1. TCR sequences are found from Table 1. In Table 1, the epitope for TCR A11Vc is listed as 8-16V, while for the rest of the TCRs it is 7-16V. Since Fig. 2c performs mutational scan over 7-16 for all TCRs, we record 7-16V as the index peptide for all TCRs.
2. Mutational scan data is based on NFAT activation heatmaps, found in Fig. 2c. The unnormalized raw data is found in the supplementary “View Supporting data values” Figure 2C sheet. We follow the minmax normalization for each TCR, defined in caption of Figure 2 to record the specific activity values, with the minima and maxima recorded from the data sheet. Note that cysteine substitution results are separately recorded in the right of the data sheet. Furthermore, for non-C substitutions, while the alphabetic AA order is maintained for the substituted amino acid, in recording the data in the 18X10 (as opposed to 20X10, or 19X10, excluding only C) grid for each TCR, C and the WT amino acids are missing for each position. So, the set of substituted amino acids is different for each position, and that is not accurately recorded in the grid row amino acid name, since the amino acids cannot be common for all columns.
3. Following the legend in Fig. 2c, we minmax normalize the results using the controls for each TCR: Minimum (Jurkat Background) and Maximum (PMA/I Avg), noted separately on the right side of the grid in the spreadsheet. The index peptide activity is also found in the same location. Some peptide activities attain a small negative value after this normalization, we set them to zero in our record.