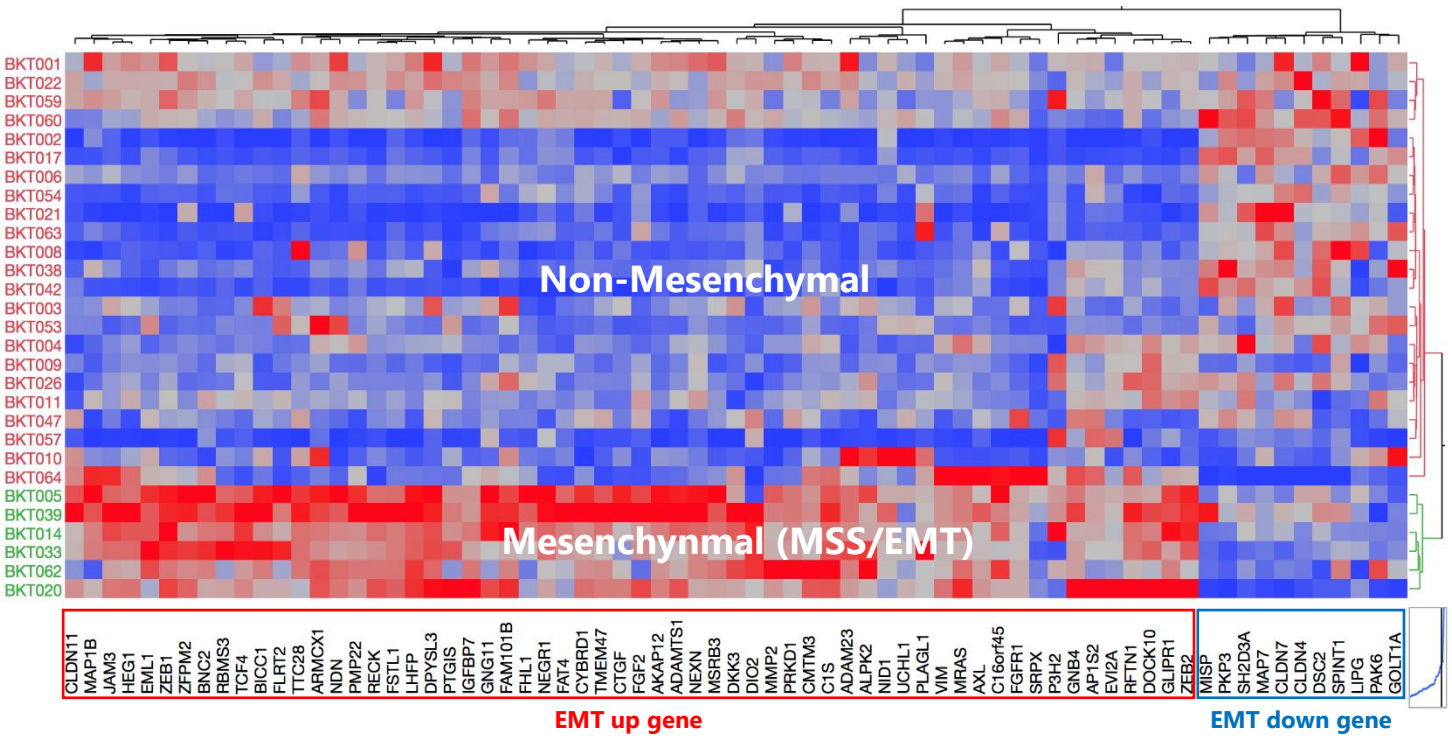
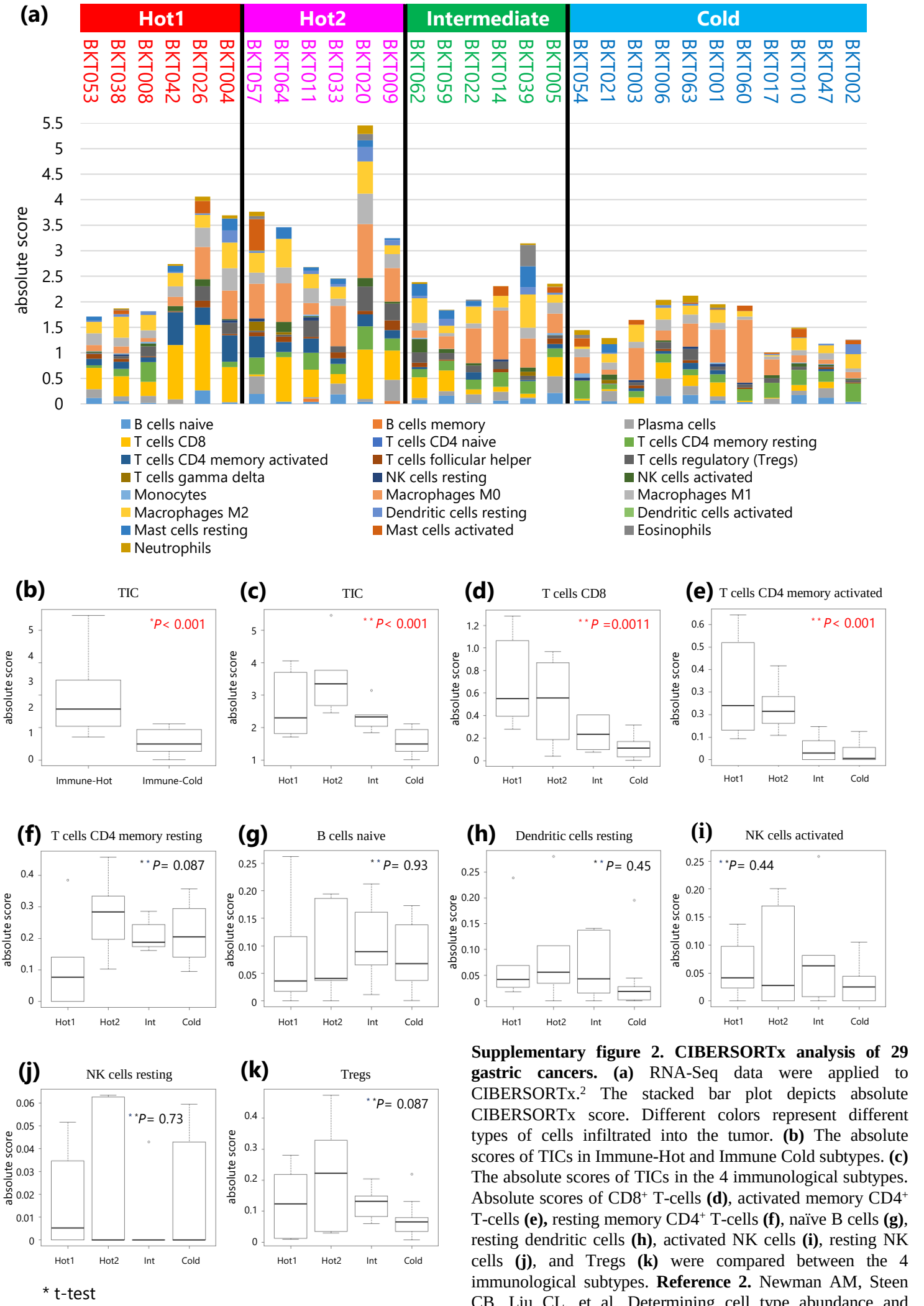


Supplementary figure 1. Hierarchical clustering of 29 gastric cancers for epithelial-mesenchymal transition (EMT).
According to the expression analysis of 71 genes reported by the Asian Cancer Research Group (ACRG), gastric cancer was divided into Mesenchymal or Non-Mesenchymal subtypes.[1]

Reference

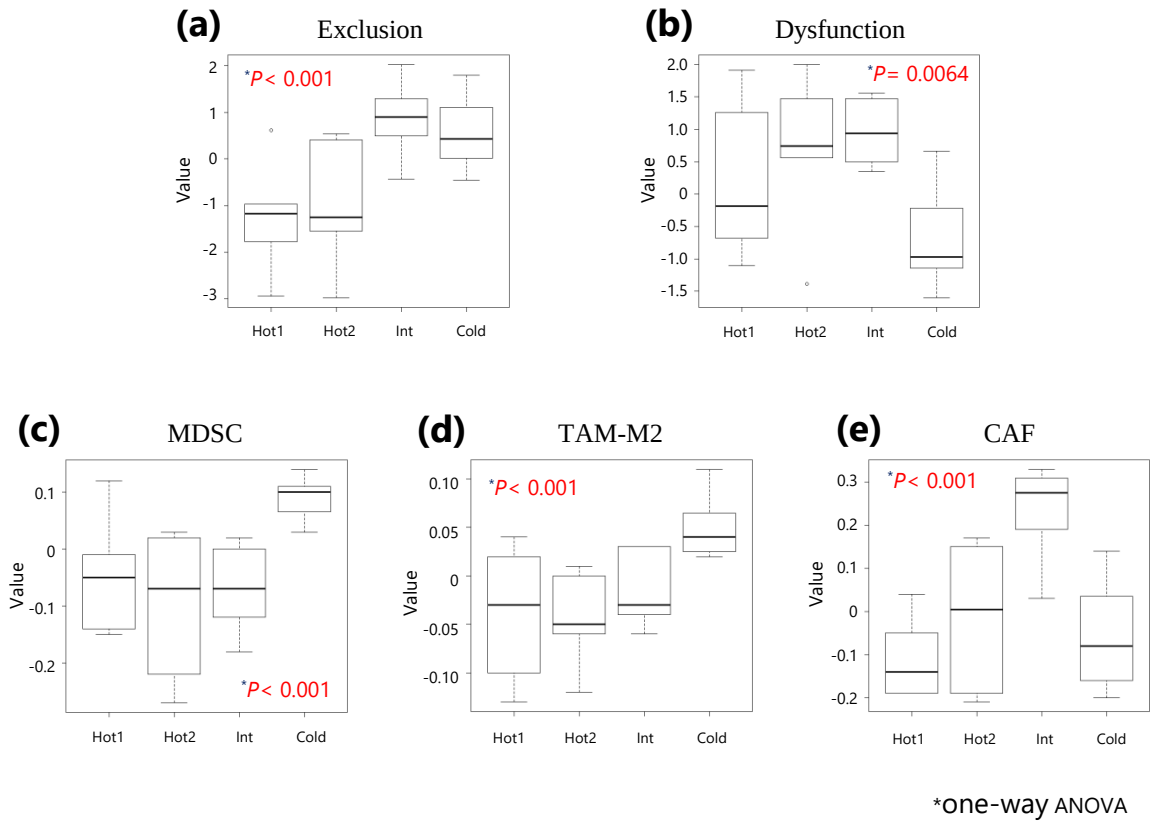
1. Lee J, Cristescu R, Kim KM, *et al.* Development of mesenchymal subtype gene signature for clinical application in gastric cancer. *Oncotarget*. 2017;**8**:66305-66315.



* t-test

* *one-way ANOVA

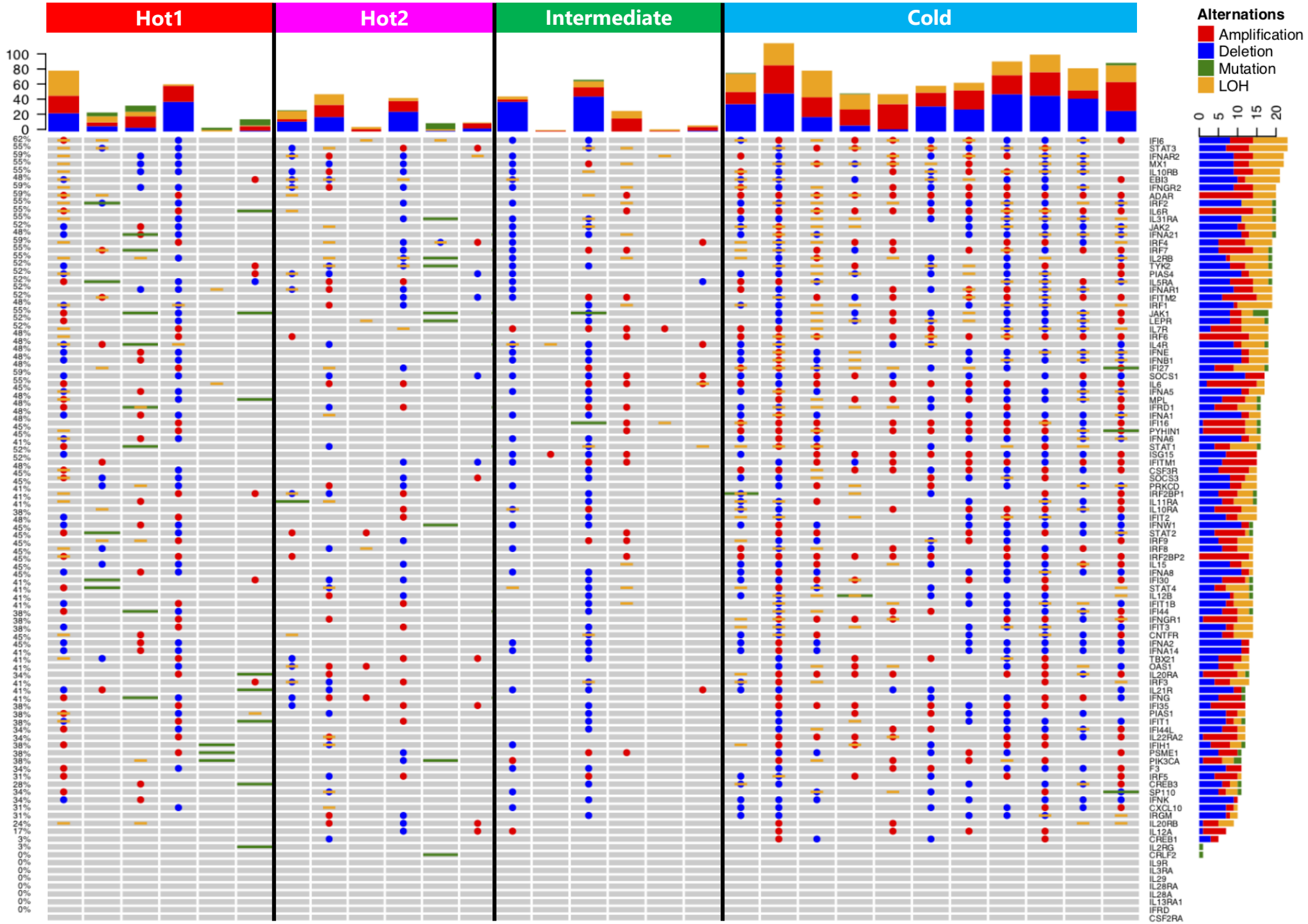
Supplementary figure 2. CIBERSORTx analysis of 29 gastric cancers. (a) RNA-Seq data were applied to CIBERSORTx.[2] The stacked bar plot depicts absolute CIBERSORTx score. Different colors represent different types of cells infiltrated into the tumor. **(b)** The absolute scores of TICs in Immune-Hot and Immune Cold subtypes. **(c)** The absolute scores of TICs in the 4 immunological subtypes. Absolute scores of $CD8^+$ T-cells **(d)**, activated memory $CD4^+$ T-cells **(e),** resting memory $CD4^+$ T-cells **(f)**, naïve B cells **(g)**, resting dendritic cells **(h)**, activated NK cells **(i)**, resting NK cells **(j)**, and Tregs **(k)** were compared between the 4 immunological subtypes. **Reference 2.** Newman AM, Steen CB, Liu CL, et al. Determining cell type abundance and expression from bulk tissues with digital cytometry. Nature Biotechnology. 2019;37:773-782.



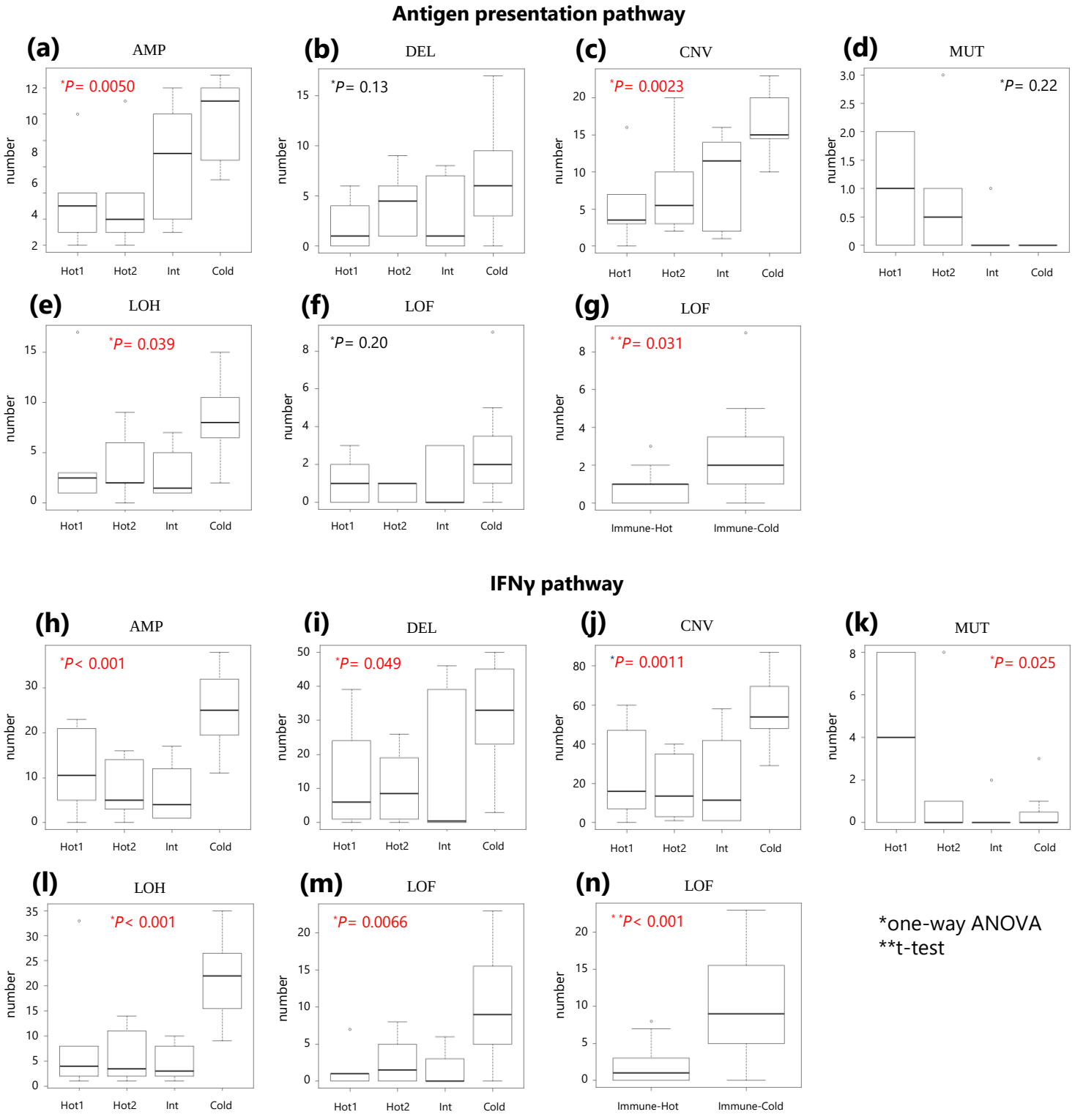
Supplementary figure 3. TIDE analysis of 29 gastric cancers.
The immunosuppressive tumor microenvironment was evaluated on the basis of gene expression using the TIDE web application (http://tide.dfci.harvard.edu/.).[3] **(a)** Exclusion values of TIDE for the 4 immunological subtypes, **(b)** Dysfunction values of TIDE for the 4 immunological subtypes, **(c)** MDSC signatures, **(d)** TAM-M2, **(e)** CAF signatures.

Reference

3. Jiang P, Gu S, Pan D, *et al.* Signatures of T cell dysfunction and exclusion predict cancer immunotherapy response. *Nature Medicine*. 2018;**24**:1550-1558.



Supplementary figure 4. Summary of nucleotide and copy number variants found in the IFNγ pathway. Stacked bar plot summarizing the total numbers of amplification, deletion, mutation, and LOH per patient (longitudinal) or per gene (horizontal). Different colors represent different types of nucleotide variants, red for amplification, blue for deletion, green for mutation and yellow for LOH.



Supplementary figure 5. Nucleotide and copy number variants found in the antigen presentation pathway and IFNγ pathway.

(a) The numbers of amplified genes (AMP) associated with antigen presentation pathway in the 4 immunological subtypes.

(b) The numbers of deleted genes (DEL) related to the antigen presentation pathway in the 4 immunological subtypes.

(c) Copy number variants (CNV) associated with the antigen presentation pathway between 4 immunological subtypes.

(d) The numbers of gene mutations (MUT) associated with the antigen presentation pathway between 4 immunological subtypes.

(e) The numbers of loss of heterozygosity (LOH) associated with the antigen presentation pathway between 4 immunological subtypes.

(f) The numbers of loss of function of genes (LOF) associated with the antigen presentation pathway between 4 immunological subtypes.

(g) The numbers of LOF associated with the antigen presentation pathway between Immune-Hot and Immune-Cold subtypes.

(h) The numbers of AMP associated with the IFNγ pathway between 4 immunological subtypes.

(i) The numbers of DEL associated with the IFNγ pathway between 4 immunological subtypes.

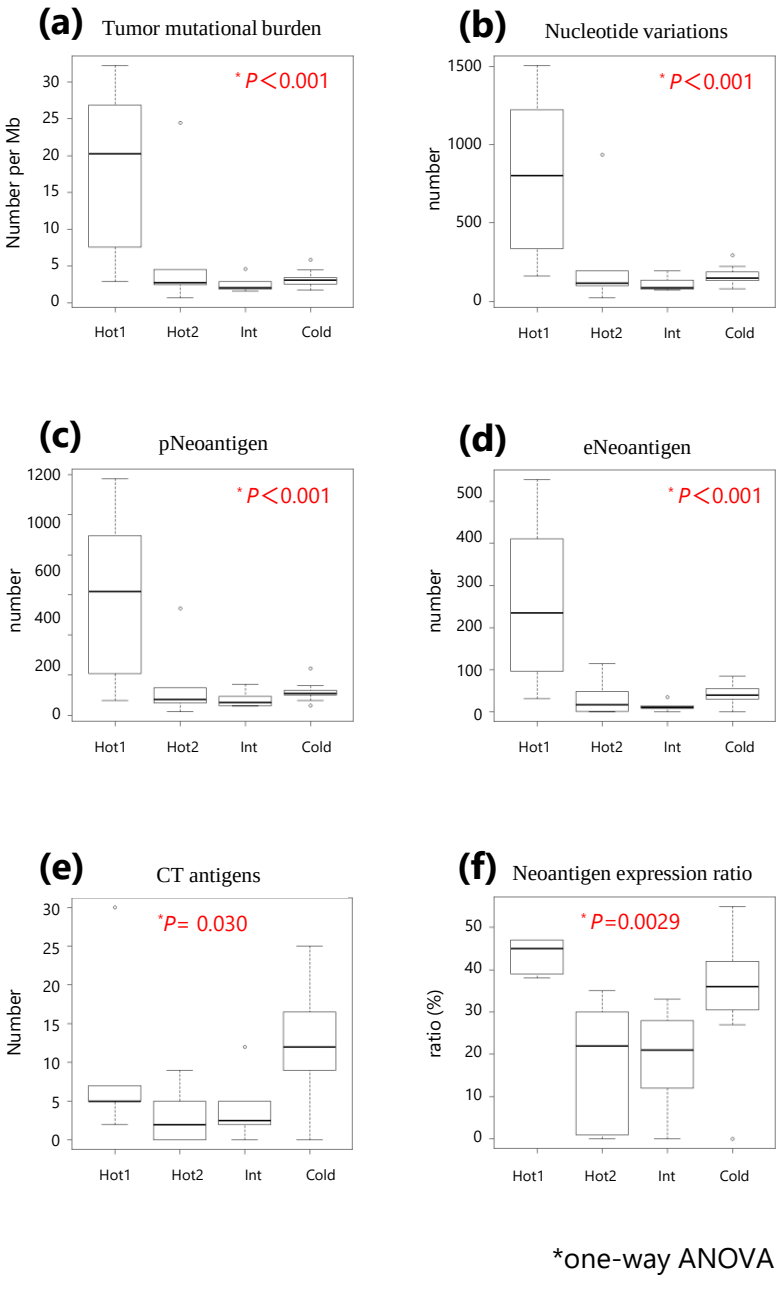
(j) The numbers of CNV associated with the IFNγ pathway between 4 immunological subtypes.

(k) The numbers of MUT associated with the IFNγ pathway between 4 immunological subtypes.

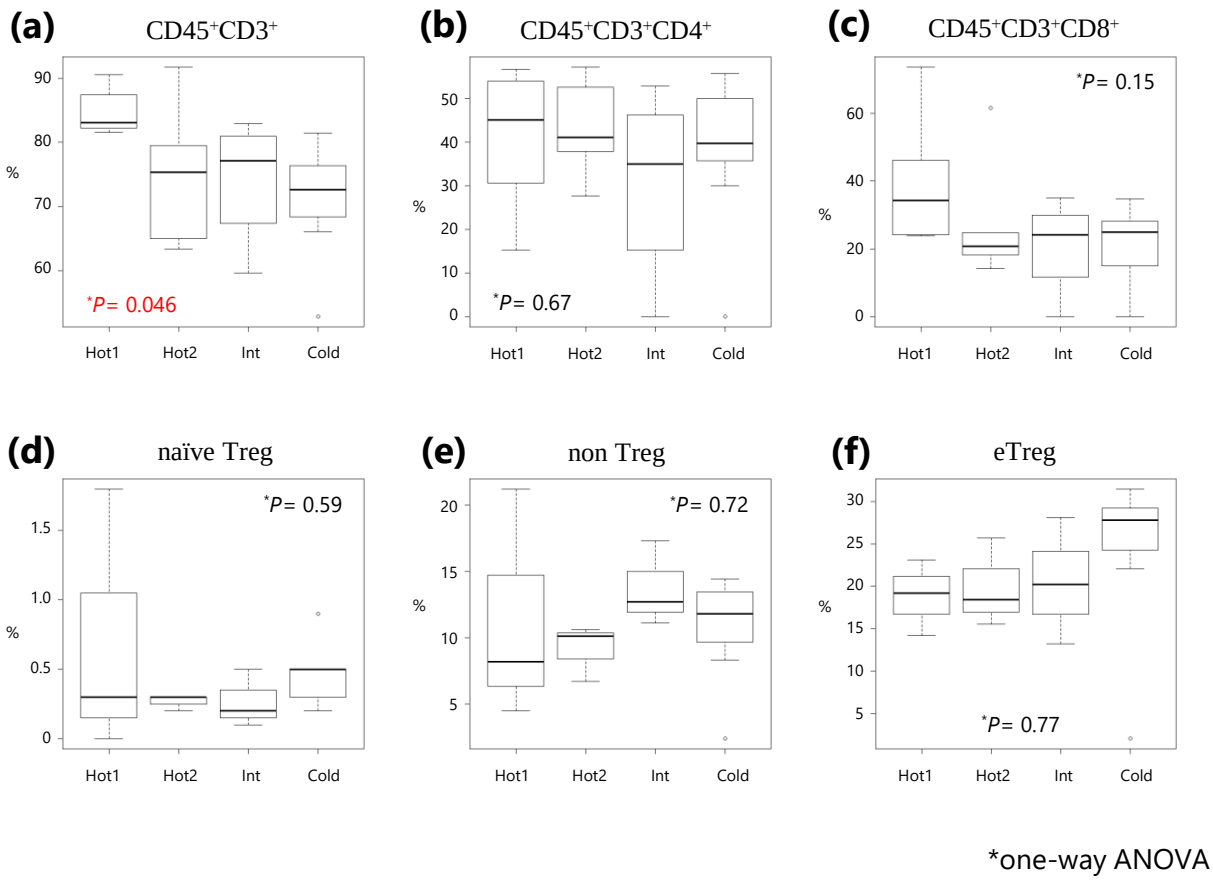
(l) The numbers of LOH associated with the IFNγ pathway between 4 immunological subtypes.

(m) The numbers of LOF associated with the IFNγ pathway between 4 immunological subtypes.

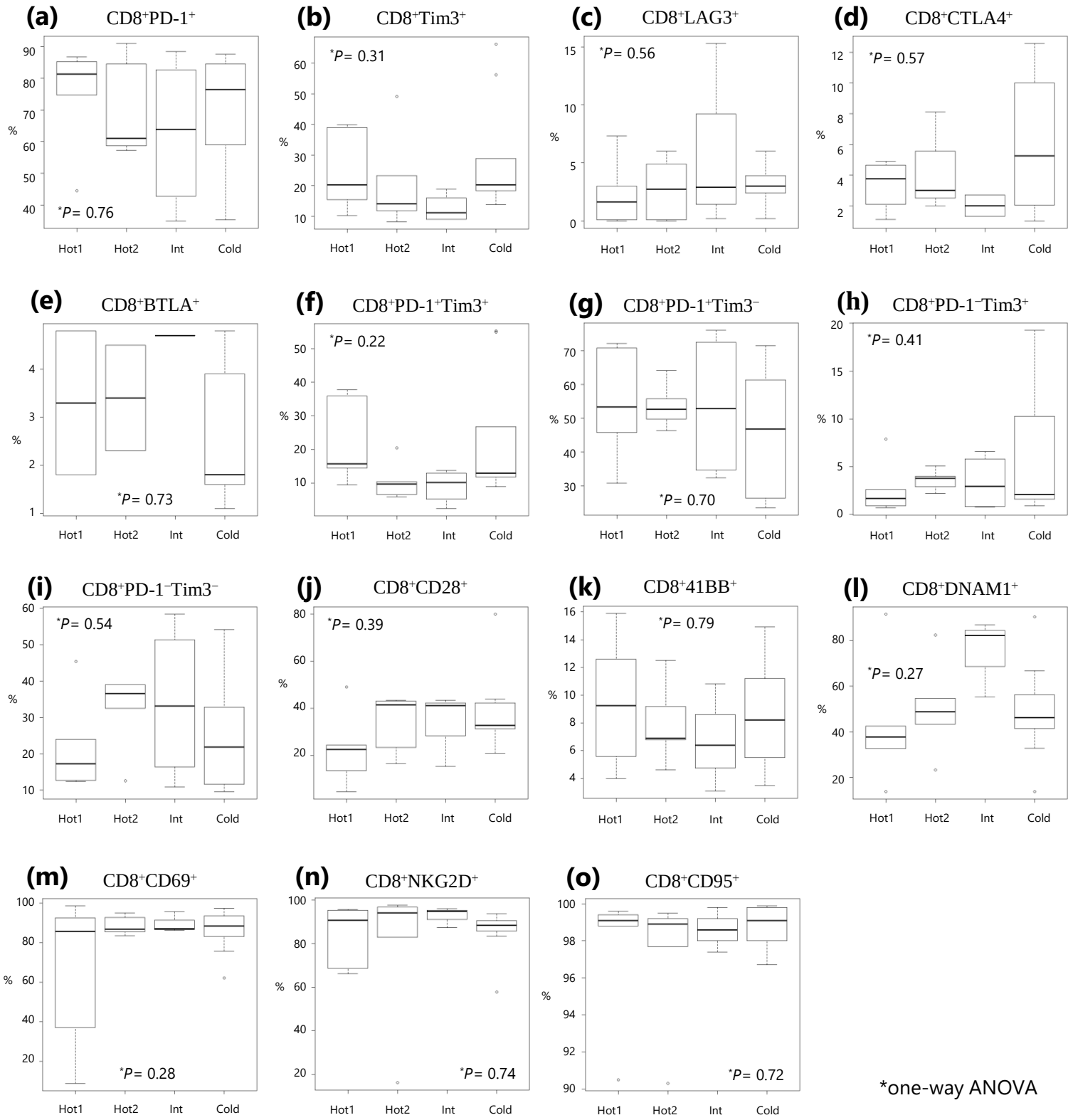
(n) The numbers of LOF associated with the IFNγ pathway between Immune-Hot and Immune-Cold subtypes.



Supplementary figure 6. Neoantigens and CT antigens.
(a) Tumor mutational burden (TMB) between the 4 immunological subtypes.
(b) The numbers of nucleotide variations between the 4 immunological subtypes.
(c) The numbers of predicted neoantigens (pNeoAg) between 4 immunological subtypes.
(d) The numbers of expressed neoantigens (eNeoAg) between 4 immunological subtypes.
(e) The numbers of CT antigens between 4 immunological subtypes.
(f) The neoantigen expression ratios in Immune-Hot and Immune-Cold subtypes.

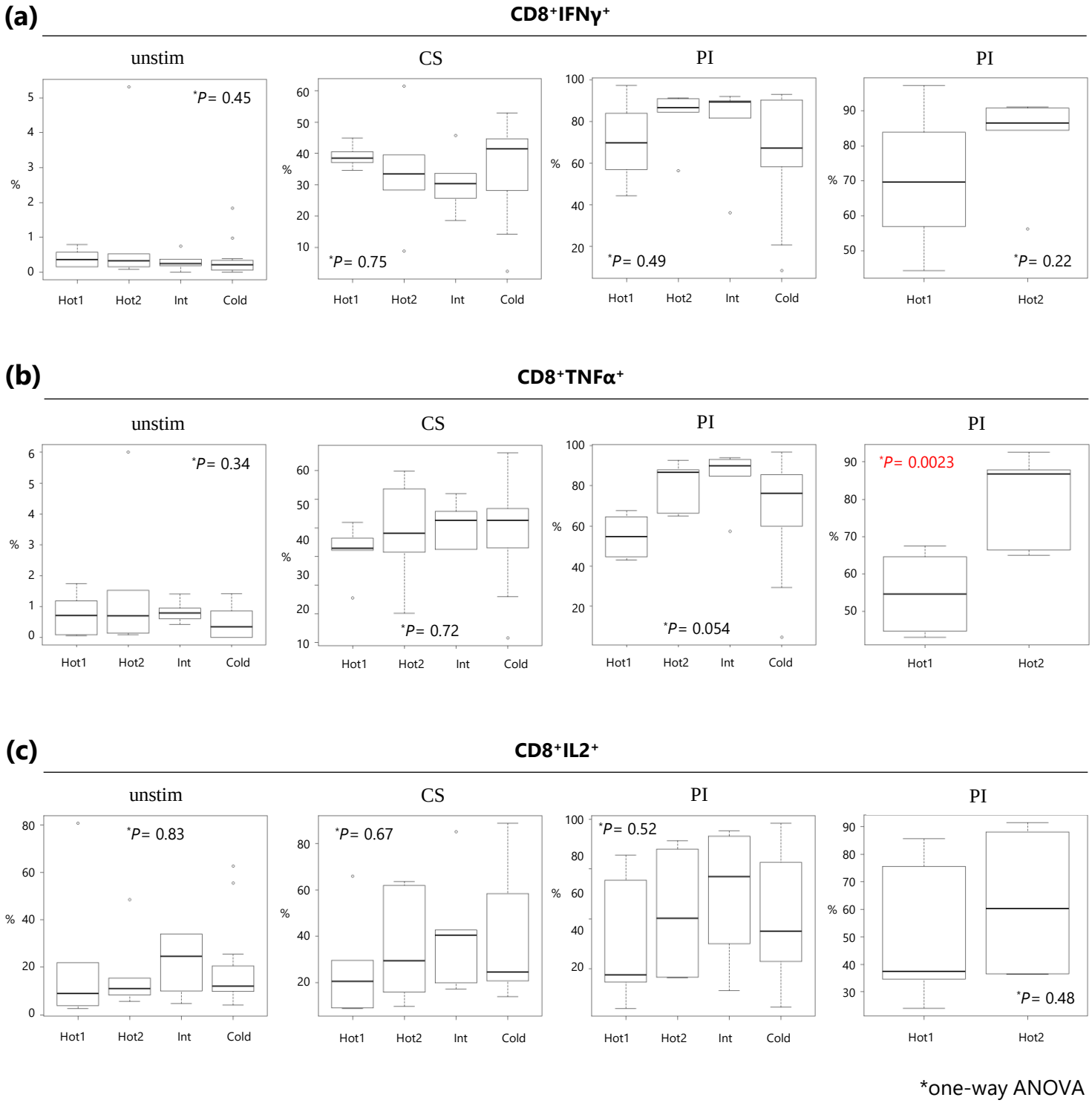


Supplementary figure 7. FACS analysis of TICs.
(a) The percentages of $CD45^+CD3^+$ T-cells in tumor infiltrating cells (TICs) between 4 immunological subtypes.
(b) The percentages of $CD45^+CD3^+CD4^+$T-cells in TICs between 4 immunological subtypes.
(c) The percentages of $CD45^+CD3^+CD8^+$T-cells in TICs between 4 immunological subtypes.
(d) The percentages of $CD45^+CD3^+CD4^+Foxp^+CD45RA^+$ naive regulatory T cells (naive Treg) in TICs between 4 immunological subtypes.
(e) The percentages of $CD45^+CD3^+CD4^+Foxp^+CD45RA^-$ nonTregs in TICs between 4 immunological subtypes.
(f) The percentages of $CD45^+CD3^+CD4^+Foxp^{++}CD45RA^-$ effector Tregs (eTreg) in TICs between 4 immunological subtypes.



Supplementary figure 8. CD8⁺ T-cell phenotypes.

(a) The percentages of CD8⁺PD-1⁺ T-cells in TICs between 4 immunological subtypes.
(b) The percentages of CD8⁺Tim3⁺ T-cells in TICs between 4 immunological subtypes.
(c) The percentages of CD8⁺LAG3⁺ T-cells in TICs between 4 immunological subtypes.
(d) The percentages of CD8⁺CTLA4⁺ T-cells in TICs between 4 immunological subtypes.
(e) The percentages of CD8⁺BTLA⁺ T-cells in TICs between 4 immunological subtypes.
(f) The percentages of CD8⁺PD-1⁺Tim3⁺ T-cells in TICs between 4 immunological subtypes.
(g) The percentages of CD8⁺PD-1⁺Tim3⁻ T-cells in TICs between 4 immunological subtypes.
(h) The percentages of CD8⁺PD-1⁻Tim3⁺ T-cells in TICs between 4 immunological subtypes.
(i) The percentages of CD8⁺PD-1⁻Tim3⁻ T-cells in TICs between 4 immunological subtypes.
(j) The percentages of CD8⁺CD28⁺ T-cells in TICs between 4 immunological subtypes.
(k) The percentages of CD8⁺4-1BB⁺ T-cells in TICs between 4 immunological subtypes.
(l) The percentages of CD8⁺DNAM1⁺ T-cells in TICs between 4 immunological subtypes.
(m) The percentages of CD8⁺CD69⁺ T-cells in TICs between 4 immunological subtypes.
(n) The percentages of CD8⁺NKG2D⁺ T-cells in TICs between 4 immunological subtypes.
(o) The percentages of CD8⁺CD95⁺ T-cells in TICs between 4 immunological subtypes.



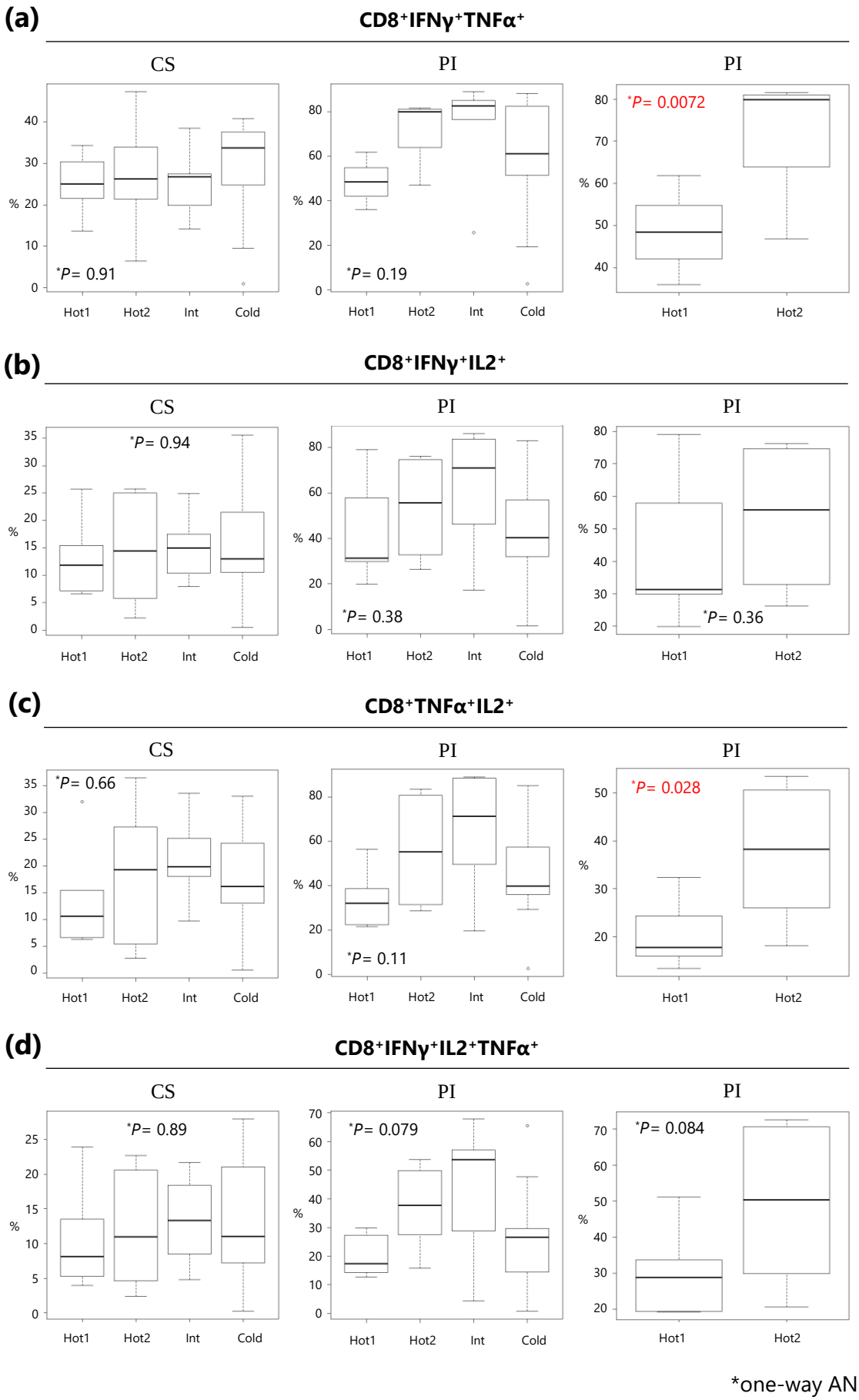
*one-way ANOVA

Supplementary figure 9. Cytokine production of CD8⁺ T-cells.

(a) The percentages of CD8⁺IFNγ⁺ T-cells without stimulation (Unstim), with CytoStim (CS) or PMA/ionomycin (PI) stimulation in TICs between 4 immunological subtypes. The difference in IFNγ production between Hot1 and Hot2 was evaluated.

(b) The percentages of CD8⁺TNFα⁺ T-cells without stimulation (Unstim), with CytoStim (CS) or PMA/ionomycin (PI) stimulation in TICs between 4 immunological subtypes. The difference in TNFα production between Hot1 and Hot2 was evaluated.

(c) The percentages of CD8⁺IL-2⁺ T-cells without stimulation (Unstim), with CytoStim (CS) or PMA/ionomycin (PI) stimulation in TICs between 4 immunological subtypes. The difference in IL-2 production between Hot1 and Hot2 was evaluated.



*one-way ANOVA

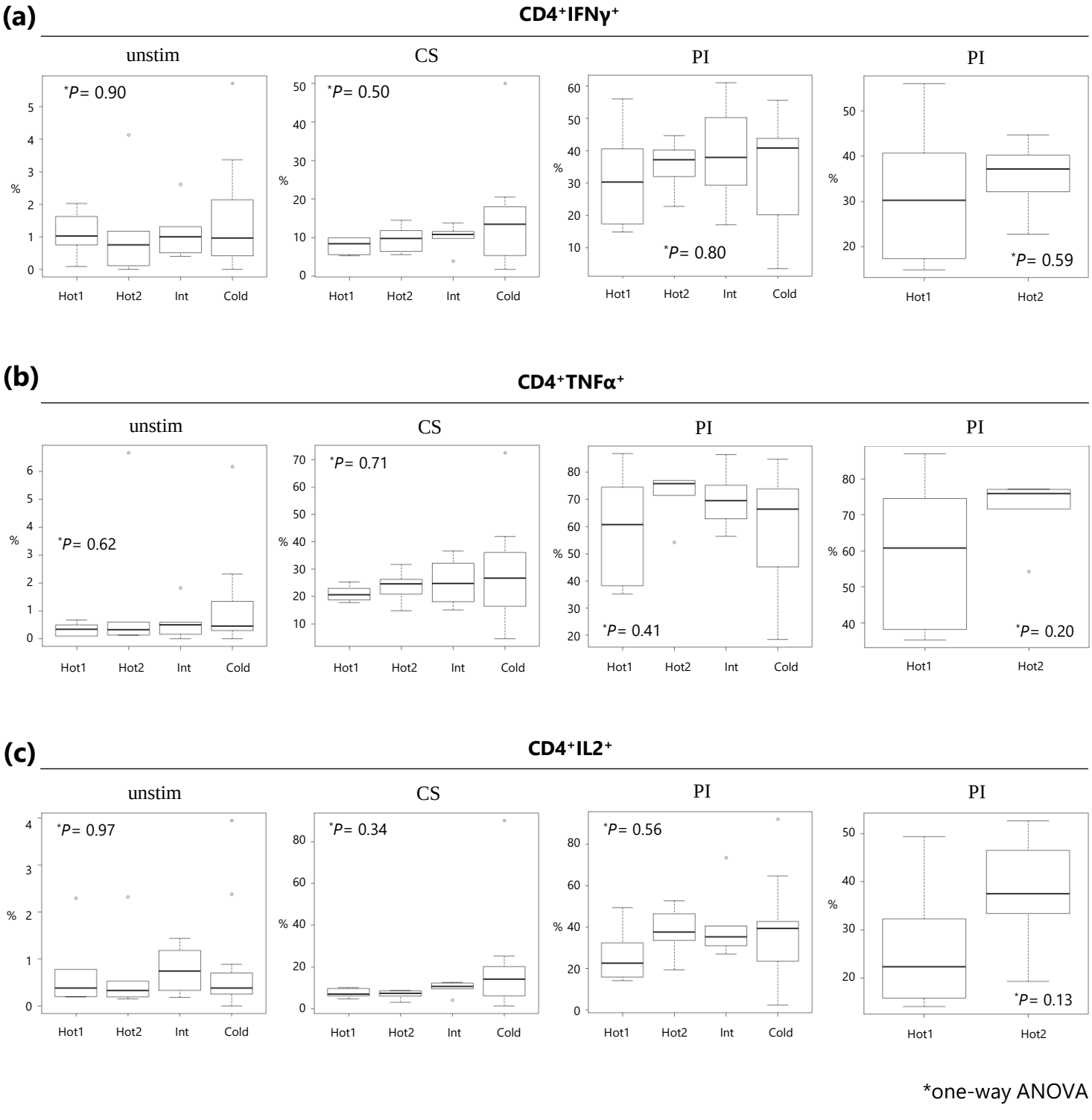
Supplementary figure 10. Polyfunctional CD8⁺ T-cells.

(a) The percentages of CD8⁺ T-cells producing IFNγ and TNFα were evaluated after CytoStim(CS) or PMA/ionomycin (PI) stimulation. The difference in the percentages of double producers between Hot1 and Hot2 was evaluated.

(b) The percentages of CD8⁺ T-cells producing IFNγ and IL-2 were evaluated after CS or PI stimulation. The difference in the percentages of double producers between Hot1 and Hot2 was evaluated.

(c) The percentages of CD8⁺ T-cells producing TNFα and IL-2 were evaluated after CS or PI stimulation. The difference in the percentages of double producers between Hot1 and Hot2 was evaluated.

(d) The percentages of CD8⁺ T-cells producing IFNγ, TNFα and IL-2 were evaluated after CS or PI stimulation. The difference in the percentages of triple producers between Hot1 and Hot2 was evaluated.

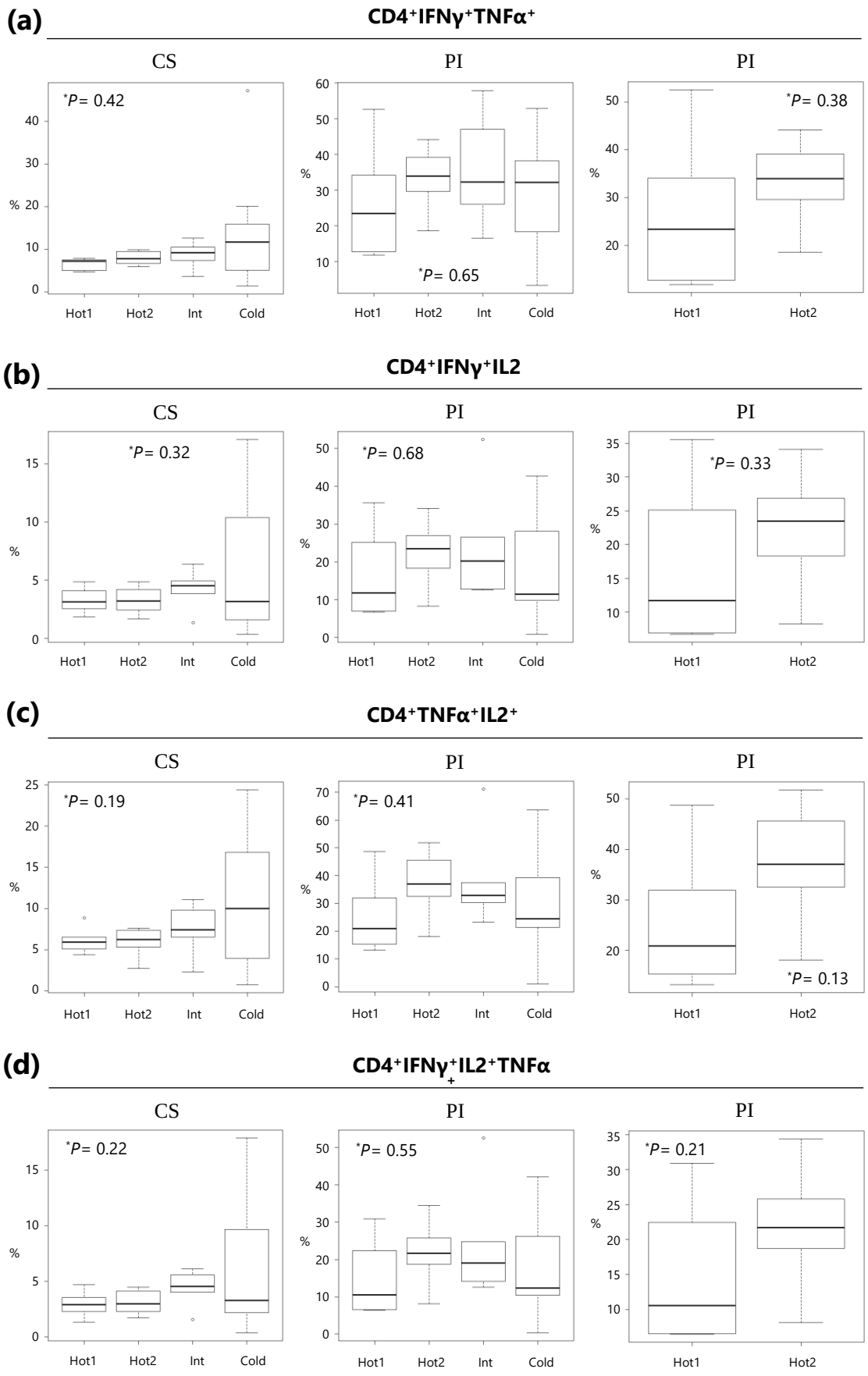


Supplementary figure 11. Cytokine production of CD4⁺ T-cells.

(a) The percentages of $CD4^+IFN\gamma^+$ T-cells without stimulation (Unstim), with CytoStim (CS) or PMA/ionomycin (PI) stimulation in TICs between 4 immunological subtypes. The difference in IFNγ production between Hot1 and Hot2 was evaluated.

(b) The percentages of $CD4^+TNF\alpha^+$ T-cells without stimulation (Unstim), with CytoStim (CS) or PMA/ionomycin (PI) stimulation in TICs between 4 immunological subtypes. The difference in TNFα production between Hot1 and Hot2 was evaluated.

(c) The percentages of $CD4^+IL\text{-}2^+$ T-cells without stimulation (Unstim), with CytoStim (CS) or PMA/ionomycin (PI) stimulation in TICs between 4 immunological subtypes. The difference in IL-2 production between Hot1 and Hot2 was evaluated.



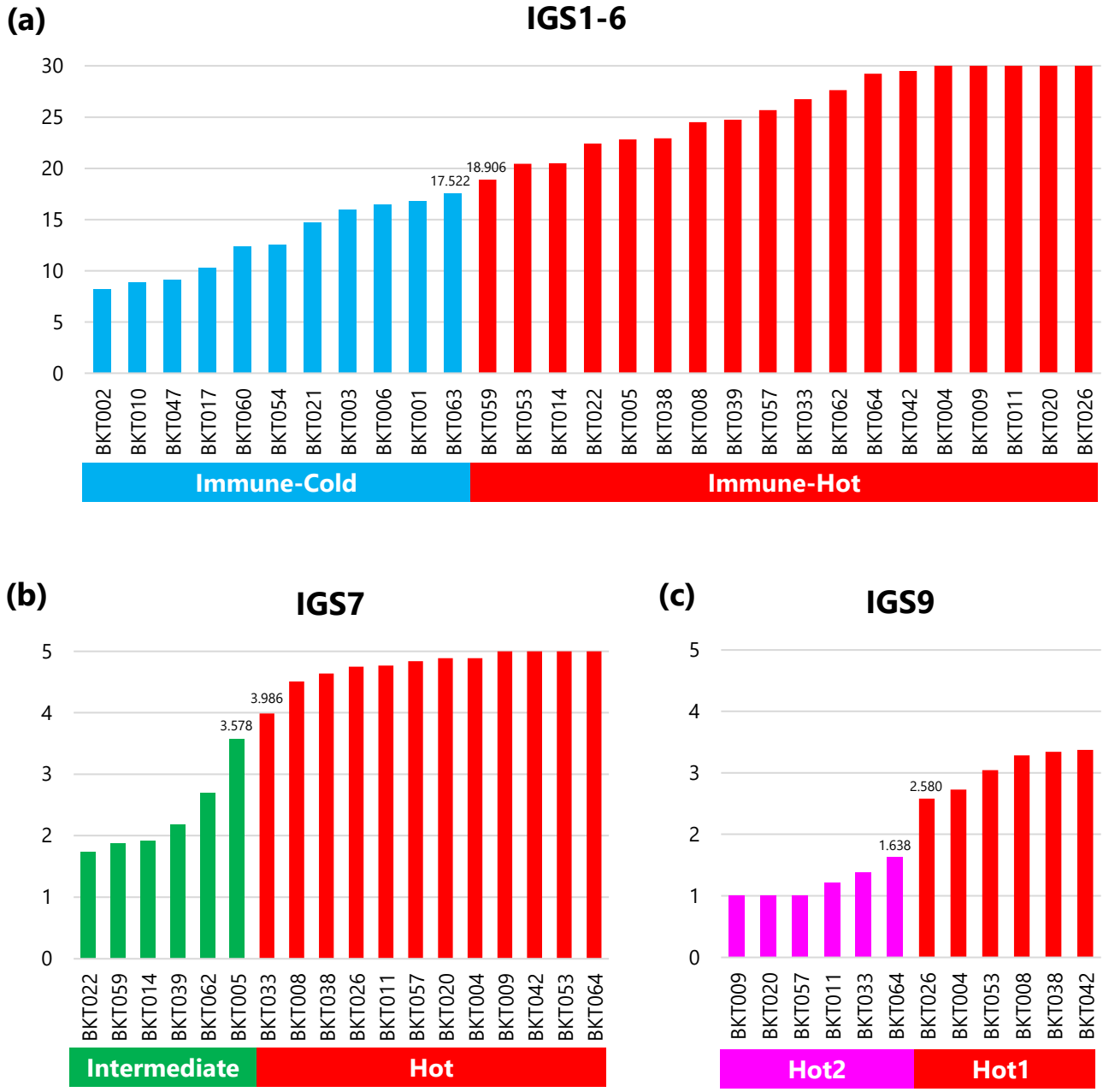
Supplementary figure 12. Polyfunctional CD4⁺ T-cells.

(a) The percentages of CD4⁺ T-cells producing IFNγ and TNFα were evaluated after CytoStim(CS) or PMA/ionomycin (PI) stimulation. The difference in the percentages of double producers between Hot1 and Hot2 was evaluated.

(b) The percentages of CD4⁺ T-cells producing IFNγ and IL-2 were evaluated after CS or PI stimulation. The difference in the percentages of double producers between Hot1 and Hot2 was evaluated.

(c) The percentages of CD4⁺ T-cells producing TNFα and IL-2 were evaluated after CS or PI stimulation. The difference in the percentages of double producers between Hot1 and Hot2 was evaluated.

(d) The percentages of CD4⁺ T-cells producing IFNγ, TNFα and IL-2 were evaluated after CS or PI stimulation. The difference in the percentages of triple producers between Hot1 and Hot2 was evaluated.



Supplementary figure 13. Immunogram scores for immunological classification.
(a) Immune-Hot and Immune-Cold tumors were distinguished by the sum of immunogram scores of innate immunity (IGS1), priming and activation (IGS2), T cells (IGS3), IFNγ response (IGS4), inhibitory cells (IGS5), and inhibitory molecules (IGS6).
(b) Intermediate and Hot tumors were defined by IGS7 (recognition of tumor cells).
(c) IGS9 (Glycolysis) was used to discriminate Hot1 from Hot2 tumors.