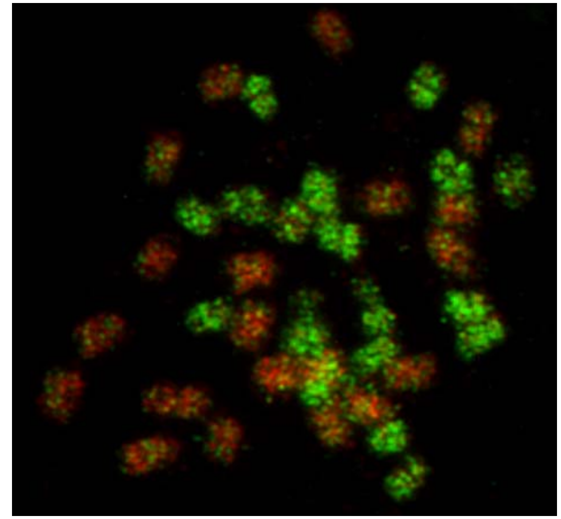
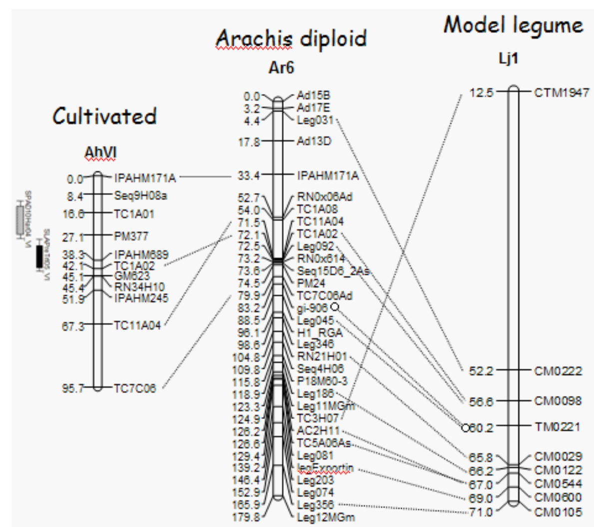
Groundnut genetics, genomics and molecular breeding.





Genomic Resources in groundnut

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NSF, Generation Challenge Program
Collaborators, V. Penmetsa, A. Farmer, Mei Yuan,

Steve Knapp – University of Georgia, USA
USDA, National Peanut Board,
Generation Challenge Program,Peanut Foundation
Collaborators, E. Nagy, C. Taylor

Genomic Resources in groundnut

Generation

Main GCP Projects

Unlocking the genetic diversity in peanut's wild relatives with genomic and genetic tools.

Improving tropical legume productivity for marginal environments in sub-Saharan Africa – TLI.

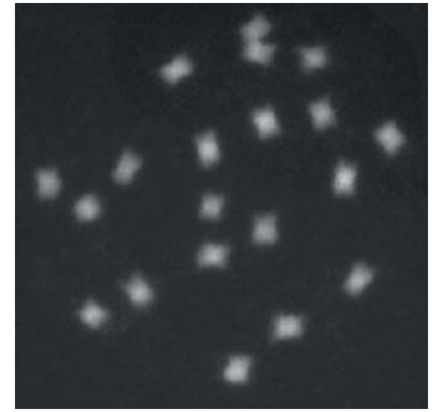
Project Rationale

Origin of cultivated peanut

Diploid species with A-genome

$n = 10 \times n = 10$

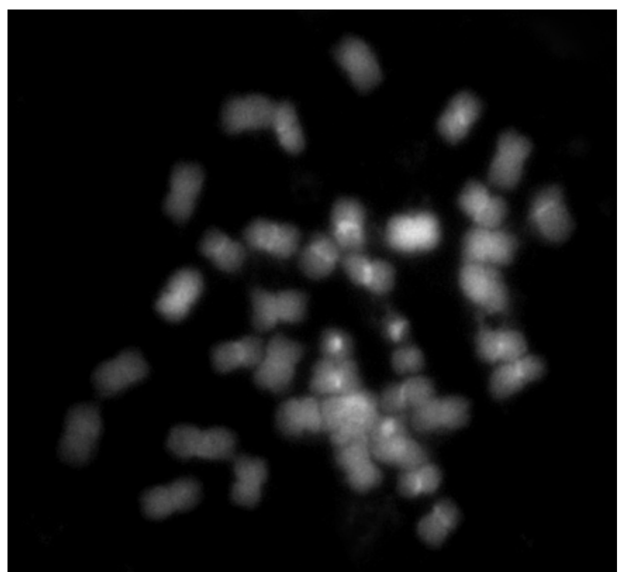
Diploid species with B-genome



Sterile AB hybrid 2n = 20

Genetic bottle-neck !

Spontaneous duplication



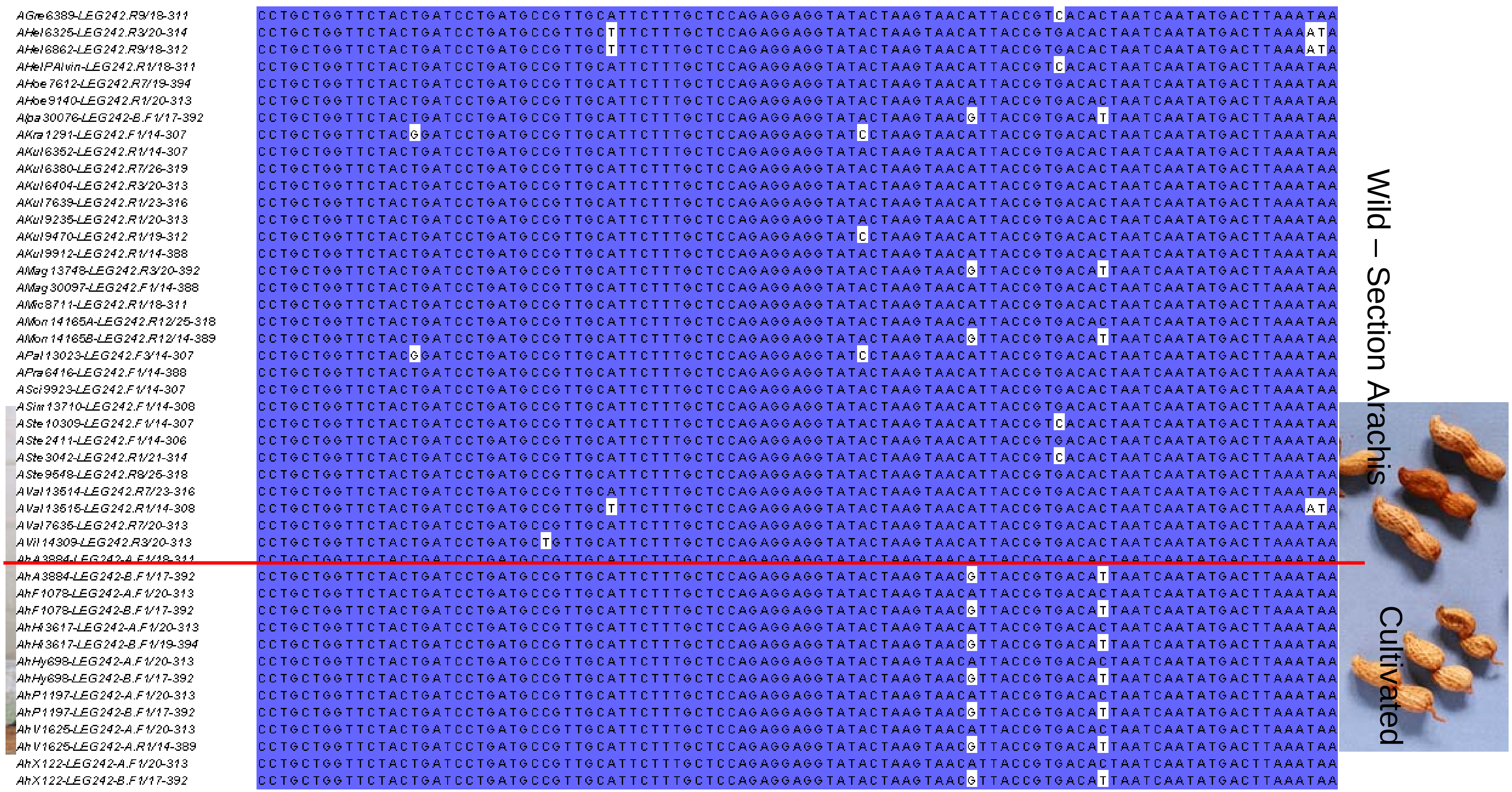
Arachis hypogaea

AABB

Project Rationale

A. hypogaea		Wild species:
Few alleles	←	Many alleles
Tetraploid		Diploid

Wild alleles bring many new traits and provide polymorphism for genetics



Projects Rationale

Year 2000

- Only two RFLP maps

  (both in pops incorporating wild species polymorphism)

- No maps from cultivated x cultivated populations
- 6 SSR markers published

Projects aimed for

- Development of sufficient markers for routine molecular breeding

  (even in cultivated x cultivated crosses.)

- Reference genetic maps for molecular breeding

  (within a comparative framework)

- Genomic resources for peanut research
- Use of tools in breeding programs, both for introgression of wild traits and for cultivated peanut.

Activities and results

Development of sufficient markers for routine molecular breeding.

Concentration on microsatellite markers:

PCR-based, easy-to-use, suitable for breeders

~ 40% poly.
in cultivated

Three approaches:

1) Targeted long $(TC)_n$ SSRs, most polymorphic: **410**+282=692

2) EST SSRs: ~ 1200 — Map genes but ~ <10% pol. in cultivated

2) Targeting SSRs close to resistance genes: **131** — High value

3) Development of SSRs from BAC end sequences: **1338** SSRs

? poly. in cultivated
Anchor physical map

Result – A total of ~3300 SSRs now available

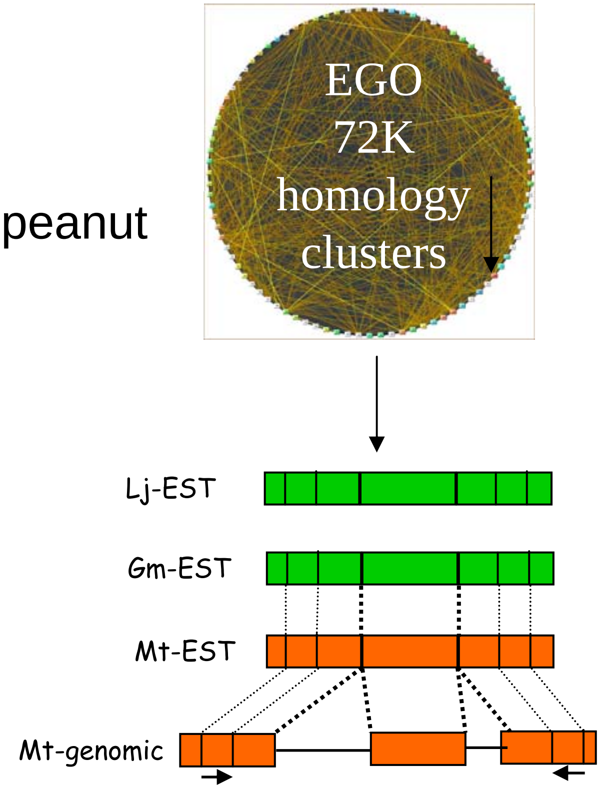
Activities and results

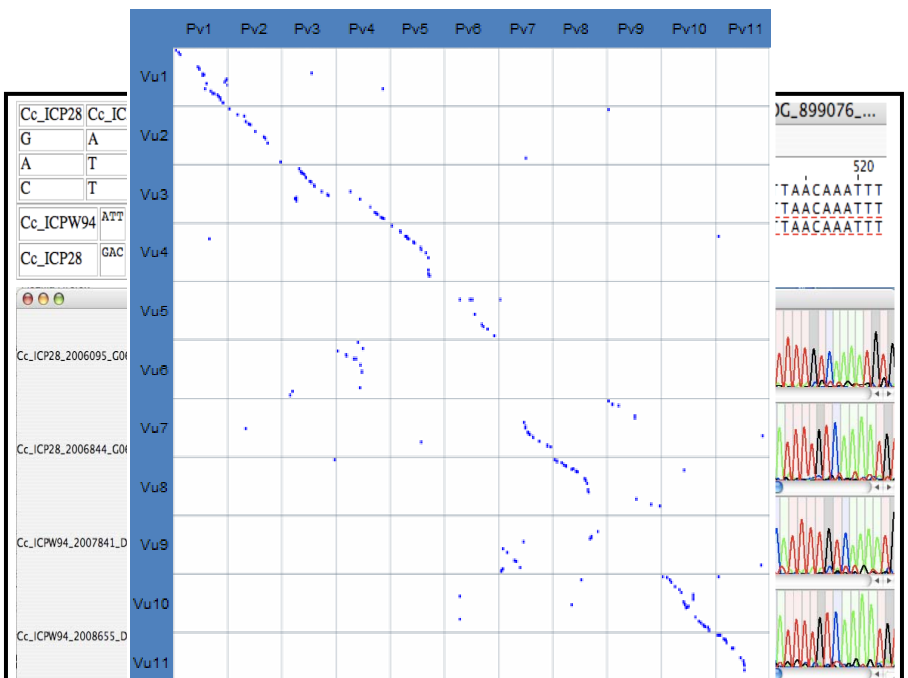
Reference genetic maps for molecular breeding - A comparative gene-rich framework

Orthologous Genetic Markers in 6 legume crops

Low copy genes SNP intron-markers ~ 379 in diploid peanut

Genotyping using Illumina platform





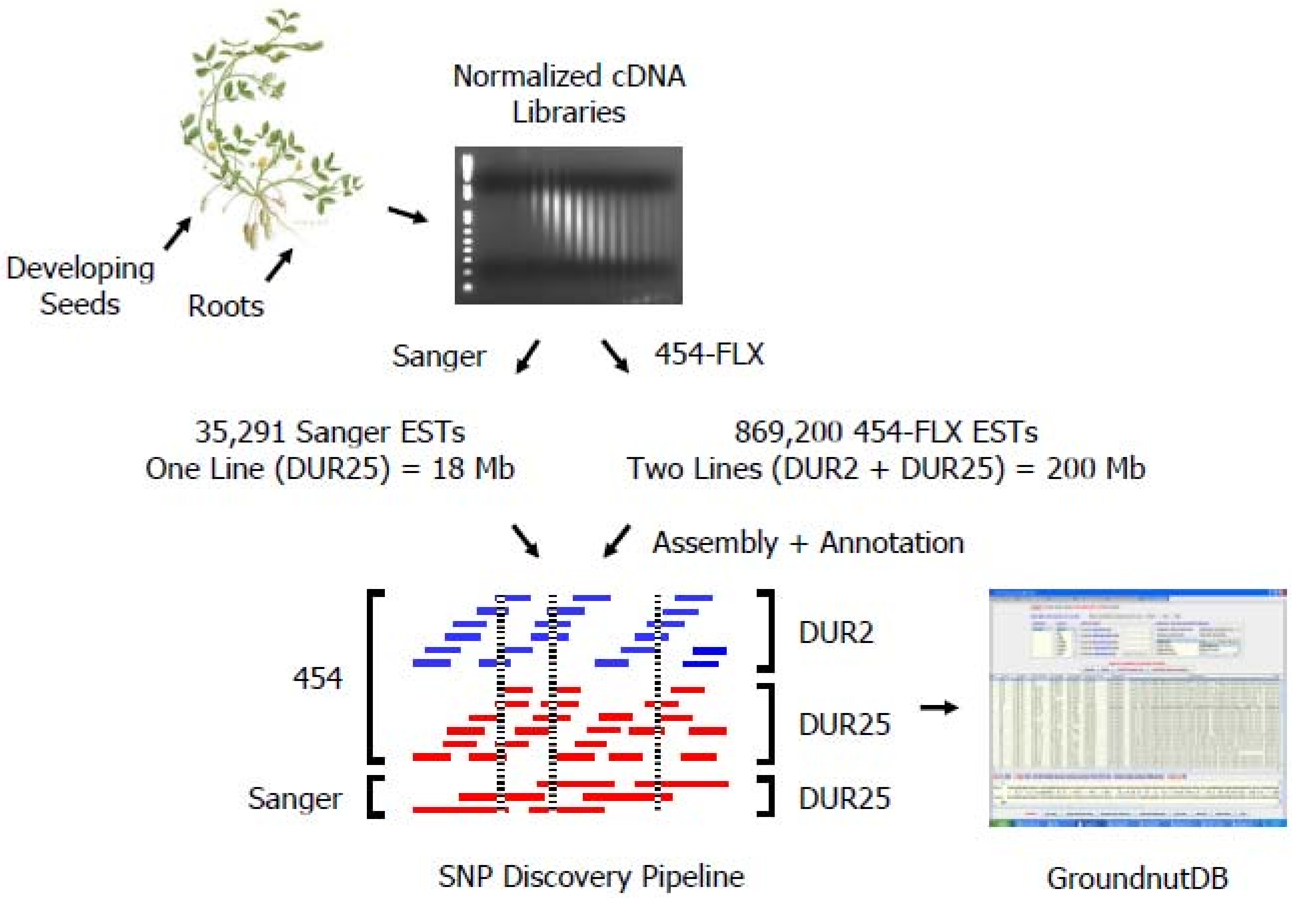
example plot, Arachis data out soon!

Expected result –
Peanut integrated into a unified genetic system for legumes

Collaborator activities

Genomic resources for peanut research – high density gene SNP map

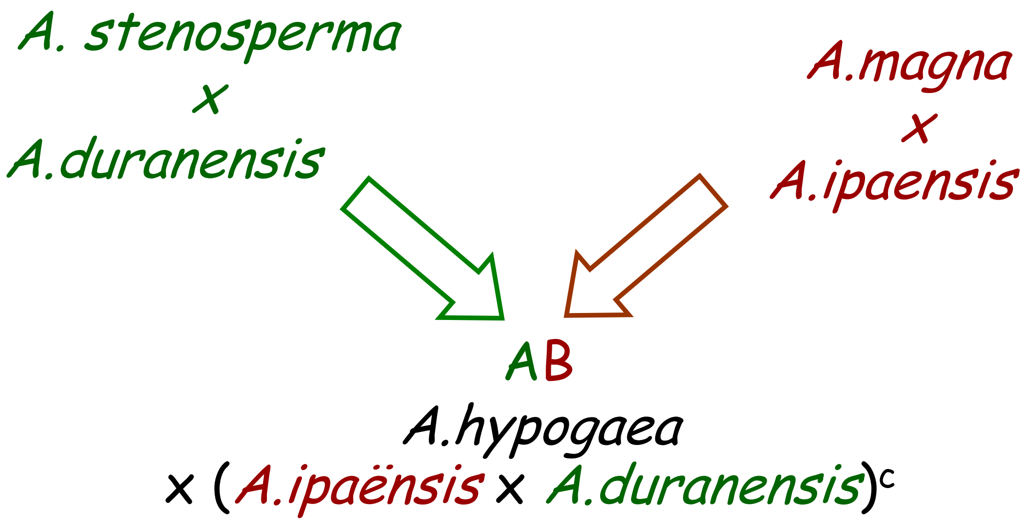
1,536 SNPs Golden Gate Array for diploid peanut (*A. duranensis*)



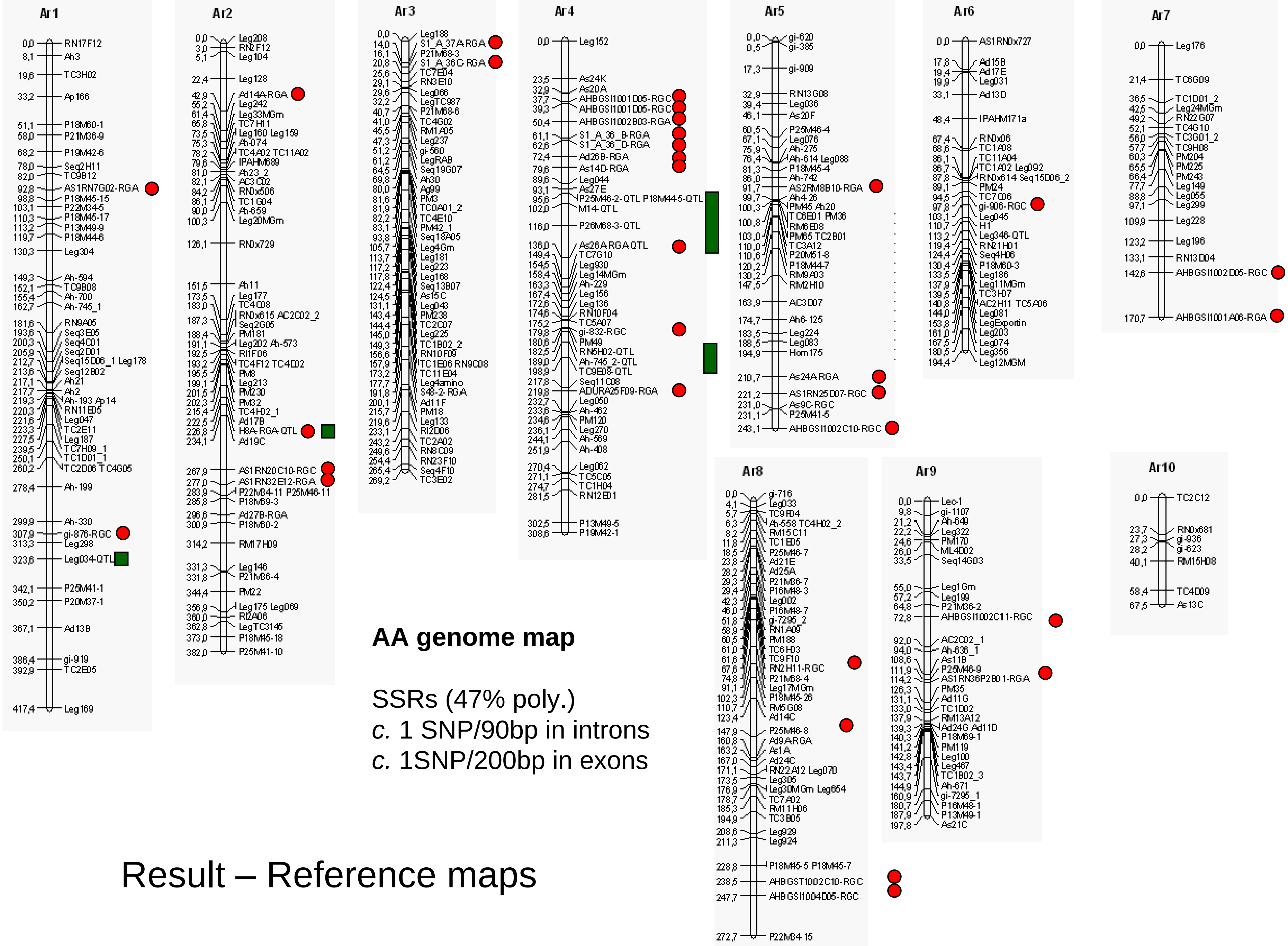
Array being tested important parentals / accessions in GCP projects

Activities and results

Reference genetic maps for molecular breeding – Reference populations



Result – RIL reference populations for genetic mapping publicly available



AA genome map

SSRs (47% poly.)
c. 1 SNP/90bp in introns
c. 1SNP/200bp in exons

Result – Reference maps

Activities and results

Genomic resources for peanut research - BAC libraries and physical map

A.duranensis

BAC (*Hind*III)
c. 80,000 clones
110kb média de inserto
c. 6.5x

40,000 BAC end sequences
Coverage being increased
Building of physical map

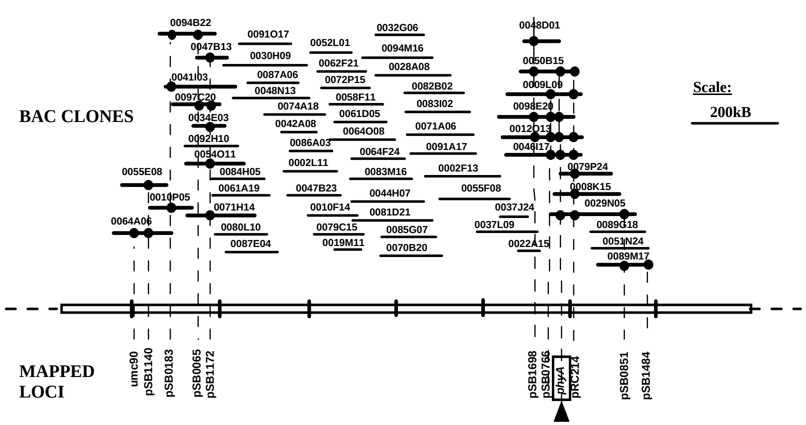
A.ipaensis

BAC (*Hind*III)
c. 80,000 clones
100kb média de inserto
c. 6.5x

AB
A. hypogaea

Tiffrunner BAC (random shear)

Physical map of RGA regions

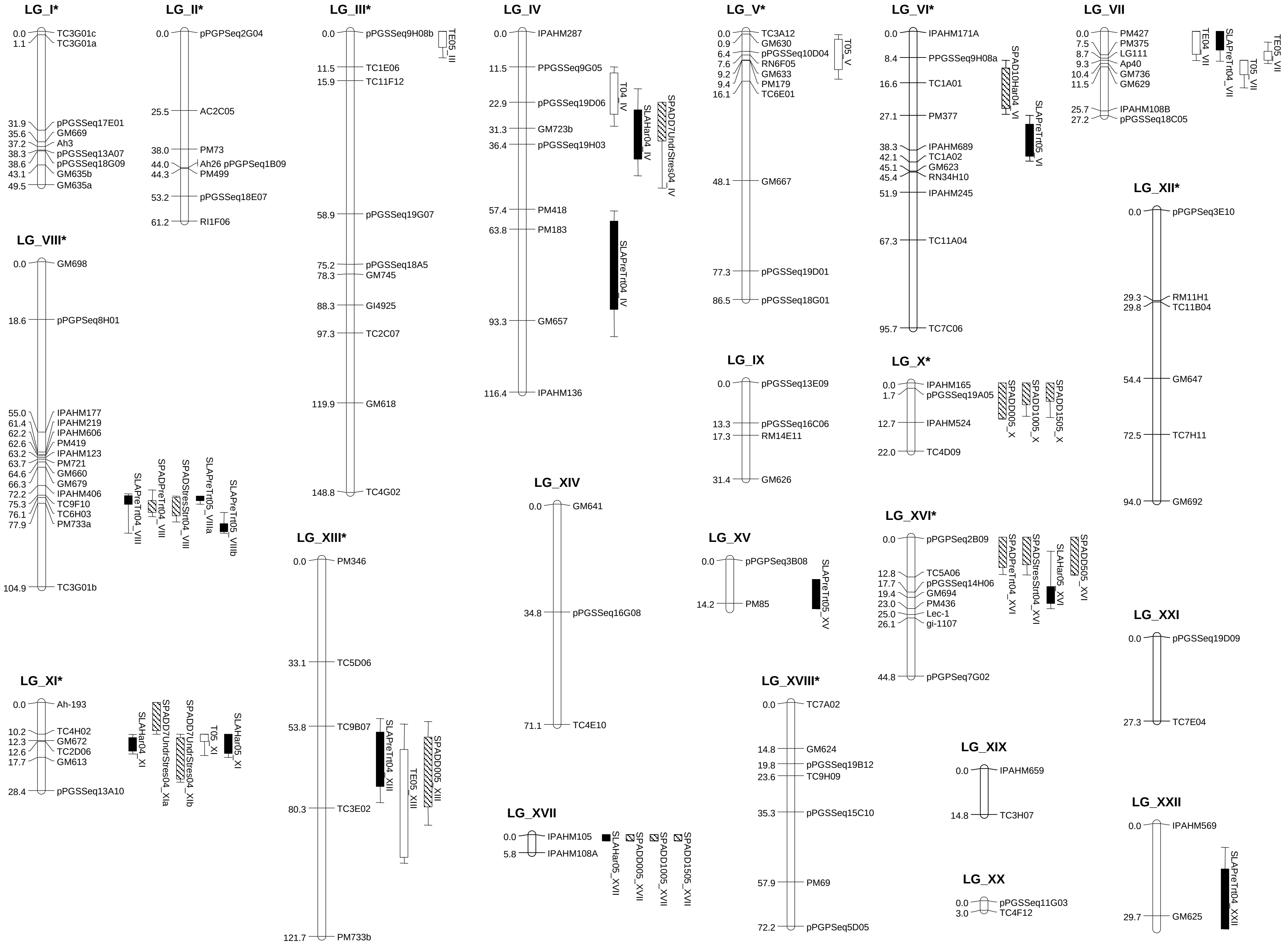


Expected results -

High-quality genetically-anchored physical maps available for whole peanut A-genome

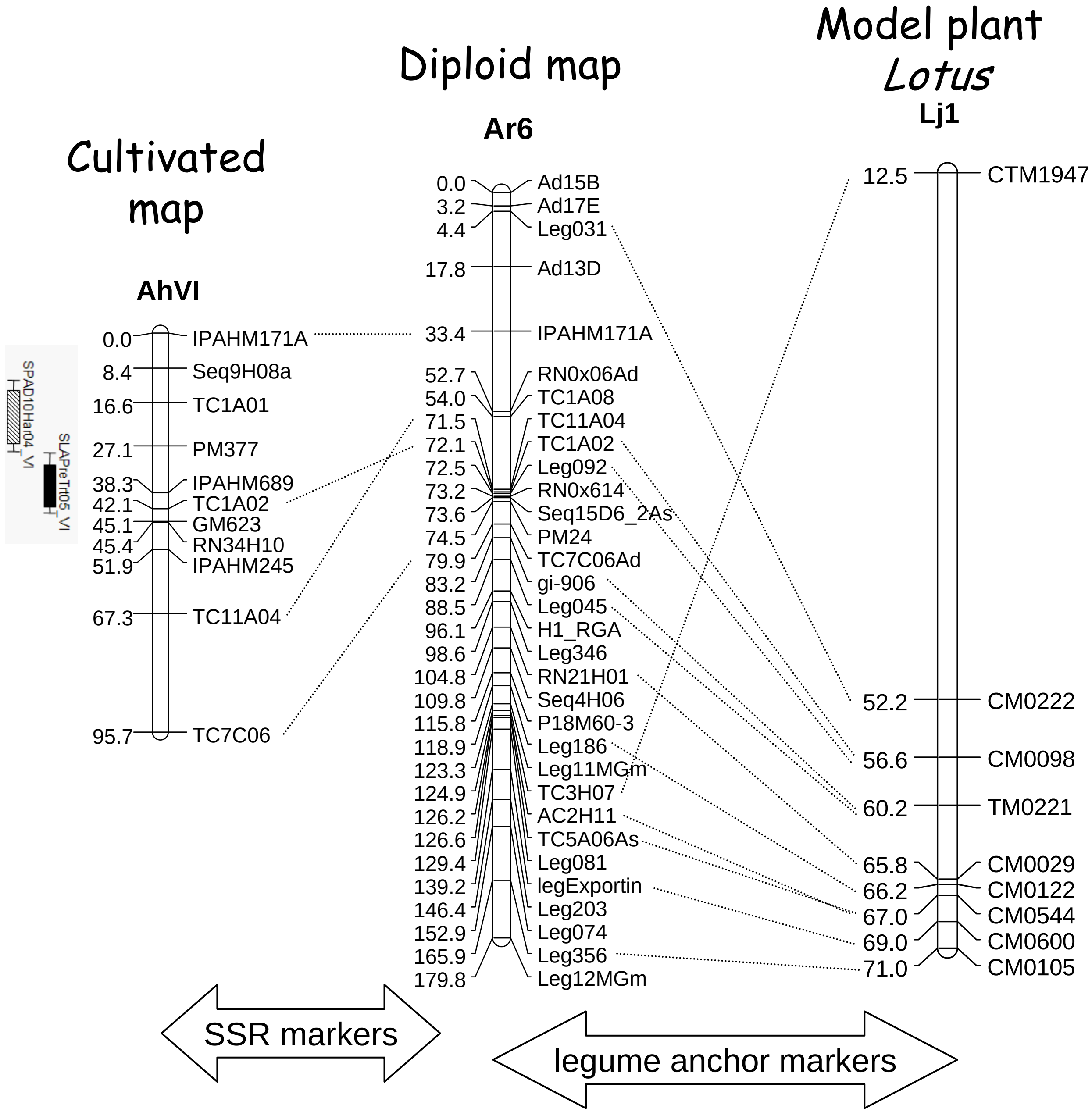
and for cultivated RGA regions

Product delivery and impact on users. – first cultivated groundnut maps



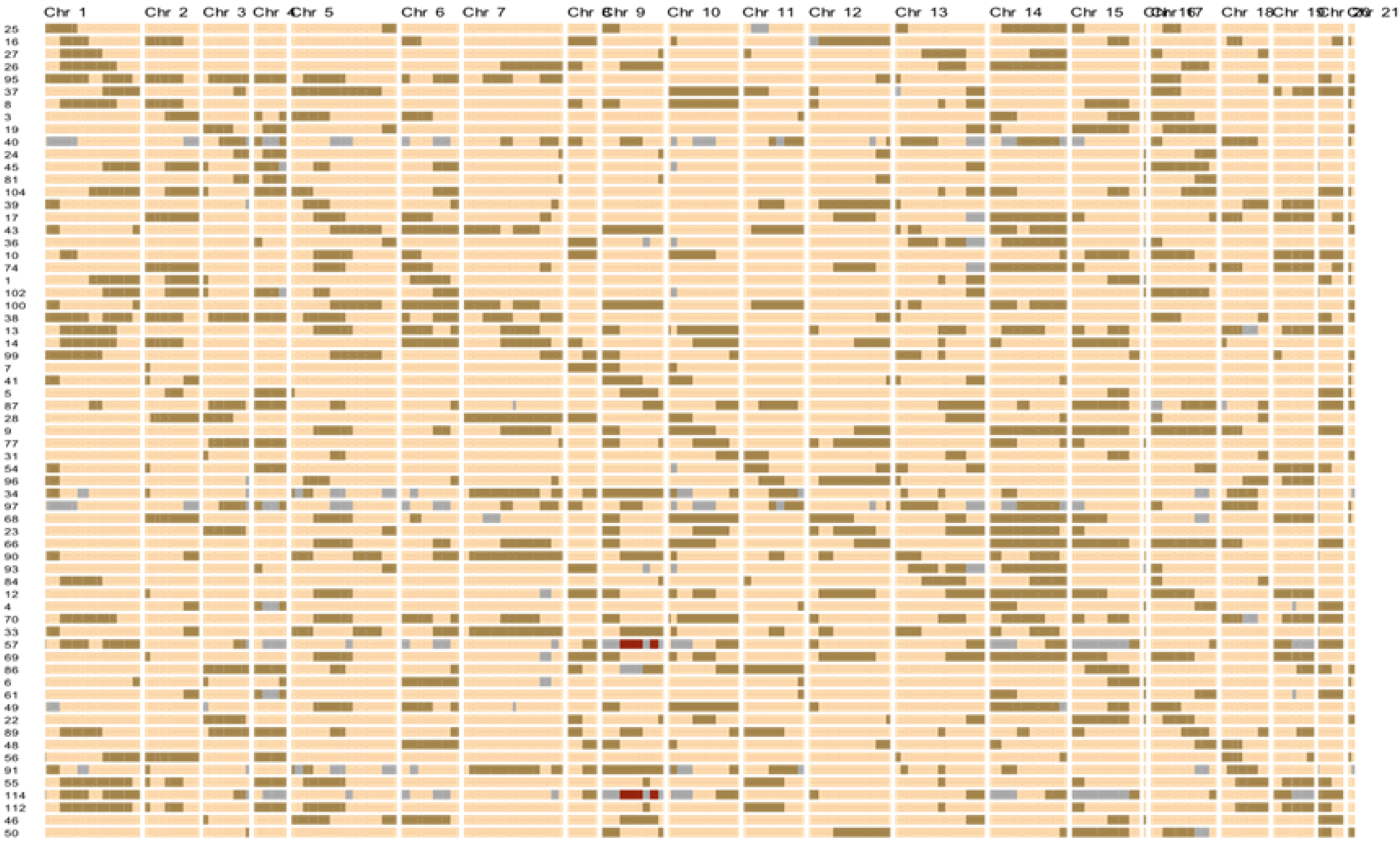
Product delivery and impact on users.

– Reference A map enables more leverage of data



Product delivery and impact on users.

Introduction of wild genes into breeding programs



Application of molecular tools for controlled wild introgression into Peanut cultivated germplasm in Senegal. J-F. Rami, O. Ndoye et. al.

Summary

- Groundnut genomic resources have increased dramatically.

  More markers
  BAC libraries
  Physical map resources

- Groundnut tetraploidy and low polymorphism remain limiting factors

- *Future work*

  Full characterisation of markers – definition of working high poly. set
  Fullest possible integration of the resources