCN	OSMR	0.15	0.00	0.14	0.00	0.00	0.06
DCN	GDF-15	0.16	0.00	0.00	0.06	0.00	0.14
DCN	CST3	0.17	0.00	0.06	0.00	0.00	0.15
DCN	MEPE	0.32	0.00	0.00	0.00	0.00	0.32
DCN	VCAM1	0.38	0.00	0.19	0.00	0.00	0.26
DCN	IGFBP-7	0.49	0.00	0.32	0.16	0.00	0.18
DCN	PLC	0.99	0.00	0.10	0.07	0.90	0.85
GDF-15	DCN	0.16	0.00	0.00	0.06	0.00	0.14
GDF-15	TNF-R1	0.23	0.00	0.06	0.00	0.00	0.21
GDF-15	LTBR	0.16	0.00	0.08	0.00	0.00	0.12
GDF-15	ST2	0.28	0.00	0.00	0.00	0.00	0.28
GDF-15	IL-6RA	0.15	0.00	0.00	0.00	0.00	0.15
GDF-15	CCL24	0.21	0.00	0.00	0.00	0.00	0.21
GDF-15	VCAM1	0.24	0.00	0.00	0.00	0.00	0.24
GDF-15	IGFBP-7	0.31	0.00	0.00	0.00	0.00	0.31
GDF-15	PGF	0.34	0.00	0.00	0.00	0.00	0.34
GDF-15	CST3	0.57	0.00	0.00	0.00	0.00	0.57
IGFBP-7	DCN	0.49	0.00	0.32	0.16	0.00	0.18
IGFBP-7	GDF-15	0.31	0.00	0.00	0.00	0.00	0.31
IGFBP-7	VCAM1	0.19	0.00	0.10	0.00	0.00	0.13
IGFBP-7	PLC	0.35	0.00	0.12	0.23	0.00	0.13

IGFBP-7	CST3	0.62	0.00	0.10	0.00	0.00	0.60
IL-18BP	TNF-R1	0.26	0.00	0.06	0.00	0.00	0.25
IL-18BP	ST2	0.27	0.00	0.00	0.00	0.00	0.27
IL-18BP	NCR1	0.17	0.00	0.00	0.00	0.00	0.17
IL-18BP	VCAM1	0.32	0.00	0.06	0.00	0.00	0.31
IL-18BP	IL-6RA	0.18	0.00	0.00	0.00	0.00	0.18
IL-18BP	TNFSF13B	0.20	0.00	0.00	0.00	0.00	0.20
IL-18BP	CCL23	0.17	0.00	0.06	0.00	0.00	0.16
IL-18BP	CCL24	0.19	0.00	0.05	0.00	0.00	0.18
IL-6RA	TNF-R1	0.69	0.00	0.06	0.00	0.00	0.68
IL-6RA	LTBR	0.20	0.00	0.07	0.00	0.00	0.18
IL-6RA	ST2	0.33	0.00	0.00	0.00	0.00	0.33
IL-6RA	GDF-15	0.15	0.00	0.00	0.00	0.00	0.15
IL-6RA	OSMR	0.41	0.00	0.00	0.00	0.00	0.41
IL-6RA	VCAM1	0.37	0.00	0.00	0.00	0.00	0.37
IL-6RA	AOC3	0.24	0.00	0.00	0.00	0.00	0.24
IL-6RA	IL-18BP	0.18	0.00	0.00	0.00	0.00	0.18
IL-6RA	CCL23	0.19	0.00	0.09	0.00	0.00	0.15
IL-6RA	CCL24	0.25	0.00	0.00	0.00	0.00	0.25
IL-6RA	TNFRSF4	0.29	0.00	0.07	0.00	0.00	0.27
IL-6RA	TNFSF13B	0.41	0.00	0.07	0.00	0.00	0.39
LTBR	TNF-R1	0.80	0.58	0.70	0.00	0.00	0.80
LTBR	GDF-15	0.16	0.00	0.08	0.00	0.00	0.12
LTBR	IL-6RA	0.20	0.00	0.07	0.00	0.00	0.18
LTBR	TNFRSF4	0.21	0.60	0.00	0.00	0.00	0.46
LTBR	AOC3	0.23	0.00	0.00	0.00	0.00	0.23
LTBR	NCR1	0.24	0.00	0.00	0.00	0.00	0.24
LTBR	VCAM1	0.53	0.00	0.00	0.00	0.00	0.53
LTBR	TNFSF13B	0.84	0.00	0.00	0.00	0.60	0.62
MEPE	DCN	0.32	0.00	0.00	0.00	0.00	0.32
MEPE	TNF-R1	0.21	0.00	0.00	0.00	0.00	0.21
MEPE	PLC	0.17	0.00	0.00	0.00	0.00	0.17
NCR1	TNF-R1	0.17	0.00	0.00	0.00	0.00	0.17
NCR1	LTBR	0.24	0.00	0.00	0.00	0.00	0.24
NCR1	ST2	0.37	0.00	0.00	0.00	0.00	0.37
NCR1	PGF	0.17	0.00	0.00	0.00	0.00	0.17
NCR1	IL-18BP	0.17	0.00	0.00	0.00	0.00	0.17
NCR1	TNFSF13B	0.20	0.00	0.07	0.00	0.00	0.18
NCR1	VCAM1	0.20	0.00	0.00	0.00	0.00	0.20
NCR1	TNFRSF4	0.29	0.00	0.00	0.00	0.00	0.29
NCR1	AOC3	0.65	0.00	0.00	0.00	0.00	0.65
NRP1	TNF-R1	0.28	0.00	0.06	0.00	0.00	0.26
NRP1	AOC3	0.24	0.00	0.00	0.00	0.00	0.24
NRP1	TNFSF13B	0.27	0.00	0.00	0.00	0.00	0.27
NRP1	TNFRSF4	0.33	0.00	0.00	0.00	0.00	0.33
NRP1	VCAM1	0.37	0.00	0.08	0.00	0.00	0.34
NRP1	PLC	0.60	0.00	0.10	0.00	0.00	0.57
NRP1	PGF	0.99	0.00	0.00	0.27	0.00	0.99
OSMR	DCN	0.15	0.00	0.14	0.00	0.00	0.06
OSMR	TNF-R1	0.17	0.00	0.08	0.00	0.00	0.14
OSMR	VCAM1	0.20	0.00	0.10	0.00	0.00	0.14
OSMR	IL-6RA	0.41	0.00	0.00	0.00	0.00	0.41
PGF	TNF-R1	0.28	0.00	0.00	0.00	0.00	0.28
PGF	GDF-15	0.34	0.00	0.00	0.00	0.00	0.34
PGF	NRP1	0.99	0.00	0.00	0.27	0.00	0.99
PGF	NCR1	0.17	0.00	0.00	0.00	0.00	0.17
PGF	VCAM1	0.51	0.00	0.00	0.00	0.00	0.51

PGF	PLC	0.21	0.00	0.07	0.00	0.00	0.19
PGF	TNFSF13B	0.38	0.00	0.00	0.00	0.00	0.38
PGF	CST3	0.24	0.00	0.00	0.00	0.00	0.24
PLC	DCN	0.99	0.00	0.10	0.07	0.90	0.85
PLC	TNF-R1	0.17	0.00	0.07	0.00	0.00	0.14
PLC	NRP1	0.60	0.00	0.10	0.00	0.00	0.57
PLC	VCAM1	0.17	0.57	0.08	0.00	0.00	0.27
PLC	IGFBP-7	0.35	0.00	0.12	0.23	0.00	0.13
PLC	MEPE	0.17	0.00	0.00	0.00	0.00	0.17
PLC	PGF	0.21	0.00	0.07	0.00	0.00	0.19
SERPINA5	TNFSF13B	0.19	0.00	0.00	0.00	0.00	0.19
ST2	TNF-R1	0.23	0.00	0.00	0.00	0.00	0.23
ST2	CST3	0.16	0.00	0.00	0.00	0.00	0.16
ST2	TNFRSF4	0.24	0.00	0.00	0.00	0.00	0.25
ST2	TNFSF13B	0.25	0.00	0.06	0.00	0.00	0.23
ST2	VCAM1	0.25	0.00	0.08	0.00	0.00	0.22
ST2	IL-18BP	0.27	0.00	0.00	0.00	0.00	0.27
ST2	GDF-15	0.28	0.00	0.00	0.00	0.00	0.28
ST2	AOC3	0.32	0.00	0.00	0.00	0.00	0.32
ST2	CCL24	0.32	0.00	0.06	0.00	0.00	0.31
ST2	IL-6RA	0.33	0.00	0.00	0.00	0.00	0.33
ST2	NCR1	0.37	0.00	0.00	0.00	0.00	0.37
TNF-R1	PLC	0.17	0.00	0.07	0.00	0.00	0.14
TNF-R1	NCR1	0.17	0.00	0.00	0.00	0.00	0.17
TNF-R1	OSMR	0.17	0.00	0.08	0.00	0.00	0.14
TNF-R1	CCL23	0.18	0.00	0.06	0.00	0.00	0.16
TNF-R1	MEPE	0.21	0.00	0.00	0.00	0.00	0.21
TNF-R1	GDF-15	0.23	0.00	0.06	0.00	0.00	0.21
TNF-R1	ST2	0.23	0.00	0.00	0.00	0.00	0.23
TNF-R1	CST3	0.24	0.00	0.07	0.00	0.00	0.22
TNF-R1	IL-18BP	0.26	0.00	0.06	0.00	0.00	0.25
TNF-R1	PGF	0.28	0.00	0.00	0.00	0.00	0.28
TNF-R1	NRP1	0.28	0.00	0.06	0.00	0.00	0.26
TNF-R1	CCL24	0.31	0.00	0.06	0.00	0.00	0.29
TNF-R1	AOC3	0.32	0.00	0.00	0.00	0.00	0.32
TNF-R1	TNFSF13B	0.56	0.00	0.00	0.00	0.00	0.56
TNF-R1	VCAM1	0.60	0.00	0.00	0.00	0.00	0.60
TNF-R1	IL-6RA	0.69	0.00	0.06	0.00	0.00	0.68
TNF-R1	LTBR	0.80	0.58	0.70	0.00	0.00	0.80
TNF-R1	TNFRSF4	0.84	0.00	0.00	0.00	0.00	0.84
TNFRSF4	TNF-R1	0.84	0.00	0.00	0.00	0.00	0.84
TNFRSF4	LTBR	0.21	0.60	0.00	0.00	0.00	0.46
TNFRSF4	ST2	0.24	0.00	0.00	0.00	0.00	0.25
TNFRSF4	NRP1	0.33	0.00	0.00	0.00	0.00	0.33
TNFRSF4	NCR1	0.29	0.00	0.00	0.00	0.00	0.29
TNFRSF4	VCAM1	0.27	0.00	0.00	0.00	0.00	0.27
TNFRSF4	AOC3	0.40	0.00	0.00	0.00	0.00	0.40
TNFRSF4	IL-6RA	0.29	0.00	0.07	0.00	0.00	0.27
TNFRSF4	TNFSF13B	0.45	0.00	0.08	0.00	0.00	0.43
TNFSF13B	TNF-R1	0.56	0.00	0.00	0.00	0.00	0.56
TNFSF13B	LTBR	0.84	0.00	0.00	0.00	0.60	0.62
TNFSF13B	ST2	0.25	0.00	0.06	0.00	0.00	0.23
TNFSF13B	NRP1	0.27	0.00	0.00	0.00	0.00	0.27
TNFSF13B	NCR1	0.20	0.00	0.07	0.00	0.00	0.18
TNFSF13B	VCAM1	0.52	0.00	0.07	0.00	0.00	0.50
TNFSF13B	AOC3	0.28	0.00	0.00	0.00	0.00	0.28
TNFSF13B	SERPINA5	0.19	0.00	0.00	0.00	0.00	0.19
TNFSF13B	IL-6RA	0.41	0.00	0.07	0.00	0.00	0.39

TNFSF13B	CCL23	0.19	0.00	0.09	0.00	0.00	0.15
TNFSF13B	IL-18BP	0.20	0.00	0.00	0.00	0.00	0.20
TNFSF13B	CCL24	0.23	0.00	0.00	0.00	0.00	0.23
TNFSF13B	PGF	0.38	0.00	0.00	0.00	0.00	0.38
TNFSF13B	TNFRSF4	0.45	0.00	0.08	0.00	0.00	0.43
VCAM1	DCN	0.38	0.00	0.19	0.00	0.00	0.26
VCAM1	TNF-R1	0.60	0.00	0.00	0.00	0.00	0.60
VCAM1	LTBR	0.53	0.00	0.00	0.00	0.00	0.53
VCAM1	ST2	0.25	0.00	0.08	0.00	0.00	0.22
VCAM1	GDF-15	0.24	0.00	0.00	0.00	0.00	0.24
VCAM1	NRP1	0.37	0.00	0.08	0.00	0.00	0.34
VCAM1	OSMR	0.20	0.00	0.10	0.00	0.00	0.14
VCAM1	NCR1	0.20	0.00	0.00	0.00	0.00	0.20
VCAM1	PLC	0.17	0.57	0.08	0.00	0.00	0.27
VCAM1	IGFBP-7	0.19	0.00	0.10	0.00	0.00	0.13
VCAM1	CCL23	0.25	0.00	0.05	0.00	0.00	0.24
VCAM1	TNFRSF4	0.27	0.00	0.00	0.00	0.00	0.27
VCAM1	IL-18BP	0.32	0.00	0.06	0.00	0.00	0.31
VCAM1	IL-6RA	0.37	0.00	0.00	0.00	0.00	0.37
VCAM1	CST3	0.38	0.00	0.06	0.00	0.00	0.37
VCAM1	CCL24	0.42	0.00	0.14	0.00	0.00	0.36
VCAM1	AOC3	0.48	0.00	0.07	0.00	0.00	0.47
VCAM1	PGF	0.51	0.00	0.00	0.00	0.00	0.51
VCAM1	TNFSF13B	0.52	0.00	0.07	0.00	0.00	0.50

Supplementary table 5. Association of significant proteins with immune function indices.

Protein	Nadir CD4 (p-value)	CD4 (p-value)	Viral Load (p-value)	
AOC3	0.484	0.53	0.25	
CCL23	0.216	0.071	0.81	
CCL24	0.345	0.477	0.31	
CST3	0.063	0.021	0.14	CST3 is highest in those with lowest CD4
DCN	0.828	0.126	0.03	DCN is highest in those with undetectable viral load
GDF-15	0.006	0.429	0.83	GDF-15 is highest in those with lowest nadir CD4
IGFBP-7	0.248	0.623	0.57	
IL-18BP	0.498	0.004	0.11	IL-18BP is highest in those with lowest CD4
IL-6RA	0.424	0.042	0.83	IL-6RA is highest in those with lowest CD4
LTBR	0.244	0.056	0.53	
MEPE	0.846	0.086	0.11	
NCR1	0.501	0.036	0.82	NCR1 is highest in those with lowest CD4
NRP1	0.28	0.49	0.18	
OSMR	0.282	0.28	0.18	
PGF	0.654	0.184	0.95	
PLC	0.208	0.023	0.28	PLC is highest in those with lowest CD4
REG1A	0.118	0.061	0.18	
SERPINA5	0.023	0.063	0.13	SERPINA5 is highest in those with nadir CD4 of 50-199
ST2	0.057	0.179	0.36	
TNF-R1	0.476	0.007	0.71	TNF-R1 is highest in those with lowest CD4
TNFRSF4	0.941	0.006	0.53	TNFRSF4 is highest in those with lowest CD4
TNFSF13B	0.74	0.142	0.75	
VCAM1	0.924	0.274	0.05	