1. (6 pts) The *cox1* gene encodes cytochrome oxidase subunit 1, a protein that is essential for oxidative phosphorylation. This gene is in the mitochondrial genome. Undergraduate students in Dr. Birky’s lab sequenced 588 bp of the *cox1* gene from four clones belonging to a species of asexual bdelloid rotifer. Most of the 588 sites were invariant in the four sequences; the sequences shown below include *only* the variable sites, colored for your convenience.

1. What proportion of the 588 sequenced sites are variable? (1 pt)

2. Calculate the nucleotide diversity of this species; carry your calculation to four decimal places. Show your calculations. (3 pts)

3. Assuming that all of the base sequence differences are neutral and that the mutation rate is $10^{-9}$ mutations per site per gamete, calculate the effective population size of this species. (2 pts)

**Note about the clone names:** These four clones got their names because they came from wet leaves in a house gutter in Columbus, Ohio; temporary streams in Helvetia and Round Valley, Arizona; and Shmoo Pool, a temporary rock pool in Virginia Dale, Colorado that looks like a shmoo in outline.
2. (4 pts) Use the 260-bp segment of Drosophila Adh DNA sequences in lecture Section 18a p. 12 to compare *D. virilis* and *D. melanogaster*, using the FIF allele of *D. melanogaster*.

(a) For these two species, calculate the observed sequence difference \(d\) and the corrected sequence divergence \(K\) using the Jukes-Cantor correction. (2 pts)

\[d = \underline{\quad}\]

\[K = \underline{\quad}\]

(b) If these two species separated 63 million years ago, calculate the rate of sequence evolution. (2 pts)