



# Marking Success



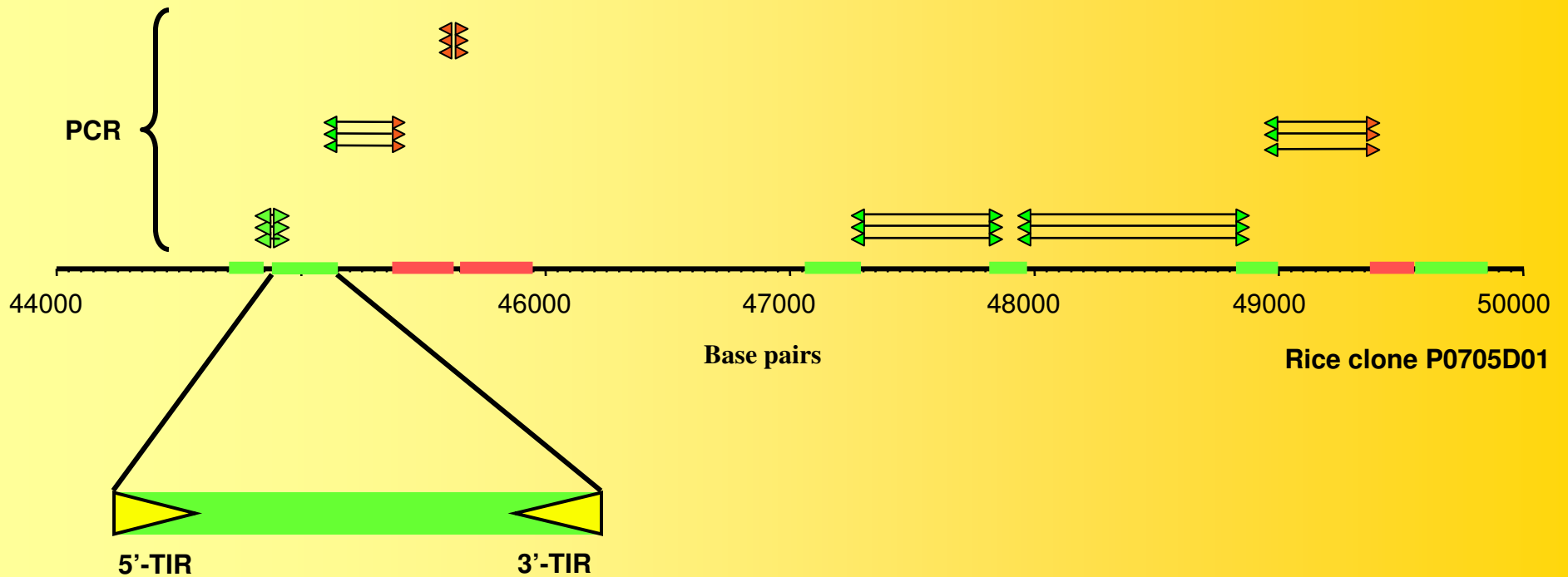
## What are IMP markers?

- Developed by and exclusive to DNA LandMarks
- Inter-MITE Polymorphism (IMP) markers are based on Miniature Inverted-repeat Transposable Elements (MITEs)
- MITEs are short interspersed DNA transposons with terminal inverted repeats (TIRs),
- Small size (< 500 bp), conserved TIRs, high A+T content
- Several distinct families: Tourist-like, Stowaway-like
- In plants highly associated with genes (flanking regions, introns)
- Present in plants, fungi, vertebrates, fishes, insects
- Abundant in plants (several thousand copies per genome)

## Basis of the IMP Technology

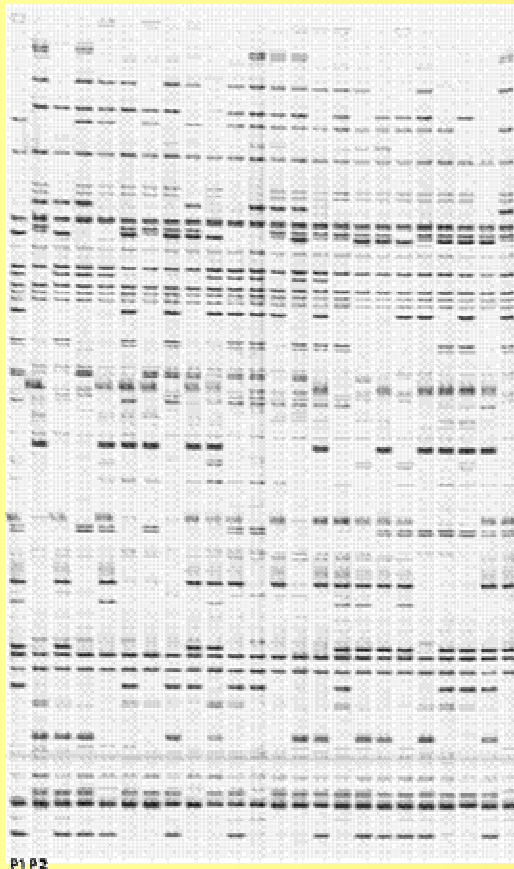
MITE-*Stowaway*-like element 

MITE-*Tourist*-like element 

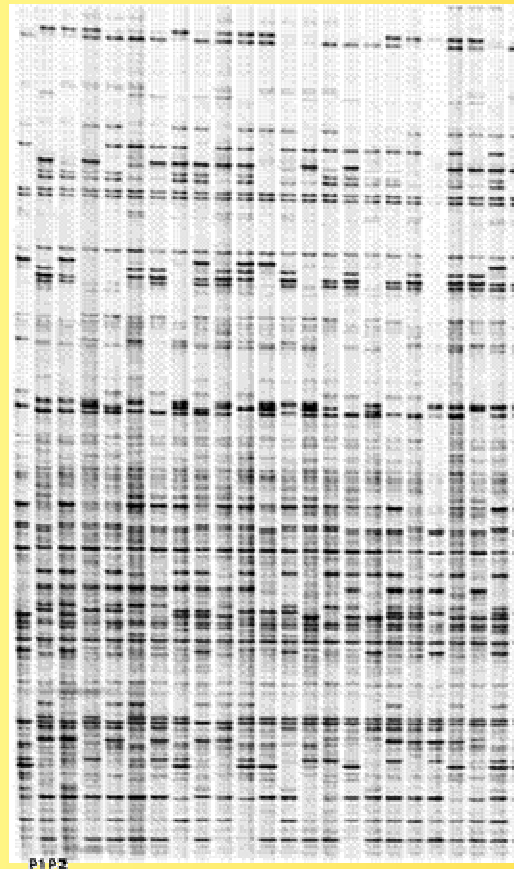


## Naturally multiplexed – Low cost/data point

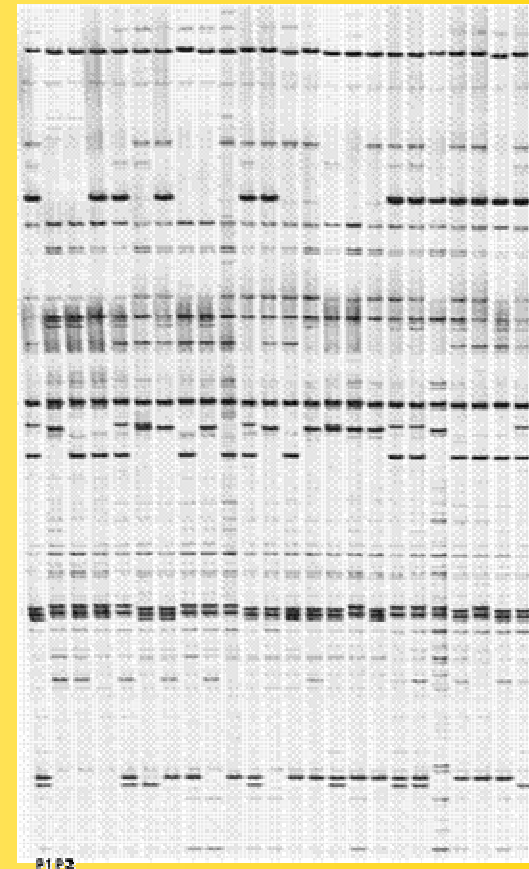
IMP-26



IMP-41



IMP-31

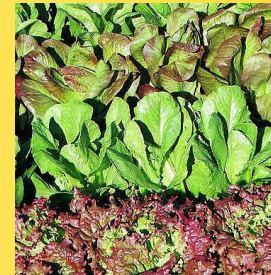


IMPs in maize: Fragments run from 500 bp - 1.1 kb in length

## Cross-species applicability

- DLM has mined various genomes for consensus sequences used to develop IMP primers
- Current IMP library includes 64 markers
- MITE families show up in abundance in all genomes we have tested to date
- Between 50-60% of IMP primers will amplify in a new species
- Polymorphism levels vary by crop
- On average an IMP primer will yield 10 markers from a single PCR
- With a quick, inexpensive pilot DLM can usually generate a few hundred markers for a new crop
- Even greater range possible if sequences of new families were mined – e.g. Solanaceae, Cucurbits, Asteraceae

Recent examples:



Lettuce



Potato



Petunia



Tomato



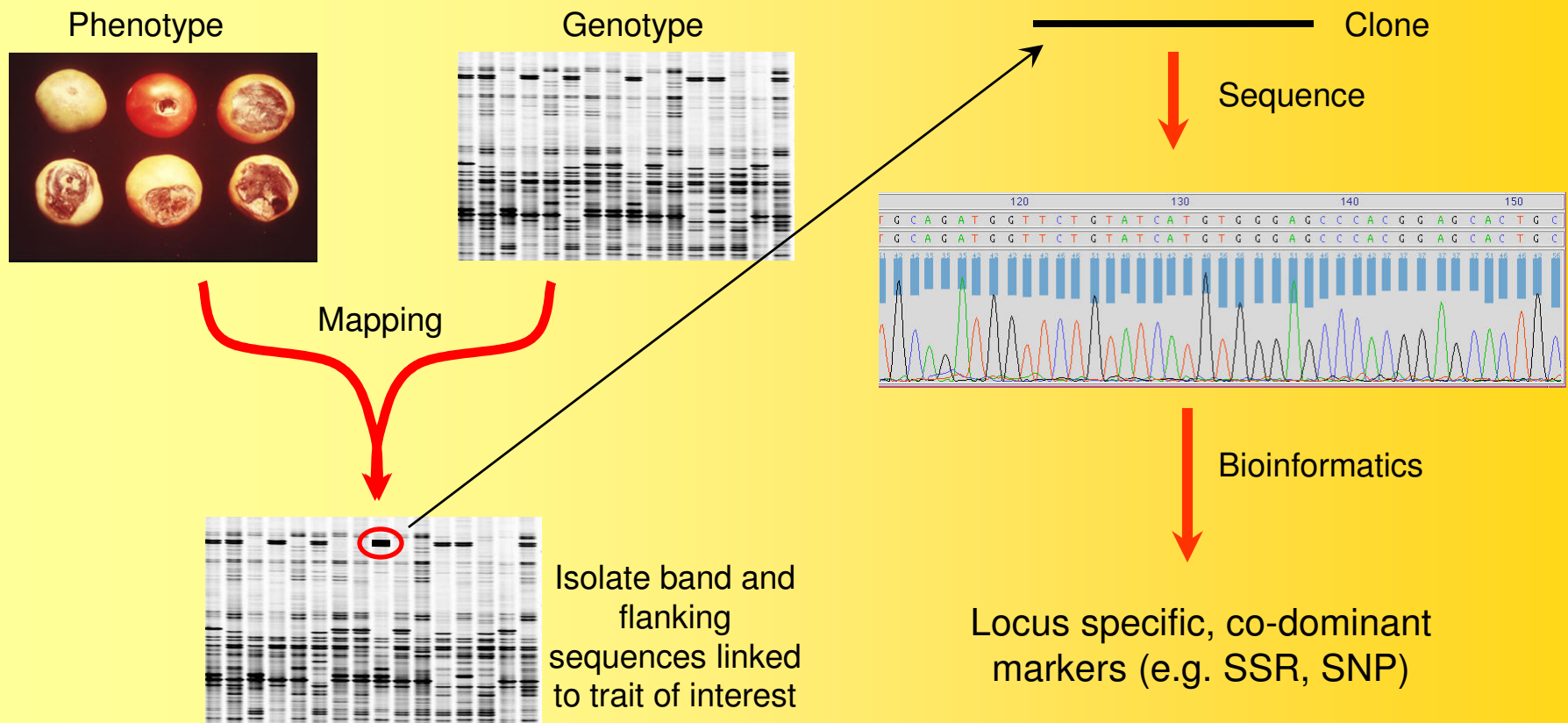
Lobolly Pine

## **IMP applications in marker-assisted breeding**

- Fingerprinting
  - Variety protection
  - Germplasm characterization
  - Identity preservation – quality control
- Trait conversion – recurrent parent genome selection
- QTL mapping & trait-linked marker development
  - Map IMP bands to key traits of interest
  - Potentially convert linked bands to locus-specific markers (future development of technology)

# Trait-linked marker development

- IMPs are very efficient for mapping traits of interest



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## Single Nucleotide Polymorphism (SNP)

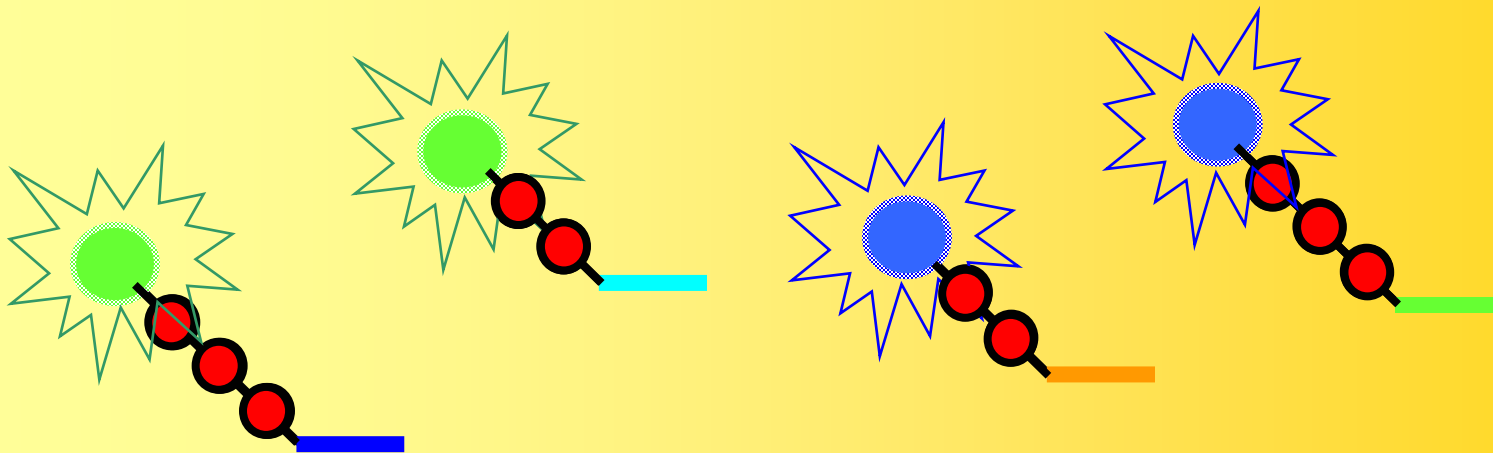
CCTGTTAA **T**GGTACATT

CCTGTTAA **C**GGTACATT

- ❑ Co-dominant marker system
- ❑ Most prolific of all marker types
- ❑ Very efficient and inexpensive to use once developed
- ❑ Holds enormous potential for multiplexing
- ❑ ABI SNPLex technology multiplexes 48 SNPs in a single reaction
- ❑ 96-plex is in development and will soon be released
- ❑ Cost is below a dollar per datapoint
- ❑ DLM is at the forefront of this technology

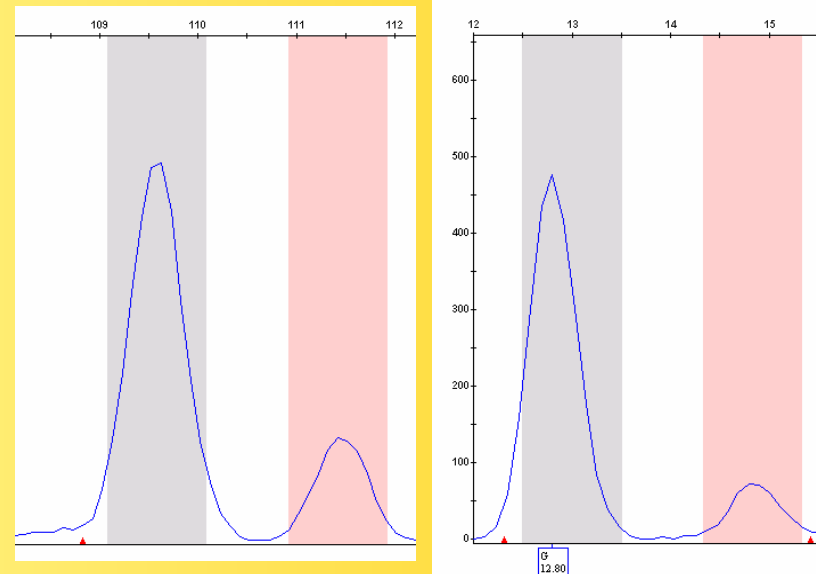
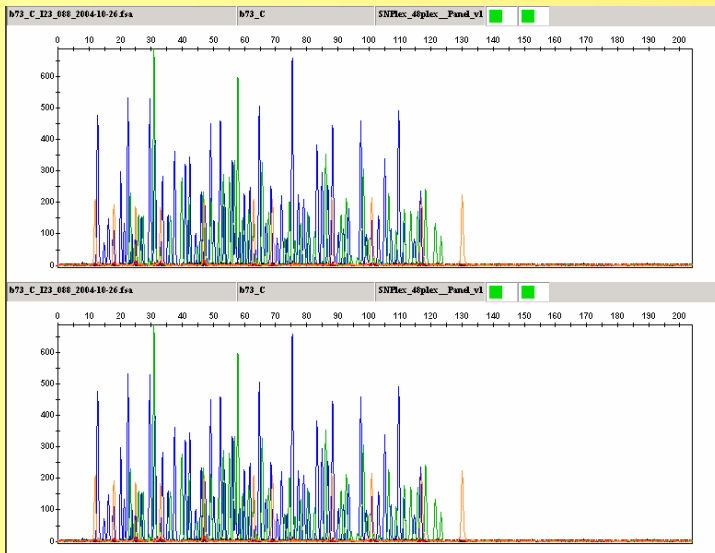
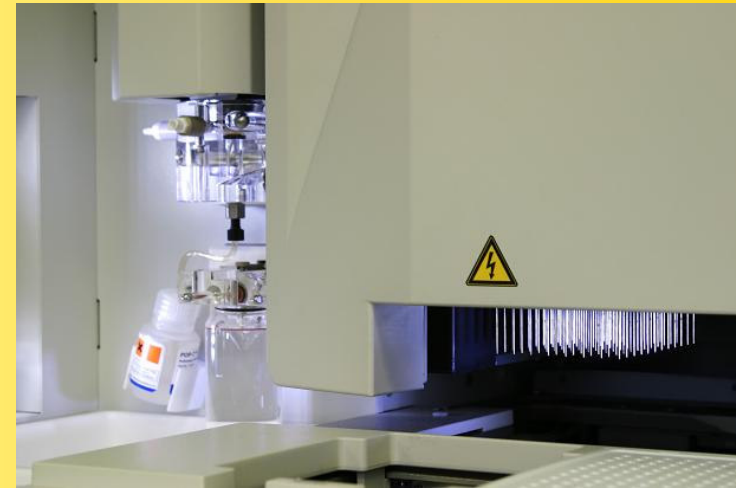
## SNPlex Technology

- Based on Oligonucleotide Ligation Assay (OLA)
- Hybridize amplified products to ZipChutes (universal reporter probes)
- ZipChutes are eluted then loaded onto the 3730XL
- ZipChutes are tagged with mobility modifiers which allow separation along a microcapillary even in a dense multiplex
- Also tagged with fluorescent dyes
- Combination of colour and size separations allows very high-throughput when run on a 3730 XL – over 400,000 dp/day



## SNPlex Technology

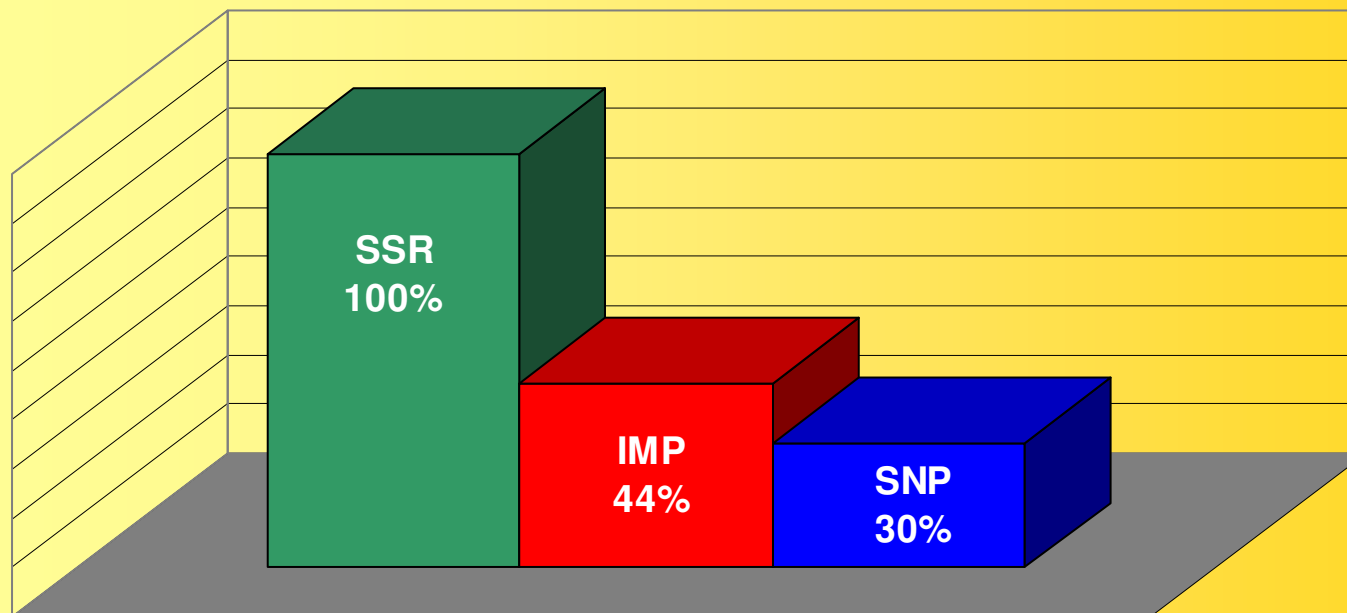
- ❑ ZipChutes are loaded onto ABI3730XL
- ❑ Output of raw data demonstrates the density of the multiplex
- ❑ Can zoom in on individual data points for closer study



## Marker technology development

- Each generation of technology becomes increasingly more powerful but also less costly

**Trait Conversion Cost Comparison**  
(Corn)



Note: Costs quoted are estimates only. Actual cost will vary on a project by project basis.