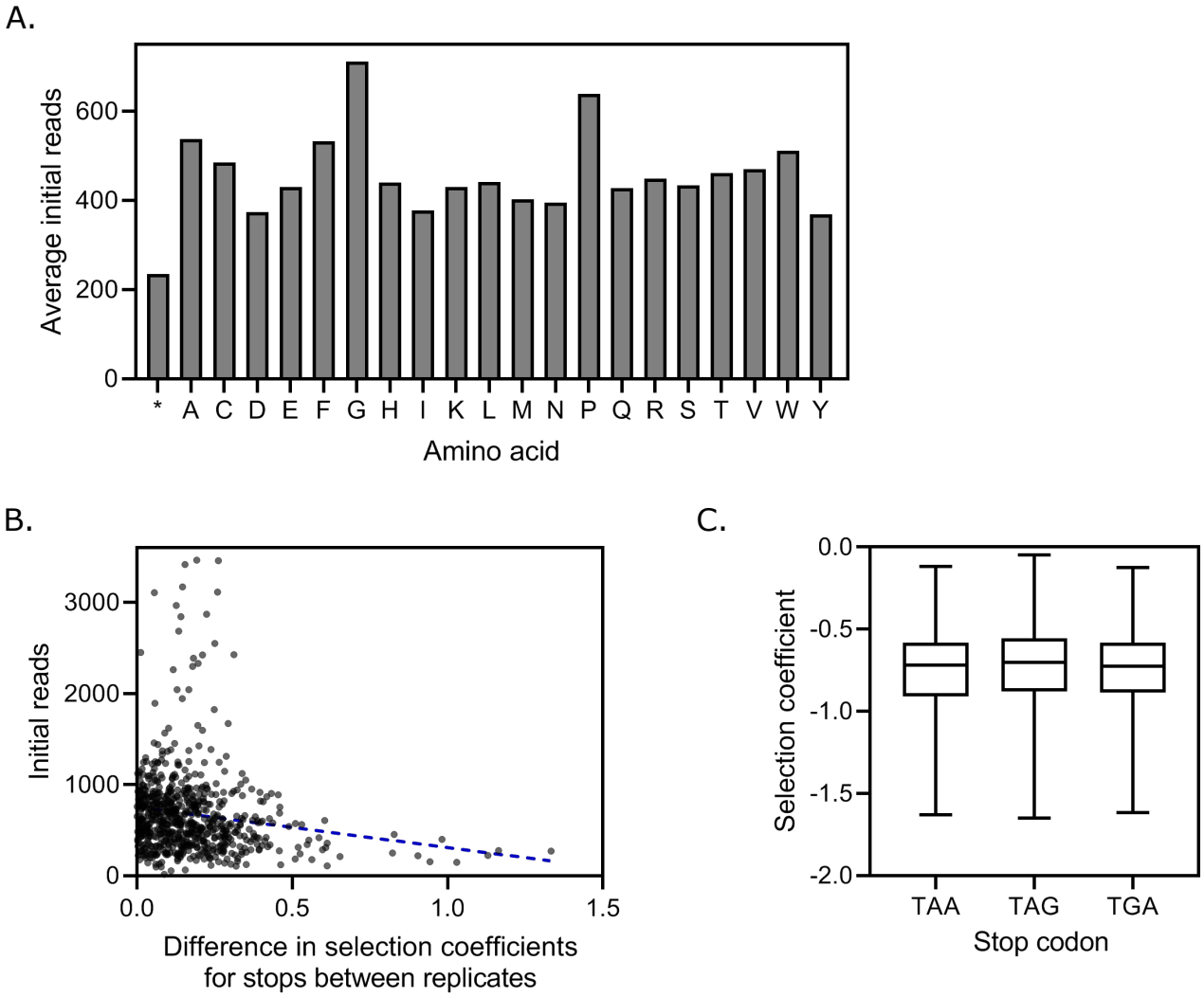

Figure 1 – figure supplement 3. A. The average initial reads measured per codon for each amino acid. B. The difference in the selection coefficients between stops in the two standard replicates compared to the initial reads for the corresponding stop in replicate 1. The blue dashed line indicates the line of best fit. $R^2 = 0.022$, $p < 0.0001$. C. The distribution of selection coefficients for each stop codon in standard replicate 1.