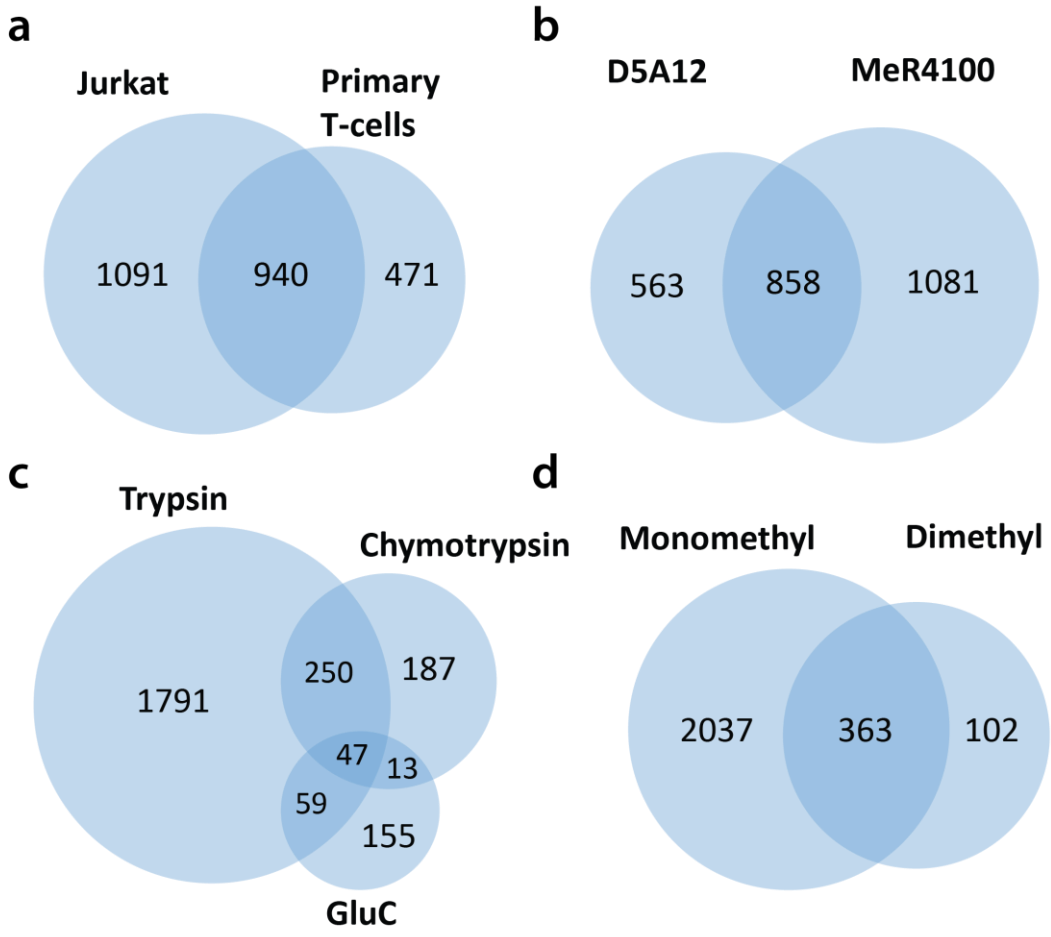
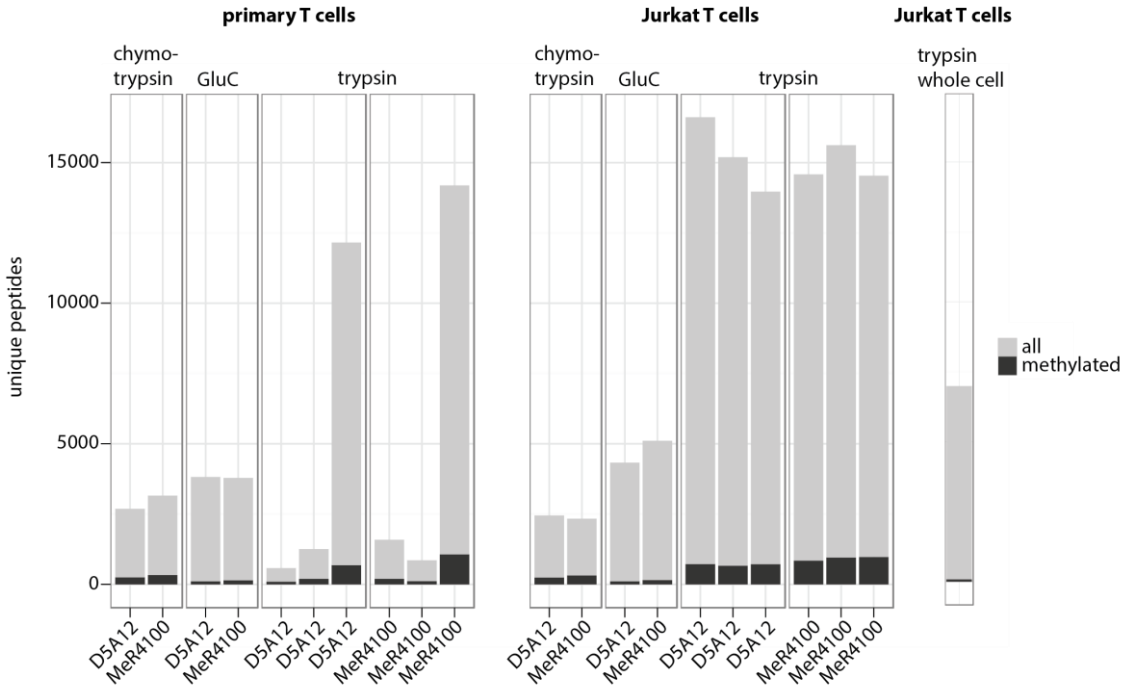
Supplementary Figure 1



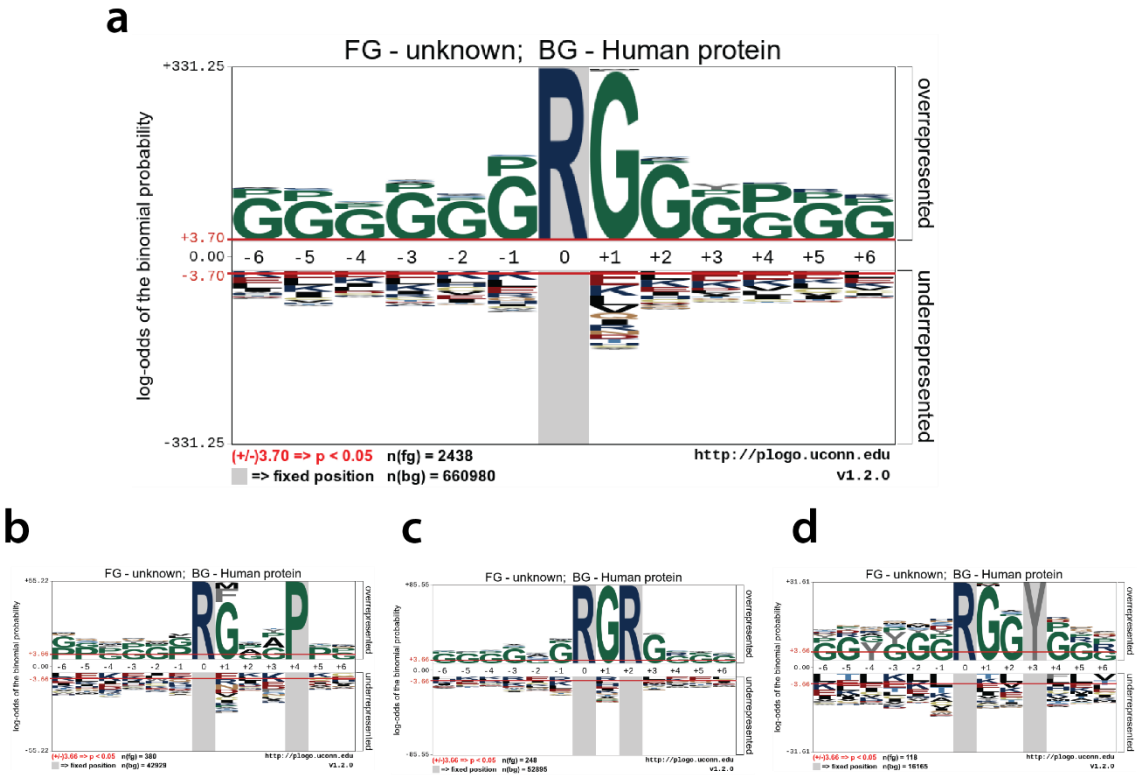
Supplementary Figure 1: Breakdown of all identified arginine methylation sites. (a) Overlap between identified arginine methylation sites in Jurkat T cells and primary T cells. (b) Arginine methylation sites identified by each antibody. (c) Arginine methylation sites identified after digestion with trypsin, chymotrypsin or GluC. (d) Type of arginine methylation site identified.

Supplementary Figure 2



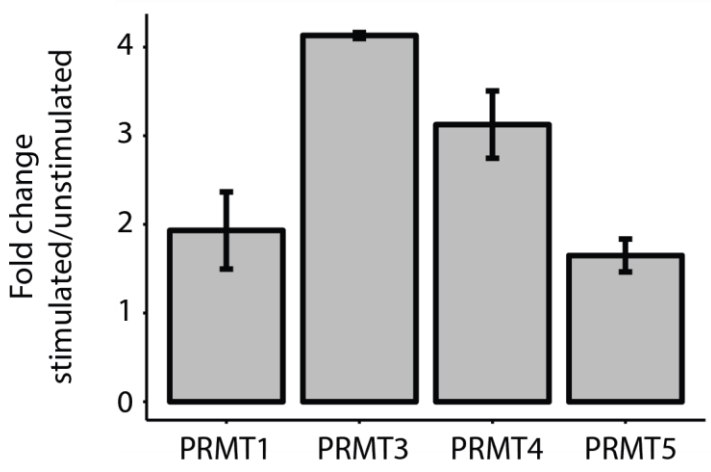
Supplementary Figure 2: Unique peptides identified across all immuno-affinity purifications, grouped by protease (chymotrypsin, GluC or trypsin) and source material (Jurkat T cells or primary T cells). For comparison, results from a representative iMethyl-SILAC labelled whole cell lysate are shown.

Supplementary Figure 3



Supplementary Figure 3: Arginine methylation sequence context. All methylation sites were analysed with pLOGO to generate a motif. Significantly over represented amino acids were fixed to explore motif sub-sets. (a) Sequence motif generated from all arginine methylation sites. (b) Proline at +4 was fixed to explore the (P)Rxxx(P) motif. (c) Arginine at +2 was fixed to explore the RxR motif. (d) Tyrosine at +3 was fixed.

Supplementary Figure 4



Supplementary Figure 4: PRMTs quantified during T-lymphocyte stimulation. Fold changes (stimulated/unstimulated) measured by mass spectrometry were averaged across all biological replicates. Bars are ±1SD.