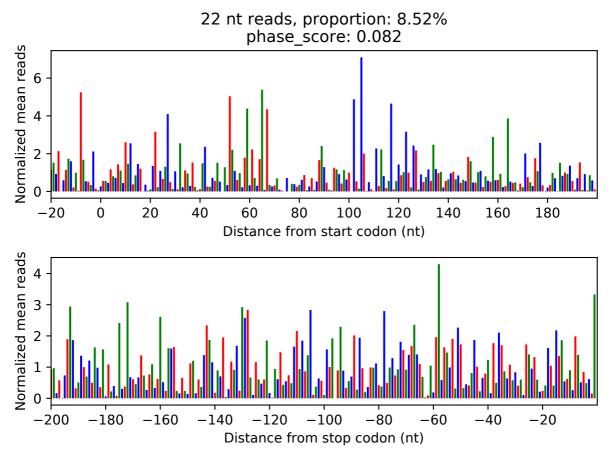
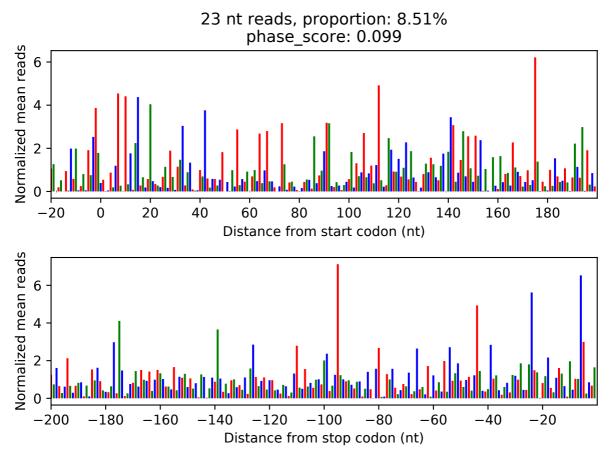
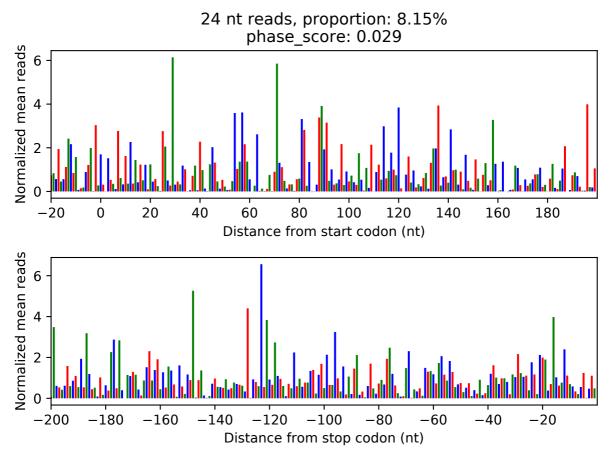
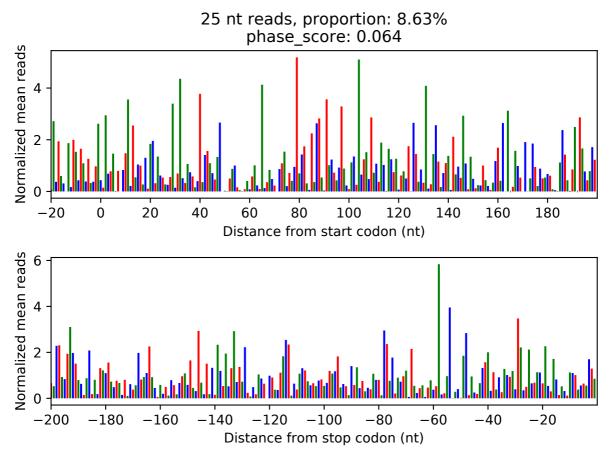


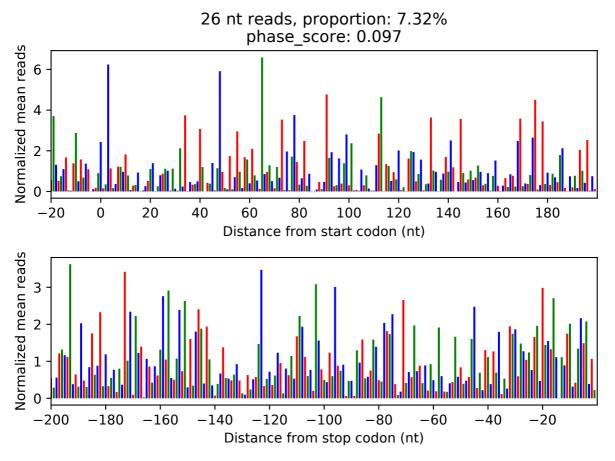
21 nt reads, proportion: 7.06% phase score: 0.042 Normalized mean reads 10.0 7.5 5.0 2.5 0.0 20 40 0 60 80 160 180 -20100 120 140 Distance from start codon (nt) Normalized mean reads -200-180-160-140-100-80-60 -40-20-120Distance from stop codon (nt)

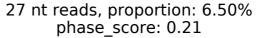


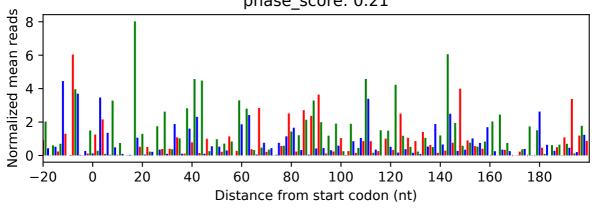


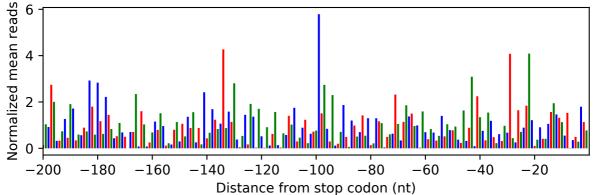


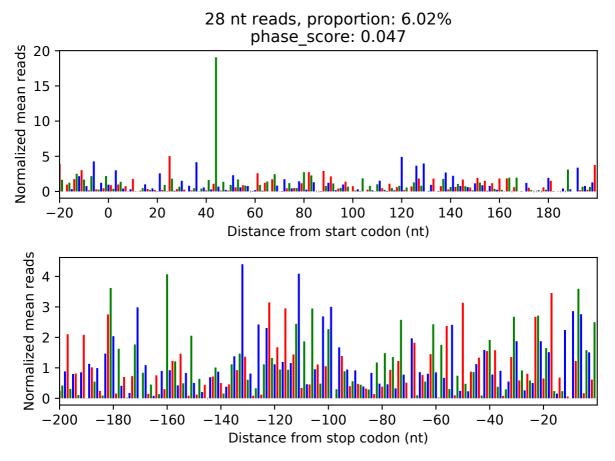


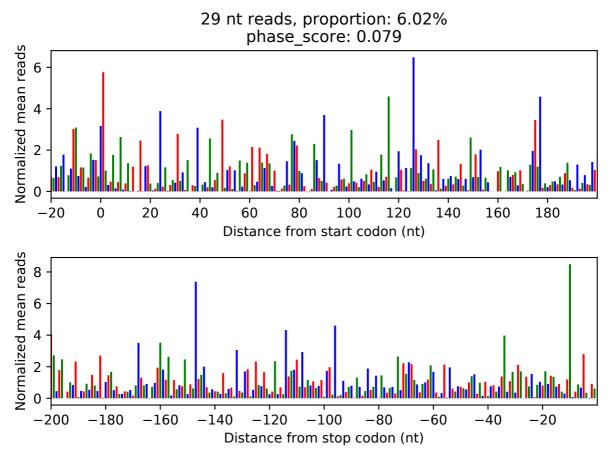


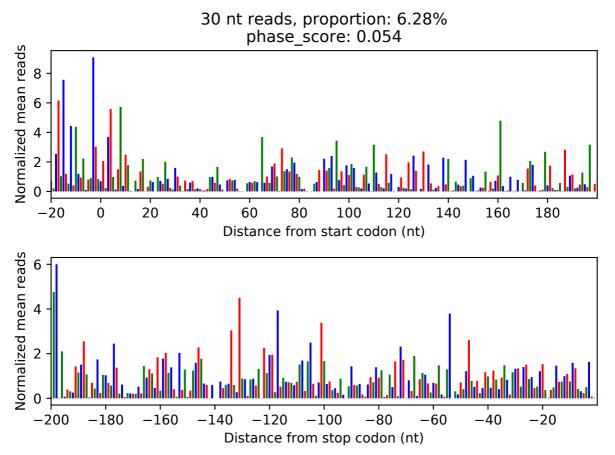




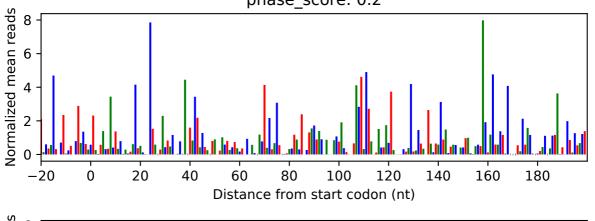


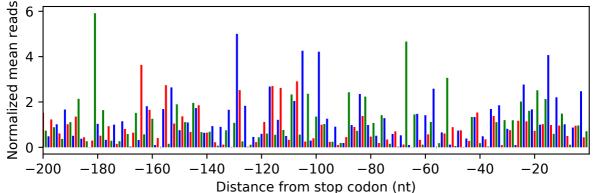


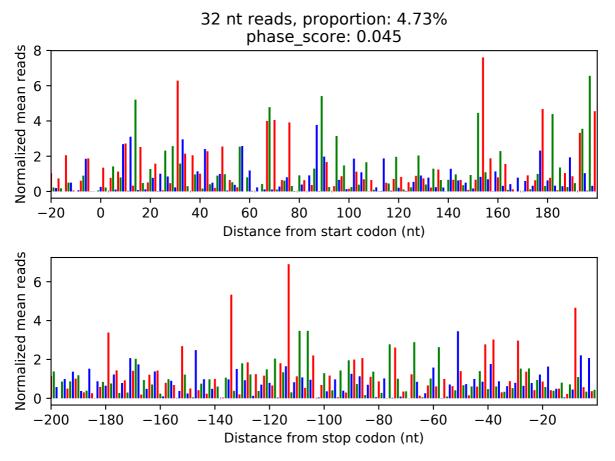


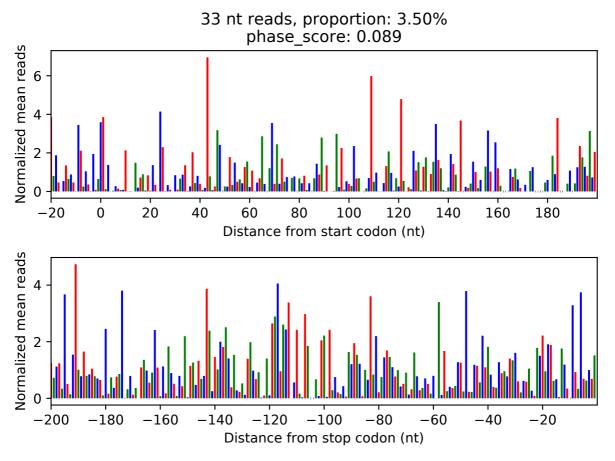


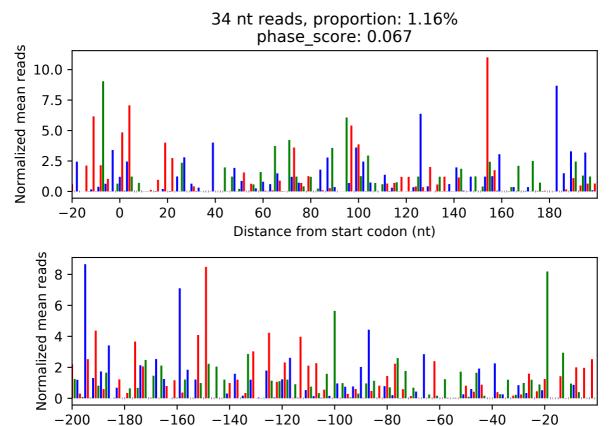
31 nt reads, proportion: 5.72% phase\_score: 0.2











Distance from stop codon (nt)

