Current commercially available short tandem repeat (STR) typing kits provide capabilities for analysis of 24 different autosomal loci including the 13 CODIS (Combined DNA Index System) STR loci [1,2] plus D2S1338, D16S539, D5S818, D7S820, D13S317, FGA, vWA, D3S1358, D8S1179, D18S51, D21S11, TH01, D19S433, D12S391, TPOX, CSF1PO, and the Y-chromosome loci DYS389I, DYS391. Other polymorphic STR loci (70) or the current CODIS core loci, have been added. Data from over 500 U.S. population samples were evaluated across the 24 STR loci using Applied Biosystems (identifier, MiniFiler, NGM, NGM Select), Promega (PowerPlex 16, PowerPlex ESII 17, PowerPlex ESXI 17, PowerPlex 18D), and Qiagen (ESFIII, ESFIII SE, OptiX) kits. Allele ranges and locus characteristics for the 24 common STR loci are discussed. The probability of identity (P) with different sets of loci is illustrated to help assess the benefits of adding loci to the current 13 CODIS core loci.

Results and Discussion

STR-locus allele frequencies were generated from 552 U.S. samples as previously described during concordance testing [16]. In total, over 1450 samples have been examined with more than a dozen different STR kits. Information from various subsets of this data are shown on this poster. The table on the left ranks the 24 autosomal STR loci by their probability of identity, which is a measure of locus diversity determined by the square of the observed genotypic frequencies with a lower number indicating a higher power of discrimination. The table on the right calculates the random match probabilities (RMP) values for various combinations of loci. Impact of new loci on kinship calculations is illustrated with the figure on the bottom right. Adding more loci improves kinship association in parent-offspring trios. The table below displays the observed allele frequencies from a combined set of 552 U.S. samples consisting of 240 White Americans, 162 Caucasians, 139 Hispanics, and 2 Asians. The most common allele for each locus is listed in bold text.

Observed Allele Frequencies for 552 U.S. Population Samples