

Program Upgrade Bulletin

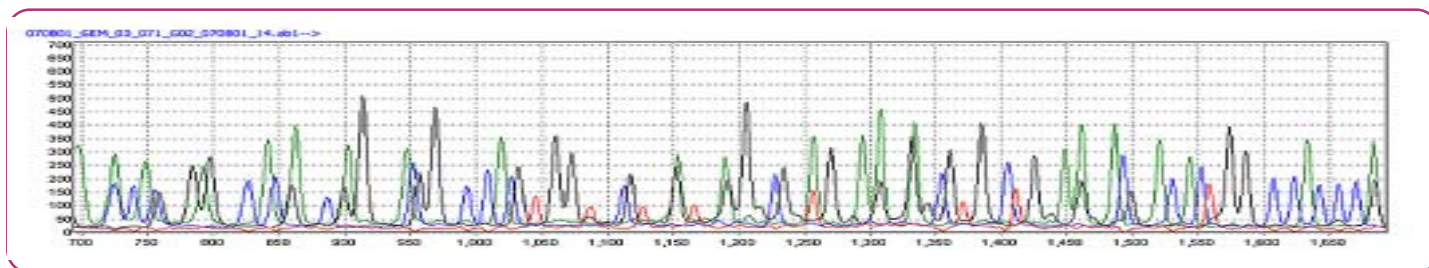
June, 2006

Mutation
Surveyor[®]
Mutation
Explorer[®]

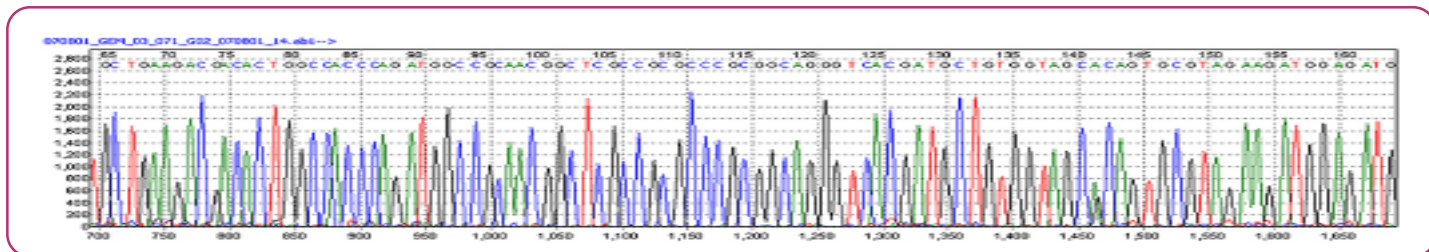
We are pleased to announce the following enhancements are now included in Mutation Surveyor and Mutation Explorer v. 3.0:

Mobility Correction for ABI 3700 systems

Raw Data

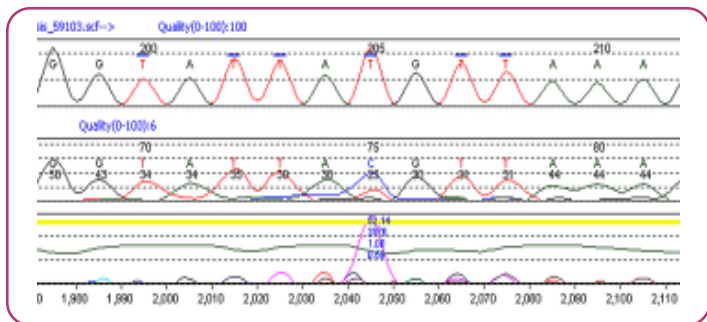


Re-Processed Data



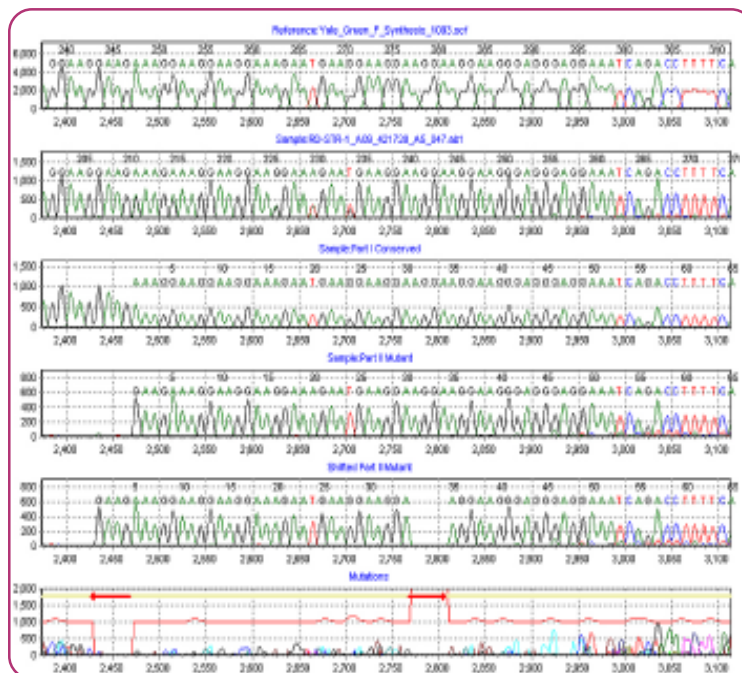
Both programs now include a "Raw data" re-processing and base calling feature to correct mobility issues frequently observed with the newer Applied Bio Systems Sequence instrumentation and KB basecaller.

Automated Methylation Detection



Mutation Surveyor now utilizes its unique physical trace comparison technology to detect methylation in CpG islands. The GenBank sequence of the DNA of interest is used as a "ruler" to report nucleotide changes, including methylations and mutations. The methylation function of Mutation Surveyor utilizes the GenBank sequence text or derivatives of the sequence text and converts it into a synthetic reference sequence. This synthetic reference sequence is then physically compared to the sample sequence traces from bisulfite-treated DNA to find nucleotide differences.

Enhanced Het-Indel Detection



Improved Indel detection algorithm can differentiate tandem Het-Indels.

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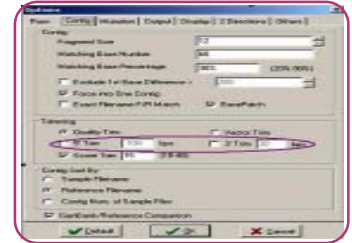
6 The Business Centre, Harvard Way, Kimbolton, Cambs PE28 0NJ
Tel: 0845 1300 950, Fax 0845 1300 960, www.biogene.com

Program Upgrade Bulletin Mutation Surveyor & Mutation Explorer v 3.0

Heterozygote & Methylation Quantification

Config	Sample	GenBank	Base Size	Standard1	Standard2	Mutation	SC Drop	SC Incr
1F (18)	ACE_01021_08_A02	ACE_A01	123206	0% - ACE_01021_08	95.43% - ACE_01021_08	T → A	23.96%	99.43%
1F (18)	ACE_01021_08_B06	ACE_A01	123206	0% - ACE_01021_08	95.43% - ACE_01021_08	T → A	86%	18.22%
1F (18)	ACE_01021_08_B05	ACE_A01	123206	0% - ACE_01021_08	90% - ACE_01021_08	T → A	35.1%	90%
1F (18)	ACE_01021_08_C01	ACE_A01	123206	0% - ACE_01021_08	90% - ACE_01021_08	T → A	19.64%	100%
1F (18)	ACE_01021_08_A04	ACE_A01	123229	0% - ACE_01021_08	90% - ACE_01021_08	G → A	14.22%	90%
1F (18)	ACE_01021_08_C01	ACE_A01	123229	0% - ACE_01021_08	90% - ACE_01021_08	G → A	18.92%	9.688%
1F (18)	ACE_01021_08_A01	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	28.17%
1F (18)	ACE_01021_08_A02	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	54.45%
1F (18)	ACE_01021_08_A04	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	90%
1F (18)	ACE_01021_08_B06	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	49.72%
1F (18)	ACE_01021_08_B05	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	28.58%
1F (18)	ACE_01021_08_B01	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	35.63%
1F (18)	ACE_01021_08_B02	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	38.81%
1F (18)	ACE_01021_08_B04	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	26.45%
1F (18)	ACE_01021_08_B05	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	26.75%
1F (18)	ACE_01021_08_C01	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	28.54%
1F (18)	ACE_01021_08_C02	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	26.65%
1F (18)	ACE_01021_08_C03	ACE_A01	123230	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	28.74%
1F (18)	ACE_01021_08_A02	ACE_A01	123226	0% - ACE_01021_08	90% - ACE_01021_08	T → G	0%	90%

Trimming Options



Trim data by quality of base score or by Bp in either the 3' & 5' direction.

Mutation Surveyor now quantitates the percent of methylation as well as the percent heterozygosity based upon the change in intensity, or dropping factor.

Project Comparison

New editors permit rapid conversion to cDNA.



New .gbk & .seq editors permit easy conversion to cDNA

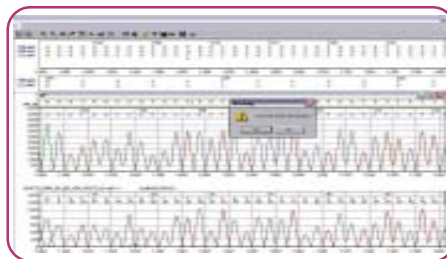
Automatic Linkage to Data Base

ID	Gene	Gene Symbol	Mutation ID	Mutation	Position	Score	Contig	Mutation
1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
2	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
3	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
4	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
5	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
6	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
7	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
8	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
9	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
10	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
11	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
12	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
13	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
14	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
15	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1
16	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1

Version 3.0 features a new data table for exporting to your Lims or other data base. User can select from multiple fields.

Base Call Editing

Erroroneous base calls can now be edited. Mutation Surveyor also employs an "intelligent" base call editor that seeks the same position in all traces within the batch and automatically edits that position's base call.



Gene	Position	Reference	Sample	Match
ACE_01021_08_A01	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A02	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A03	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A04	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A05	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A06	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A07	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A08	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A09	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A10	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A11	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A12	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A13	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A14	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A15	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A16	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A17	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A18	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A19	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A20	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match

SGP Comparison feature compares 2 projects indicating concordance between analysts or references.

Color-Coded Reporting of SNPs & other mutations

Gene	Position	Reference	Sample	Mutation
ACE_01021_08_A01	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A02	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A03	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A04	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A05	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A06	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A07	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A08	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A09	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A10	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A11	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A12	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A13	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A14	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A15	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A16	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A17	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A18	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A19	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match
ACE_01021_08_A20	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	103-SE02000-1-F-ab1	Match

Reports non-synonymous or missense mutations.

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