ANOMALIES IN 67 Y-CHROMOSOME STR LOCI

Nicole Bryant, Chelsea Joseph and Zach Wolfenbarger

Human Origins Genotyping Laboratory, Arizona Research Laboratories, The University of Arizona, Tucson, AZ

The Human Origins Genotyping Laboratory (HOGL) provides Y-chromosome STR testing services for IBM's and National Geographic's Genographic Project (https://www3.nationalgeographic.com/genographic/) and Family Tree DNA (www.familytreeDNA.com). HOGL currently genotypes 67 STR loci on the human Y-chromosome. Over the course of nine years and over 100,000 male samples, we have observed unique anomalies at a number of loci. These anomalies include regional deletion events, locus-specific deletion events, duplications, micro-alleles and single nucleotide polymorphisms in the flanking sequences. HOGL has implemented standardized protocols to help identify anomalous behavior at loci during fragment analysis. Here we present a summary of anomalous alleles, focusing on several specific loci including: DYS391, DYS449, DYS437 and DYS439. We assessed the occurrence of anomalies within Y-chromosome haplogroups to further assist in identifying patterns within lineages.

*Corresponding Author

Human Origins Genotyping Laboratory, Arizona Research Laboratories, The University of Arizona, Keating Building, Room 111, 1657 E Helen St, Tucson, AZ 85721, coli@email.arizona.edu