## SUCCESSFUL SNP GENOTYPING BY MALDI-TOF MASS SPECTOMETRY WITH DNA EXTRACTED FROM HUMAN BLOOD SERUM SAMPLES WITH DNA IQ™ CASEWORK PRO KIT FOR MAXWELL® 16

Rainer Schubbert, Sarah Kössel, Britta Gätjens, Katrin Juling Eurofins Medigenomix GmbH, Anzinger Str. 7a, 85560 Ebersberg, Germany

Human blood serum samples contain small and varying amounts of DNA, since the DNA carrying blood cells were separated from the samples. Furthermore, the DNA is partially fragmented and hence, the quality of DNA extracted from serum samples is rather low. Although serum samples are not the first choice samples for a genetic study, it can be necessary to yield their DNA and to analyse genetic markers on it.

Recently, we were asked to genotype 200 human blood serum samples at 26 point mutations (SNPs) in a clinical patient study. Since the DNA traces in serum samples resemble forensic traces we tried to catch the DNA by a forensic DNA extraction method, the Promega DNA IQ™ Casework Pro Kit for Maxwell® 16.

Subsequently, the DNA was used for genotyping with MassARRAY® SNP genotyping system (Sequenom®). This system requires only a small and low-quality spike of DNA and analyses up to 40 SNPs in one multiplex reaction.

Here, we present our data from the successful genotyping of the serum DNA with very high calling rates and reliable and reproducible results. **%**