# Immunopeptidomic analysis reveals that deamidated HLA-bound peptides arise predominantly from deglycosylated precursors

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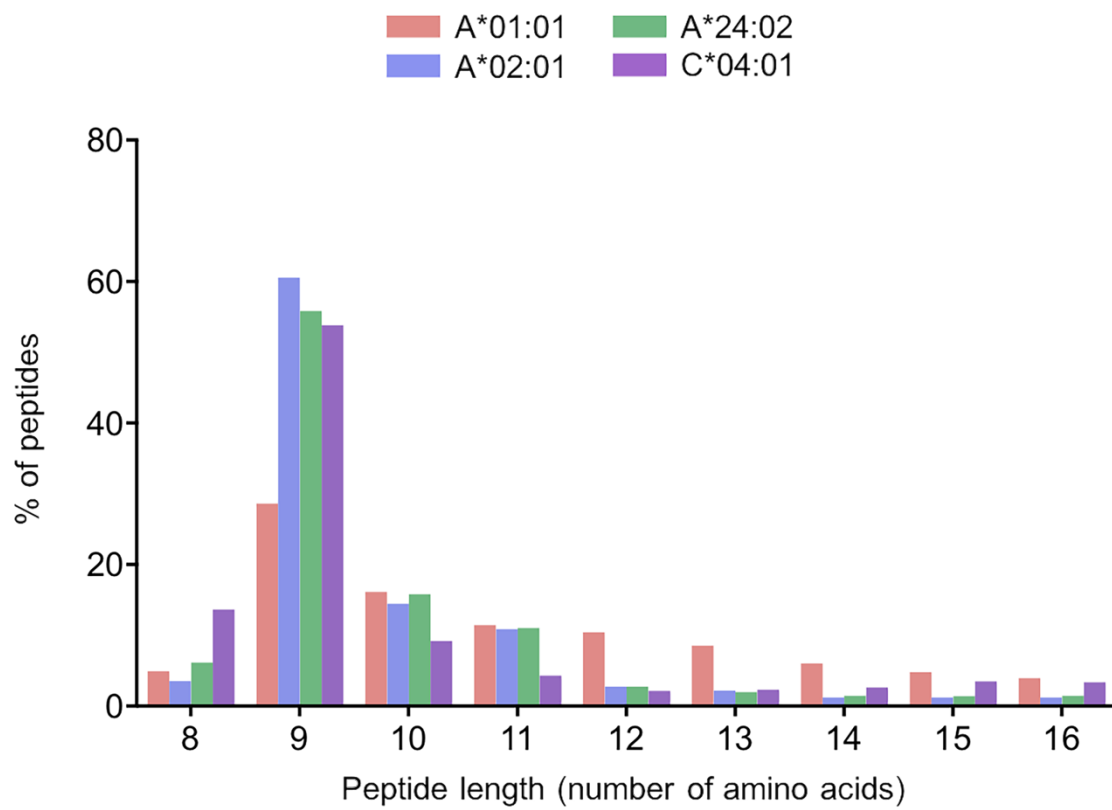
## SUPPLEMENTAL DATA

**Figure S1. Length distribution (of 8-16mers) of pHLA-I peptide repertoire from C1R cells expressing A\*01:01, A\*02:01, A\*24:02 or C\*04:01.**
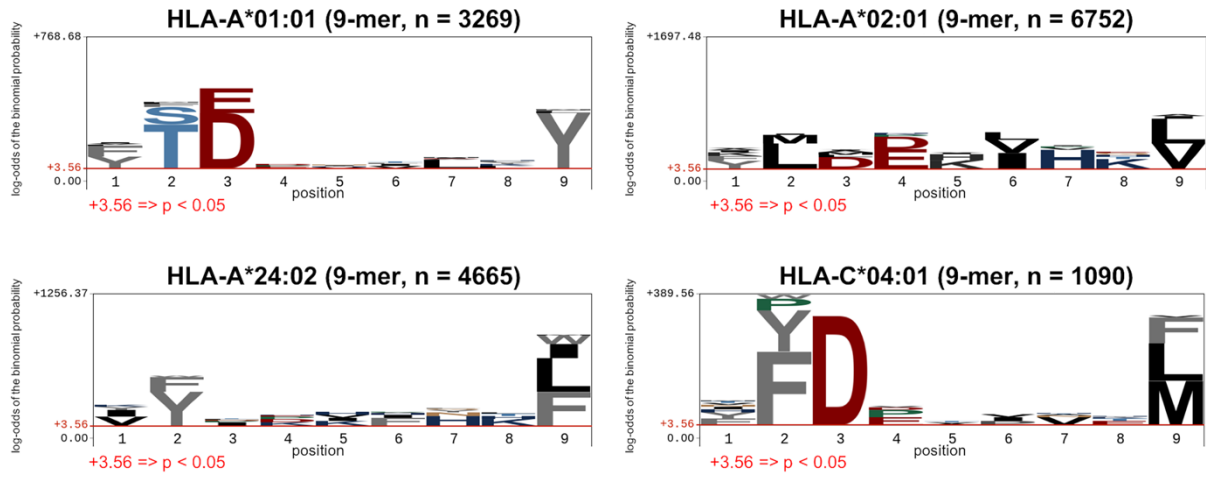
**Figure S2. Motif analysis on 9mer peptides from HLA-A*01:01, A*02:01, A*24:02 and C*04:01.** The motif analysis was generated by using pLogo (1). Amino acids above the red threshold line indicate that the log-odds of the binomial probability is significant.
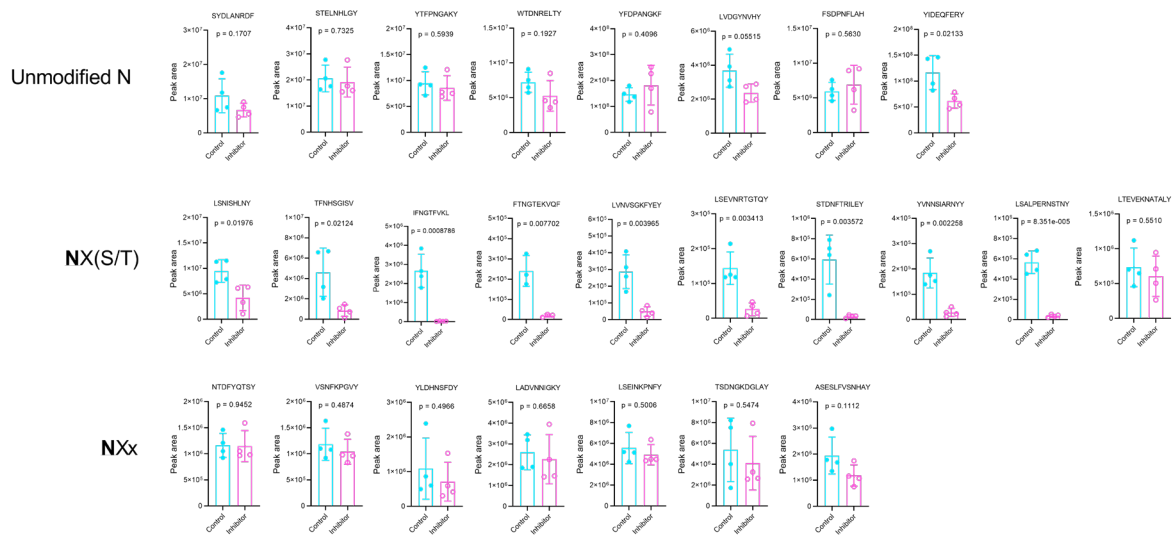
**Figure S3. MRM peak areas for peptides detected from control versus inhibitor (Z-VAD-FMK) treated samples.** Unmodified N: peptides with an Asn residue but bearing no PTMs. **N**X(S/T): peptides with a deamidated Asn residue and bearing the N-linked glycosylation motif (X is any amino acid except Pro). **N**Xx: peptides with a deamidated Asn residue (x is any amino acid except Ser or Thr).

1. O'shea, J. P., Chou, M. F., Quader, S. A., Ryan, J. K., Church, G. M., and Schwartz, D. (2013) pLogo: a probabilistic approach to visualizing sequence motifs. *Nature methods* 10, 1211