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BECKMAN COULTER
Capillary Electrophoresis

One Gel, One Array, One Software

CEQ™ 8000 STR Analysis

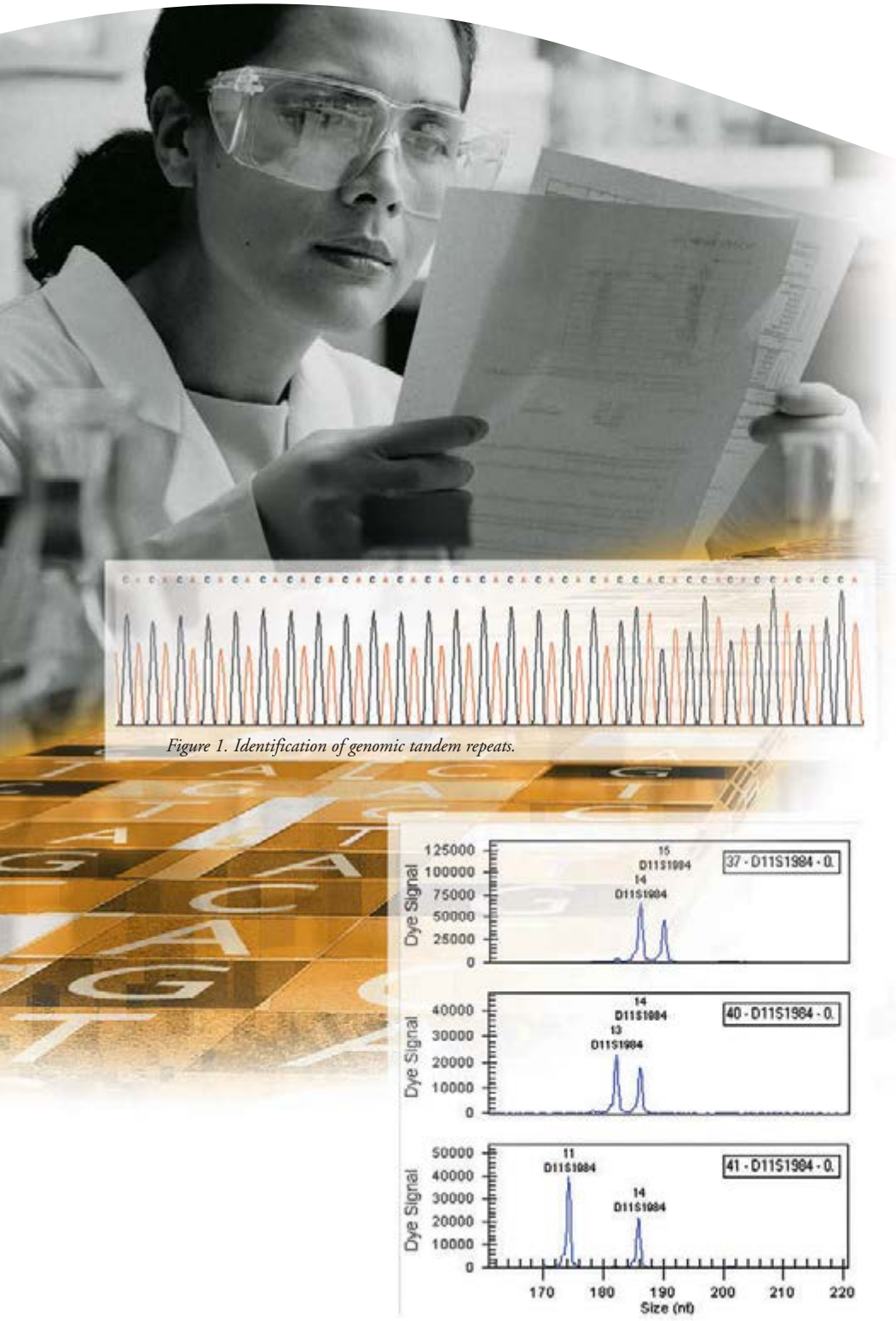

Figure 1. Identification of genomic tandem repeats.

Figure 2. Automated tandem repeat analysis.

Tandem repeat regions in DNA sequences are widespread throughout the human, plant and microbe genomes and show sufficient variability among individuals that they have become important in genetic mapping and linkage analysis. These tandemly repeated regions of DNA are typically classified into several groups depending on the size of the repeat region. Minisatellites (variable number of tandem repeats, VNTRs) have core repeats with 9-80 bp, while microsatellites (short tandem repeats, STRs) contain 2-7 bp repeats. STR markers are very abundant and well-distributed throughout the genomes, located approximately every 10-15 kb.

Identification of Tandem Repeats - Sequencing

Genomic tandem repeats are identified by dye terminator cycle sequencing (DTCS) *(Figure 1)*.

Automated Tandem Repeat Analysis - Fragment Analysis

Tandem repeats have become one of the most widely used genomic markers due to their high degree of heterozygosity and simple methodology – PCR® amplification, fragment sizing and locus / allele scoring. The CEQ™ 8000 Genetic Analysis System provides accurate and high precision sizing of the amplified fragments for automated allele and locus identification. It identifies alleles even in the presence of polymerase artifacts such as stutter and plus A peaks.

The electropherograms may be viewed individually, overlaid or stacked to facilitate data comparison. CEQ™ DNA Size Standard-400 or Size Standard-600 are used for fragment sizing *(Figure 2)*.

CEQ™ DTCS Quick Start Kit

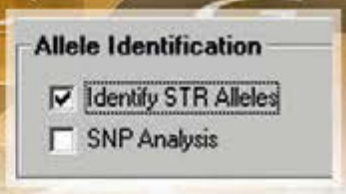

Figure 3. STRs may be identified by size allowing alleles to be identified.

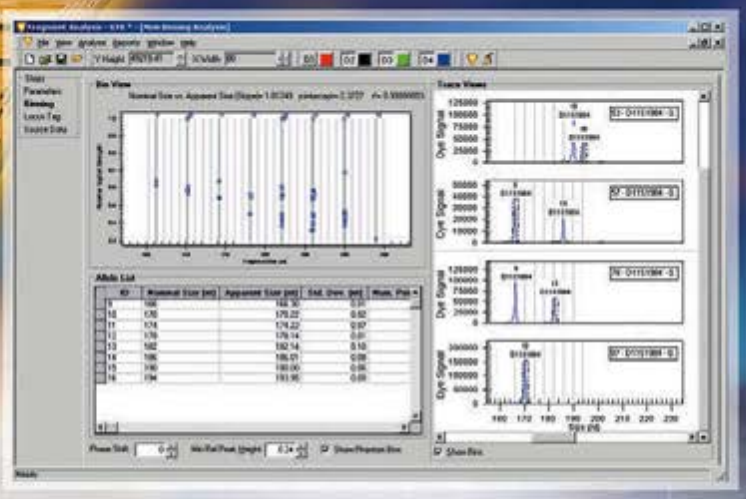

Figure 4. Locus Tag are automatically generated using the integrated Binning software.

Figure 5. Exported STR genotype table.

Individual ID	D11S1984 A1	D11S1984 A2
37-D11S1984	14	15
40-D11S1984	13	14
41-D11S1984	11	14
42-D11S1984	12	13
43-D11S1984	14	15
44-D11S1984	13	14
46-D11S1984	15	15
47-D11S1984	15	15
48-D11S1984	11	12

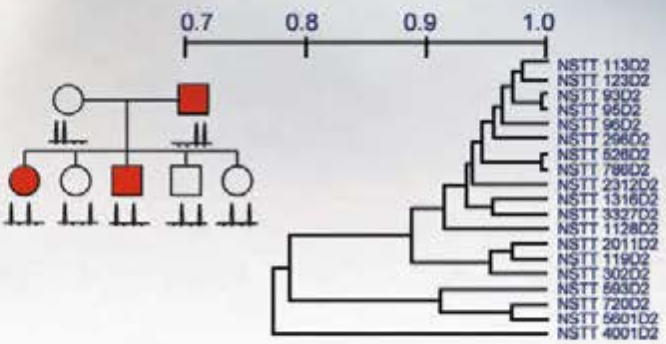

Figure 6. The results are easily used for phylogenetic analysis.

The STR genotypes can be exported in spreadsheet format *(Figure 5)* for linkage/association studies or used for automated analysis of cancer loss of heterozygosity (LOH) / microsatellite instability (MI) or phylogenetic analysis *(Figure 6)*.

Ordering Information:

Reagents for Automated DNA Sequencing:

608120 CEQ™ DTCS Quick Start Kit

608000 CEQ™ DTCS Kit

Reagents for Short Tandem Repeat Analysis:

608098 CEQ™ DNA Size Standard Kit – 400 (for 60-400 bp)

608095 CEQ™ DNA Size Standard Kit – 600 (for 60-600 bp)

For Labeled Primers contact your local Beckman Coulter sales representative.

Hardware and Software

285501 CEQ™ 8000 Genetic Analysis System, 110/230 V With CEQ™ 8000 Software for Sequencing and Fragment Analysis

285590 CEQ™ 8000 Migration Package (from CEQ™ 2000XL)

CEQ™ Supplies

608087 CEQ™ DNA Separation Capillary Array, 33cm × 75 mm

608082 CEQ™ Sample Loading Buffer (SLS), 6.0 ml

608010 CEQ™ Separation Gel 1

608012 CEQ™ Sequencing Separation Buffer, 4/pk

609844 CEQ™ Separation Buffer Plates, Nonsterile, without lids, 300 µl/well, 100/pk

609801 Sample Microtiter Plates, 25/pk, V-bottom, Thermal cycler compatible, 200 µl/well

* *The PCR process is covered by patents owned by Roche Molecular Systems, Inc. and F. Hoffman-La Roche, Ltd.*

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