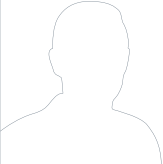
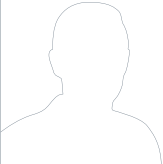
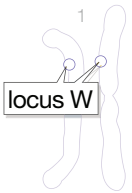
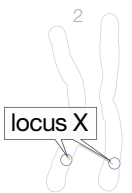
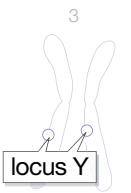
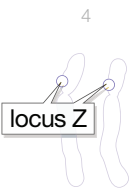


STR

A **Short Tandem Repeat (STR)** is a region of DNA composed of a short sequence of nucleotides repeated many times. Since the number of repeated sequences in a given STR varies from person to person, pinpointing these variants can be useful in DNA fingerprinting.

As the name implies, the repeated stretches in STRs are short—only two to ten base pairs long. For this reason, and because they are dispersed more evenly throughout the genome than the longer Variable Number of Tandem Repeats, or VNTRs, STRs are favored by forensic labs.

Large databases of information on STRs in the general population tell analysts how much variation exists at any given STR location. That information can help forensic analysts determine the conclusiveness of a "match" between two samples. If ten percent of people have the same number of repeats at a given STR, for example, finding a match at that site is merely suggestive that two samples are a match. If two sites with the same prevalence match, the odds drop to one in a hundred that the similarity is coincidental. If 13 sites match, the odds that any two people would possess such a fingerprint are so small— about one in ten trillion—that the result can be considered a definitive match.

				
Subject B 				
Tandem repeats at each loci	12 8	9 9	11 3	5 10

Results					
	12	14	9 9	11 3	5 10
	12	8	9 9	11 3	5 10