

STRait RAZOR v2.0: THE IMPROVED STR ALLELE IDENTIFICATION TOOL – RAZOR

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STRait Razor (the STR Allele Identification Tool – Razor) was developed as a bioinformatic software tool to detect short tandem repeat (STR) alleles in massively parallel sequencing (MPS) raw data. The method of detection used by STRait Razor allows it to make reliable allele calls for all STR types in a manner that is similar to that of capillary electrophoresis. STRait Razor v2.0 incorporates several new features and improvements upon the original software, such as a larger default locus configuration file that increases the number of detectable loci (now including X-chromosome STRs and Amelogenin), an enhanced custom locus list generator, a novel output sorting method that highlights unique sequences for intra-repeat variation detection, and a genotyping tool that emulates traditional electropherogram data. Users also now have the option to choose whether the program detects autosomal, X-chromosome, Y-chromosome, or all STRs. Concordance testing was performed, and allele calls produced by STRait Razor v2.0 were completely consistent with those made by the original software. This poster will explain the new features of STRait Razor v2.0 and their impact on forensic DNA analysis.