



Figure 2 - Figure Supplement 2. Distribution, enrichment profile and physicochemical properties of variants after selection on 10G, BL21 and BW25113.

Number of variants that were depleted ($F_N \leq 0.1$) tolerated ($F_N > 0.1$ and < 2) or enriched ($F_N \geq 2$) after selection on **(A)** *E. coli* 10G, **(B)**, BL21, and **(C)** BW25113, separated by topology of the tip domain color coded as interior loops (red), β -sheets (beige) and exterior loops (blue). **(D)** Average F_N of enriched variants ($F_N \geq 2$) for 10G (orange squares), BL21 (blue circles), and BW25113 (teal triangles) ordered left to right from lowest to highest F_N . **(E)** Alluvial distribution of enriched variants ($F_N \geq 2$) on 10G (upper), BL21 (middle) and BW25113 (bottom), showing wild type amino acids (left), their substitution (middle) and topological location on the structure (right). Each alluvial is colored based on the substituted amino acid and scaled by F_N across hosts. Violin plots comparing **(F)** change in mass, **(G)** change in hydrophilicity, and **(H)** change in hydrophobicity for grouped depleted ($F_N \leq 0.1$) tolerated ($F_N > 0.1$ and < 2) or enriched ($F_N \geq 2$) substitutions on *E. coli* 10G, BL21 and BW25113. p-values are shown if only if < 0.05 , the upper p-value is the result of a Kruskal-Wallis test among all three groups while pairwise p-values from a Wilcoxon test are shown linking each group.