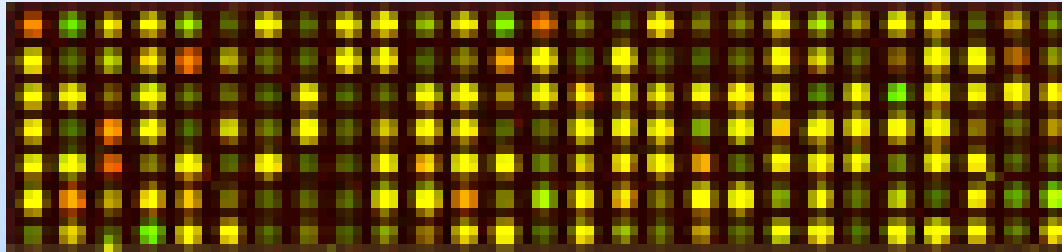


# JIC/JCVI/Cogenics *Brassica* microarray

12<sup>th</sup> January 2008

Ian Bancroft  
John Innes Centre



# Array design

## Assembly statistics:

810,254 raw ESTs

803,326 ESTs after clean-up

### Assembly conducted at 95% cut-off

Paralogues within C genome 86.5 +/- 3.6% conserved in coding regions, so should resolve

Homoeologues between A and C genomes 96.8 +/- 1.2% conserved in coding regions, so should co-assemble

94,558 unique sequences

42,642 assemblies

51,946 singletons

72,148 sequences have UniRef100 annotation

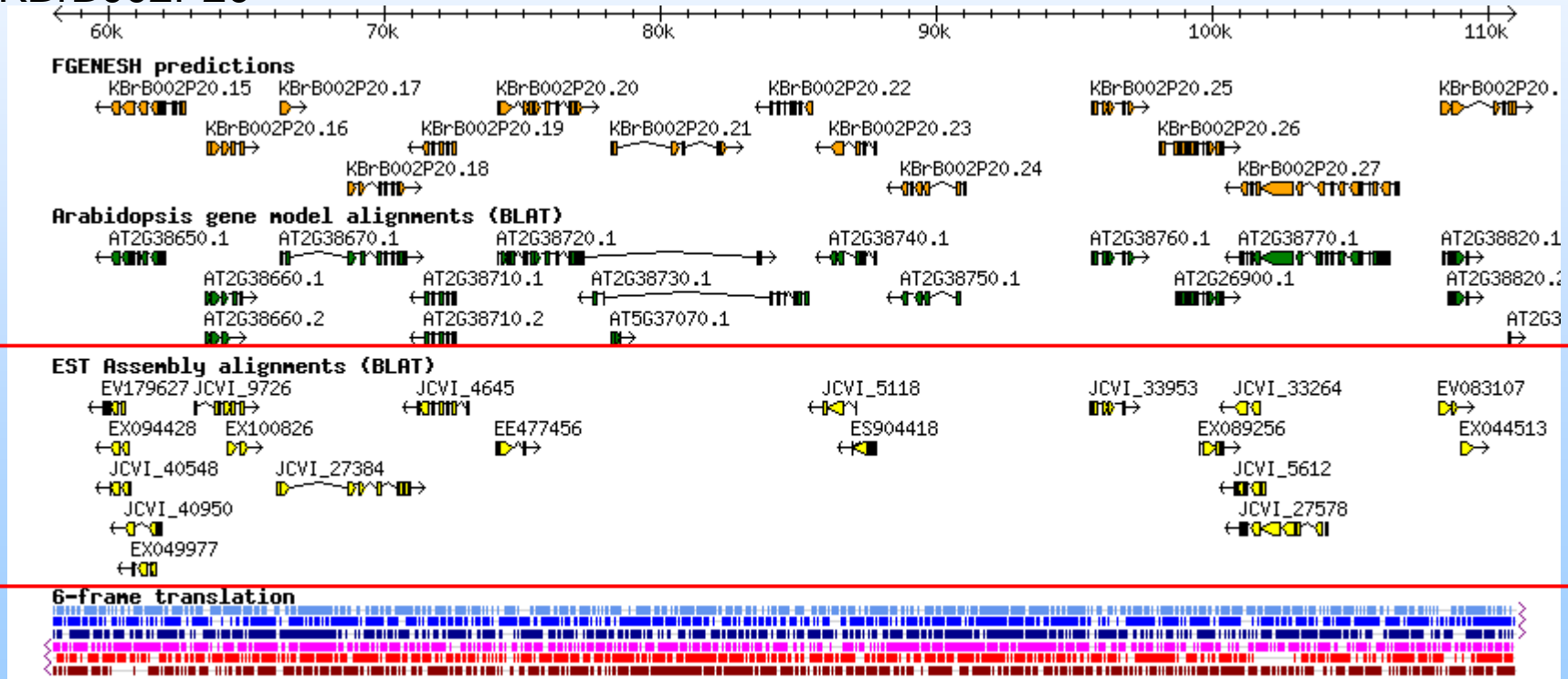
## Assemblies available from:

<ftp://149.155.100.41/pub/brassica/>

# Array design

Assemblies (and singletons) incorporated into the JIC *Brassica* genome sequence annotation (accessible via *Brassica* Genome Gateway site: <http://brassica.bbsrc.ac.uk>)

## KBrB002P20



# Array design

## Array statistics:

**Agilent 2 x 105k format** (<http://www.chem.agilent.com>)

**60-mer oligos**

**91,854 good probes designed**

81,388 probes with no cross-hybridization potential

10,466 probes have cross-hybridization potential

## Access to array:

**Freely available, but as it is an Agilent custom array, access needs to be authorised. Contact:**

**Jim Lovgren (Cogenics; USA):** [jlovgren@cogenics.com](mailto:jlovgren@cogenics.com)

**JIC Genome Lab:** [enquiries@jicgenomelab.co.uk](mailto:enquiries@jicgenomelab.co.uk)

**Commercial service provider: Cogenics**

# Array validation

## Aim:

As most ESTs in the assemblies were from *B. napus*, we aimed to confirm that homoeologues in the “diploid” species hybridize efficiently to the probes.

We anticipate no problems, as homology in coding regions is very high

*B. oleracea* - *B. napus* C genome: 99.85 +/- 0.14% conserved

*B. rapa* - *B. napus* A genome: 98.63 +/- 0.80% conserved

# Array validation

## Experiment:

Analyse leaf transcriptome in *B. oleracea* (Alboglabra A12DH), *B. rapa* (Trilocularis RO18) and reciprocal resynthesised *B. napus* produced from these lines



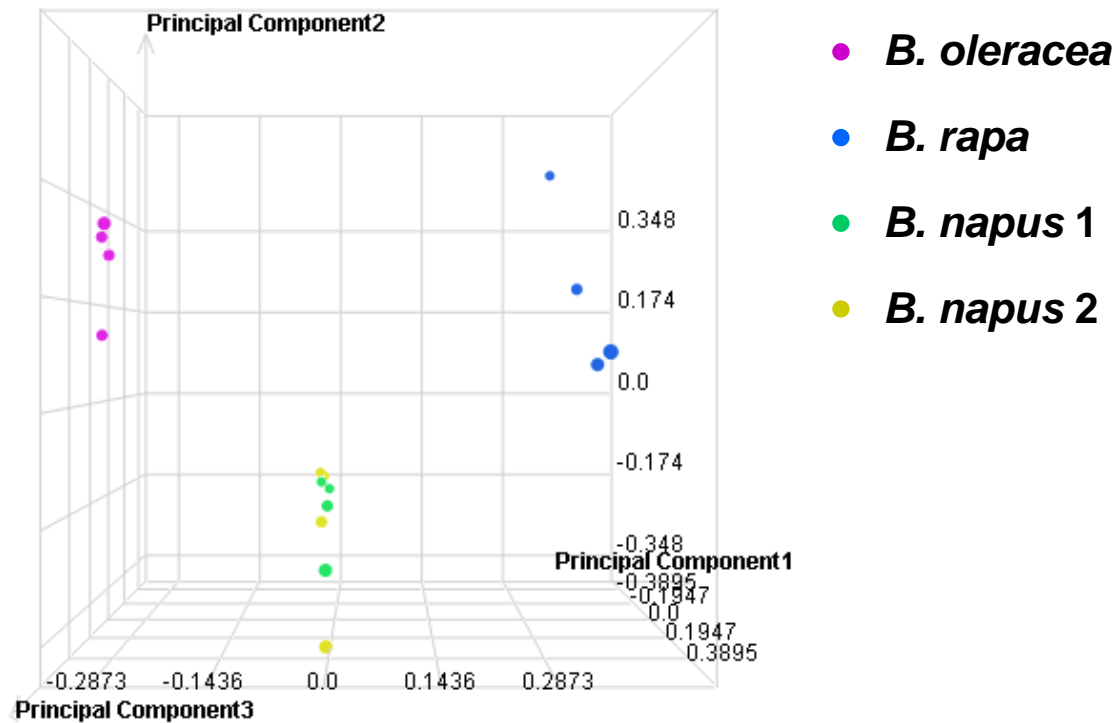
## Validation results

Quantitative differences in expression can be detected between *B. rapa* and *B. oleracea* ( $P < 0.005$ )

Quantitative differences in expression can be detected between the reciprocal resynthesised *B. napus* ( $P < 0.005$ )

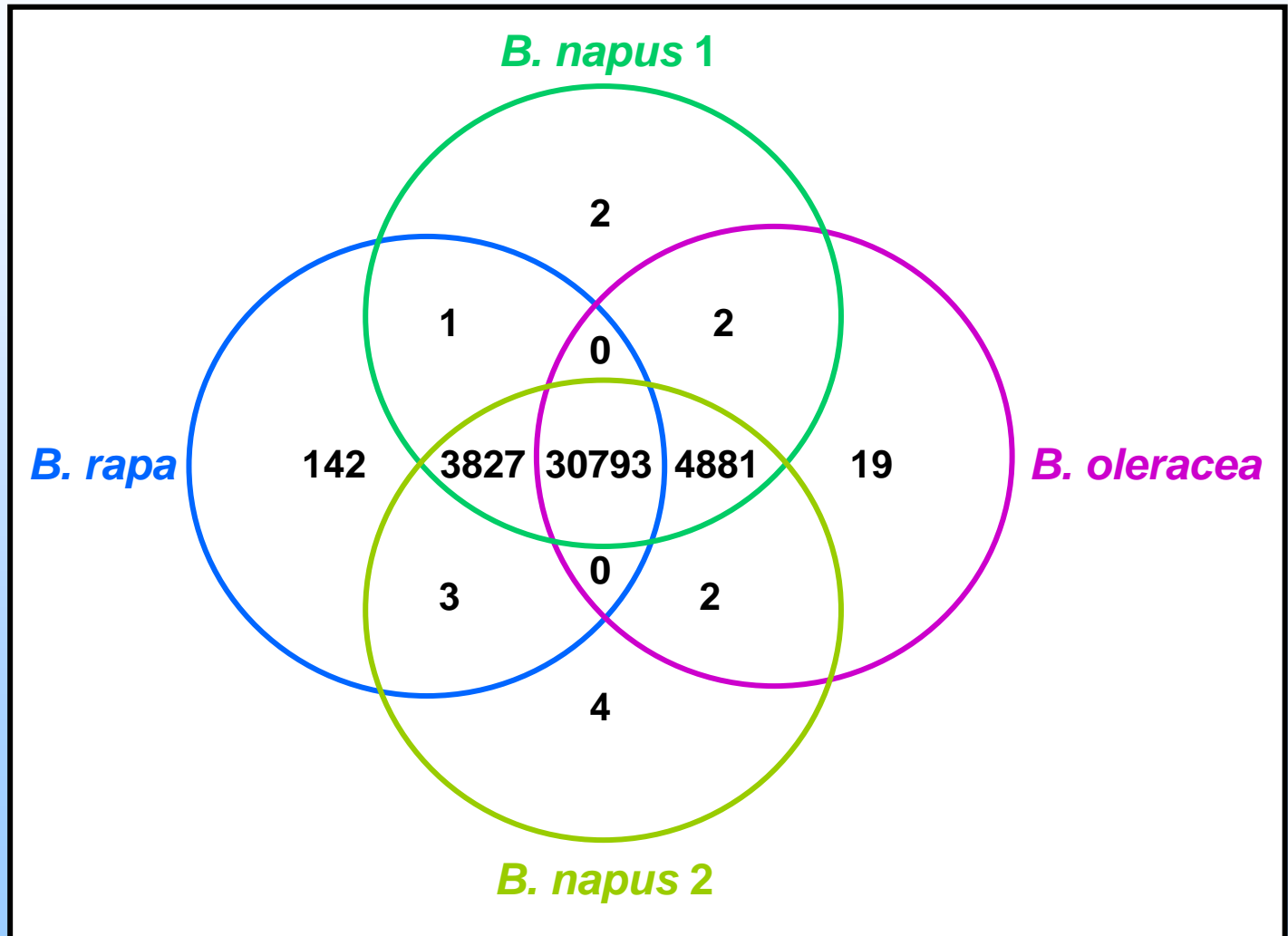
# Validation results

Principal component analysis resolves the genotypes



# Validation results

Genome-specific expression identified by qualitative analysis of  
~34,000 unigenes



Number of probes yielding significant signals in all 4 replicates

# Acknowledgements

**ESTs** - The *Brassica* genomics community

## Assemblies

JCVI: Foo Cheung, Chris Town

## Annotation

JIC: Nizar Drou, Martin Trick

## Probe and array design

Cogenics: Ed Lobenhofer

## Resynthesised *B. napus*

IAPB, Gottingen: Stefan Abel

## Biological materials for validation experiment

JIC: Fiona Fraser

## Data analysis for validation experiment

JIC, Cogenics: Andreas Magusin, Ed Lobenhofer

## For further information

### **EST assemblies:**

Chris Town  
The J. Craig Venter  
Institute  
9704 Medical Center Drive  
Rockville, MD 20850  
Tel. 301-795-7523  
cdtown@jcv.org

### **Array design:**

Ed Lobenhofer, Ph.D.  
Director, Scientific Affairs  
Cogenics™,  
100 Perimeter Parkway, Suite C  
Morrisville, NC 27560  
Telephone: 919-379-5482  
elobenhofer@cogenics.com

### **Access to array /commercial service:**

Jim Lovgren  
Product Manager  
Cogenics™,  
100 Perimeter Park Dr., Suite C  
Morrisville, NC 27560  
Direct: 919-469-7682  
Mobile: 919-538-1679  
jlovgren@cogenics.com

**Or via. JIC Genome Laboratory:** enquiries@jicgenomelab.co.uk