A Variant Analysis Software

SOFTGENETICS®

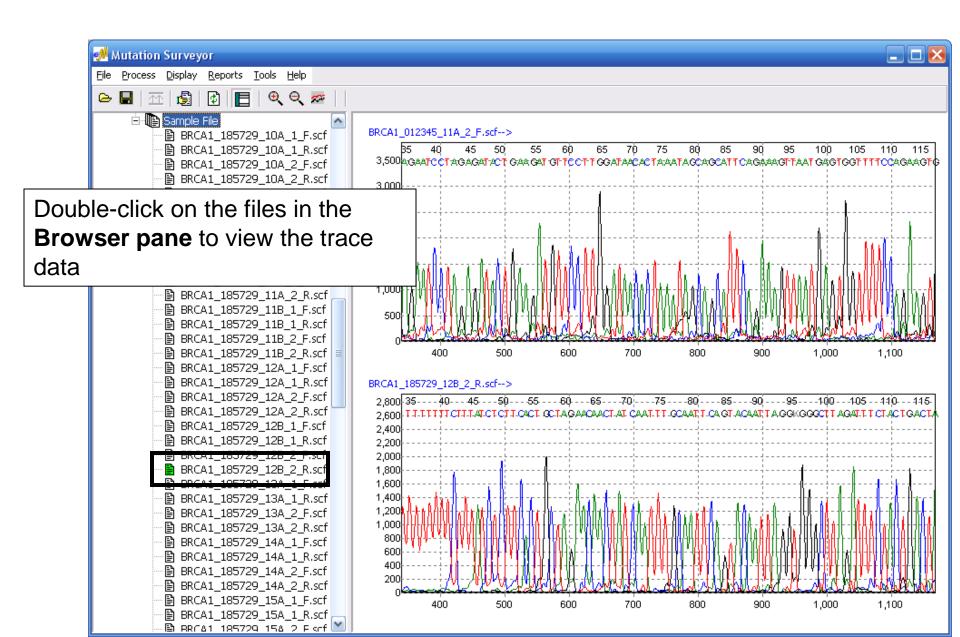
Software PowerTools for Genetic Analysis

www.softgenetics.com / info@softgenetics.com

Upload Data

Mutation Surveyor File Process Display Reports Tools Help Open Files editions of the second	Click Open Files icon in main toolbar
GenBank Sequence File(Optional) Add Remove Remove All	Add GenBank Files (GBK/SEQ) and/or Reference Files (SCF/AB1/ABI) NOTE: Both GenBank and Reference
Reference Files Add Remove Remove All	files are optional when sequences map to genes of <i>Homo sapiens</i> .
Sample Files C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10A_1_F.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10A_2_F.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10A_2_R.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10B_1_F.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10B_2_R.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10B_2_R.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10B_2_R.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10B_2_R.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_10B_2_R.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_11B_2_R.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_11A_1_F.scf C:\Data\MutationSurveyor\BRCA1\Samples\BRCA1_012345_11A_1_R.scf C:\Data\MutationSurveyOR\BRCA1\Samples\BRCA1_0123	Add Sample Files (SCF/AB1/ABI)
Samples Selected: 150 🗆 Load Grouping File OK Cancel	Click OK

Review Raw Data



Analysis Settings

File

In the main toolbar select Process \rightarrow Settings...

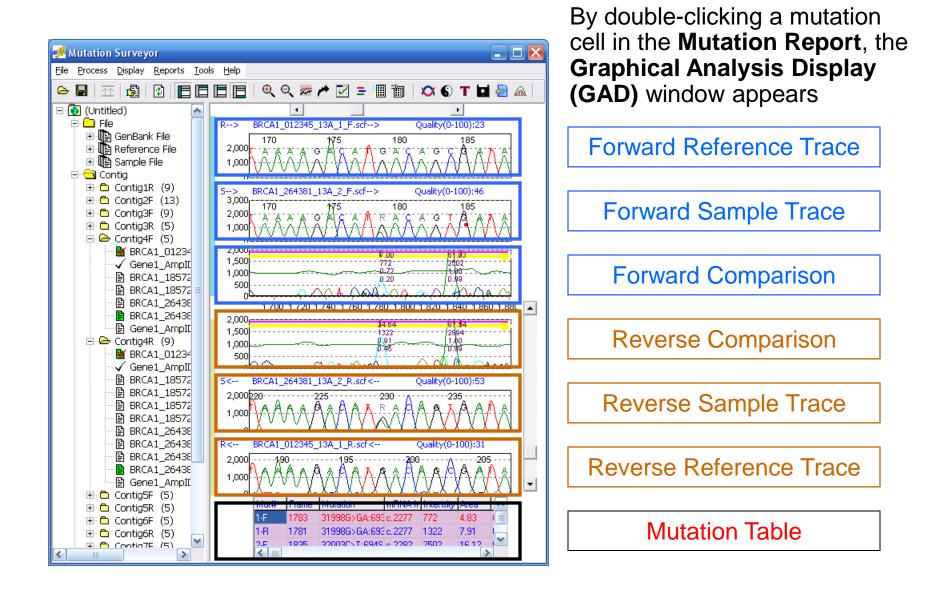
📌 Mutation Surveyor Process Display Reports Tools Help 🔍 🔍 🗫 Run E Restart BRCA1_012345_11A_2_F.scf--> 35729_10A_1_F.scf Settings... 5.5 Mutation Project Settings E DRCA1 1 BRCA1_1 Contig Mutation Output Display 2 Directions Others Raw 🖹 BRCA1_1 Contig BRCA1_1 12 Fragment Size BRCA1_1 BRCA1_1 Matching Base Number 60 🖹 BRCA1_1 Matching Base Percentage 30% (20%-90%) 🖹 BRCA1_1 Force into One Contia 🖹 BRCA1_1 Exclude 1st Base Difference > 200 🗄 🔲 BasePatch Calculate Lane Quality Within the Region of Interest Use Amplicon ID to Construct Contig • From Character 1 To 7 C Use Sample Grouping File Pairing Exact Filename F/R Match 🔲 Exact Filename Match Before F/R Trimming Quality Trim Vector Trim 5' Trim 30 🔲 3' Trim 30 bps bos Score Trim 16 (10-40) Contig Sort By: Sample Filename **Reference Filename** œ Contig Num. of Sample Files GenBank/Reference Comparison Default ΟK Cancel

For first run analysis click **Default** then **OK**

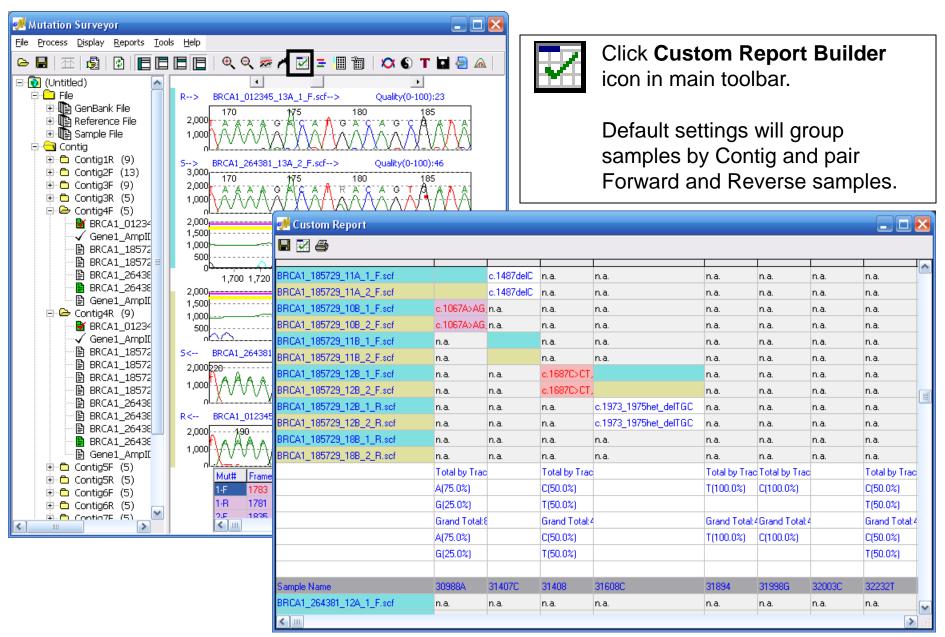
Analyze Your Data!

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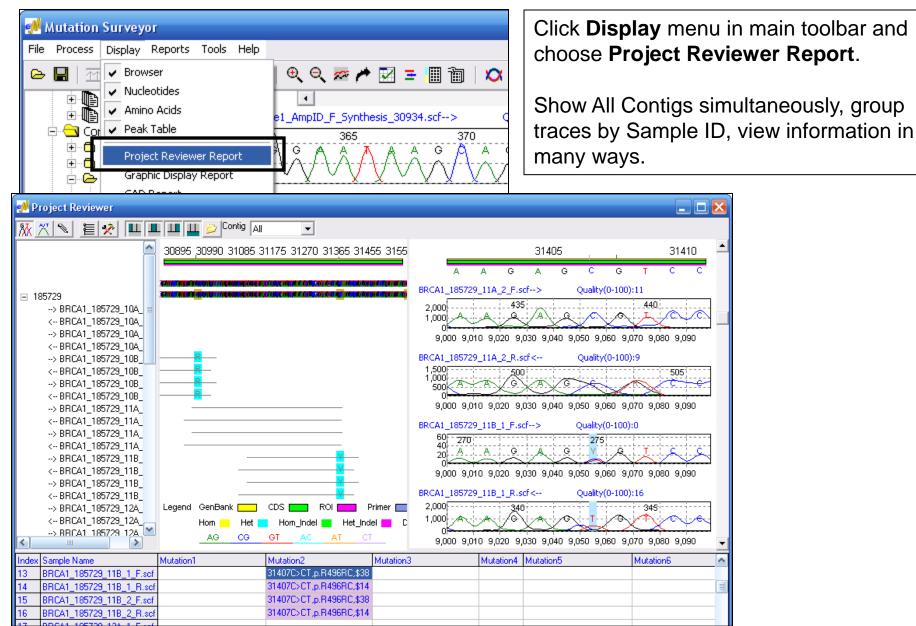
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