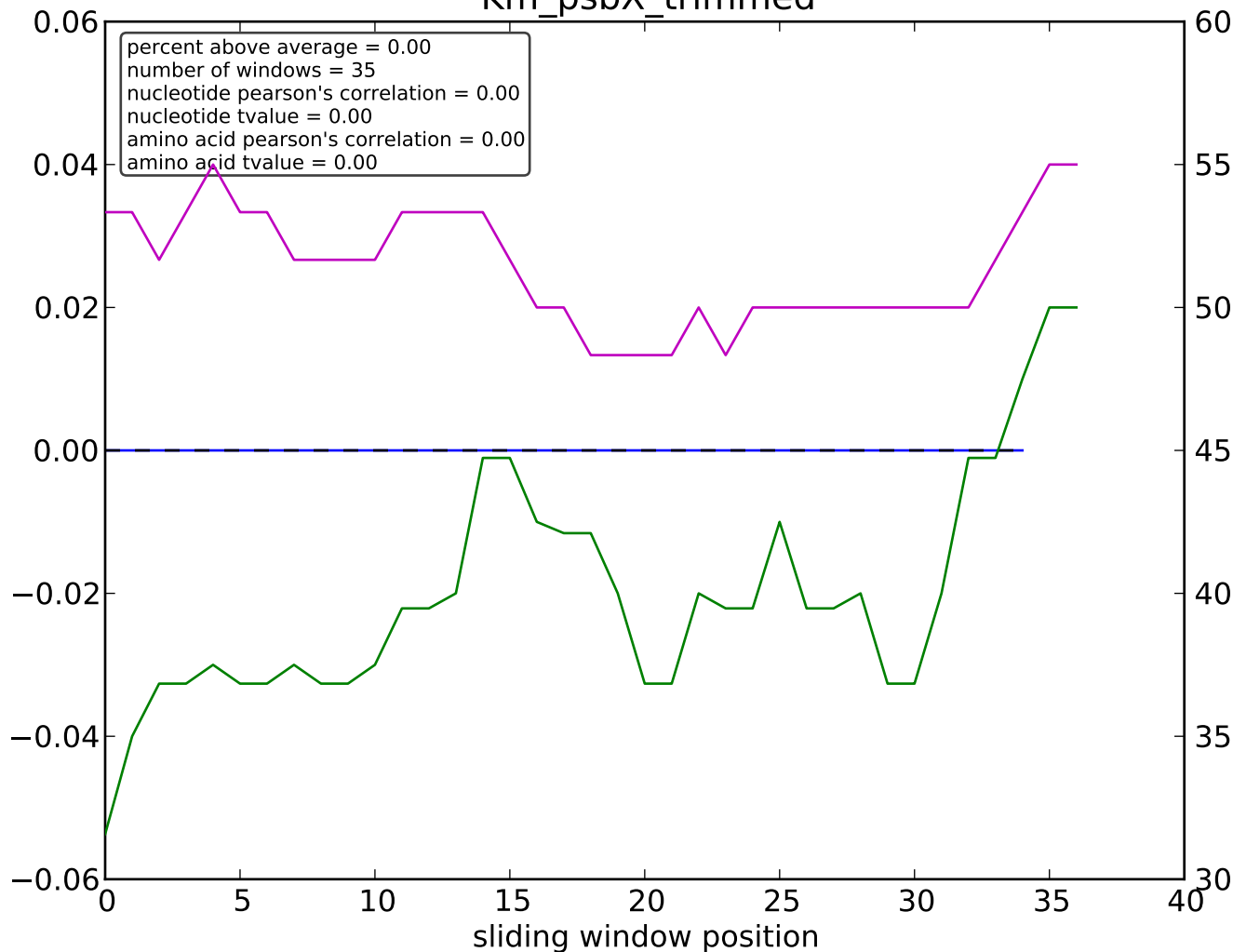


Km_psbX_trimmed

percent above average = 0.00
 number of windows = 35
 nucleotide pearson's correlation = 0.00
 nucleotide tvalue = 0.00
 amino acid pearson's correlation = 0.00
 amino acid tvalue = 0.00

percent edited residues in RNA



percent sequence identity to reference
 percent amino acid similarity to reference