

## SOME STRATEGIES TO RECOVER SGM PLUS® PROFILES FROM PROBLEMATIC EVIDENCE SAMPLES

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Forensic laboratories have to deal frequently with evidence samples that contain small amounts of DNA that, further, may be degraded. The choice of adapted extraction methods and efficient PCR protocols is therefore crucial in order to successfully amplify this material. For instance, reducing the amount of template DNA and increasing the number of PCR cycles can sometimes greatly improve the results. Similarly, doubling the amount of *Taq* Polymerase and adding albumin in the PCR-mix may help with the typing of some problematic samples.

We re-analyzed 170 samples, which initially gave inconclusive SGM Plus® profiles, using such strategies. The totality of these samples were first re-amplified using the initial extract. In a second run, samples for which enough material was left (about 40%) were re-extracted, generally following a different protocol. All the alleles reported in this work were detected a minimum of three times in replicate amplifications from the same or from different extracts.

At the end, a SGM Plus® profile fulfilling the Swiss national data base criteria (6 and 8 STRs for single and mixed profiles, respectively) was obtained for 78 out of the 170 samples considered (46%). The success rate per sample type and a description of illustrative cases demonstrating the usefulness of these strategies are presented in the poster.