

Expanded View Figures

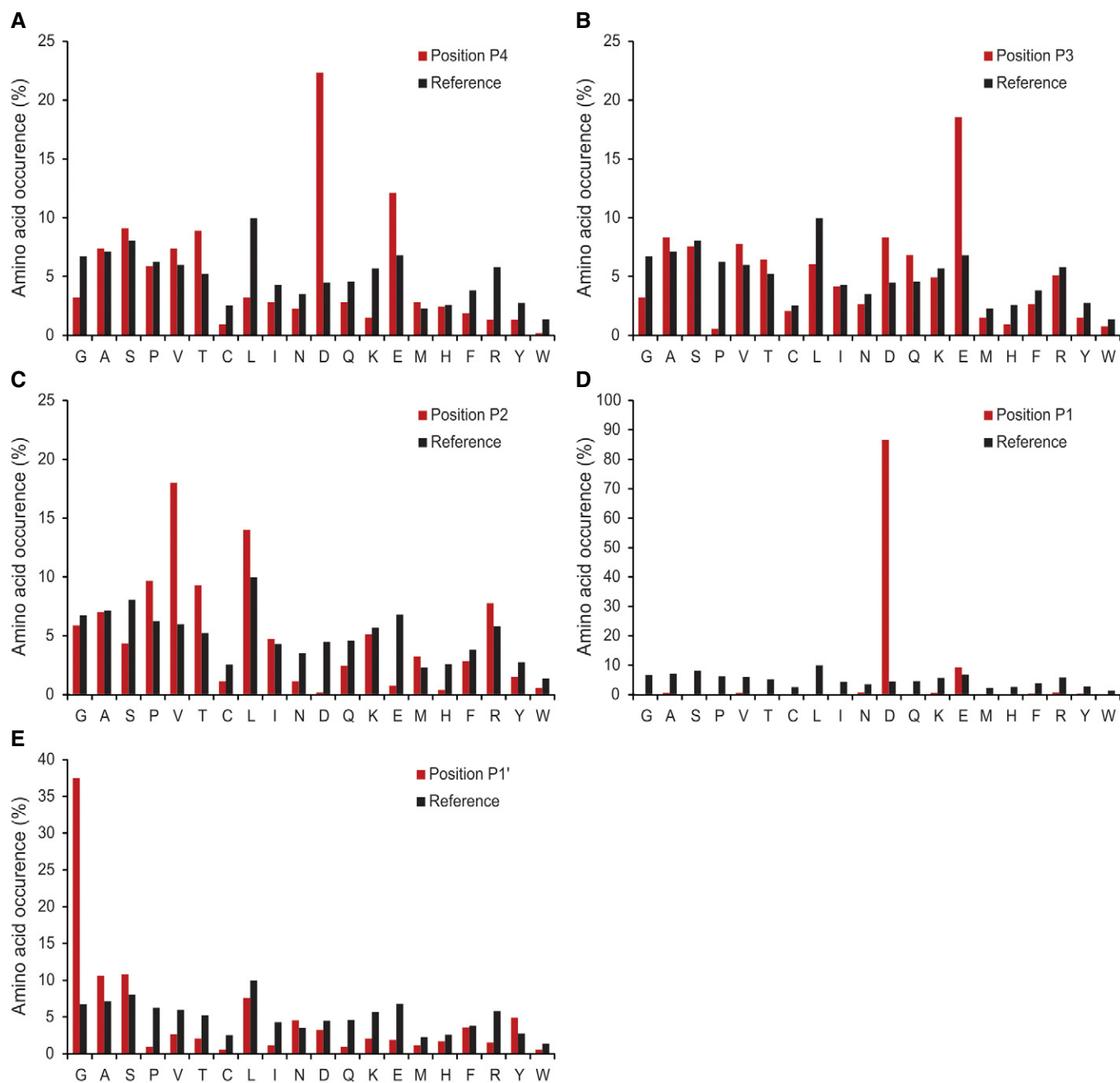


Figure EV1. Caspase-7 cleavage specificity profiling.

A-E The amino acid frequency distribution of caspase-7 P4 to P1' sites compared with the human proteome amino acid frequency distribution.

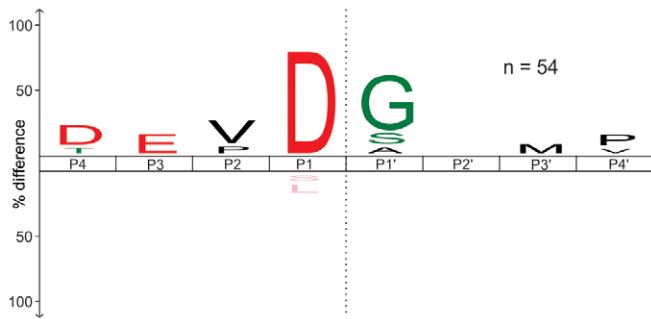


Figure EV2. Correlation of DIPPS caspase-7 specificity with apoptotic cleavages.
Matching cleavage site identifications between DIPPS and DegraBase with representative number of identified cleavage sites (*n*-values).

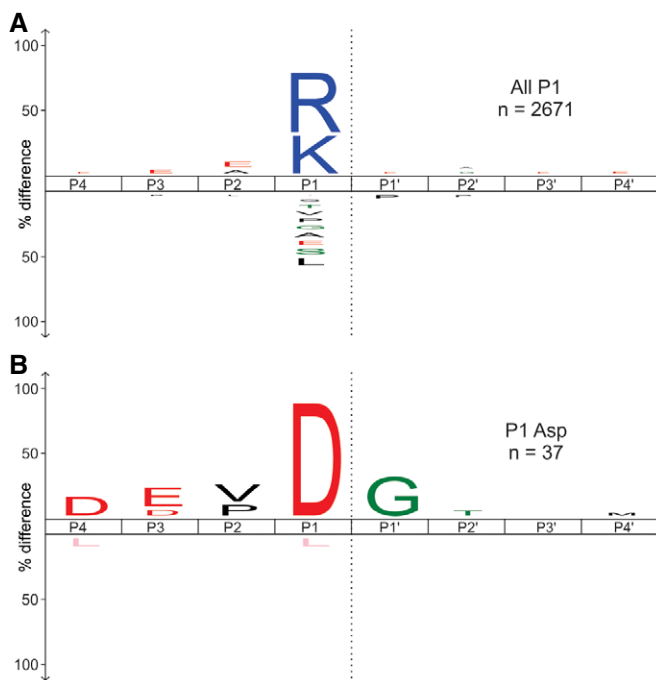


Figure EV3. Cleavage specificity profile of caspase-7 after the secondary digestion of extracted gel pieces with trypsin.
A The first digestion of the gel pieces with caspase-7 was followed by the trypsin digestion. The cleavage specificity profile after the second digestion is presented in the upper panel.
B In the lower panel, the cleavage profile is only shown for P1 Asp cleavage sequences. The representative number of the cleavage sites used for the cleavage fingerprint construction is presented as *n*-values. The scissile peptide bond between P1 and P1' is indicated as a gray dashed line. *P*-value used for the iceLogo construction was 0.05.

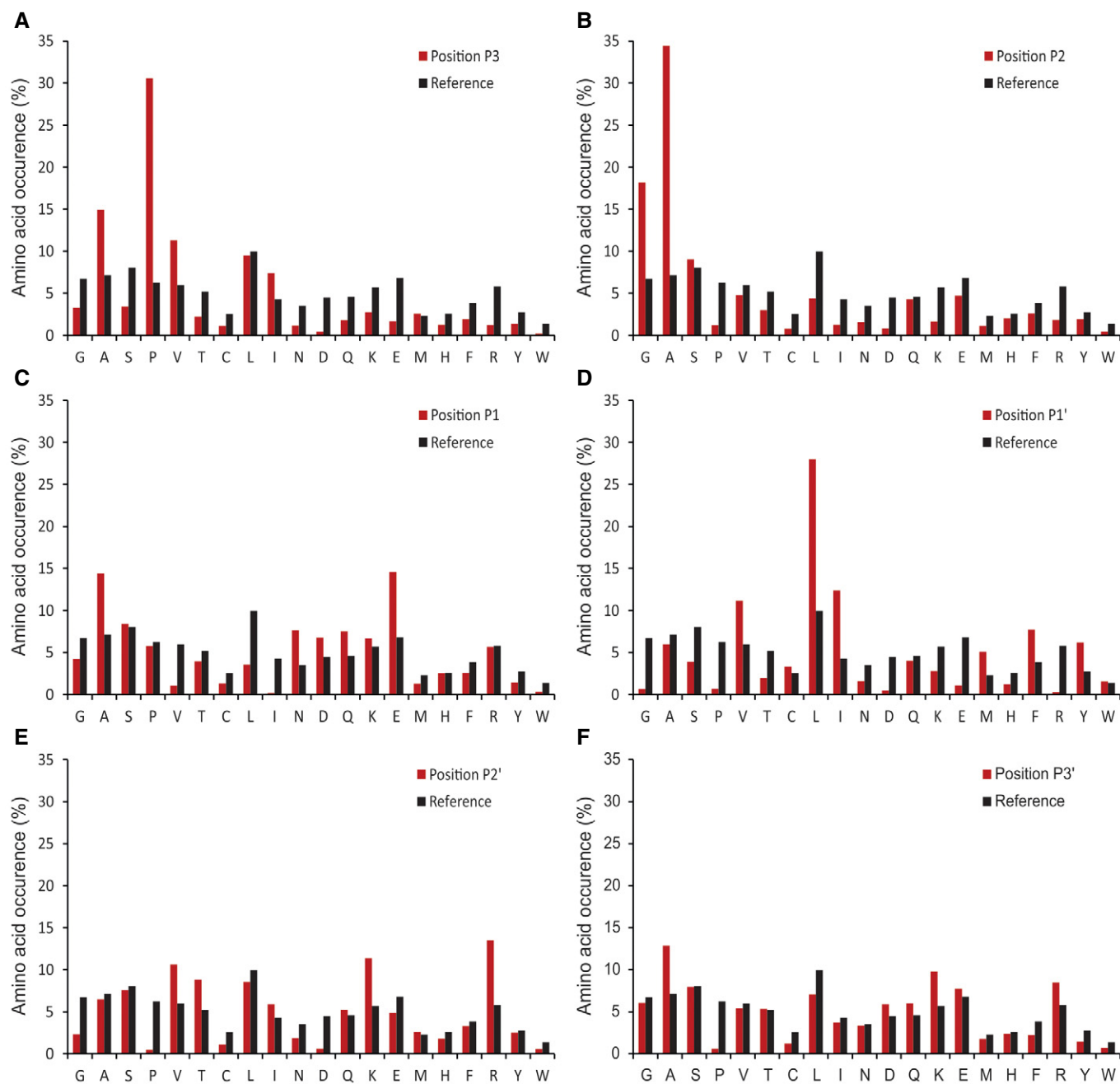


Figure EV4. MMP-3 cleavage specificity profiling.

A–F The frequency distribution of MMP-3 P3 to P3' sites compared with the human proteome amino acid frequency distribution.

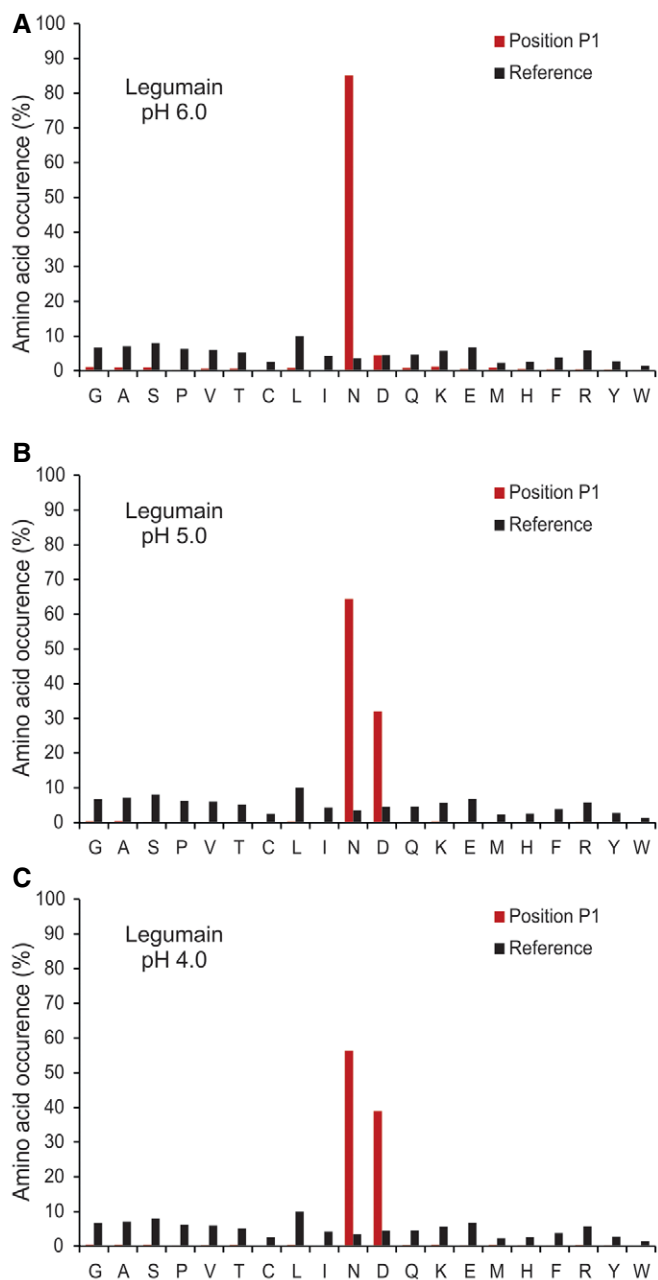


Figure EV5. Legumain cleavage specificity profiling.

A–C The frequency distribution of legumain P1 site at (A) pH 6.0, (B) pH 5.0, and (C) pH 4.0 compared with the human proteome amino acid frequency distribution.