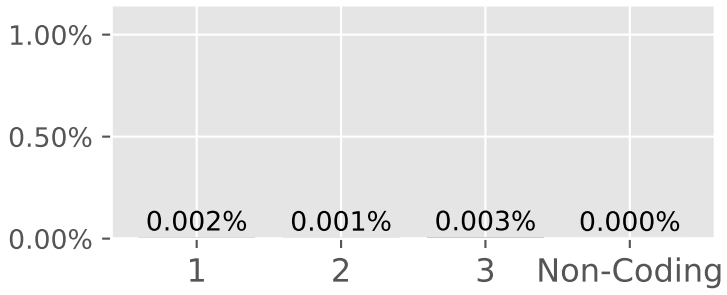
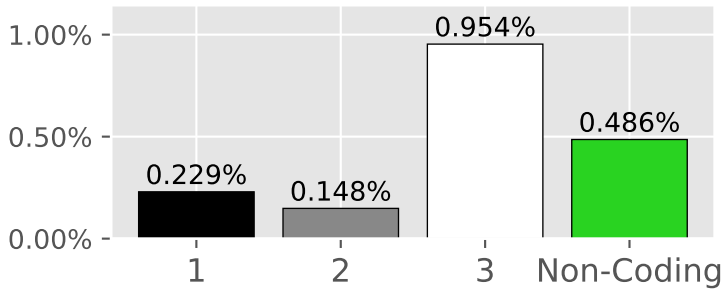
Rare mutation frequencies across codon positions
(each bar normalized by total number of positions in that category)

Number of Mutated Positions / Number of Positions

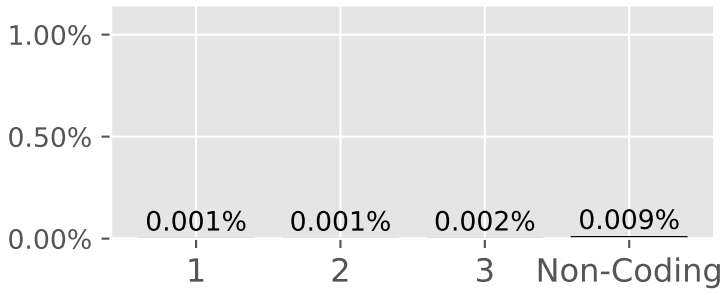
CAMP: LoFreq



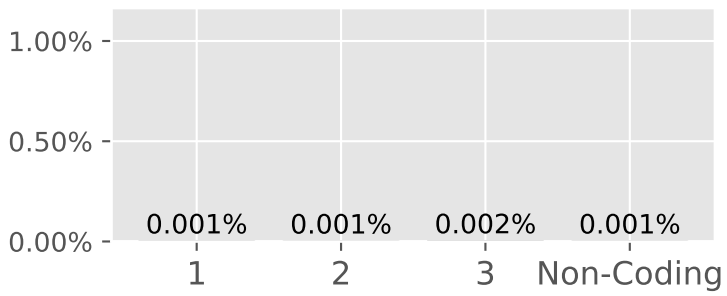
BACT1: LoFreq



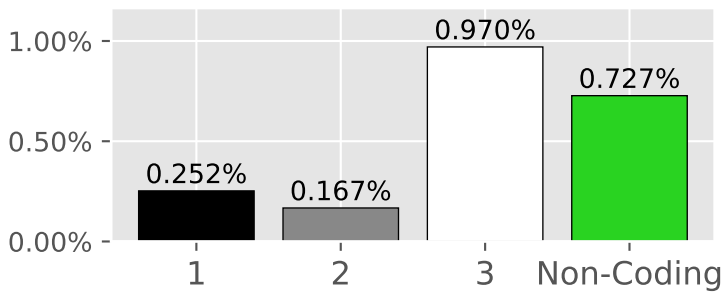
BACT2: LoFreq



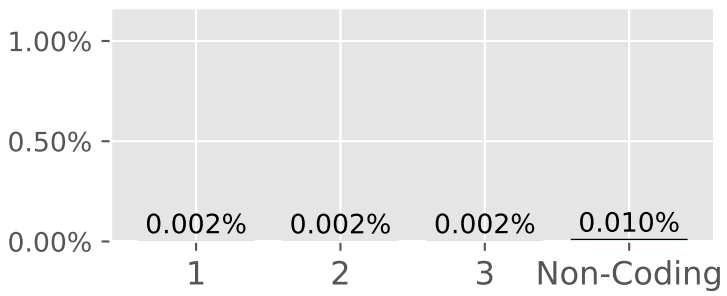
CAMP: naïve, p = 2%



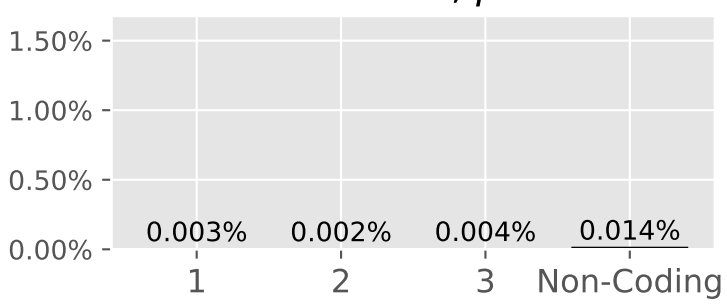
BACT1: naïve, p = 2%



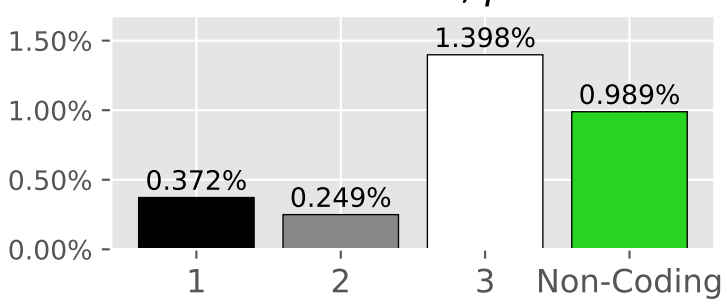
BACT2: naïve, p = 2%



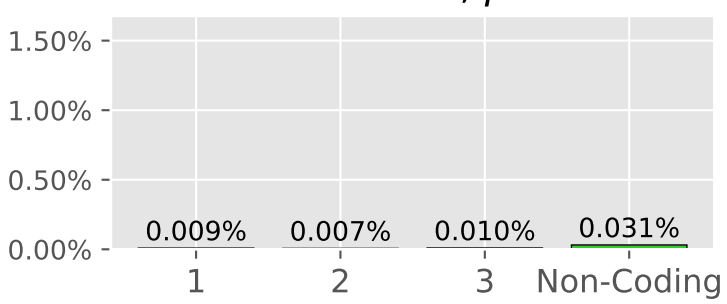
CAMP: naïve, p = 1%



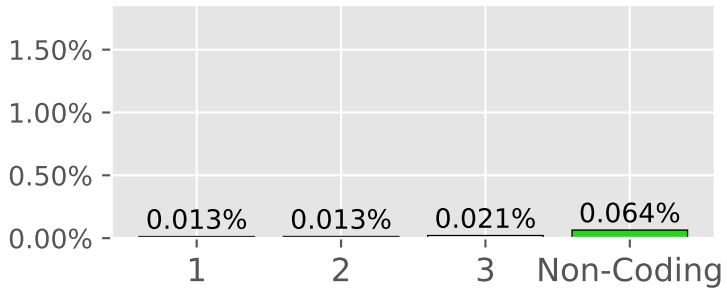
BACT1: naïve, p = 1%



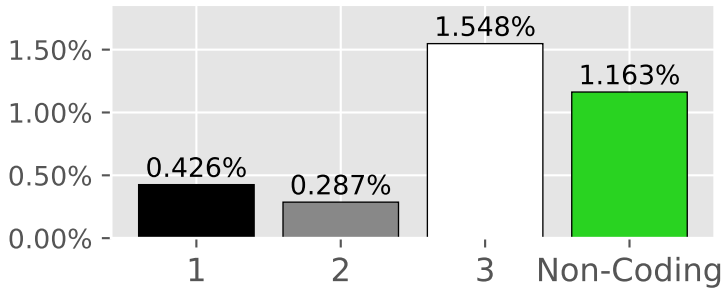
BACT2: naïve, p = 1%



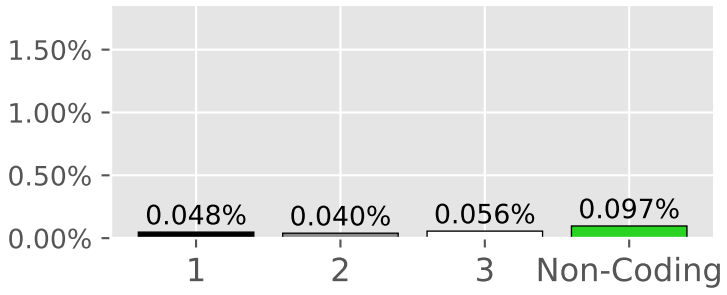
CAMP: naïve, p = 0.5%



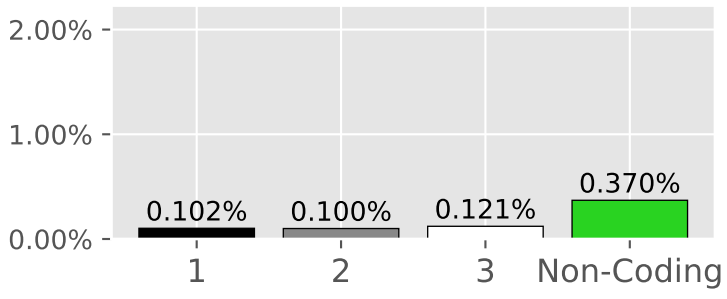
BACT1: naïve, p = 0.5%



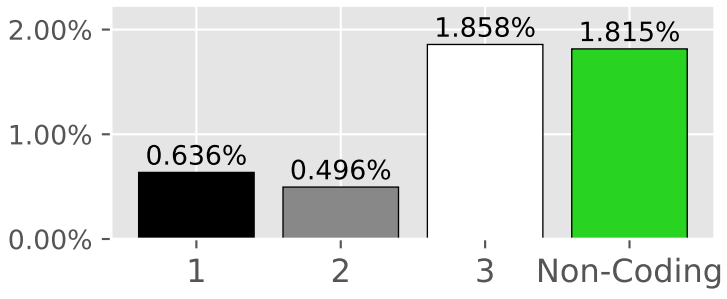
BACT2: naïve, p = 0.5%



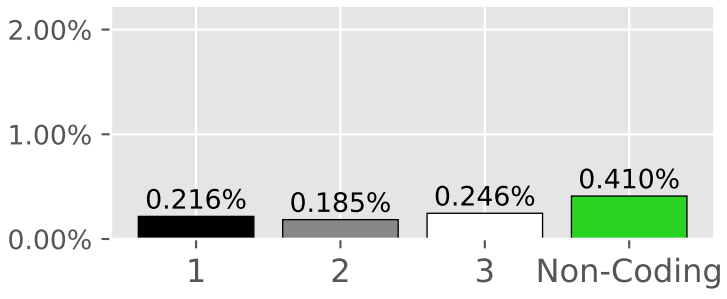
CAMP: naïve, p = 0.25%



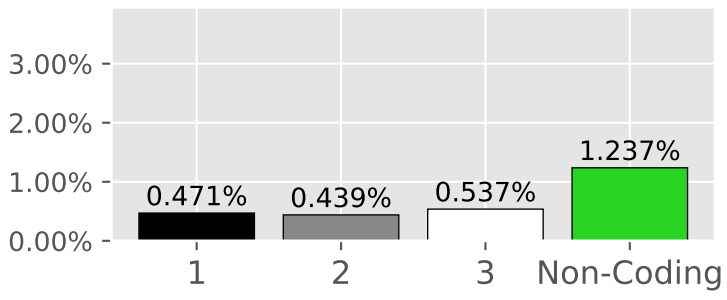
BACT1: naïve, p = 0.25%



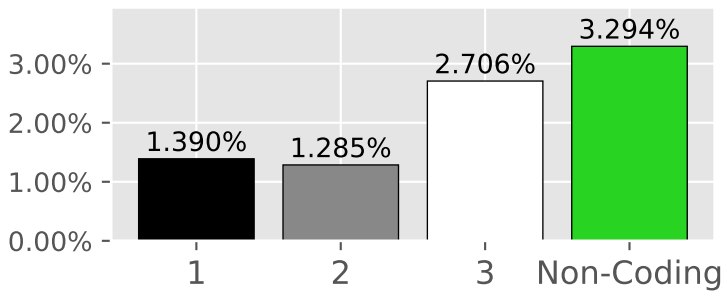
BACT2: naïve, p = 0.25%



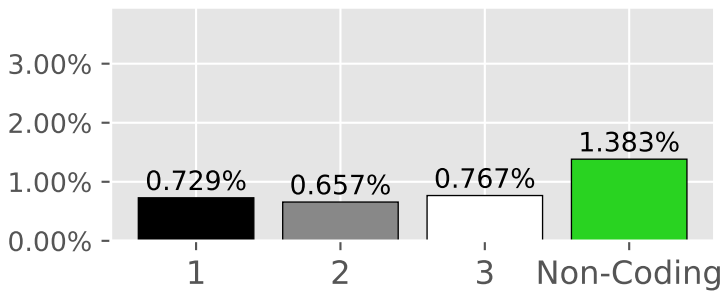
CAMP: naïve, p = 0.15%



BACT1: naïve, p = 0.15%



BACT2: naïve, p = 0.15%



Codon Position