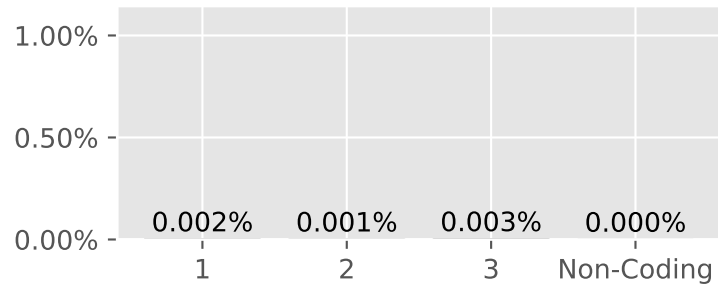
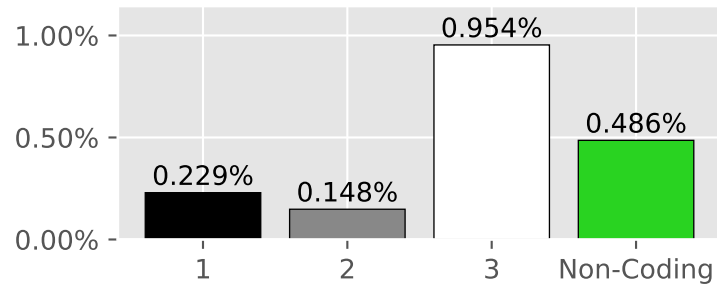


Rare mutation frequencies across codon positions (each bar normalized by total number of positions in that category)

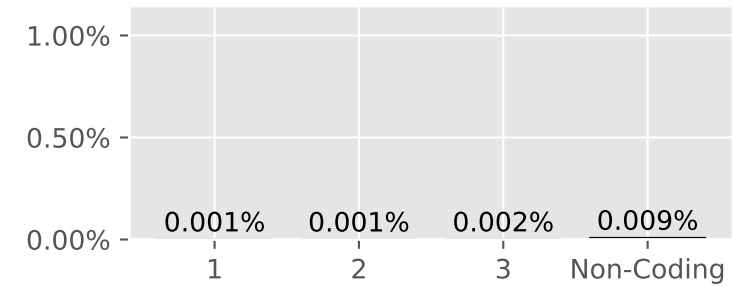
CAMP: LoFreq



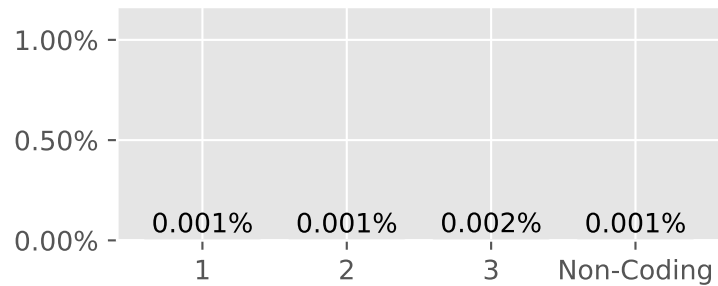
BACT1: LoFreq



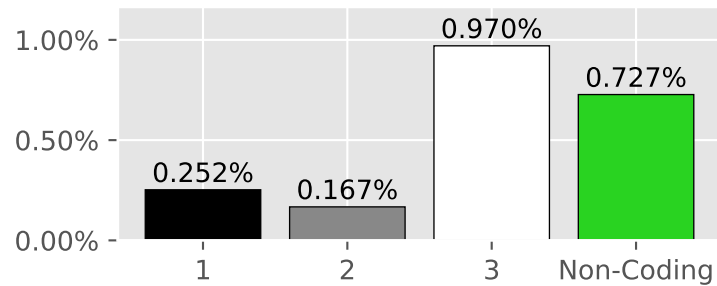
BACT2: LoFreq



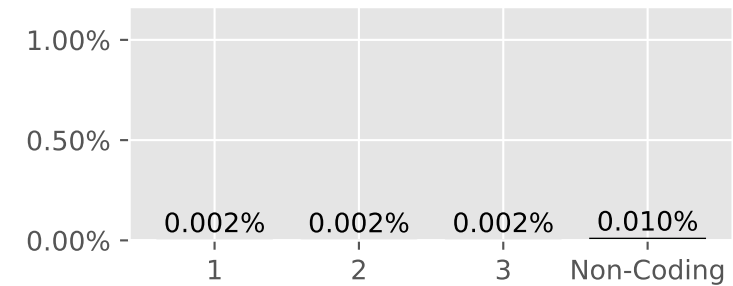
CAMP: naïve, $p = 2\%$



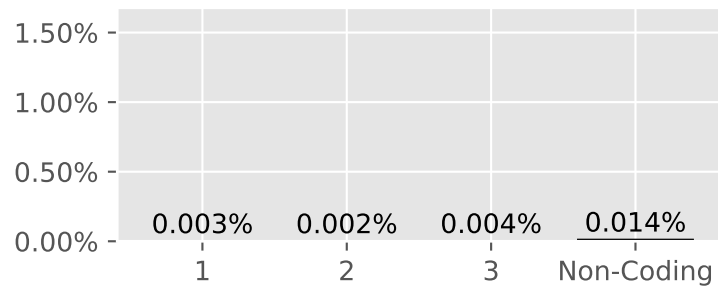
BACT1: naïve, $p = 2\%$



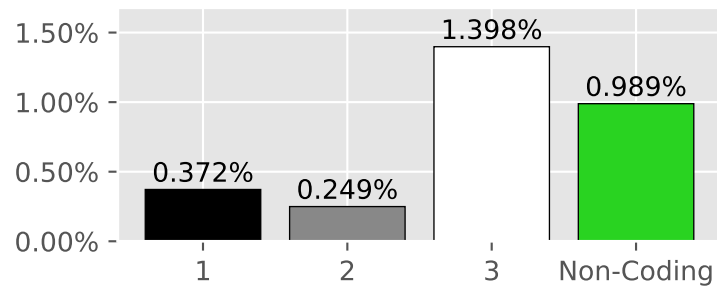
BACT2: naïve, $p = 2\%$



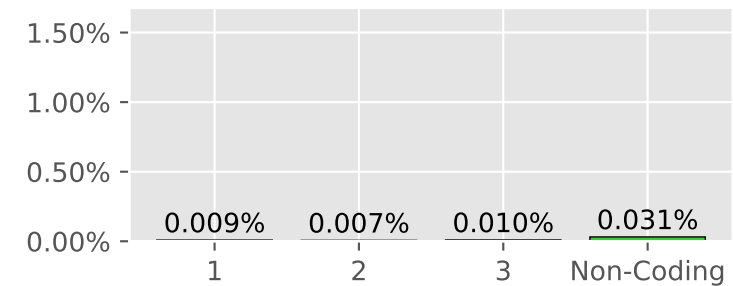
CAMP: naïve, $p = 1\%$



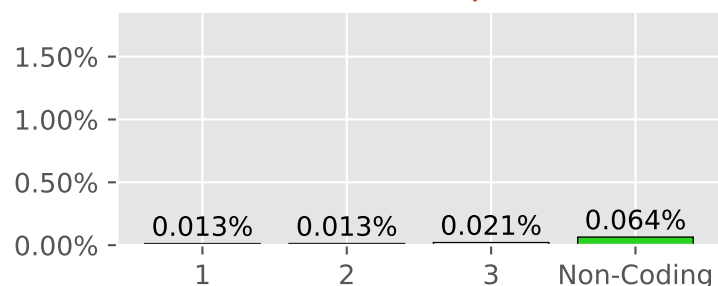
BACT1: naïve, $p = 1\%$



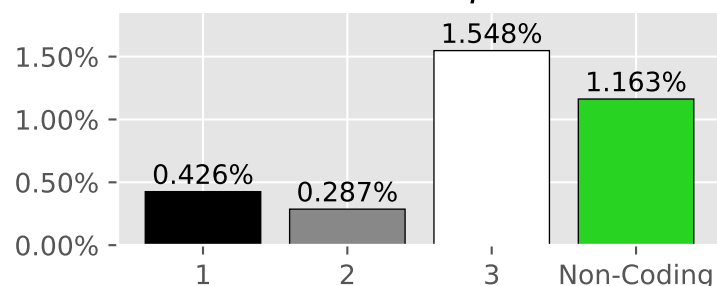
BACT2: naïve, $p = 1\%$



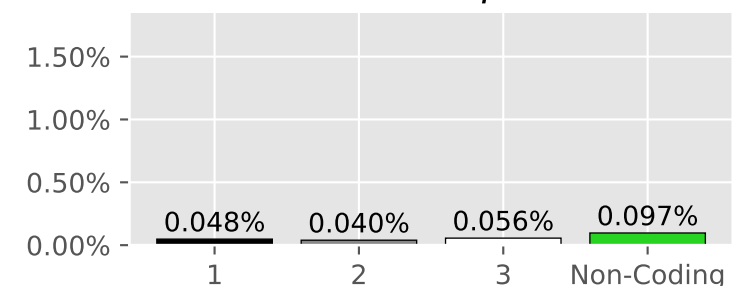
CAMP: naïve, $p = 0.5\%$



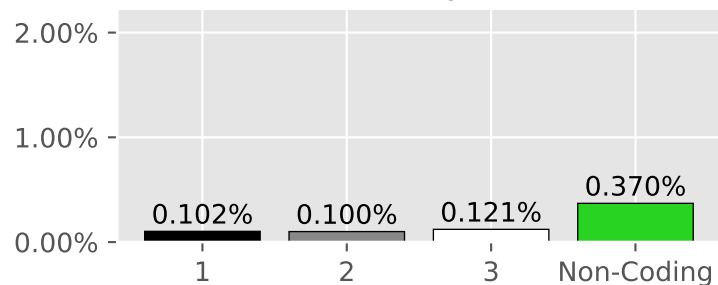
BACT1: naïve, $p = 0.5\%$



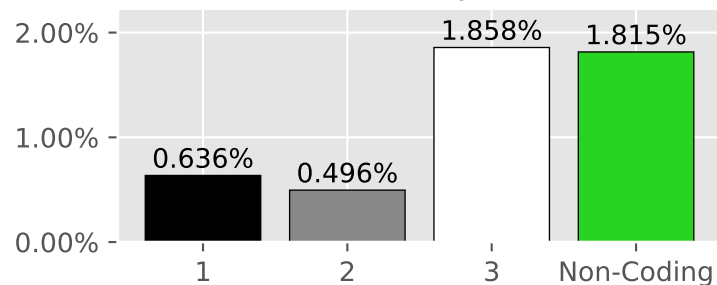
BACT2: naïve, $p = 0.5\%$



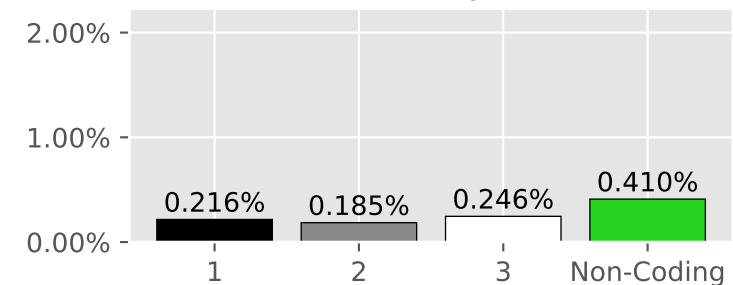
CAMP: naïve, $p = 0.25\%$



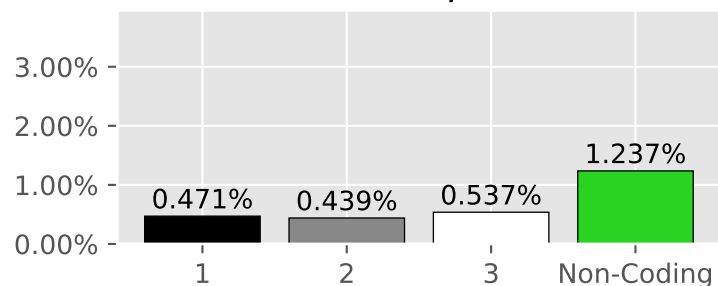
BACT1: naïve, $p = 0.25\%$



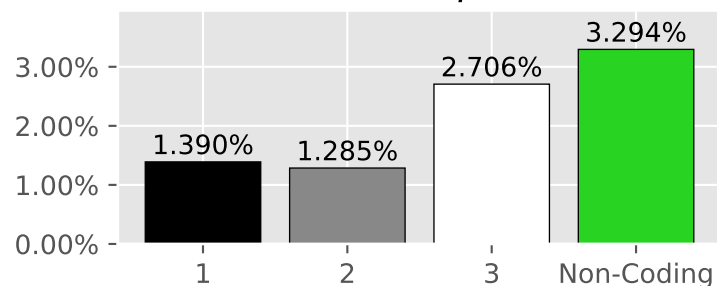
BACT2: naïve, $p = 0.25\%$



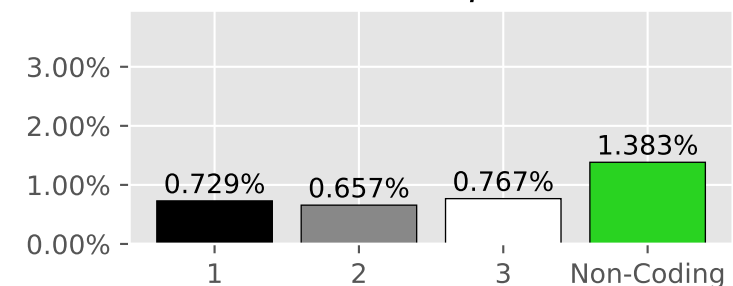
CAMP: naïve, $p = 0.15\%$



BACT1: naïve, $p = 0.15\%$



BACT2: naïve, $p = 0.15\%$



Codon Position