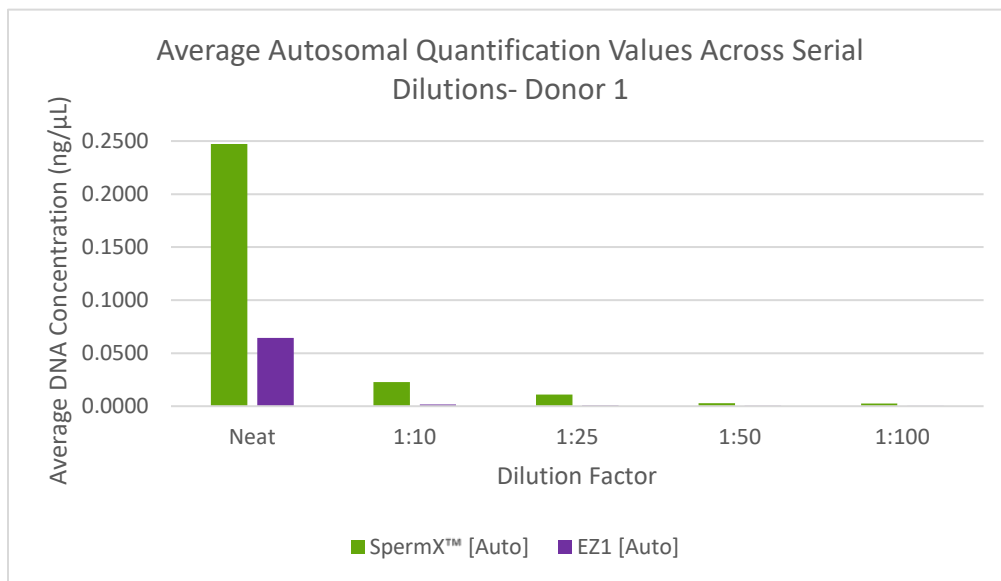


# Differential Extraction Sensitivity Study

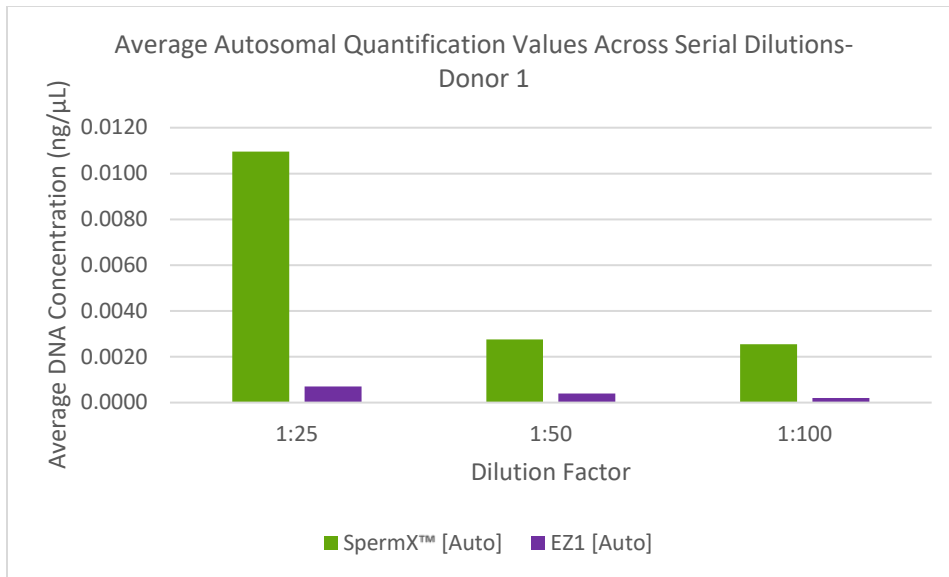
## Palm Beach County Sheriff's Office

### Sensitivity (Serial Dilution) Study

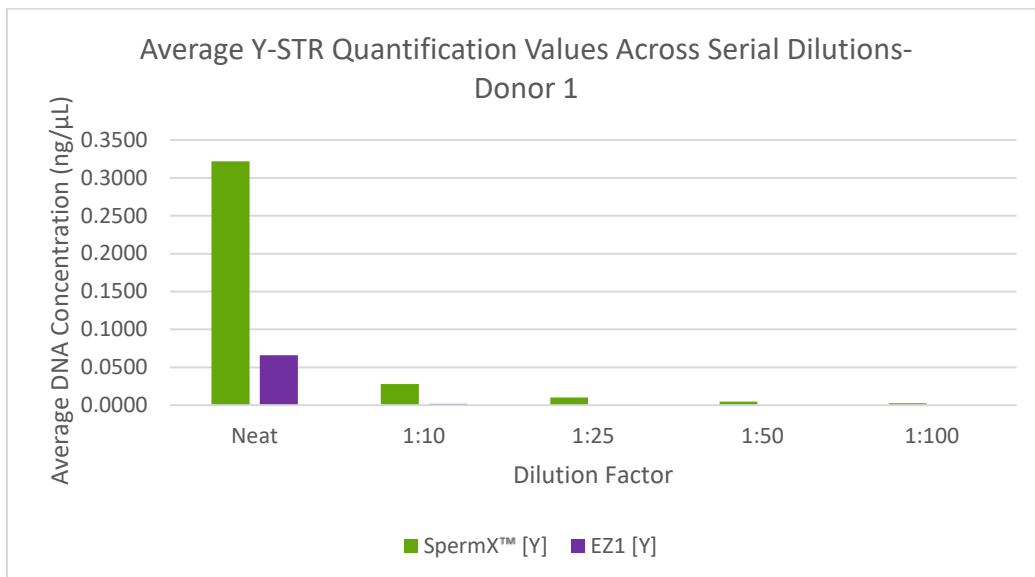
Two semen dilution series (neat, 1:10, 1:25, 1:50, and 1:100) were prepared from two male donors (Donor 1 and Donor 2) to assess DNA recovery and STR profile completeness (allele recovery). Each dilution was extracted in duplicate using both the Gentueri SpermX™ GenSpin Differential Extraction Protocol and the laboratory's currently validated differential Extraction Protocol (EZ1 Advanced XL). For each dilution, half a swab was processed per extraction method. Samples were analyzed to evaluate the sensitivity of the SpermX GenSpin protocol relative to the laboratory's current differential extraction method. Profile completeness across the serial dilutions was evaluated to determine the extent of allele recovery at decreasing DNA concentrations for each extraction method.



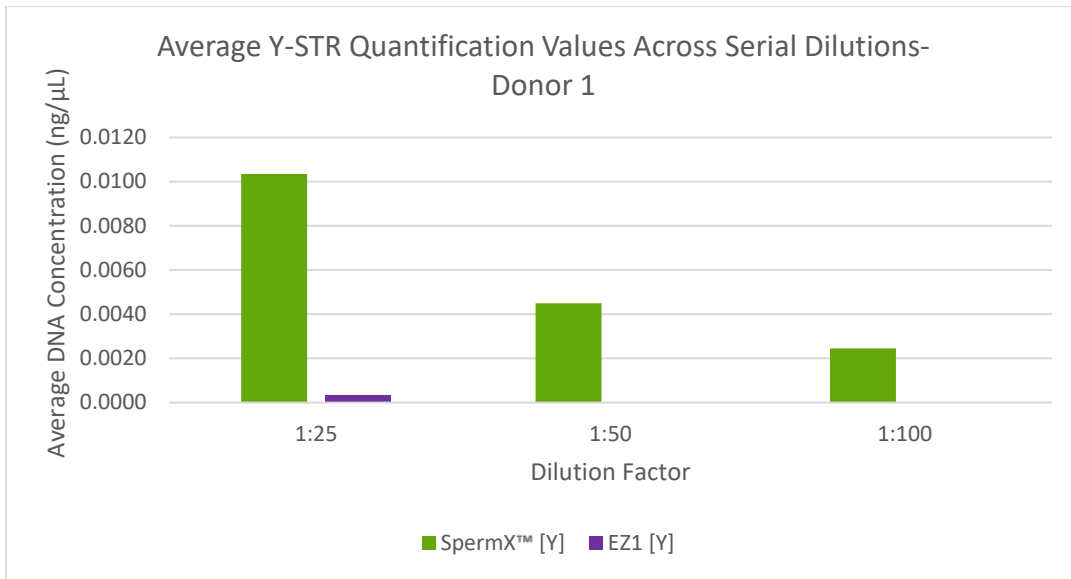
Comparison of the average autosomal quantification values (ng/µL) across a serial dilution series (neat, 1:10, 1:25, 1:50, and 1:100) of male donor 1, obtained using the SpermX™ GenSpin and the laboratory's current differential extraction method with Promega PowerQuant® analysis.



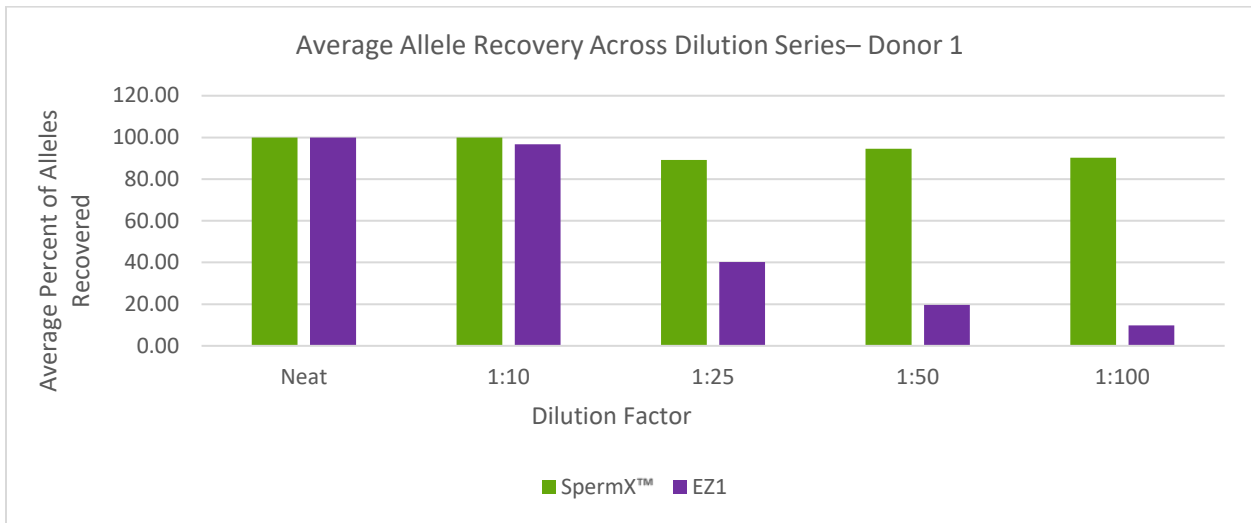
Comparison of the average autosomal quantification values (ng/μL) across a serial dilution series (1:25, 1:50, and 1:100) of male donor 1, obtained using SpermX™ GenSpin and the laboratory's current differential extraction method with Promega PowerQuant® analysis.



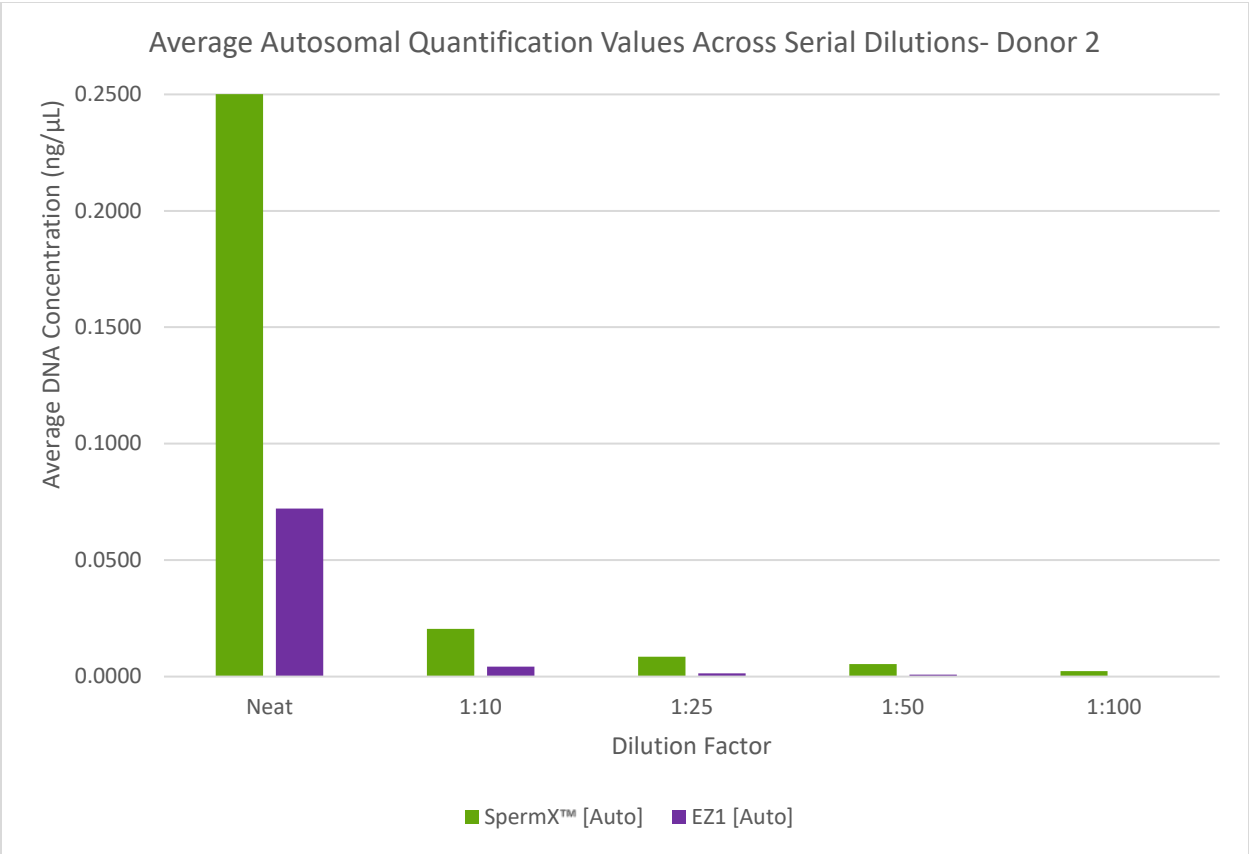
Comparison of the average Y-STR quantification values (ng/μL) across a serial dilution series (neat, 1:10, 1:25, 1:50, and 1:100) of male donor 1, obtained using the SpermX™ GenSpin and the laboratory's current differential extraction method with Promega PowerQuant® analysis.



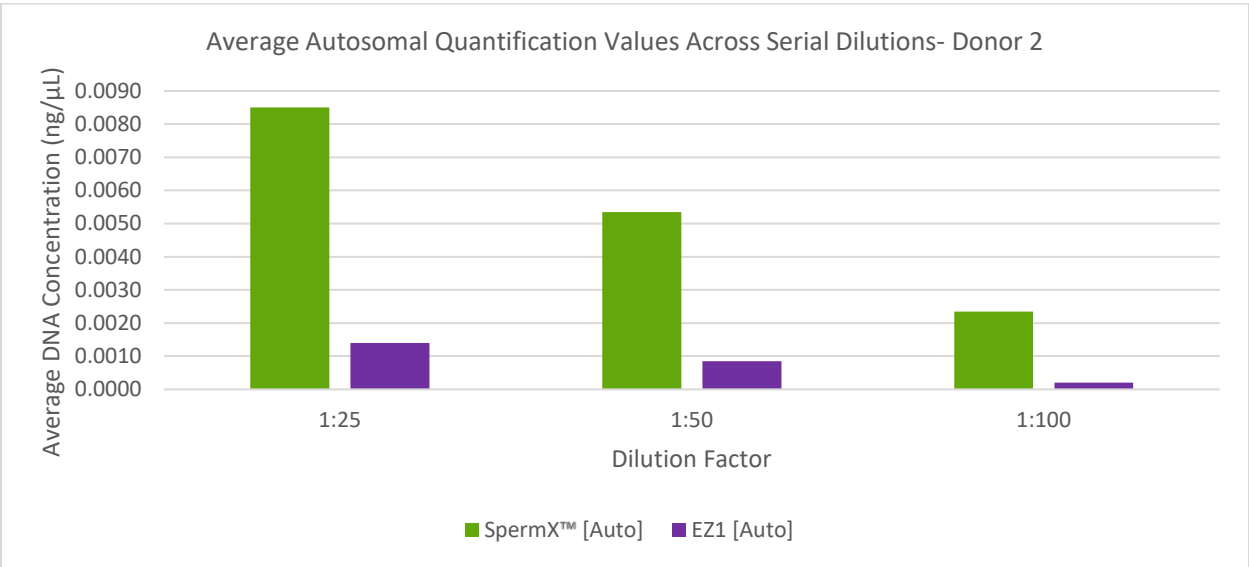
Comparison of the average Y-STR quantification values (ng/μL) across a serial dilution series (1:25, 1:50, and 1:100) of male donor 1, obtained using the SpermX™ GenSpin and the laboratory's current differential extraction method with Promega PowerQuant® analysis.



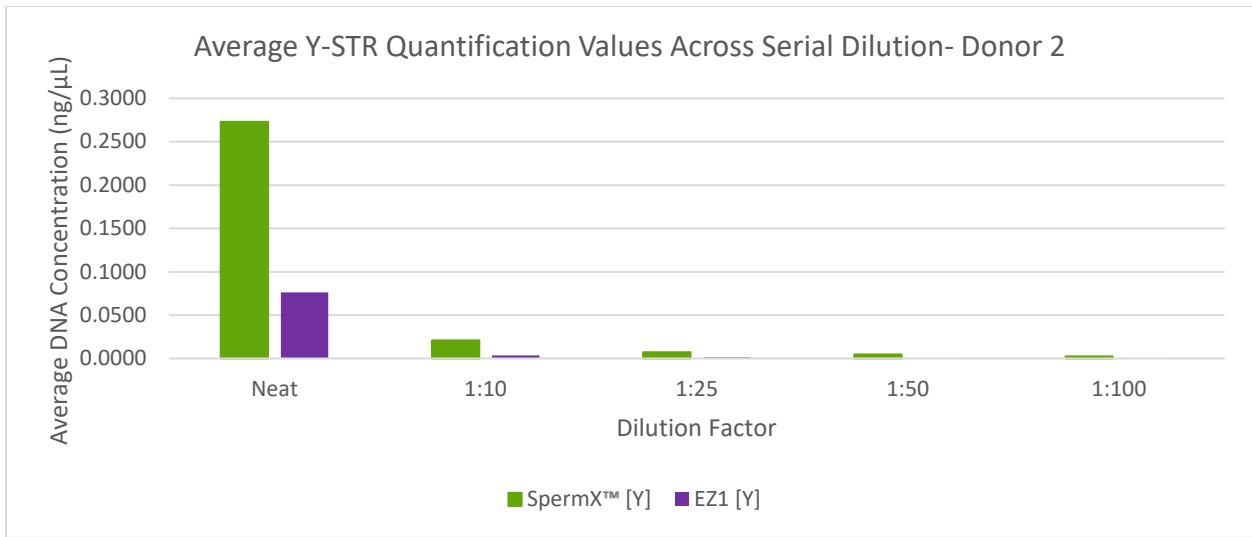
Comparison of average alleles recovery across a serial dilution series of male donor 1 using the SpermX™ GenSpin and the laboratory's current differential extraction method analyzed with Promega PowerPlex® Fusion 6C.



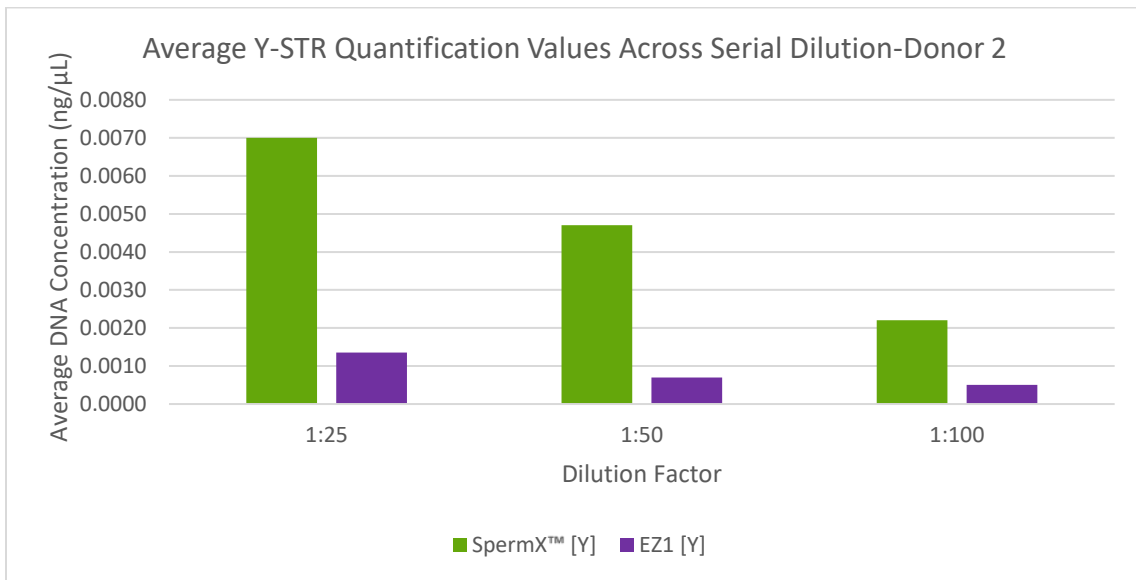
Comparison of the average autosomal quantification values (ng/μL) across a serial dilution series (neat, 1:10, 1:25, 1:50, and 1:100) of male donor 2, obtained using the SpermX™ GenSpin and the laboratory’s current differential extraction method with Promega PowerQuant® analysis.



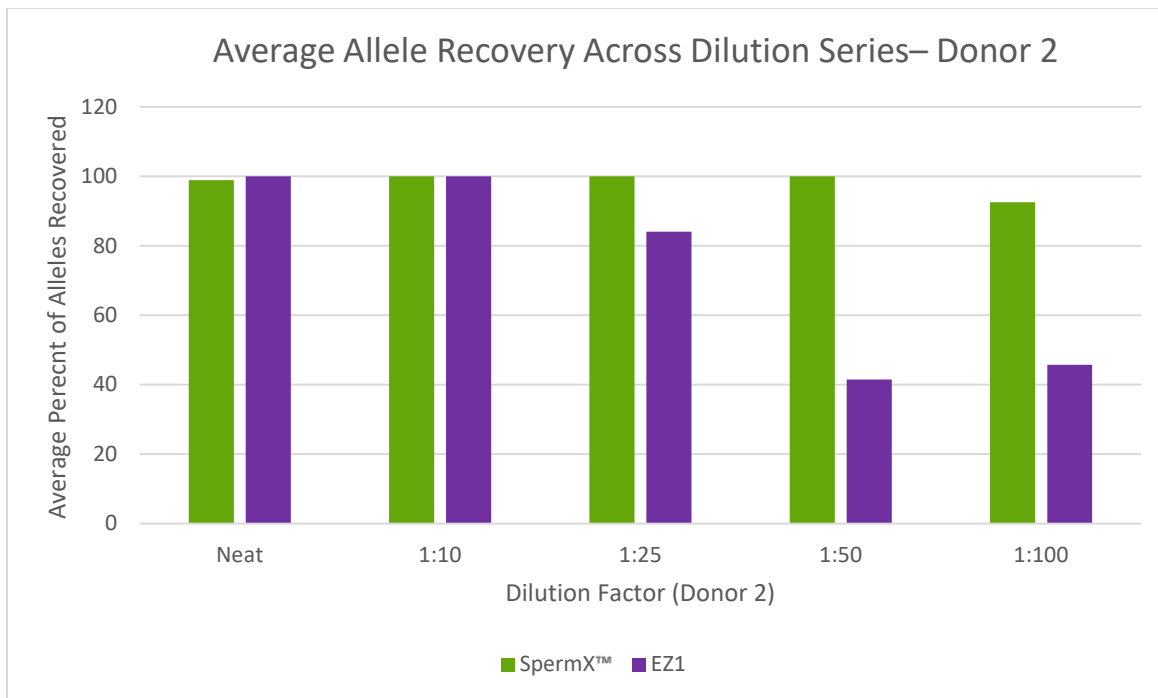
Comparison of the average autosomal quantification values (ng/μL) across a serial dilution series (1:25, 1:50, and 1:100) of male donor 2, obtained using laboratory’s current differential extraction method with Promega PowerQuant® analysis.



Comparison of the average Y-STR quantification values (ng/μL) across a serial dilution series (neat, 1:10, 1:25, 1:50, and 1:100) of male donor 2, obtained using the SpermX™ GenSpin and laboratory’s current differential extraction method with Promega PowerQuant® analysis.



Comparison of the average Y-STR quantification values (ng/μL) across a serial dilution series (1:25, 1:50, and 1:100) of male donor 2, obtained using the SpermX™ GenSpin and laboratory’s current differential extraction method with Promega PowerQuant® analysis.



Comparison of average allele recovery across a serial dilution series of male donor 2 using the SpermiX™ GenSpin and the laboratory’s current differential extraction analyzed with Promega PowerPlex® Fusion 6C.

### Summary of Findings

Across both donors, the Gentueri SpermiX™ GenSpin Differential Extraction method consistently outperformed the laboratory’s current differential extraction method in DNA recovery and allele detection. For Donor 1, SpermiX™ GenSpin yielded 3.8x–26x higher autosomal and Y-target DNA concentrations than the laboratory’s current differential extraction method, while for Donor 2, fold increases averaged 6.6x for autosomal and 5.2x for Y-target DNA. SpermiX™ GenSpin maintained measurable recovery at all dilutions, including 1:100, whereas in-house differential extraction yields were frequently near or below detection limits. SpermiX™ GenSpin preserved a high number of detectable alleles across the dilution series, with ≥89% of expected alleles observed for Donor 1 and ≥92% for Donor 2 even at the highest dilutions, compared to <50% of expected alleles detected for the laboratory’s current differential extraction method beyond the 1:25 dilution. These results indicate that Gentueri SpermiX™ GenSpin extraction method provides efficient extraction, high sensitivity, and reliable allele recovery across a wide range of DNA inputs.