

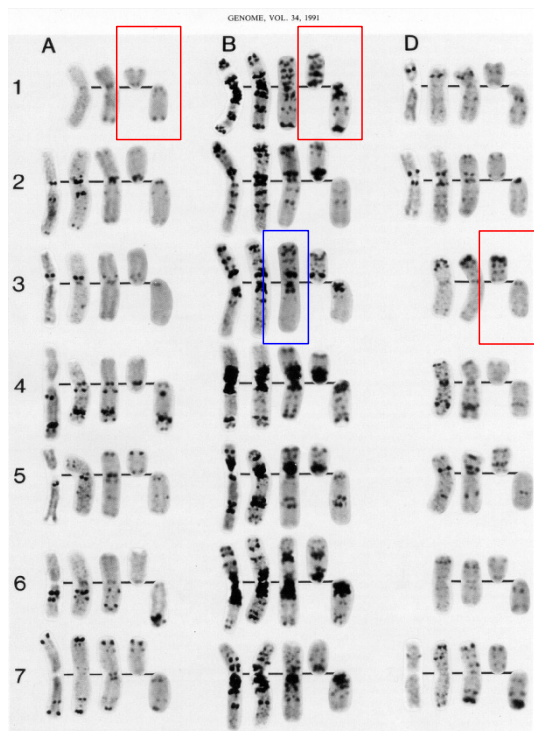
BAC Fluorescent Fingerprinting workflow at Institute of Applied Genomics, Udine (Italy)

Federica Cattonaro

IWGSC: Physical Mapping Standard Protocols Workshop

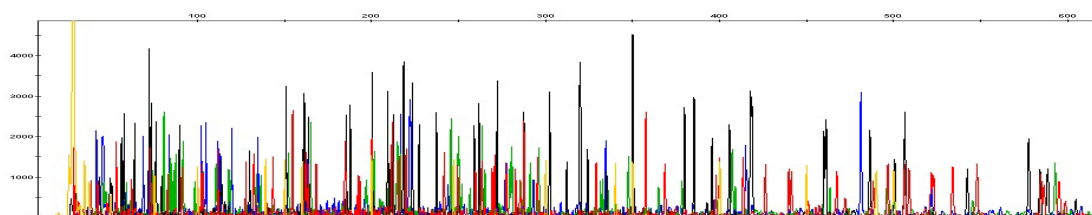
FINGERPRINTING

PAG Meeting, San Diego, January 2010



Chromosome_(arm)	Clones #	Status dic. 2009	Recipient partner
3Bv1 MTP	7740	completed	INRA
3Bv2	82176	completed	INRA
3DL	64512	completed	JIC
3DS	36864	completed	IEB
1AS	31104	completed	UZH
1BS	55296	completed	HU
1BL	92160	30720 to fingerprint	INRA
1AL	92554	Gen-Feb 2010	SABA
TOTAL	462406		

CURRENT STATUS DECEMBER 2009



Fluorescent fingerprinting improvements

automated
miniprep
protocol

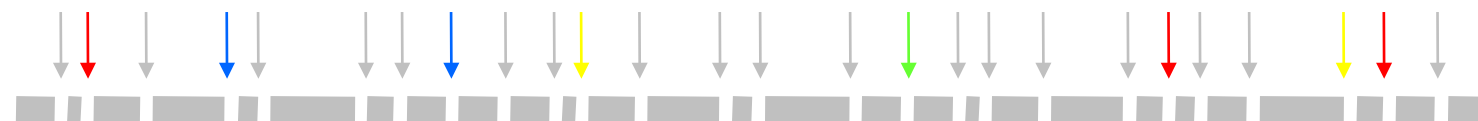
1. BAC DNA extraction and purification



miniaturized
one-tube
fingerprinting
reaction protocol

2. Multiple restriction endonuclease digestion

(4 rare cutters, *EcoRI*, *XbaI*, *BamHI*, *XhoI* and 1 frequent cutter, *HaeIII*)



3. Fragment labeling using fluorescent SNaPshot chemistry

(ddATP, ddCTP, ddGTP, ddTTP)



novel speedy
cleanup
protocol

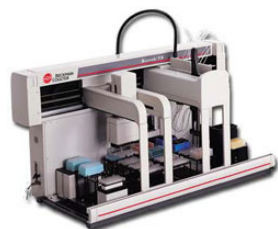
4. Post extension cleanup of unincorporated dyes

5. Electrophoresis separation and peak detection

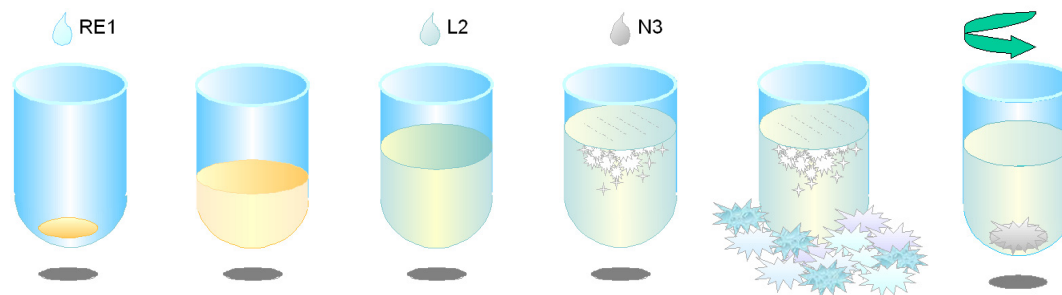
(ABI3730 capillary automated sequencer)

1. BAC DNA extraction & purification

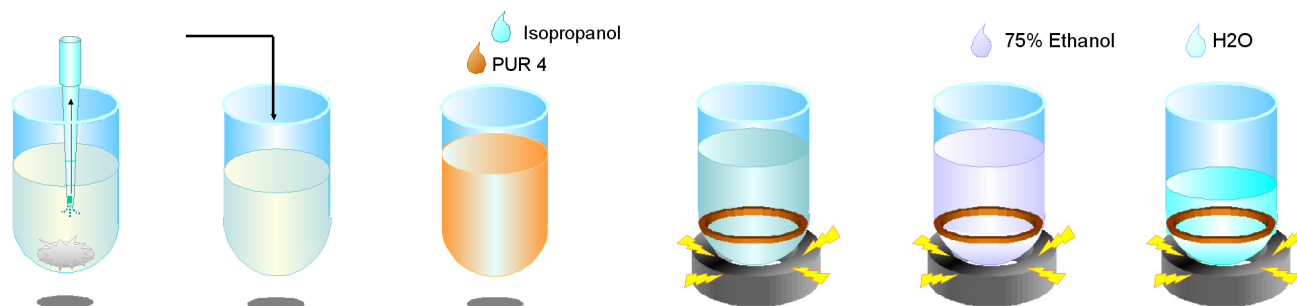
- alkaline lysis DNA extraction protocol based on **AGENCOURT® CosMCPrep® System**
- automatization of the procedure on a BECKMAN 96 head FX^p robot



phase1: alkaline lysis and flocculent pelleting



phase2: lysate transfer, SPRI purification and elution



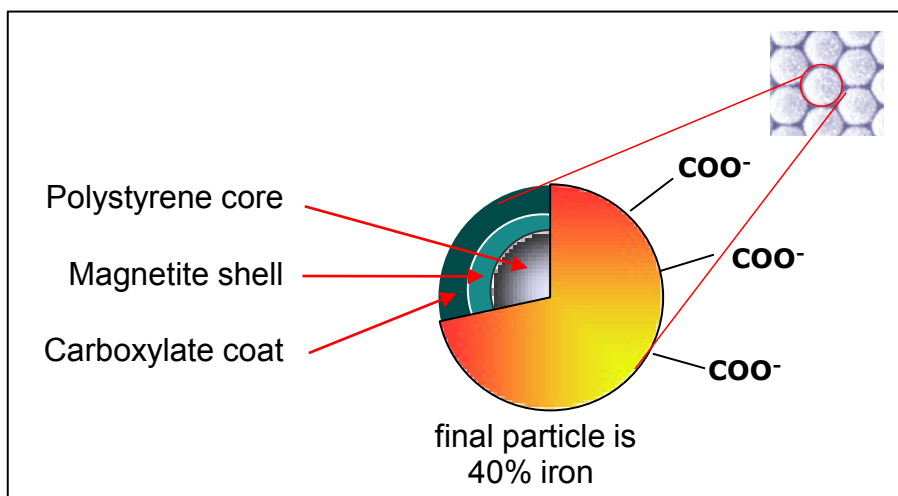
1. BAC DNA extraction & purification

Agencourt® SPRI™ technology

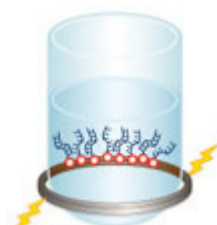
Solid Phase Reverse Immobilization

Patented technology developed at Whitehead Institute
(*Nucleic Acids Res.* 1995; 23:22)

- Polystyrene: low sedimentation rate
- Magnetite: bead pellet in magnetic field
- Carboxylic groups: reversible interaction between hydrophilic beads and nucleic acids
- Elution in aqueous solution (no chaotropic salts)



Step 1
NA Immobilization



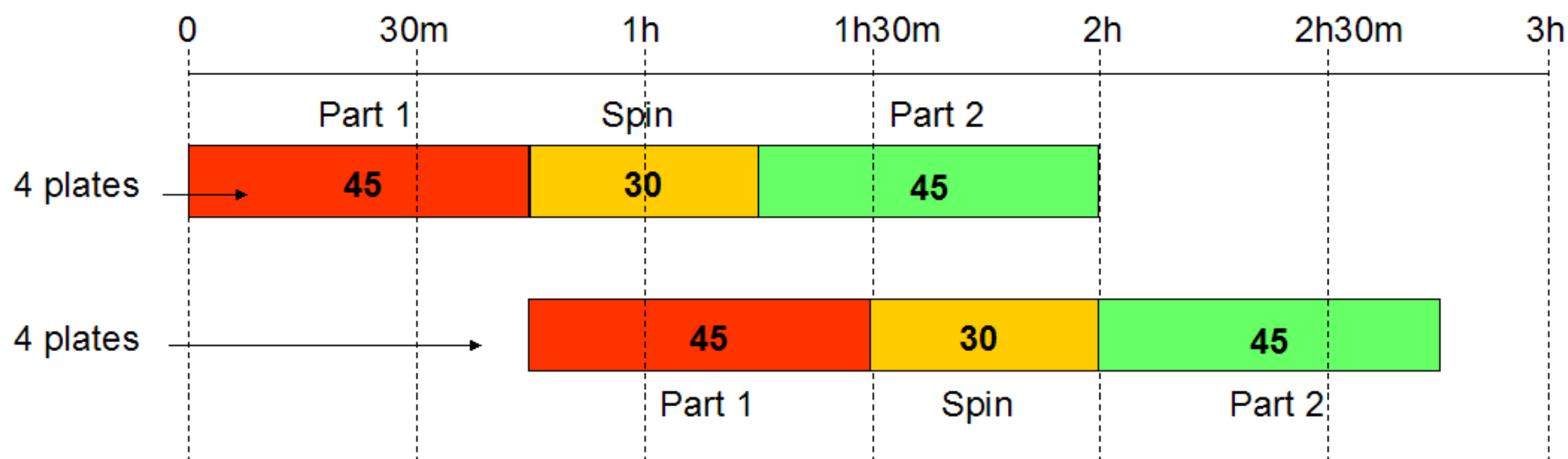
Step 2
Contaminant Removal & Wash



Step 3
NA Elution

1. BAC DNA extraction & purification

High Throughput: Overlapping Batches

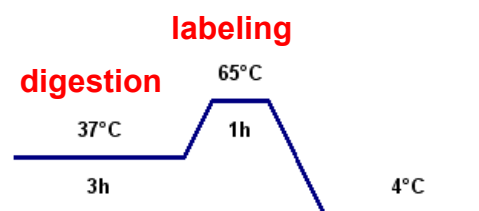


8 x 96-well plates in less than 3 hours → 4-6 384-well plates per day

BAC preparation remains the fingerprinting procedure bottleneck
(split of 384-format in 96-format)

2. One-tube digestion & labeling reactions

- Reduction of SNaPshot and restriction enzymes amounts
- SNaPshot Ready Reaction mix directly added to the digestion mixture
- Two temperature ramp incubation to perform digestion and labeling reaction in one tube



3. Post extension treatment: size standard

GeneScan™ 500 LIZ® internal Size Standard

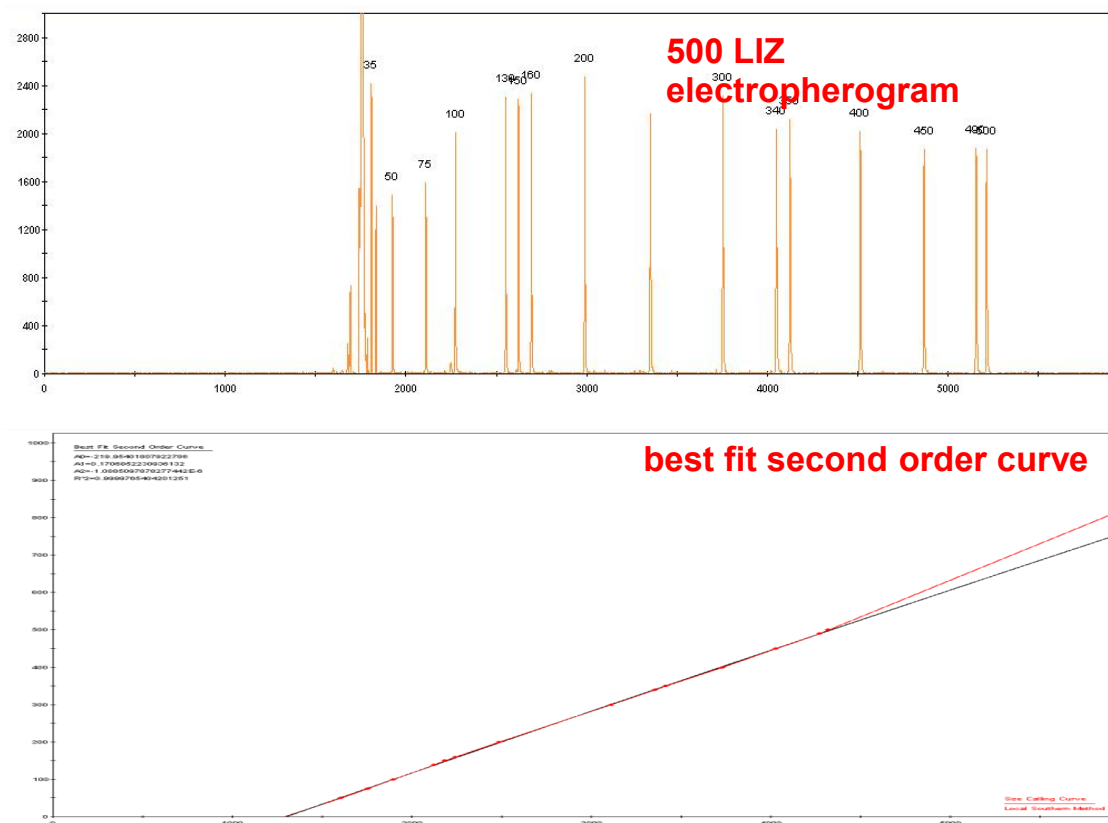
A set of DNA fragments of known sizes, labeled with an AB proprietary fluorophore (**orange**), used for determining the size of unknown DNA fragments run on ABI PRISM® DNA sequencers

GeneMapper software generate a calibration or sizing curve based upon the migration times of the known fragments in the standard.

The unknown fragments are mapped onto the curve and the sample data is converted from migration times to fragment sizes.

(The 250-bp peak shows abnormal migration and shall not be used to size samples)

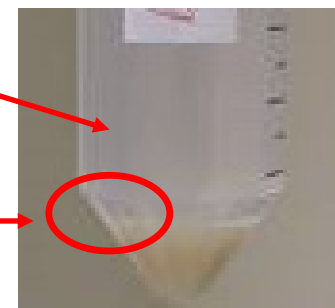
 pass  check  low quality



CCN[C+]1=C(C)C=C2C(=C1)OC(=C(C)C)C(=C2)C3=CC=CC=C3C(=C4C=CC(=C(C=C4)COC(=O)CC)C=C4)C

The **Applied Biosystems BigDye® XTerminator™ Purification Kit** is a cleanup system for DNA sequencing reactions that removes free BigDye® terminators

BDX resin: fast sedimentation rate

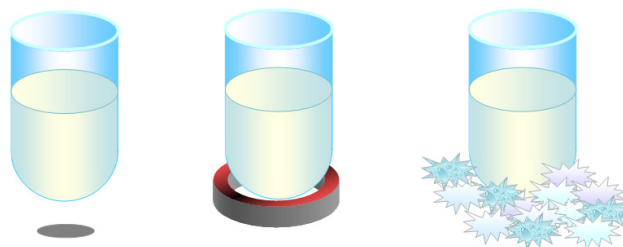


3. Post extension treatment

In collaboration with Applied Biosystems we transfer this fast and simple purification system to the fingerprinting clean up

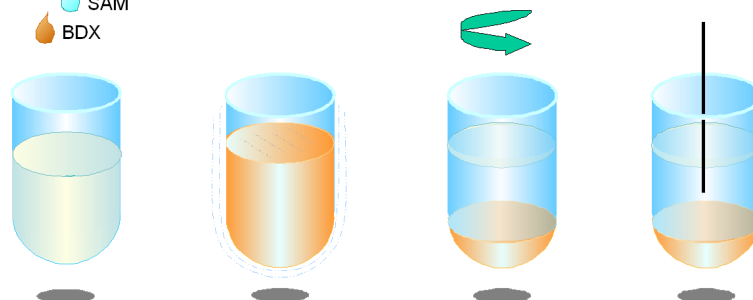
phase1: internal standard adding and sample denaturation

formamide
500LIZ



phase2: dye cleanup, resin pelleting and CE loading

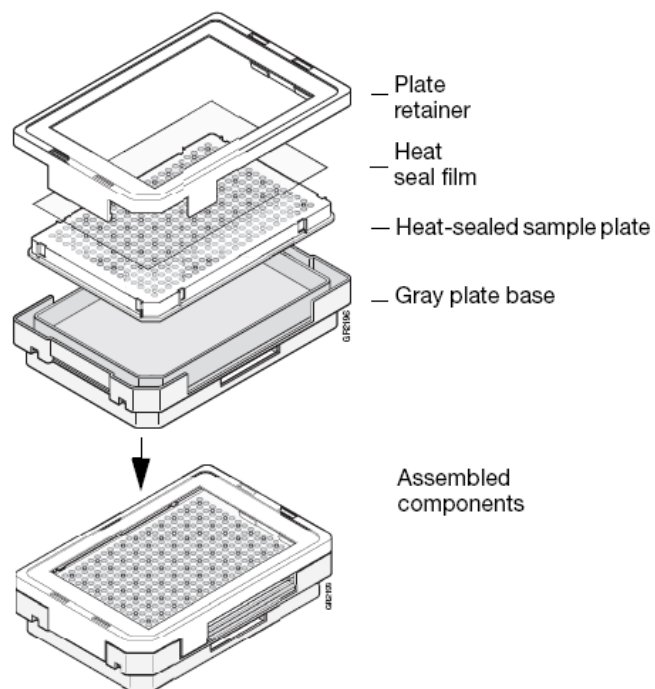
SAM
BDX



4. Fingerprinting run



- The sample sheet is automatically generated by a barcoding system during the fingerprinting pipeline
- The heat-sealed plate is assembled in a specific base-retainer box and directly loaded on the instrument



4. Fingerprinting run

The sample sheet must report the plate sealing type

GeneMapper Plate Editor

File Edit

Plate Name: TaeCsp3DShA_0001 Operator: magni

Plate ID: TaeCsp3DShA_0001 Owner: magni

Plate Sealing: **Heat Sealing** Scheduling: 1234

Well	Sample Name	Comment	Sample Type	Size Standard	Panel	Analysis Method
A01	TaeCsp3DShA_0001A01		Sample	GS500(-250)LIZ	None	Fingerprints
B01	TaeCsp3DShA_0001B01		Sample	GS500(-250)LIZ	None	Fingerprints
C01	TaeCsp3DShA_0001C01		Sample	GS500(-250)LIZ	None	Fingerprints
D01	TaeCsp3DShA_0001D01		Sample	GS500(-250)LIZ	None	Fingerprints
E01	TaeCsp3DShA_0001E01		Sample	GS500(-250)LIZ	None	Fingerprints
F01	TaeCsp3DShA_0001F01		Sample	GS500(-250)LIZ	None	Fingerprints

Description

Ok Cancel

4. Fingerprinting run

The sample sheet must report the specific instrument protocol

GeneMapper Plate Editor

File Edit

Plate Name: Operator:

Plate ID: Owner:

Plate Sealing: Scheduling:

Well	Study	User-Defined 1	User-Defined 2	User-Defined 3	Results Group 1	Instrument Protocol 1
A01					Tae3D	Fingerprinting_BDX_new
B01					Tae3D	Fingerprinting_BDX_new
C01					Tae3D	Fingerprinting_BDX_new
D01					Tae3D	Fingerprinting_BDX_new
E01					Tae3D	Fingerprinting_BDX_new
F01					Tae3D	Fingerprinting_BDX_new

Description

Ok Cancel

4. Fingerprinting run

- An appropriate run module is needed for sample injection (from ABI)
- Oven temperature must be manually set

Run Module Editor

Run Module Description

Name: BDX_GM_36

Type: REGULAR

Template: BDX_RapidSeq36_POP7

Description:

Run Module Settings

Name	Value	Range
Oven_Temperature	66	18...70 DegC
PreRun_Voltage	15.0	0...15 kV
PreRun_Time	180	1...1800 sec
Injection_Voltage	2.0	0...15 kV
Injection_Time	15	1...90 sec
First_ReadOut_Time	200	100...16000 ms
Second_ReadOut_Time	200	100...16000 ms
Run_Voltage	15.0	0...15 kV
Voltage_Number_Of_Steps	10	0...100 Steps
Voltage_Step_Interval	20	0...180 secs
Voltage_Tolerance	0.6	0...6.0 kV
Current_Stability	30.0	0...2000 uA
Ramp_Delay	1	1...1800 sec
Data_Delay	120	1...1800 sec
Run_Time	1200	300...14000 sec

Ok Cancel



Foundation Data Collection Version 3.0 - No User is logged in

File View Service Tools Wizards Help

GA Instruments > ga3730 > SEQUENCER3 > Manual Control

Manual Control

Send Defined Command For: Oven

Command Name	Value	Range
Set oven temperature	66.0	18.0 - 70.0 C

Comments:

Sets the oven temperature.

Send Command

5. Fingerprinting quality check

The summaries of the automatic analysis performed by GeneMapper and FPBscript are saved for each plate in txt format

```
C:\WINDOWS\system32\cmd.exe
C:\scripts>for /L %i in (1 1 100) do "C:\scripts\Genemapper analysis report.bat"
C:\scripts>"C:\scripts\Genemapper analysis report.bat"
C:\scripts>C:\scripts\report_gen_phiga.pl --dir "\\sequencer0\sequences" --outdir "\\Sequencer0\Analisi Reports\fingerprints"
C:\scripts>C:\scripts\report_gen_phiga.pl --dir "\\sequencer1\sequences" --outdir "\\Sequencer1\Analisi Reports\fingerprints"
Processing \\sequencer1\sequences\Tae3B\TaeCsp3BFhB_0262
Report for \\Sequencer1\Analisi Reports\TaeCsp3BFhB_0182.txt
C:\scripts>C:\scripts\report_gen_phiga.pl --dir "\\sequencer2\sequences" --outdir "\\Sequencer2\Analisi Reports\fingerprints"
C:\scripts>C:\scripts\report_gen_phiga.pl --dir "\\sequencer3\sequences" --outdir "\\Sequencer3\Analisi Reports\fingerprints"
Waiting an hour
C:\scripts>C:\scripts\sleep 3600
^Cterminare il processo bat
```

Report_TaeCsp3BFhB_0182.txt - WordPad

File Modifica Visualizza Inserisci Formato ?

Clones processed by GeneMapper: 352 (91.66%)

True peak heights (count\avg):

B:	10980	avg:	5387.6
G:	9945	avg:	4074.8
Y:	9391	avg:	4073.95
R:	10417	avg:	6684.57

Background peak heights (count\avg):

B:	48020	avg:	433.47
G:	51678	avg:	113.5
Y:	52814	avg:	164.94
R:	45814	avg:	124.48

B clones with few peaks: 1 (0.26%)

G clones with few peaks: 1 (0.26%)

Y clones with few peaks: 1 (0.26%)

R clones with few peaks: 1 (0.26%)

Clones with at least a dye with few peaks: 1 (0.26%)

Clones with too many peaks: 0 (0%)

Clones with no peak: 0 (0%)

SQ passed: GM_SizeCalling goodness measure (OK < 10-15%)

Channel Intensities: true peak measure (10000rfu>OK>200rfu; 1000rfu>optimal>3000rfu)

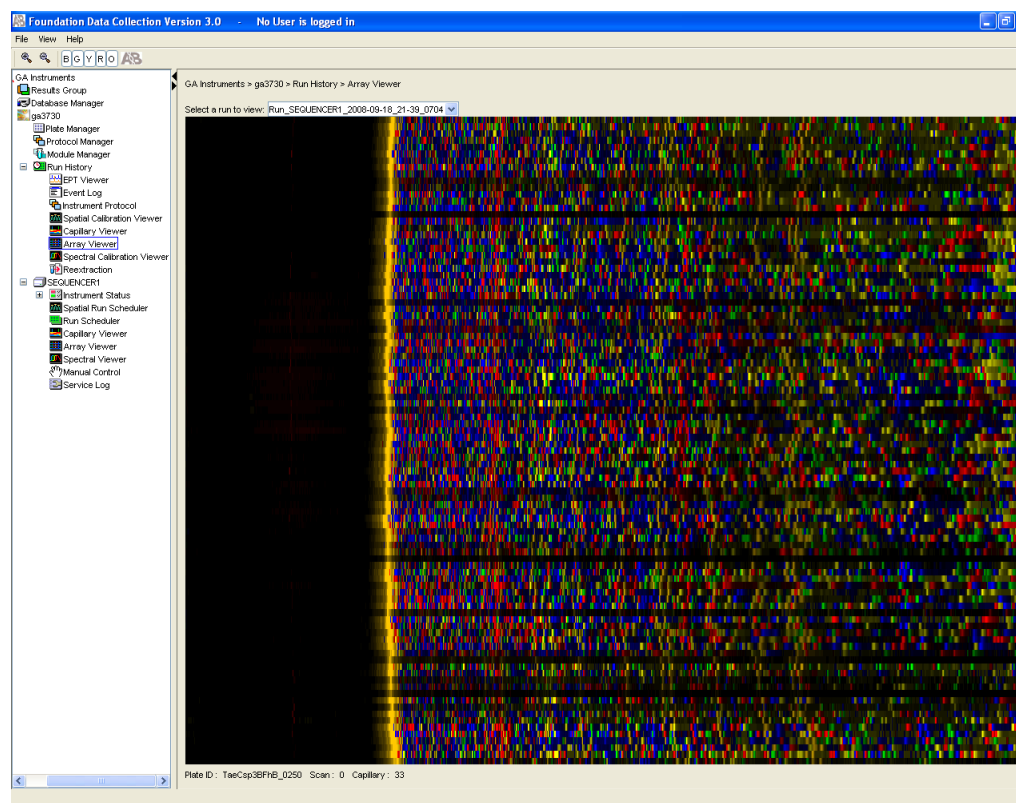
Channel Intensities: background peak measure (OK if 10% of the true peaks)

Failed samples (no DNA; no fingerprinting rxn)

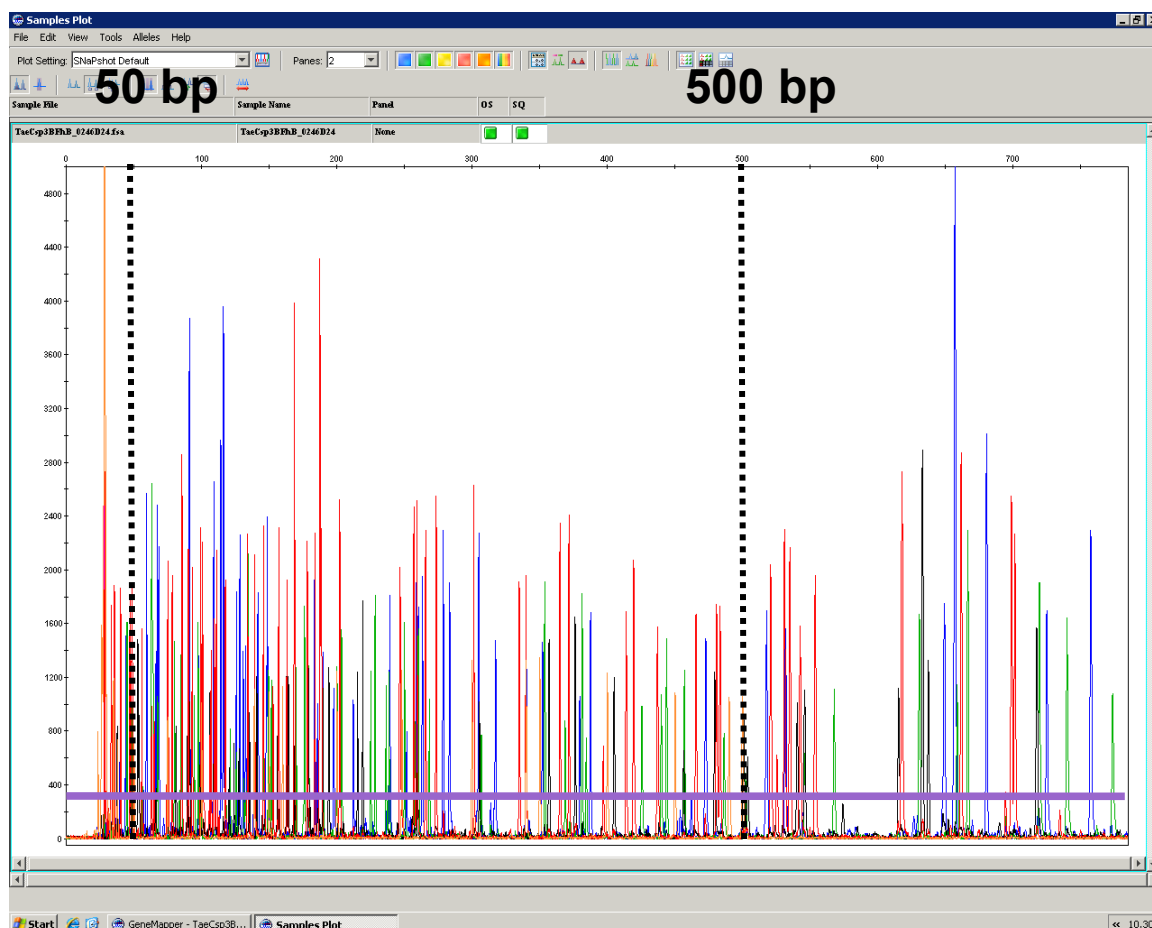
Contaminated samples (DNA mixture)

On 82176 processed fingerprints
(wheat TaeCsp3BFhB library):

- Good sized clones: **91%**
(GeneMapper SQ threshold 0.5)
- Empty/failed clones: **1.6%**
(FPB script – minBands 40)
- Cross contaminated clones: **<5%**
(GenoProfiler size matched 50%)



True signal vs. background



Fluorescence of the true peaks
1000-5000 rfu
(BDX purification improves the
signal intensities)

Background threshold
($<10\%$ of the true peaks)

- CosPrep (Agencourt) for BAC DNA extraction
- Restriction enzyme digestion
- SNaPSHOT (ABI) labelling

Weekly (5 days)
7,680-9,600

Monthly (20 days)
30,720-38,400

Annually (240 days)
368,640 - 460,800

384-well PCR



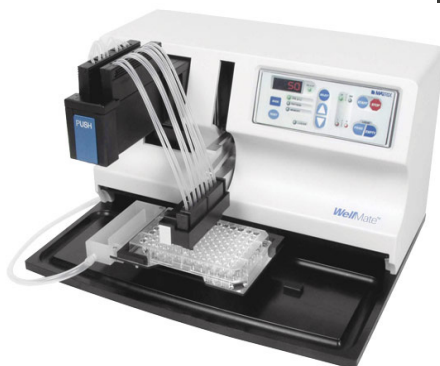
**Biomek FX
(96-head)**



ABI3730 xl



Centrifuge for microplates



Matrix WellMate Microplate Dispenser



Standard protocols

Same method, different workflows: same enzyme combination + SNAPShot labelling

UD Davis

Qiagen miniprep (filter)

96-well format

Dig+labelling

LIZ 1200

Etanol precipitation

IGA

CosPrep (SPRI technology)

384-well format

Dig/labelling in the same well

LIZ 500

BDX Technology

1. Miniprep

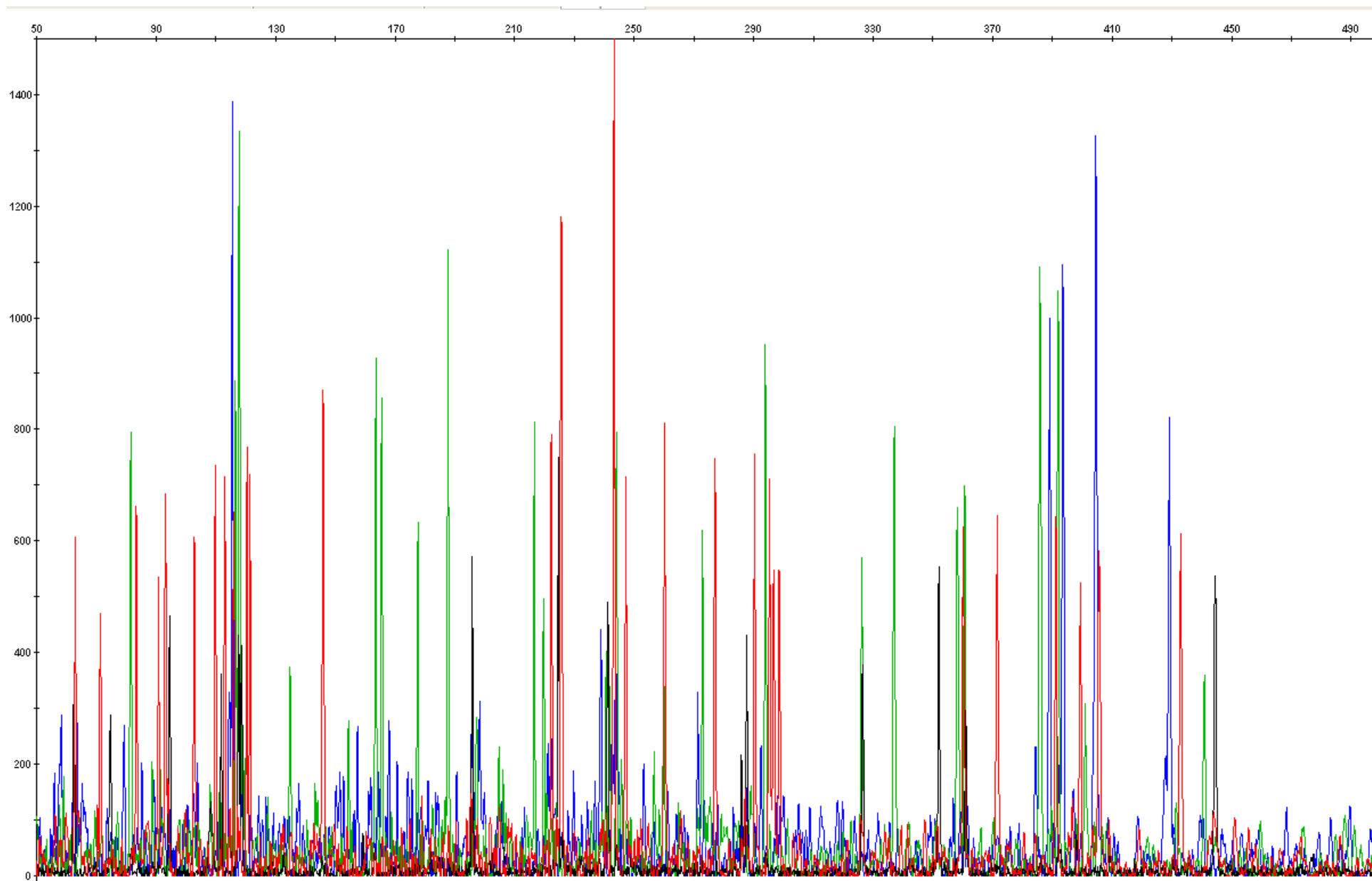
Miniprepping is the most delicate phase of the workflow

Set-up very well the bacterial growing conditions to avoid too many or too low bacterial cells:

an accurate optimization need to be done
in each lab with the aid of the kit manufacturer
(i.e. Qiagen or Beckman)

Do not prepare all the minipreps at a time: it's better to finish the entire workflow for each batch of plates

1. CONTAMINATED PATTERN: high background

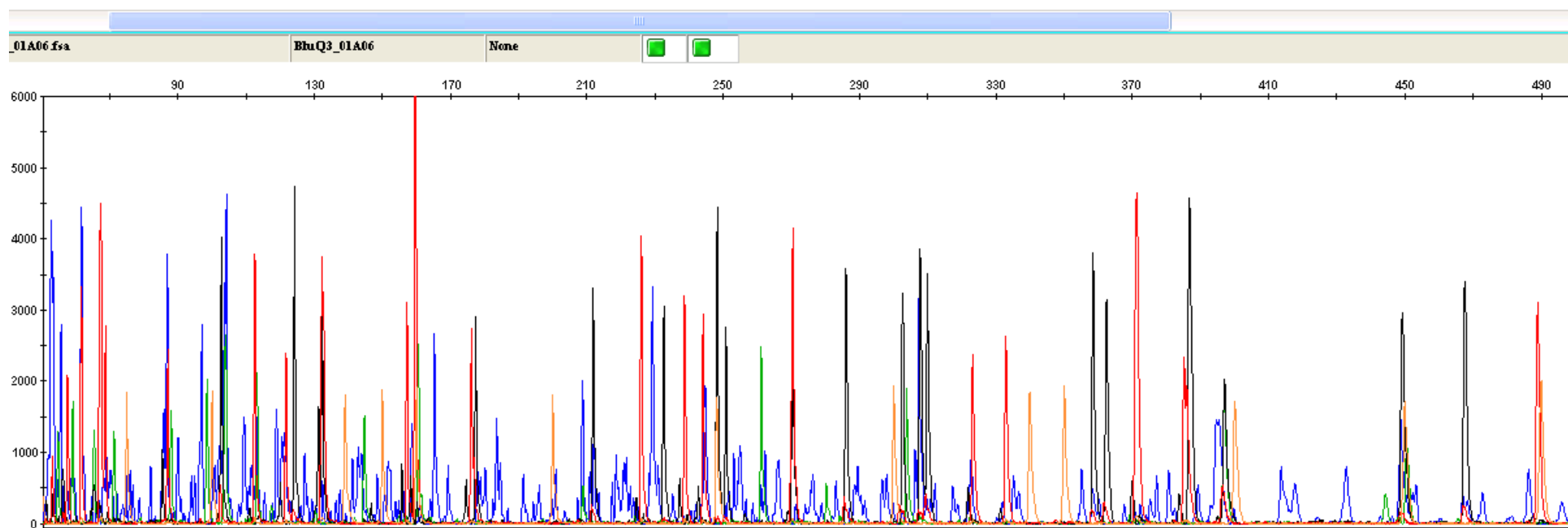
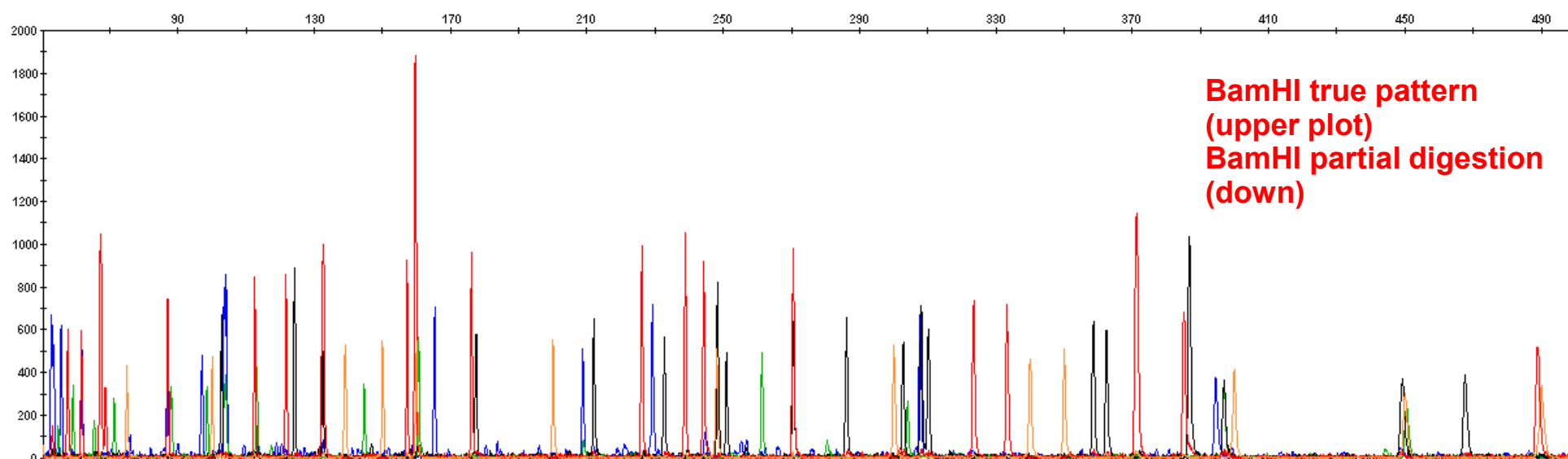


2. Restriction enzyme digestion

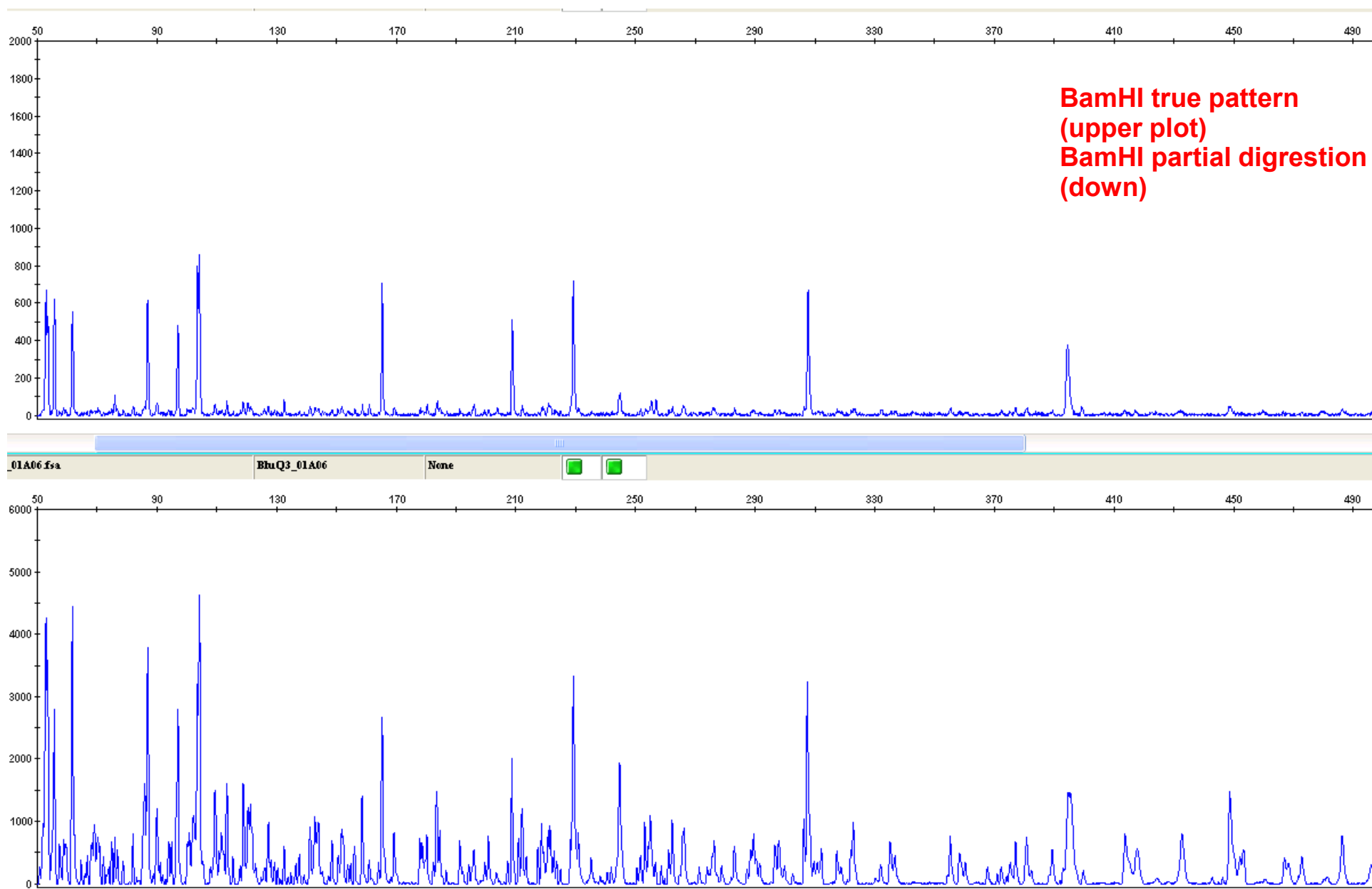
Use high fidelity restriction enzymes (i.e. New England Biolabs) to avoid star activity

Star activity=activity of restriction endonuclease under non-standard conditions that resulted in cleavage at sequences similar but not identical to their defined recognition sequences

2. PARTIAL DIGESTION: BamHI star activity (blue)



2. PARTIAL DIGESTION: BamHI star activity (blue)

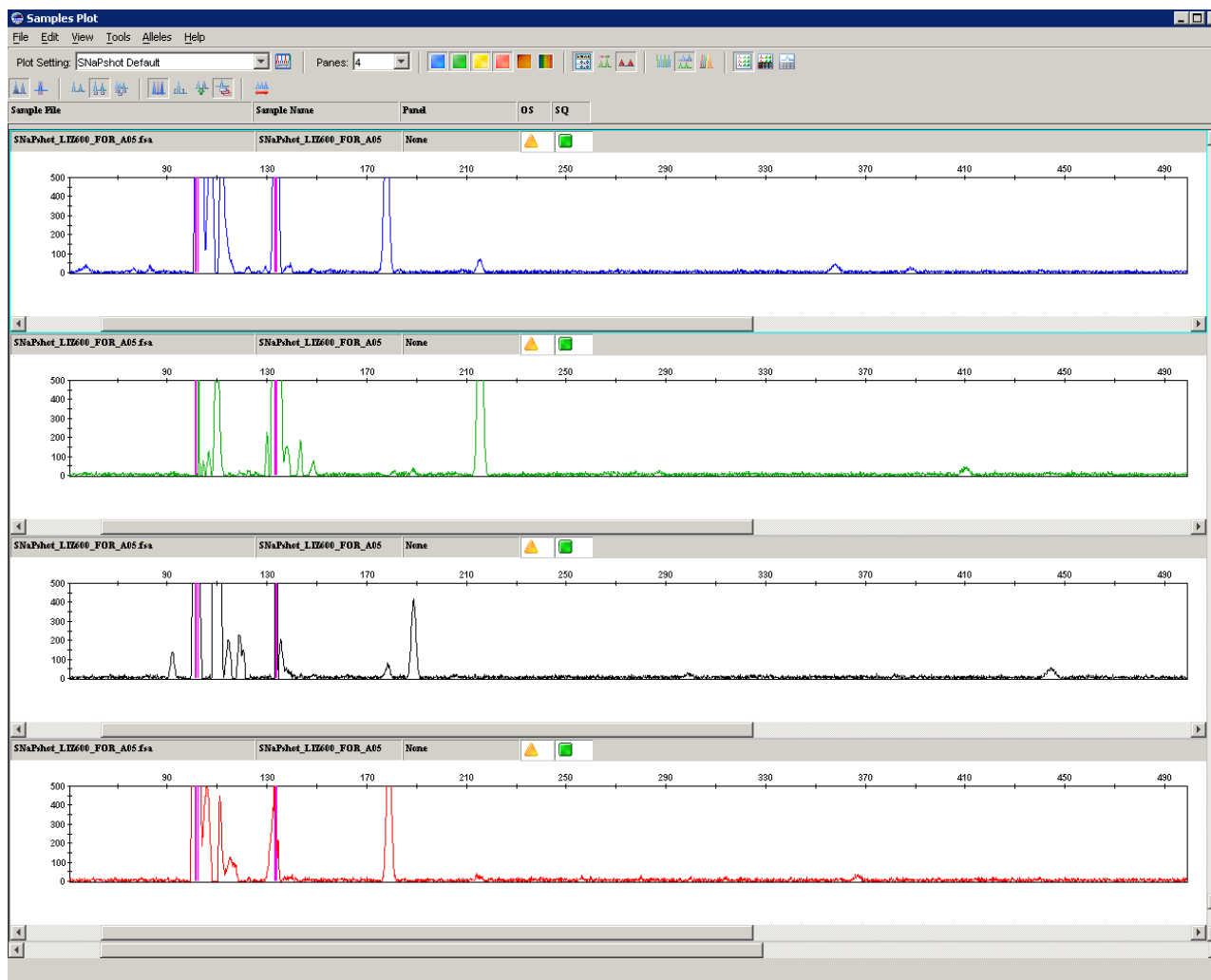


3. Dye-blob cleaning

In 96-well format the Etanol precipitation is sufficient to clean from Dye-blob

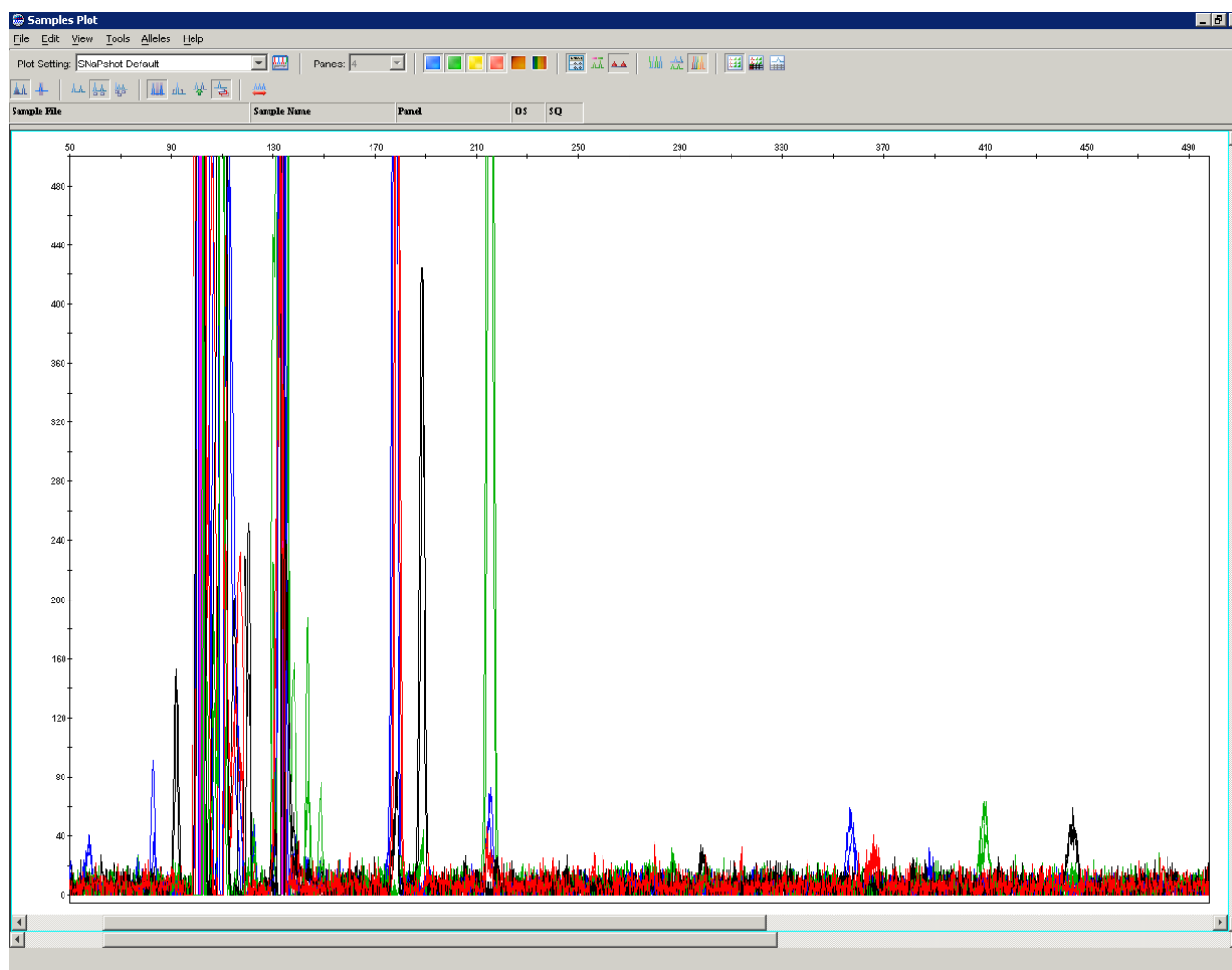
In 384-well format it's necessary to clean better from d-Rhodamine

3. Dye-blobs: SNaPshot free fluoresceinated dNTPs



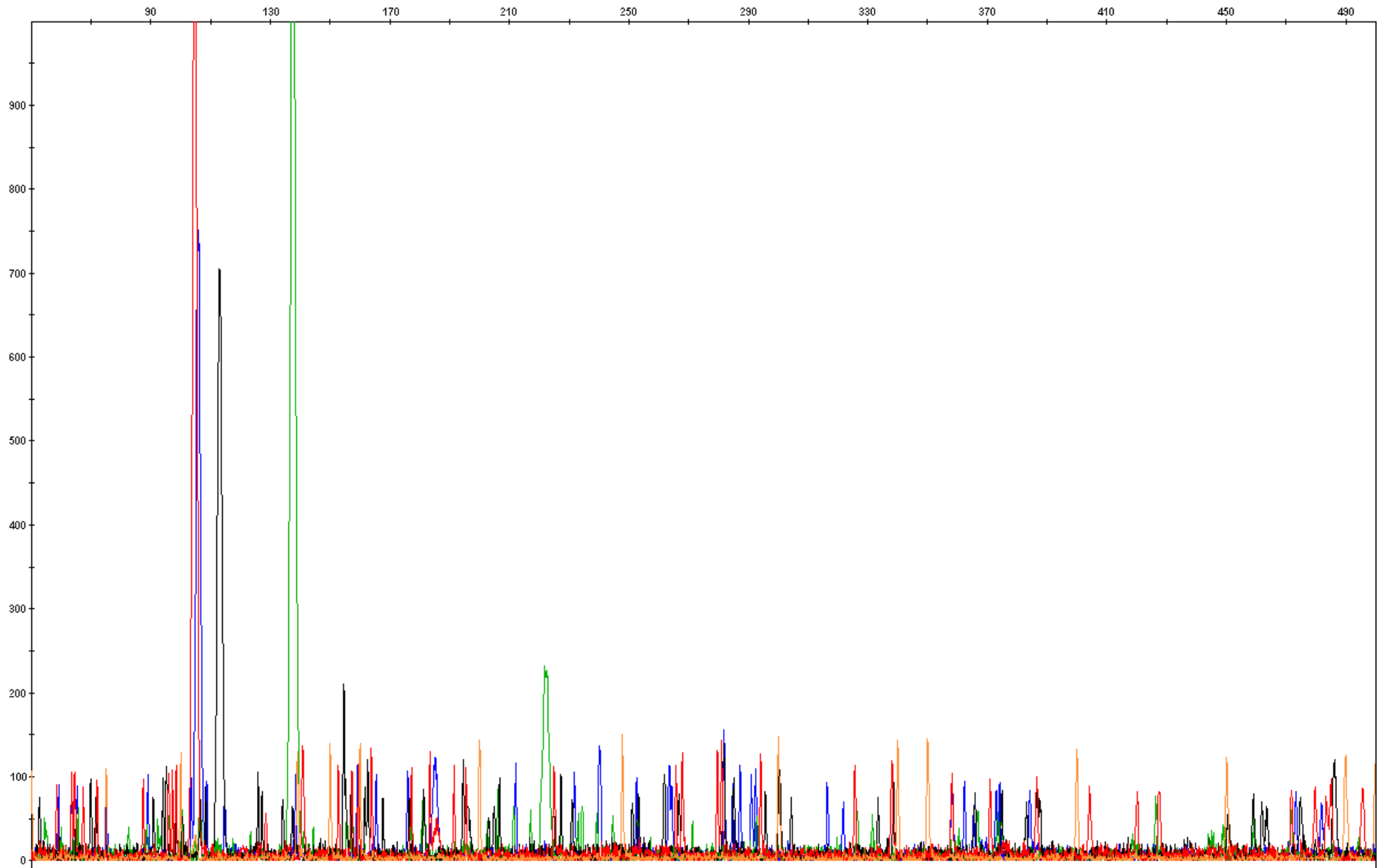
Dye blobs due to free (i.e. unincorporated) electrophoretic migration of SNaPshot fluoresceinated dNTPs

3. Dye-blobs: overlay all view



**Rhodamine dye blobs
migrate quite precisely**

3. Dye-blobs: BAC fingerprint



Conclusions

It is not easy to set-up a fingerprinting workflow (it is easier to do sequencing!)

Money investments need to be done to acquire robotics and for a first phase of optimization

A preliminary managing work need to be done to obtain the best discounts: cost per sample can be very variable, a high-throughput facility have more discount on the reagents!

**WE ARE AVAILABLE TO EVALUATE THE OPPORTUNITY TO DO
FOR YOU THE FINGERPRINTS IN SERVICE**