

ChimeRMarker™

Automated Chimerism Analysis Software



Automated Chimerism STR Analysis and Monitoring Software

- Increased Accuracy
- Streamlines Analysis Workflow
- No Data Transfer
- Longitudinal Monitoring
- Compatible with all Major Capillary Electrophoresis Systems and Chemistries

SOFTGENETICS®
Software PowerTools for Genetics Analysis

SoftGenetics, LLC
Oakwood Centre
100 Oakwood Avenue
Suite 350
State College PA 16803 USA
info@softgenetics.com
www.softgenetics.com

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ChimerMarker™ Automated Chimerism Genotyping Analysis and Monitoring Software

ChimerMarker™ software combines accurate size and allele calls (genotyping) with automated chimerism analysis. The program integrates speed and accuracy with a biologist-friendly interface. Initial analysis is typically three steps to completion.

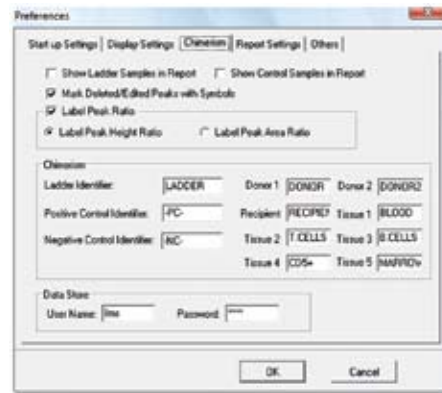
- GENOTYPING donor and recipient
- CASE SPECIFIC CHIMERISM PANEL construction
- AUTOMATED CHIMERISM CALCULATIONS and GRAPHICS.

ChimerMarker is compatible with ABI®PRISM, Beckman-CEQ™, and MegaBACE® genetic analyzers, and custom or commercially available human identification chemistries for STR genotyping (including Identifiler®, PowerPlex®16, PowerPlex®ESI).

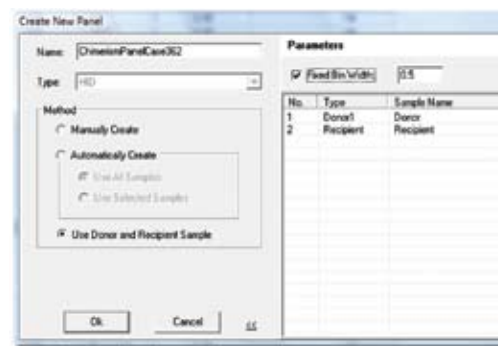
ChimerMarker software can be used to monitor chimerism level in both allogeneic and autologous stem cell transplant (SCT), hematopoietic stem cell transplant (HSCT), bone marrow transplant (BMT, post bone marrow engraftment), and peripheral blood stem cell transplant (PBSCT) samples.

Analysis Preferences, Multi-Lineage Analysis and Automated Panel Construction

The program preferences include labeling peak ratios by height or area; with multi-lineage capabilities for chimerism analysis of T-cells, B-cells, and other cell type populations. These populations may indicate graft-versus-host disease (GVHD) or graft rejection. In addition, there are functions for comparison of samples at different time points to conduct longitudinal studies and produce a comprehensive graph. Case specific panels are automatically constructed, using Donor and Recipient allele calls.



ChimerMarker recognizes up to five different tissue types with users specified identifiers for multi-lineage analysis. Analysis and calculation time are reduced since samples from multiple cell types can be analyzed at one time when a Chimerism Panel is used.

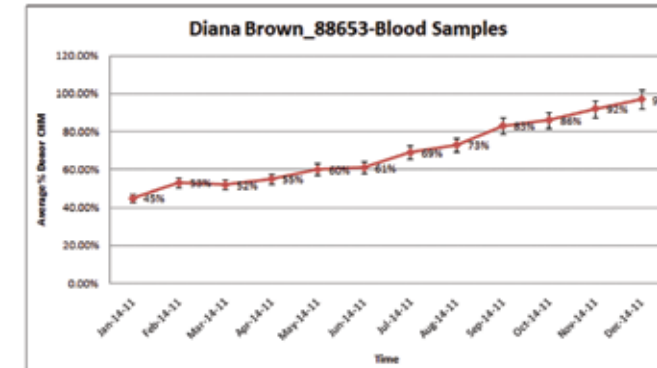
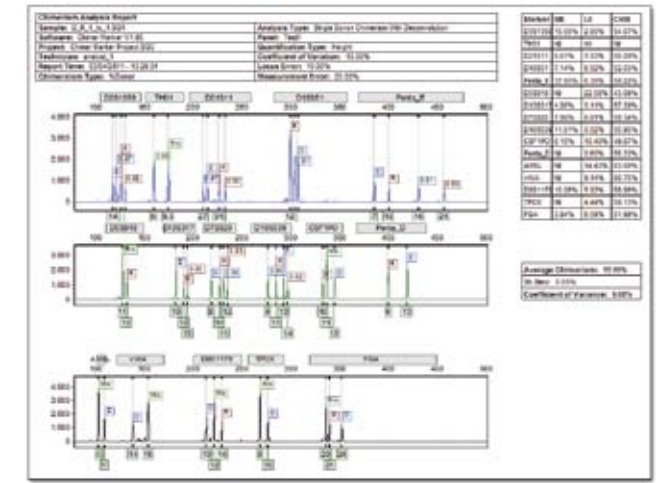


Automatically construct unique panels that will recognize donor and recipient peaks in post BMT studies.

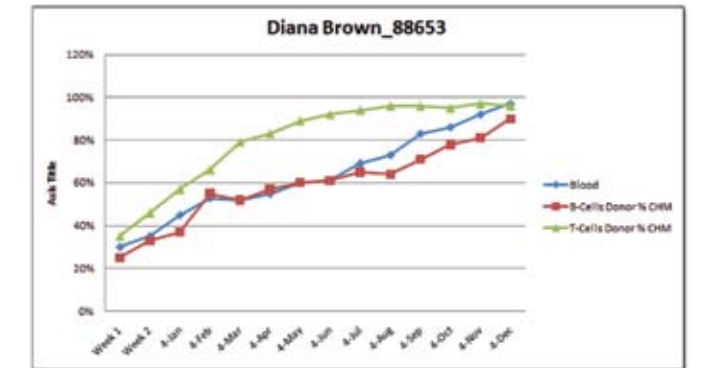


Comprehensive Report - chimerism analysis is completely linked to the main analysis screen, removing the error-prone step of data transfer from genotyping software to chimerism analysis software.

Comprehensive report for each sample at a given time point in the study; includes header, electropherograms (traces) and report table. The report header uses information from user management and the analysis settings to specify the technician, project, time, date, and parameters for electronic record keeping. The electropherograms (traces) show each dye-color separately with labels for D (donor) and R (recipient). Results displayed include quality control metrics: coefficient of variation, standard deviation, % chimerism, measurement error, and locus error for each marker; and the total average % Chimerism. Nil represents uninformative loci (all peaks are shared) and are not included in the chimerism calculations or indicates parameters could not be calculated based on data. ChimerMarker software also contains the functionality to allow the analyst to manually exclude loci from calculations if needed.



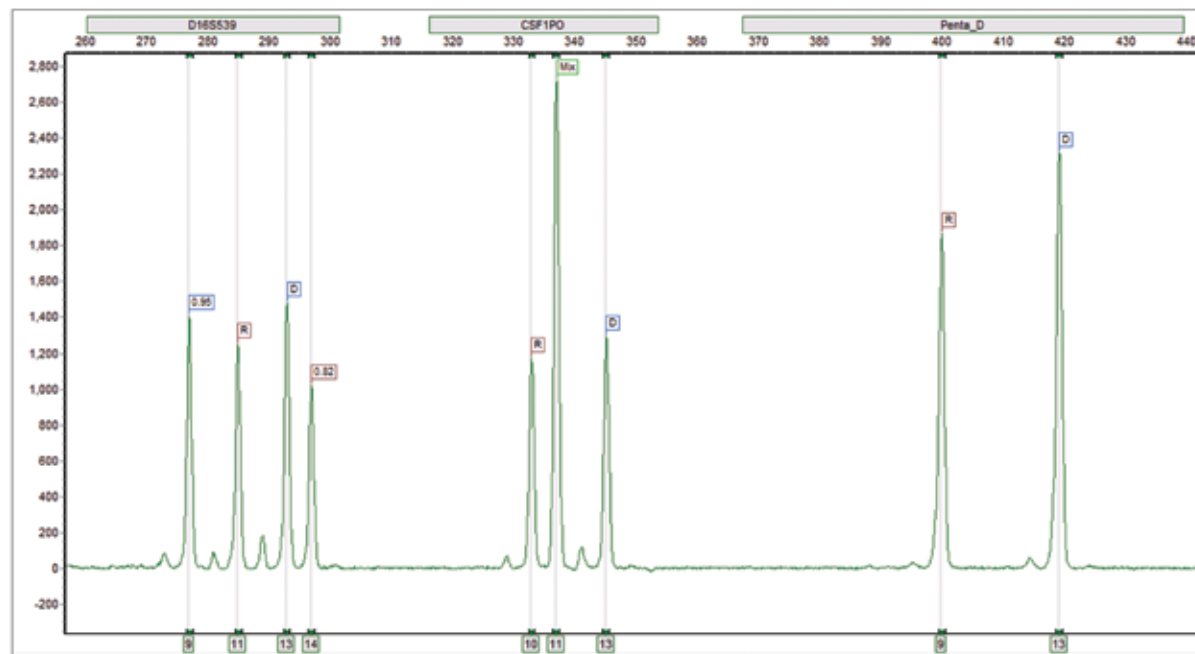
This graph is an example of a projected **Longitudinal Report** for a Post-Bone Marrow Engraftment study using a single cell type, with average percent donor chimerism monitoring over a one year period.



A projected **Multi-Lineage Analysis** graph provides visualization of the data trend in an extended monitoring period for post-bone marrow engraftment over a one year period.

ChimerMarker utilizes highly accurate size calibration and allele calling algorithms with the ability to differentiate between donor, recipient, and shared peaks in the electropherogram using the unique chimerism panel for that patient. In addition, it will also automatically calculate percent chimerism and quality metrics for each sample without the need to transfer data between software.

Peak Differentiation and Labeling – Immediate Visualization of Donor and Recipient Alleles



Post-Transplant Sample: ChimerMarker will differentiate and label peaks for Donor (D), Recipient (R), or Mixture (Mix) for shared alleles in each locus. Heterozygous Imbalances are also calculated for sister alleles of the same locus separately for donor and recipient.

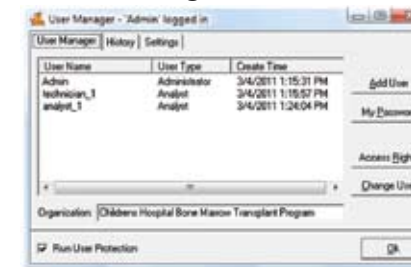
User Management and Audit Trail

User management provides control of user access rights and generates a user and audit trail for each project. Access rights for each user may be selected by the administrator – providing assurance that unauthorized individuals do not accidentally alter a project. User management also provides user ID and Organization name for the header of the final clinical research reports.

Password Protected Login



Login Record



Records Data Audit Trail



If trial disc is not present please email info@softgenetics.com for a free 30-day trial