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HR Finder

The explosion of highthroughput SNPs genotyping technologies, like Affymetrix, opened new exciting ways of investigations. Based on the method described by Woods and his collaborators (Woods et al, 2004), we have developed a new user friendly interface allowing the use of not only the 10 K but also the 100K and the 250K to seek homozygous regions in consanguineous families using only the affected members of the pedigree. HR Finder is highly customizable according to sib pairs, number of SNP per CM, number of No Call allowed... making this tool highly efficient for fast and low cost analyses.

Safe your money and only genotype the affected patient

For further information or a quote, please contact m.herman@dnavision.be