



International Center for Tropical Agriculture  
Since 1967 / *Science to cultivate change*

# *De novo* assembly of Common Bean interspecific genotypes

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Juan Garces



# INB 841: A unique introgression line

- Resulted from a cross among several introgression lines from a previous project
- Selected originally under drought
  - Expressed resistance to wilting under intense mid-season drought
  - May have rapid pod elongation
- Has been an excellent parent...progeny express:
  - Heat resistance
  - Resistance to wilting
  - Uniform and stable maturity
- We have RILs of INB 841 x RCB 293
  - Tim has evaluated for heat
  - We evaluated for drought and are repeating



0.1

*P. accutifolius*

G40001  
G40001\_def  
G35346  
G35346\_def

*P. vulgaris*

*P. coccineus*

Tree scale: 0.1

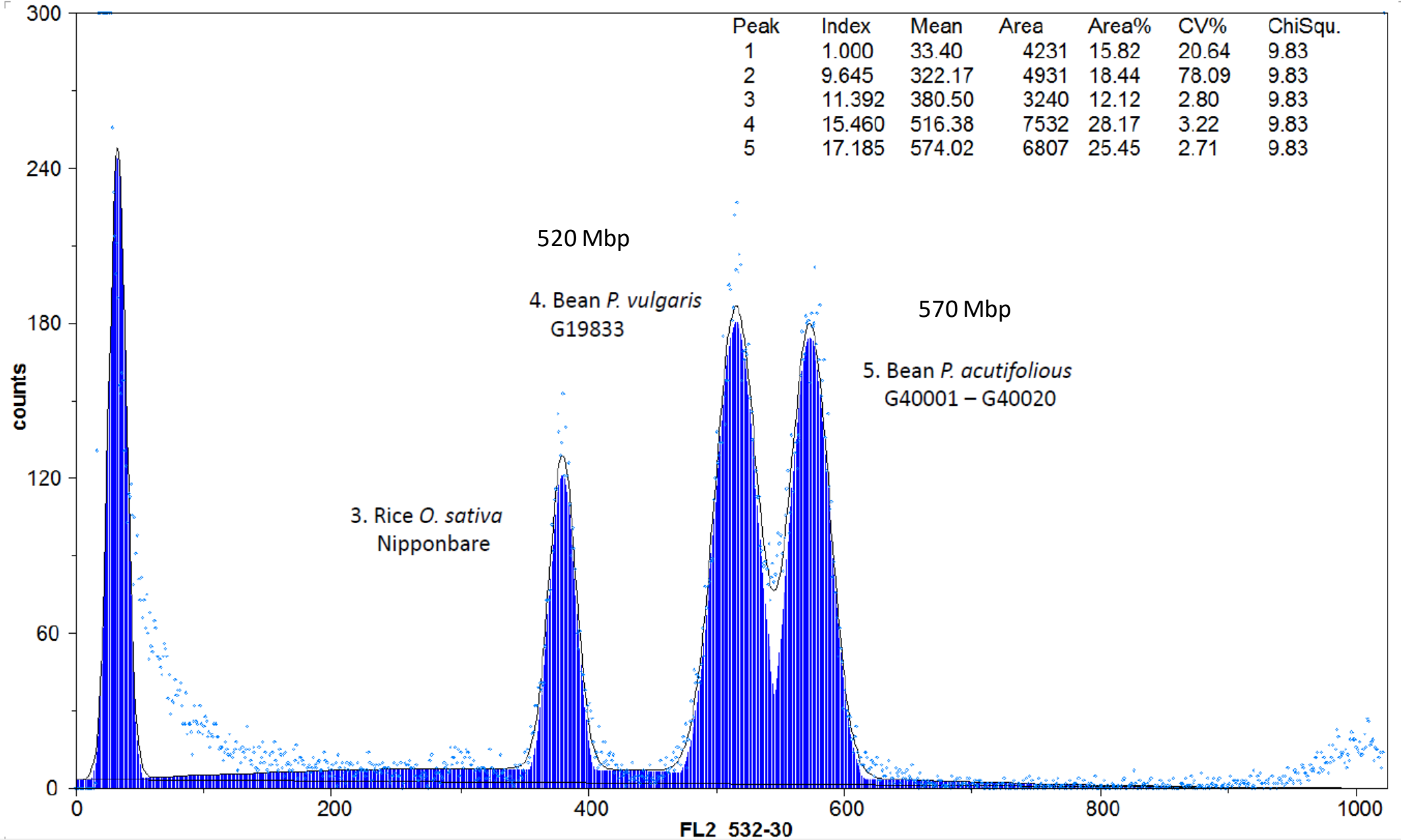
G19833  
VAP3R1  
VAP3R2  
INB834  
INB841  
VAP1R2  
VAP1R1  
RWR719  
VAP2R2  
VAP2R1

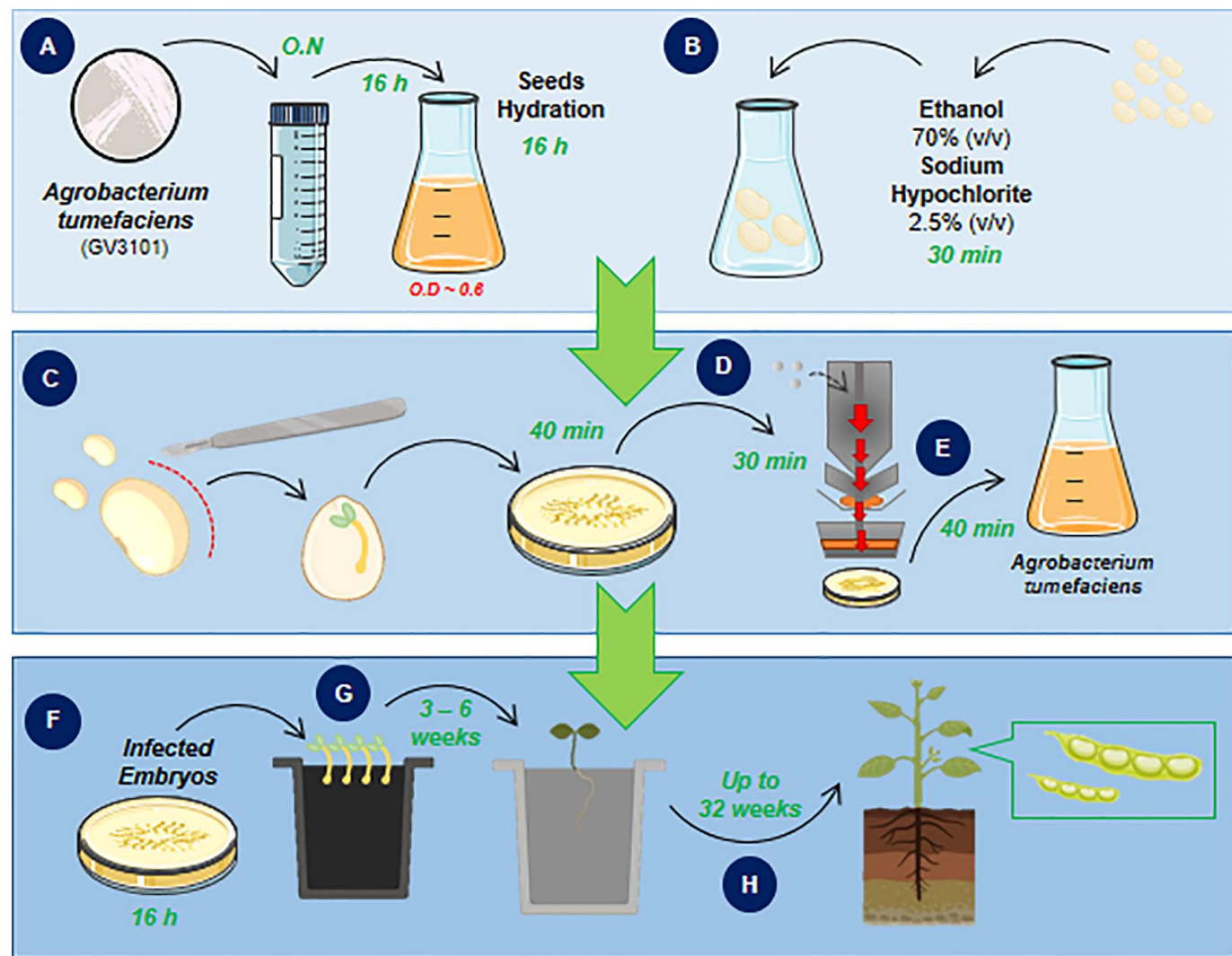
G40001

G40264

G04627  
G19833  
SRS481809.Pool5  
Sang2015\_KARDINAL  
G3696  
Sang2015\_FIERO  
Sang2015\_CAL\_EARLY  
Sang2015\_LARK  
Sang2015\_RED\_HAWK  
MSHINDT\_G0705\_GASILIDA  
Sang2015\_JALO\_EEP\_558  
MIDAS SRS481812.WildAndean  
NABE\_13 AND\_896  
NABE\_14 SRS481807.Pool6  
Sang2015\_CORNELL\_49-242  
Sang2015\_LAKER  
Sang2015\_UC\_WHITE  
Sang2015\_C-20  
Sang2015\_MATTERHORN  
Sang2015\_BAT\_90  
Sang2015\_UI\_906  
Sang2015\_MICHELITE  
Sang2015\_STAMPEDE  
Sang2015\_IT\_28  
Sang2015\_BUC\_SKIN  
Sang2015\_SIERRA  
G2333  
MEXICO\_54  
G10474  
SRS481812.WildMesa  
SRS481814.Pool1  
SRS481806.Pool3  
SRS481808.Pool2  
SRS481810.Pool4  
MD\_23-24  
HAWASSA\_DUME  
RED\_WOLAYTA  
RWR\_719  
BAT\_90  
VAX\_1  
TARS-VR-7S  
VAX\_4







# *P. acutifolius* introgression into *P. vulgaris*

Q40  
RepMasked  
MINI 300  
MAF 0.01  
Variants Group select

G40001W\_sen Vs G19833W-G10474W

G40001 WGS  
G40001 WGS\_sen  
G40001 GBS  
G40035 GBS  
G40036 GBS

AM

INB



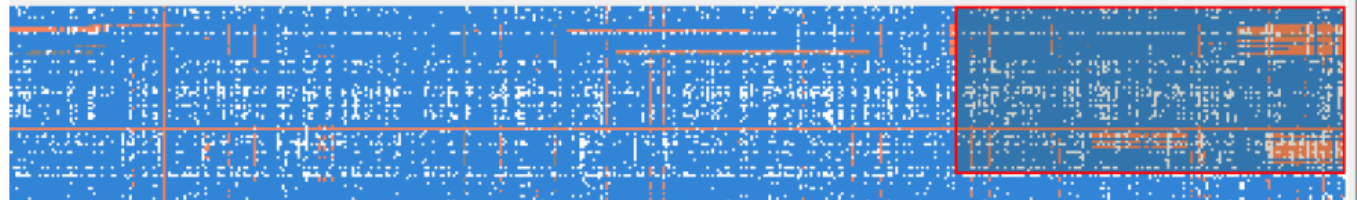
G19833W *P. vulgaris*



G40001W *P. acutifolius*

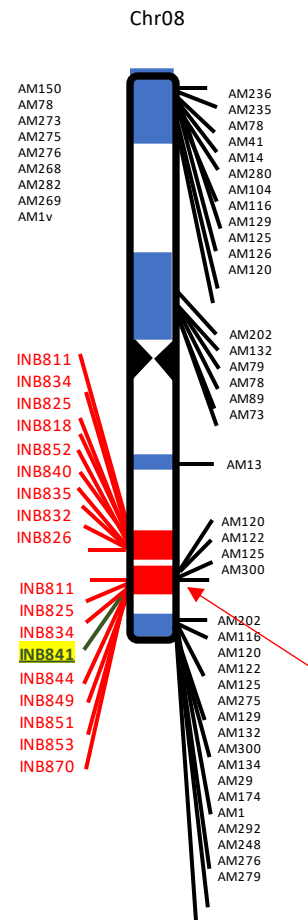


Overview



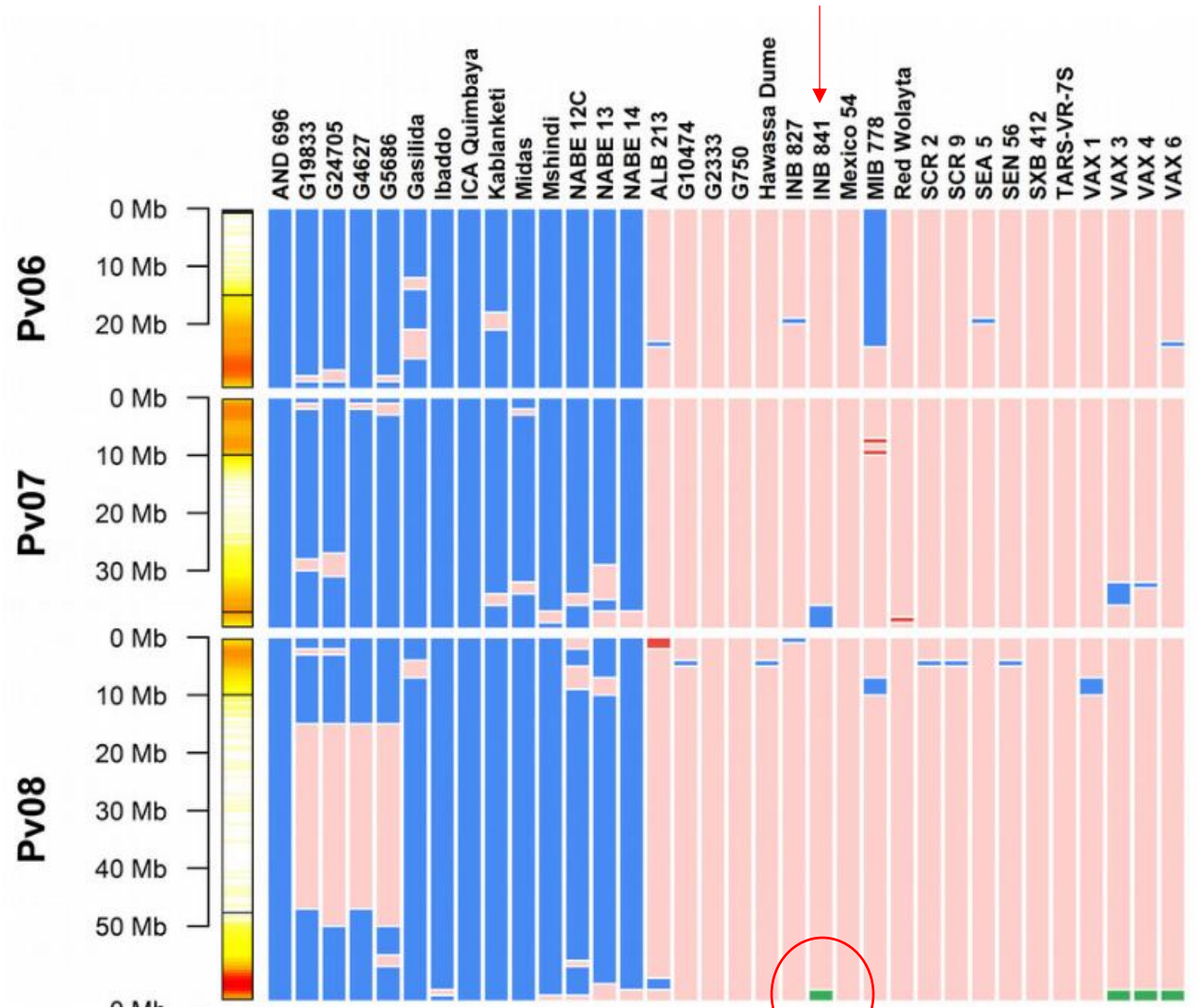
## Resequencing of Common Bean Identifies Regions of Inter-Gene Pool Introgression and Provides Comprehensive Resources for Molecular Breeding

Juan David Lobaton, Tamara Miller, Juanita Gil, Daniel Ariza, Juan Fernando de la Hoz, Alvaro Soler, Steve Beebe, Jorge Duitama, Paul Gepts, Bodo Raatz



(CIAT 2016)

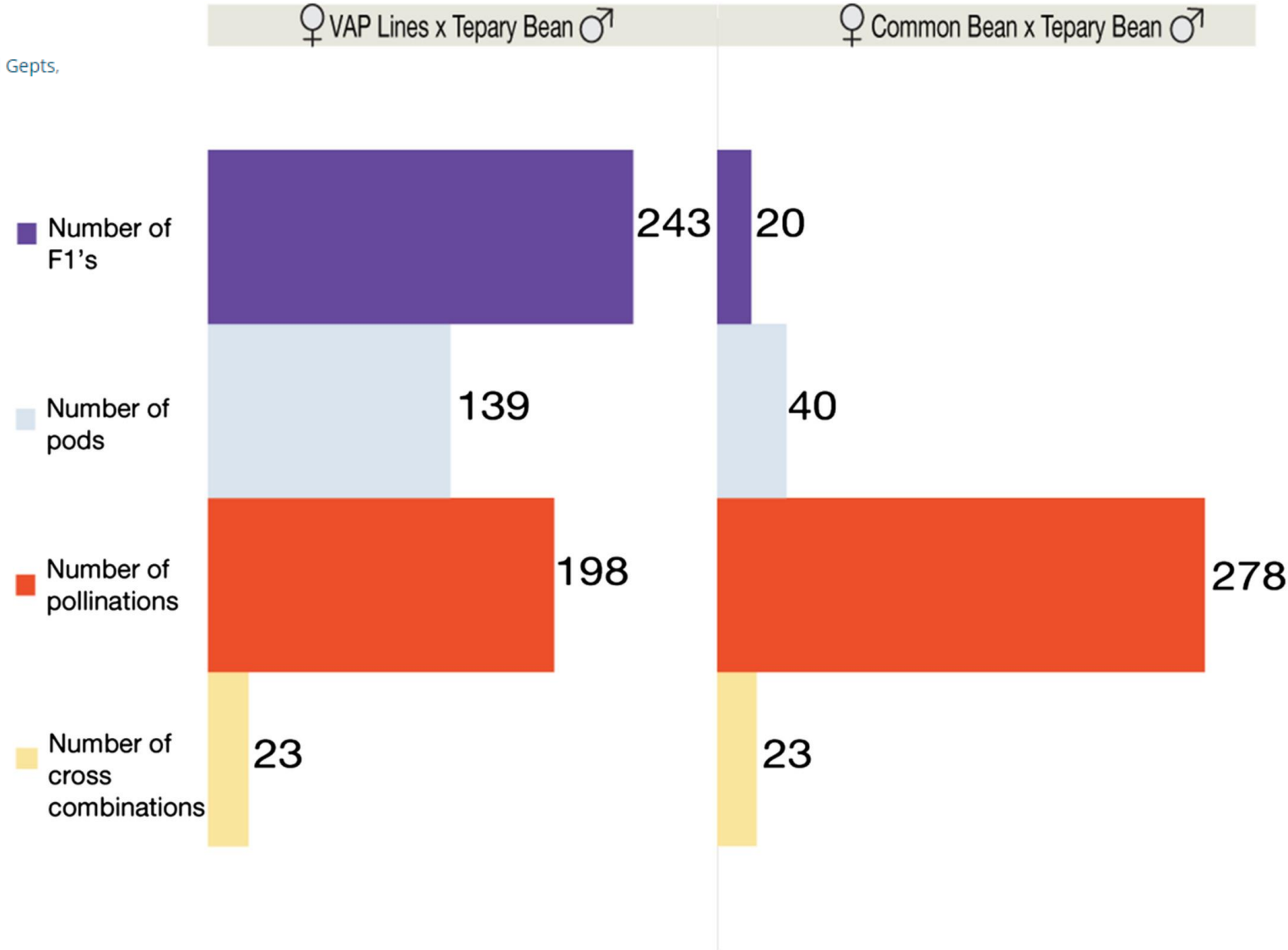
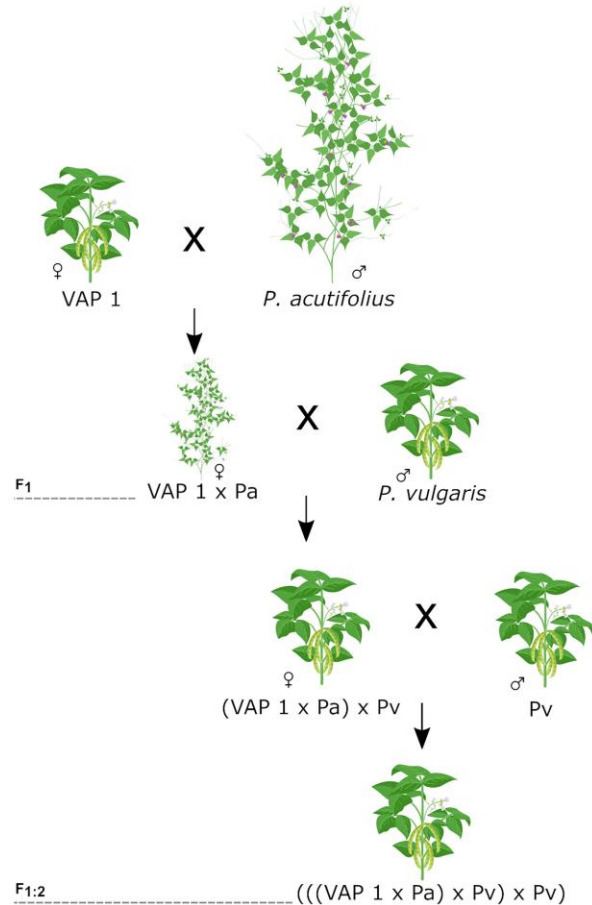
Pv08 introgression from Pa  
58,724,703 to 59,187,803



(CIAT 2018)

# Large genomic introgression blocks of *Phaseolus parvifolius* Freytag bean into the common bean enhance the crossability between tepary and common beans

Santos Barrera , Jorge C. Berny Mier y Teran, Juan David Lobaton, Roosevelt Escobar, Paul Gepts, Steve Beebe, Carlos A. Urrea



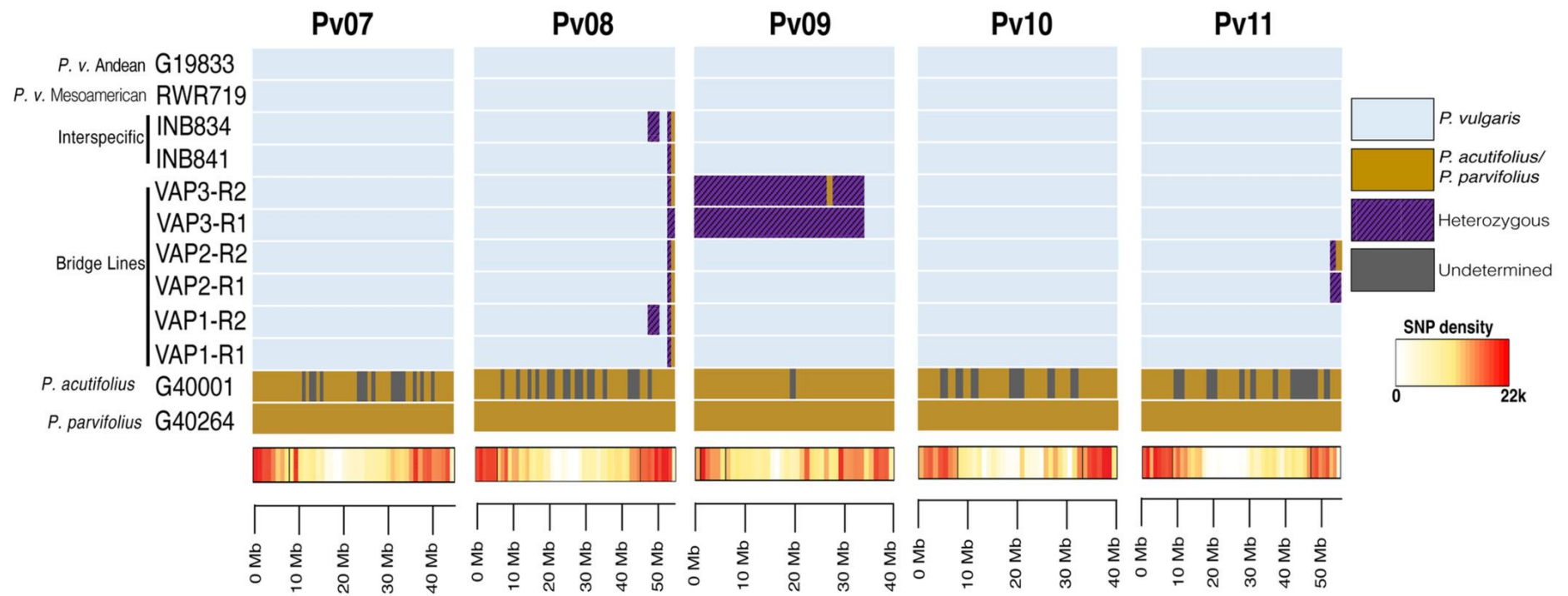
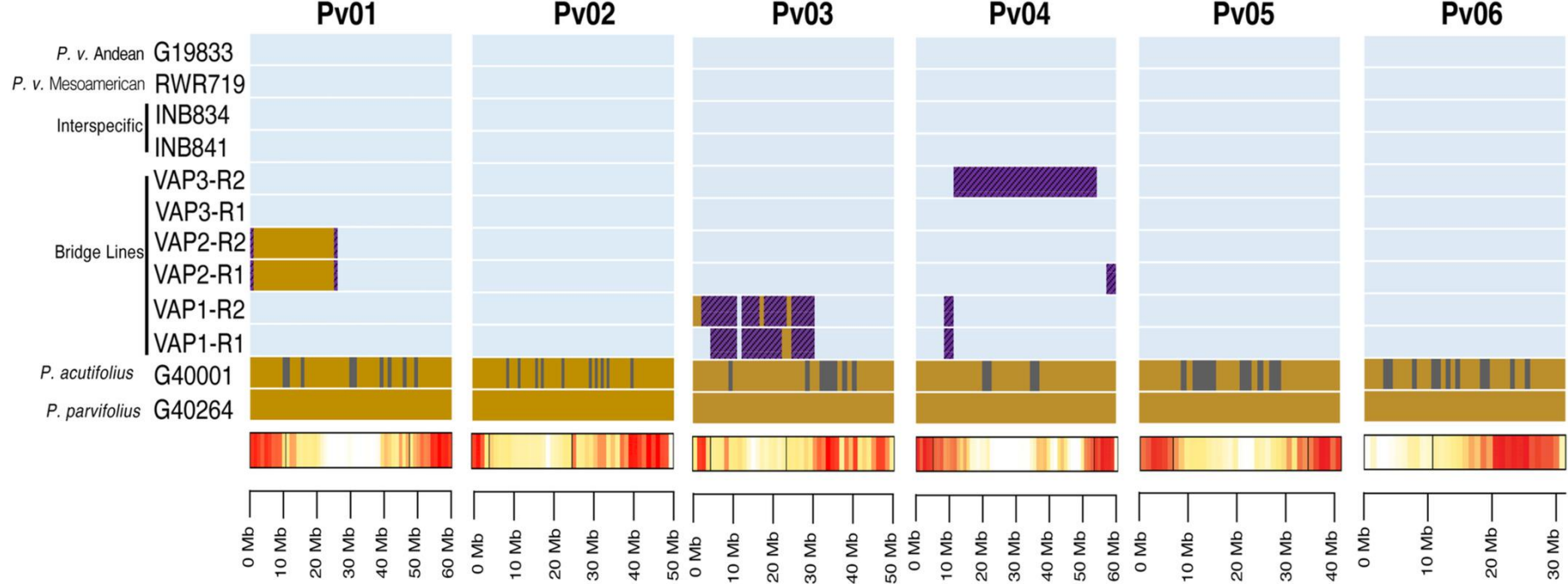


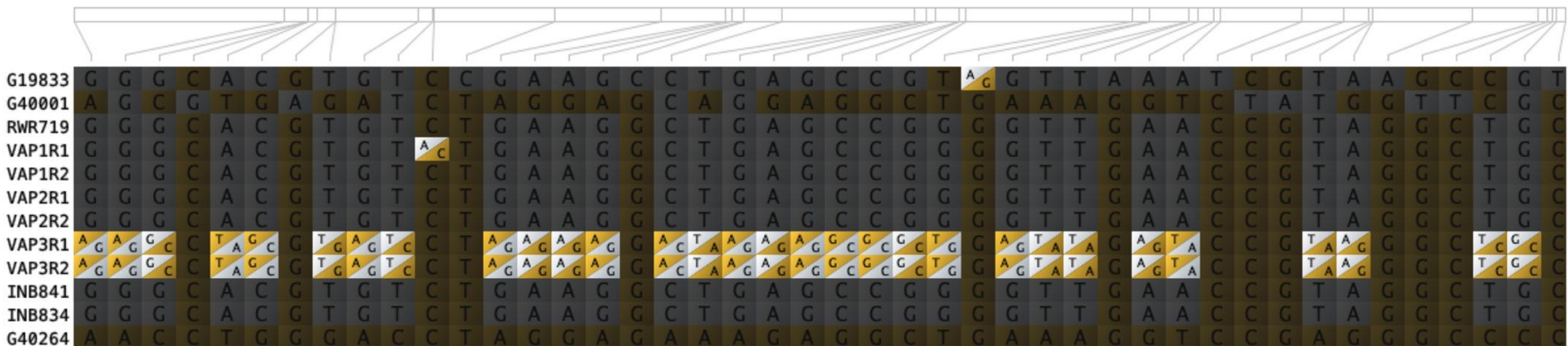
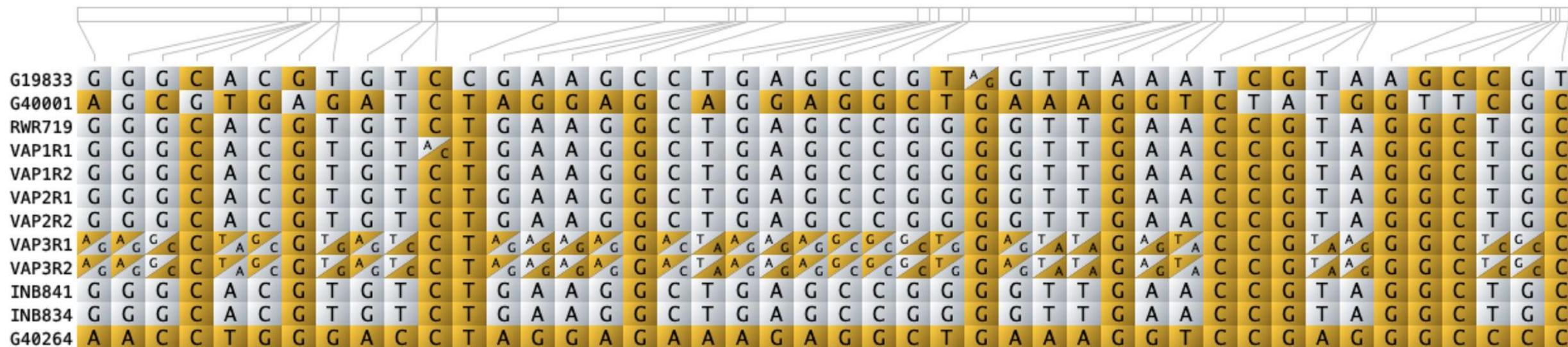
(a)



(b)





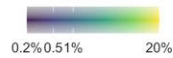


# Interspecific common bean population derived from *Phaseolus acutifolius* using a bridging genotype demonstrate useful adaptation to heat tolerance

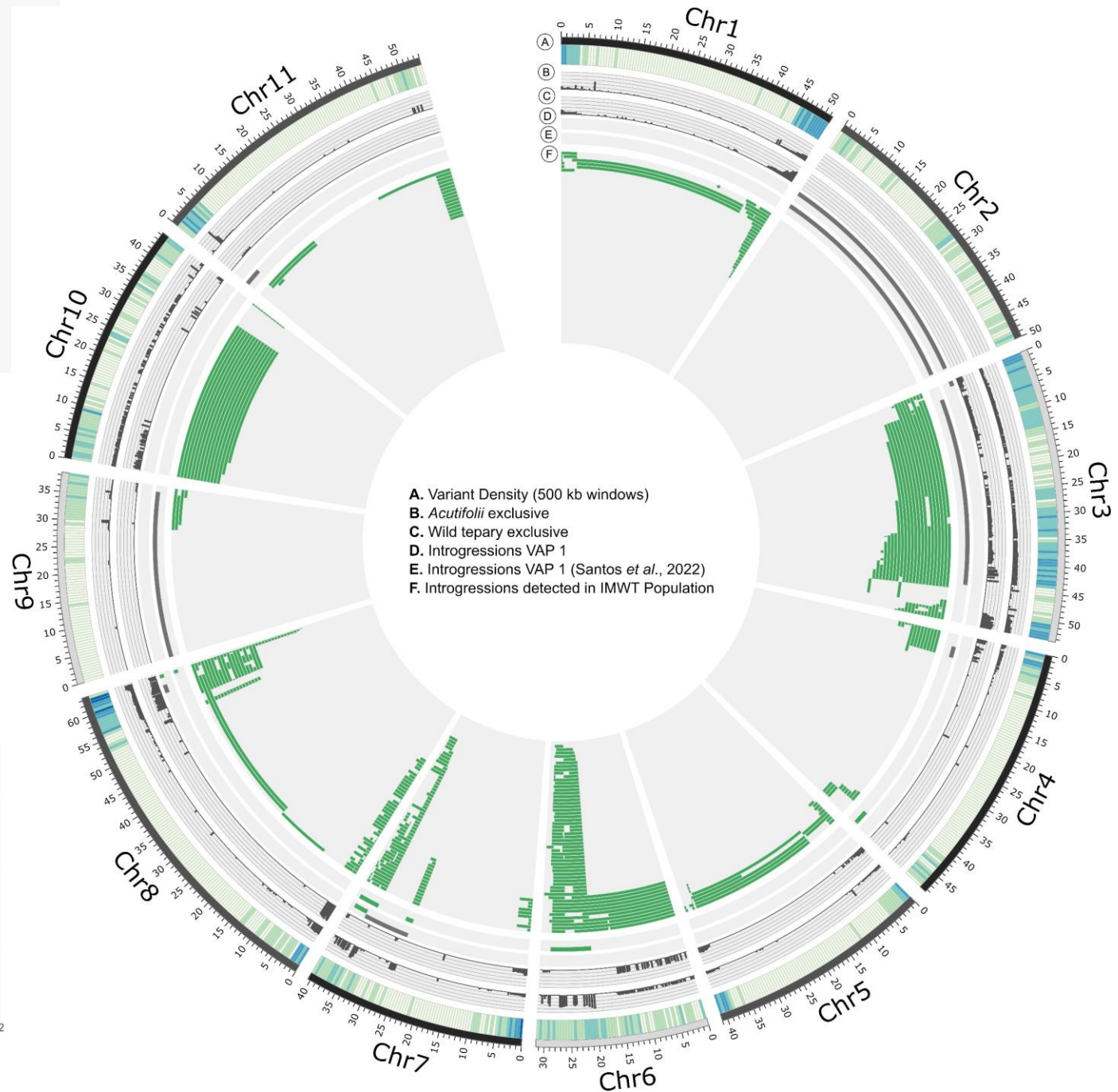
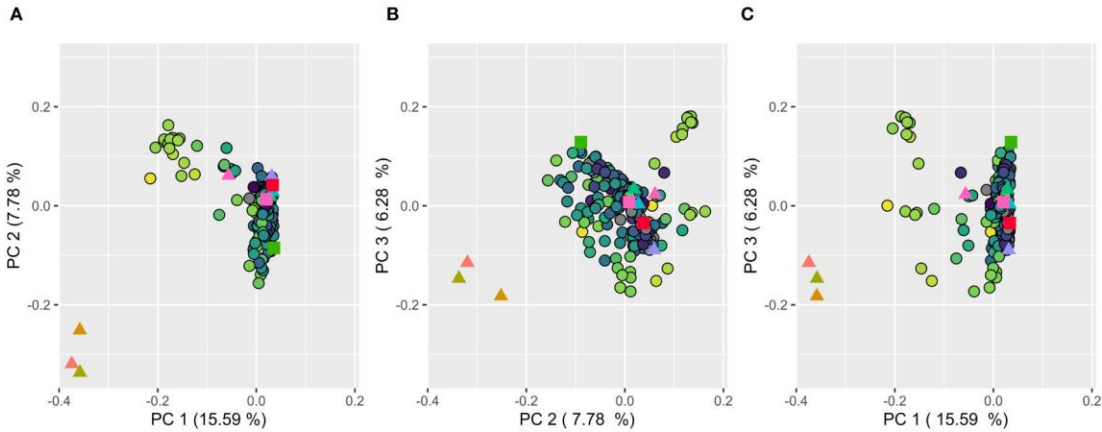
Sergio Cruz<sup>†</sup>, Juan Lobatón<sup>†</sup>, Milan O. Urban<sup>†</sup>, Daniel Ariza-Suarez<sup>†</sup>, Bodo Raatz<sup>†</sup>, Johan Aparicio<sup>†</sup>, Gloria Mosquera<sup>†</sup> and Stephen Beebe<sup>†\*</sup>

Bean Breeding Program, International Center for Tropical Agriculture (CIAT), Palmira, Colombia

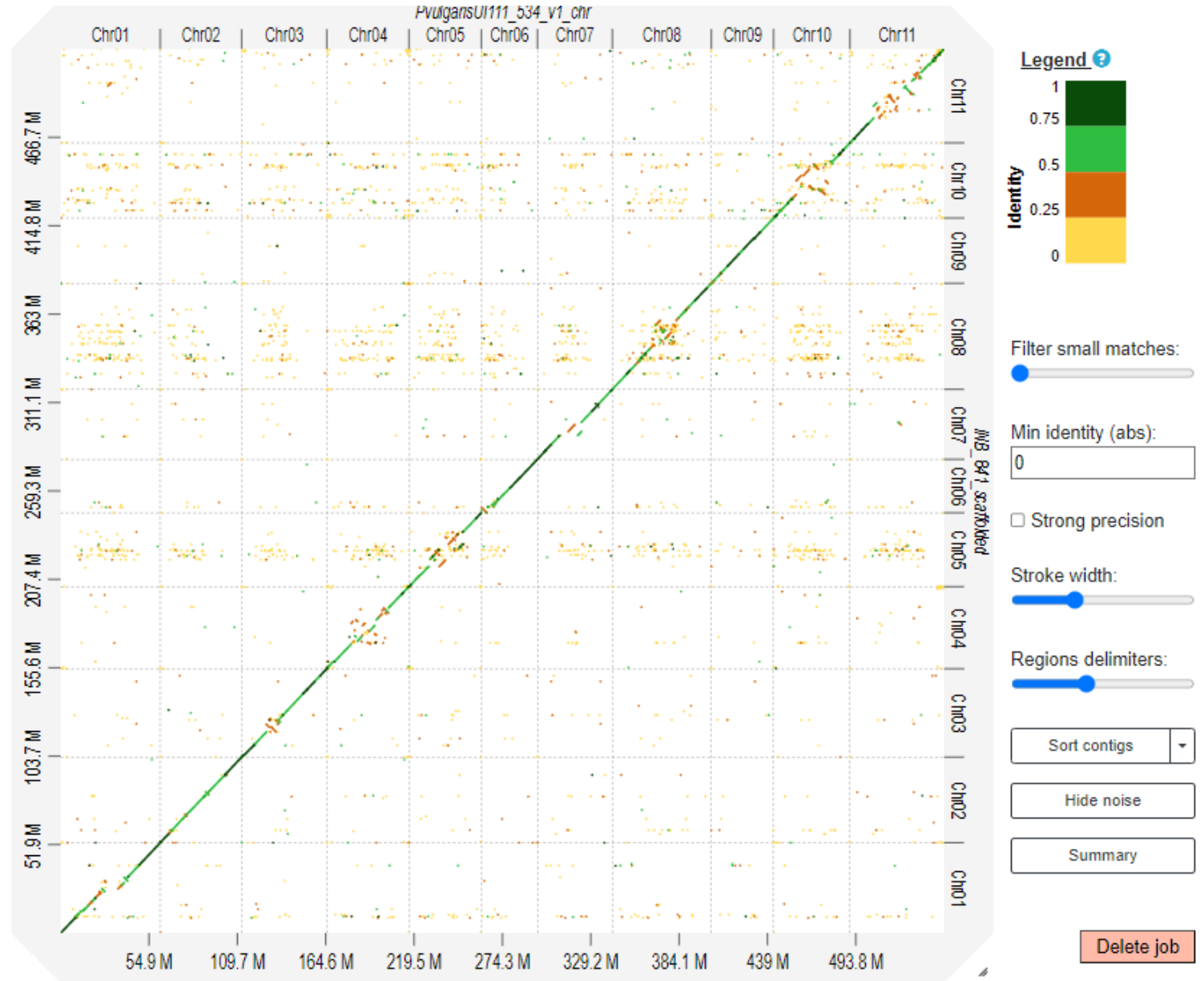
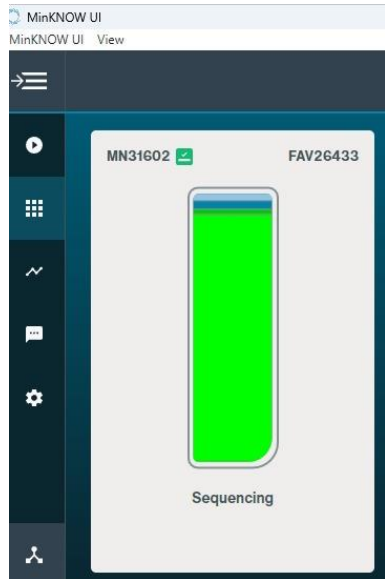
Introgression percentage (%)



Genotype



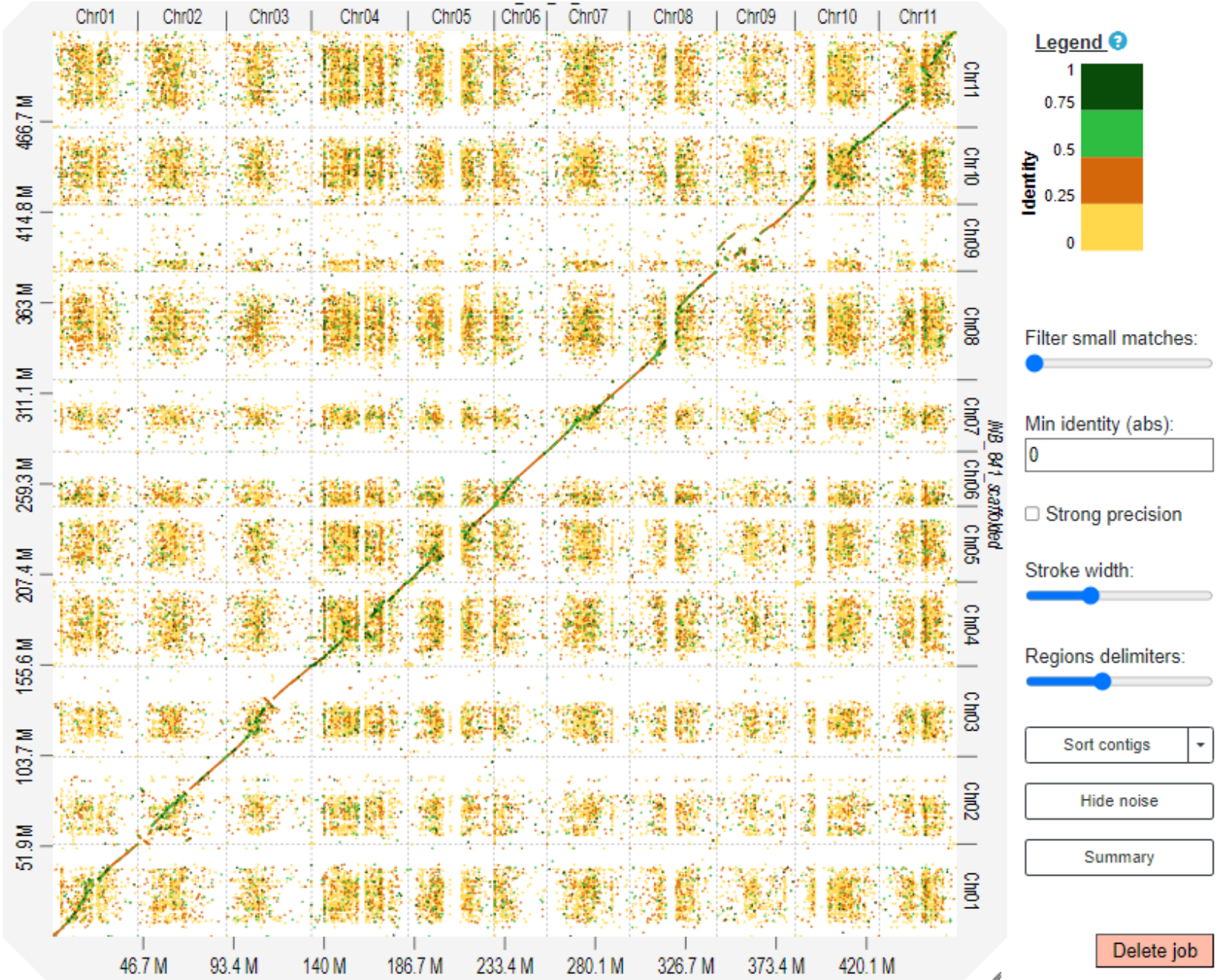
- Oxford Nanopore Long reads



# INB 841 similarity to G40001

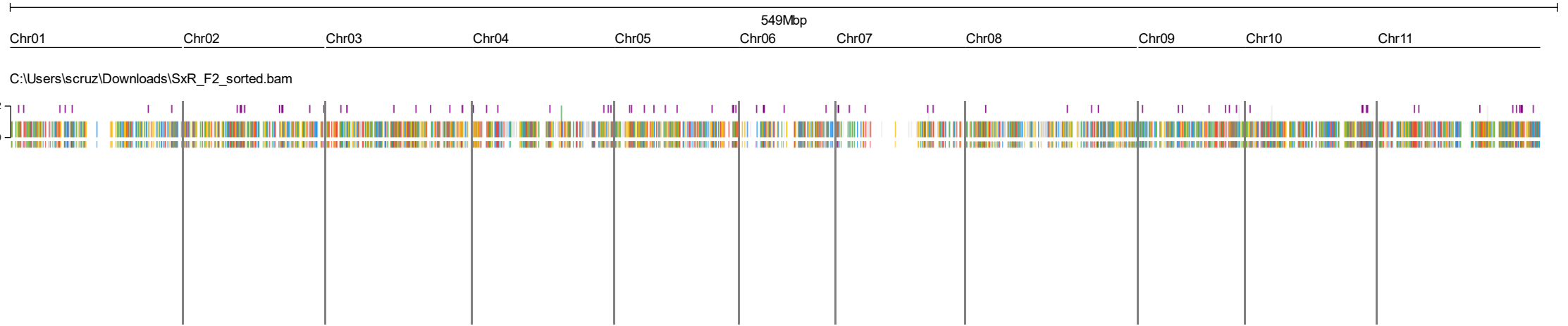
| S1         | E1         | S2         | E2         | LEN 1   | LEN2    | IDY   | Draft | G40001 | Name    | contig      | Size      |
|------------|------------|------------|------------|---------|---------|-------|-------|--------|---------|-------------|-----------|
| 6,501,270  | 6,503,778  | 6,285,522  | 6,288,034  | 2,509   | 2,513   | 99.04 | lg1   | Chr01  | 1_6.5   | tig00026363 | 1'791.309 |
| 34,491,887 | 34,493,183 | 1,066,440  | 1,067,732  | 1,297   | 1,293   | 99.69 | lg2   | Chr03  |         |             |           |
| 4,553,291  | 4,553,866  | 37,667,924 | 37,667,349 | 576     | 576     | 100   | lg5   | Chr09  |         |             |           |
| 9,312,173  | 9,315,474  | 16,553,137 | 16,556,445 | 3,302   | 3,309   | 99.27 | lg6   | Chr06  | 6_9.3   | tig00027206 | 1'811.789 |
| 51,228,967 | 51,245,170 | 54,345,630 | 54,361,834 | 16,204  | 16,205  | 99.94 | lg8   | Chr08  |         |             |           |
| 51,245,112 | 51,313,536 | 54,361,831 | 54,430,275 | 68,425  | 68,445  | 99.95 | lg8   | Chr08  |         |             |           |
| 51,293,489 | 51,371,657 | 54,410,223 | 54,488,309 | 78,169  | 78,087  | 99.36 | lg8   | Chr08  | 8_51.2  |             |           |
| 51,361,539 | 51,418,294 | 54,473,600 | 54,530,409 | 56,756  | 56,810  | 99.72 | lg8   | Chr08  |         |             |           |
| 51,418,393 | 51,438,430 | 54,530,406 | 54,550,446 | 20,038  | 20,041  | 99.89 | lg8   | Chr08  |         |             |           |
| 51,448,423 | 51,735,399 | 54,560,394 | 54,847,457 | 286,977 | 287,064 | 99.82 | lg8   | Chr08  | 8_51.4  | tig00026471 | 2'997.375 |
| 51,774,592 | 51,785,687 | 54,897,413 | 54,908,525 | 11,096  | 11,113  | 99.07 | lg8   | Chr08  |         |             |           |
| 51,785,415 | 51,795,888 | 54,908,505 | 54,918,994 | 10,474  | 10,490  | 99.04 | lg8   | Chr08  | 8_51.7  |             |           |
| 51,795,889 | 51,848,119 | 54,919,190 | 54,971,412 | 52,231  | 52,223  | 99.33 | lg8   | Chr08  |         |             |           |
| 51,932,806 | 51,942,401 | 55,060,701 | 55,070,320 | 9,596   | 9,620   | 99.09 | lg8   | Chr08  | 8_51.9  |             |           |
| 4,271,970  | 4,272,844  | 13,856,801 | 13,855,932 | 875     | 870     | 99.43 | lg9   | Chr11  |         |             |           |
| 60,019     | 64,571     | 32,472,802 | 32,468,238 | 4,553   | 4,565   | 99.01 | lg11  | Chr06  |         |             |           |
| 21,851,857 | 21,852,676 | 10,411,853 | 10,412,668 | 820     | 816     | 99.27 | lg11  | Chr11  | 11_21.8 | tig00026892 | 202.627   |

- Oxford Nanopore Long reads
  - INB841 assembly



# Scaffolding Contigs

UI111



```
12  
13 Chromosome lengths:  
14   lg1: 47,875,271bp  
15   lg10: 34,523,945bp  
16   lg11: 42,532,986bp  
17   lg2: 45,484,901bp  
18   lg3: 45,581,040bp  
19   lg4: 39,440,833bp  
20   lg5: 34,456,683bp  
21   lg6: 24,627,944bp  
22   lg7: 31,167,541bp  
23   lg8: 52,224,973bp  
24   lg9: 37,261,591bp  
25 Total length: 435,177,708bp  
26
```



# INB 841 Chr08: 8\_51.2 - 8\_51.9

tig00026471

Illumina Read depth

MUM 99% idy G40001 reference genome

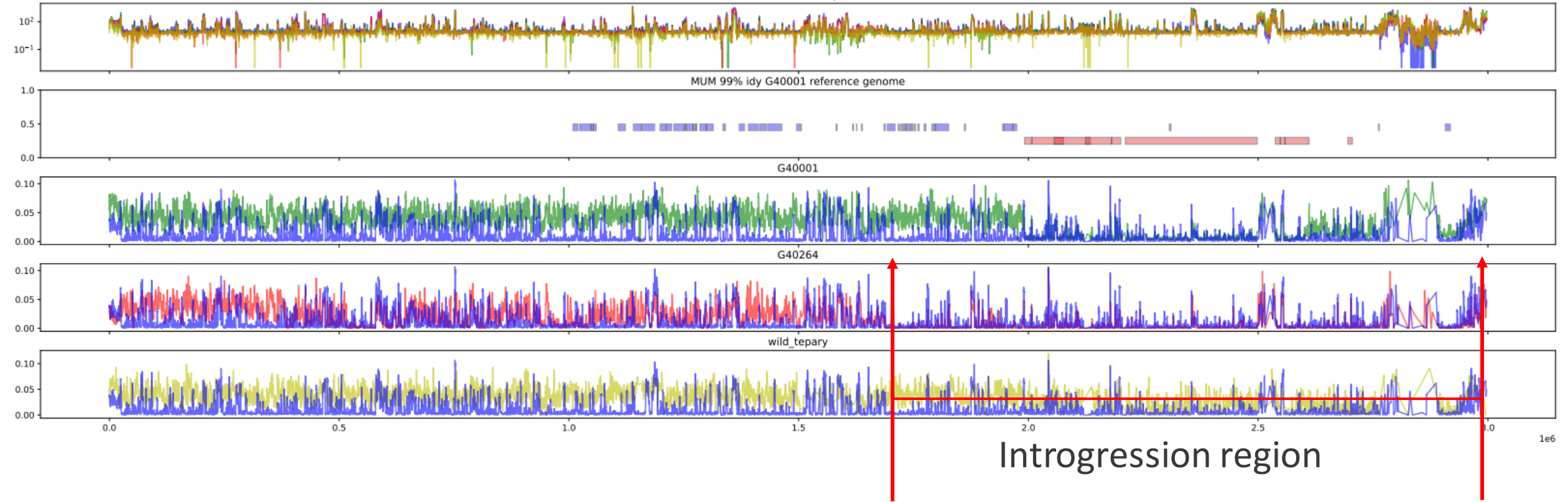
G40001

G40264

wild\_tepary

Introgression region

1e6



# Introgression region end Chr8

- Where detected 159 genes

- Four Heat shock proteins:

1. tig00026471.g316
2. tig00026471.g317
3. tig00026471.g329
4. **tig00026471.g371**

- Multiple transcription factor

Only heat shock protein with higher match for tepary than common bean

| Protein                | Species                        | E-value   | % identity | Align len | Strands | Query ID | Query from | Query to | Target from | Target to | Bitscore | # identical |
|------------------------|--------------------------------|-----------|------------|-----------|---------|----------|------------|----------|-------------|-----------|----------|-------------|
| Phacu.CVR.008G350900.1 | <i>P. acutifolius</i> v1.0     | 0         | 100        | 698       | +/+     | g371.t1  | 1          | 698      | 1           | 698       | 1413.67  | 698         |
| PvUI111.08G281200.1.p  | <i>P. vulgaris_UI111</i> v1.1  | 0         | 99         | 698       | +/+     | g371.t1  | 1          | 698      | 1           | 698       | 1400.57  | 692         |
| Phacu.WLD.009G122600.1 | <i>P. acutifolius_WLD</i> v2.0 | 2.07e-157 | 39         | 754       | +/+     | g371.t1  | 1          | 693      | 2           | 689       | 473.011  | 293         |
| Phacu.WLD.009G122600.2 | <i>P. acutifolius_WLD</i> v2.0 | 2.07e-157 | 39         | 754       | +/+     | g371.t1  | 1          | 693      | 2           | 689       | 473.011  | 293         |
| Phacu.CVR.009G131900.2 | <i>P. acutifolius</i> v1.0     | 2.07e-157 | 39         | 754       | +/+     | g371.t1  | 1          | 693      | 2           | 689       | 473.011  | 293         |
| Phacu.CVR.009G131900.1 | <i>P. acutifolius</i> v1.0     | 2.07e-157 | 39         | 754       | +/+     | g371.t1  | 1          | 693      | 2           | 689       | 473.011  | 293         |
| Phacu.CVR.009G131900.3 | <i>P. acutifolius</i> v1.0     | 2.07e-157 | 39         | 754       | +/+     | g371.t1  | 1          | 693      | 2           | 689       | 473.011  | 293         |
| Phacu.CVR.009G131900.4 | <i>P. acutifolius</i> v1.0     | 2.07e-157 | 39         | 754       | +/+     | g371.t1  | 1          | 693      | 2           | 689       | 473.011  | 293         |
| PvUI111.09G055500.1.p  | <i>P. vulgaris_UI111</i> v1.1  | 3.76e-156 | 39         | 754       | +/+     | g371.t1  | 1          | 693      | 2           | 689       | 469.544  | 291         |
| PvUI111.04G125000.1.p  | <i>P. vulgaris_UI111</i> v1.1  | 4.43e-156 | 39         | 733       | +/+     | g371.t1  | 1          | 689      | 1           | 697       | 472.626  | 287         |
| Phacu.CVR.004G162100.1 | <i>P. acutifolius</i> v1.0     | 3.98e-154 | 39         | 735       | +/+     | g371.t1  | 1          | 689      | 1           | 697       | 467.233  | 288         |
| Phacu.CVR.009G205600.1 | <i>P. acutifolius</i> v1.0     | 3.12e-142 | 38         | 725       | +/+     | g371.t1  | 1          | 694      | 1           | 705       | 436.417  | 278         |

# Contiguity quality assessment

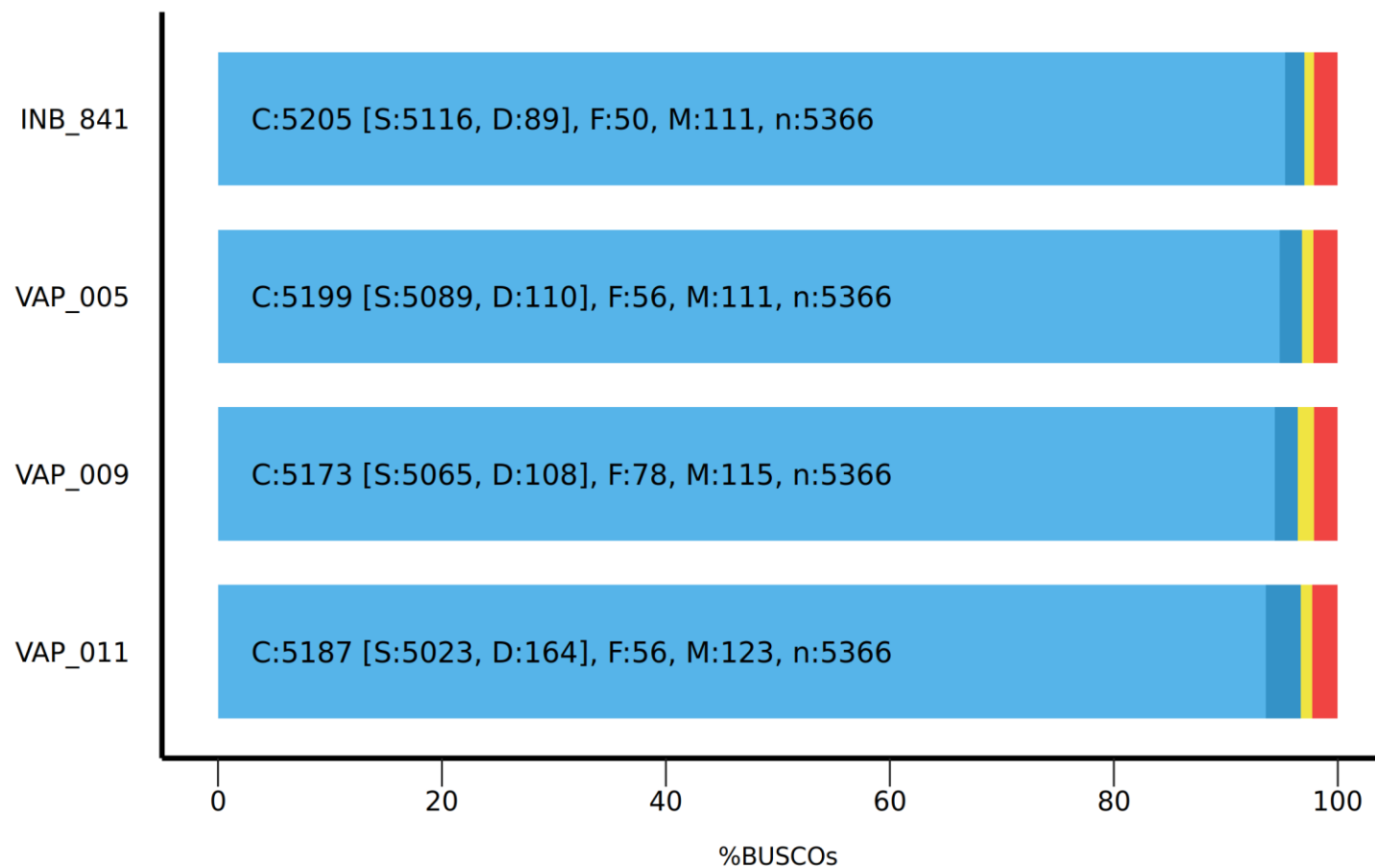
(scaffolded draft)

| <b>Assembly</b> | <b># contigs</b> | <b>Largest contig</b> | <b>Total length</b> | <b>N50</b> | <b>L50</b> |
|-----------------|------------------|-----------------------|---------------------|------------|------------|
| INB_841         | 490              | 25,457,563            | 556,673,332         | 4,756,386  | 30         |
| VAP_005         | 950              | 21,061,453            | 554,824,956         | 3,436,560  | 40         |
| VAP_009         | 383              | 25,349,498            | 556,133,646         | 5,408,703  | 26         |
| VAP_011         | 284              | 20,808,903            | 563,632,783         | 5,935,280  | 29         |

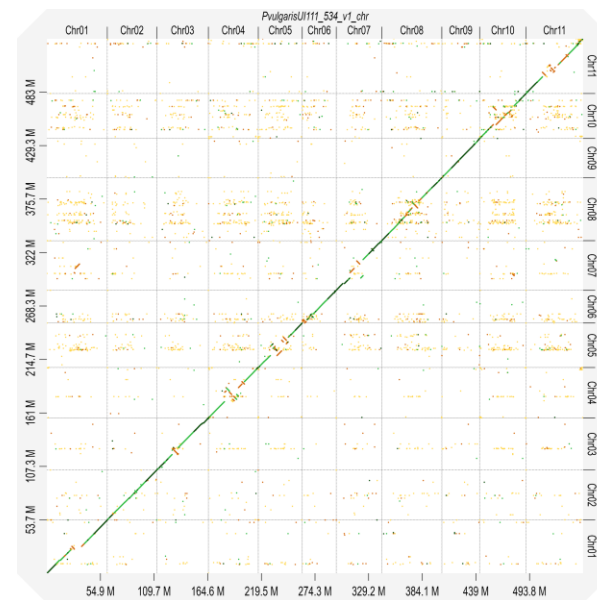
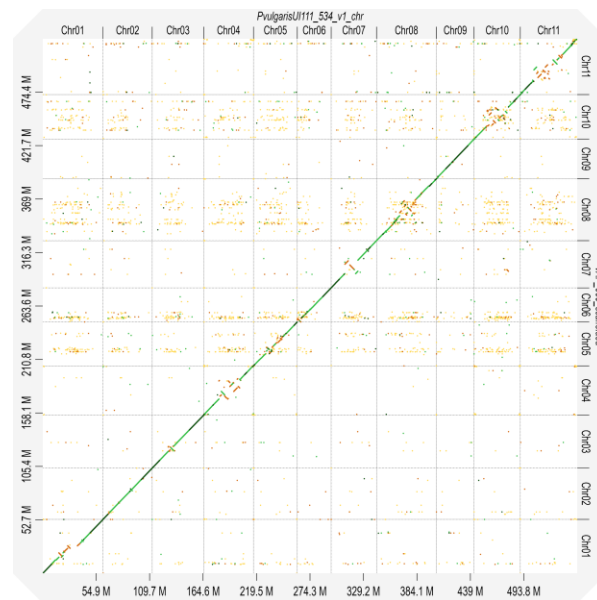
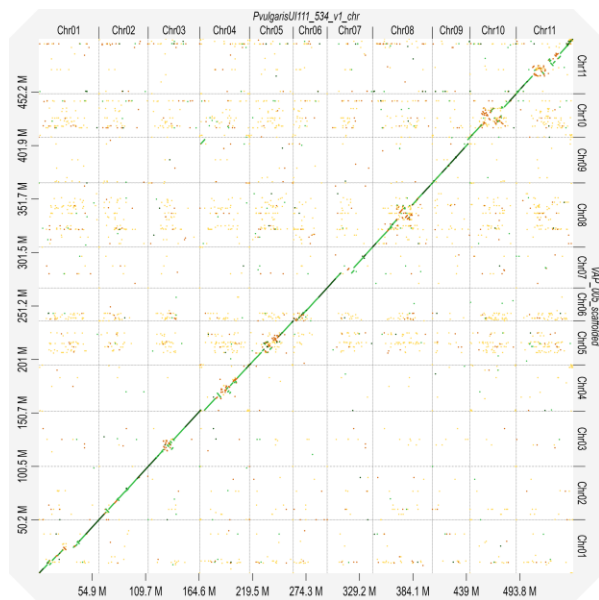
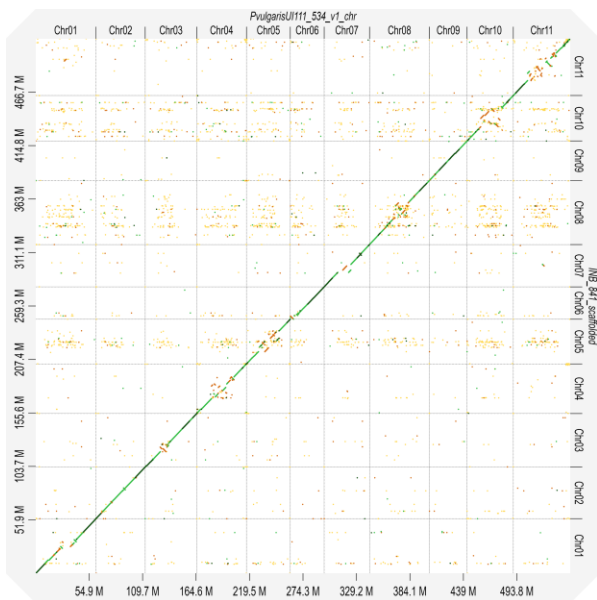
# Completeness quality assessment

(scaffolded draft)

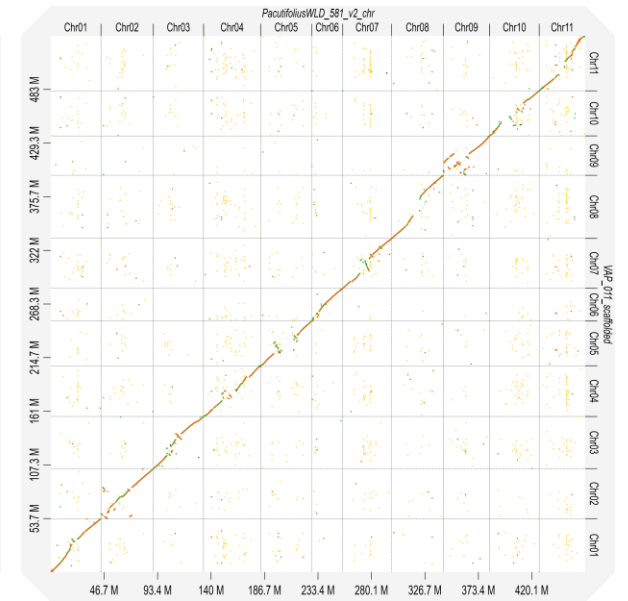
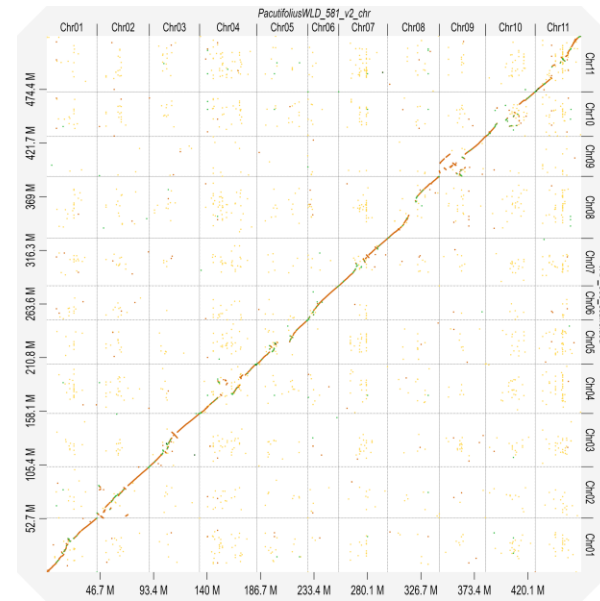
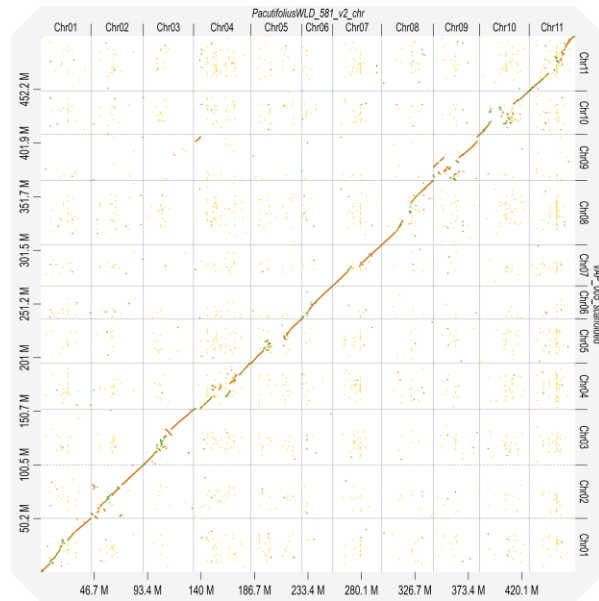
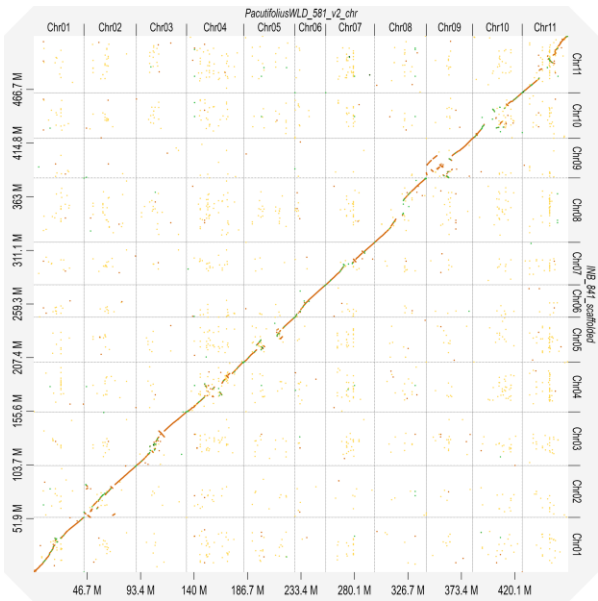
## BUSCO Assessment Results



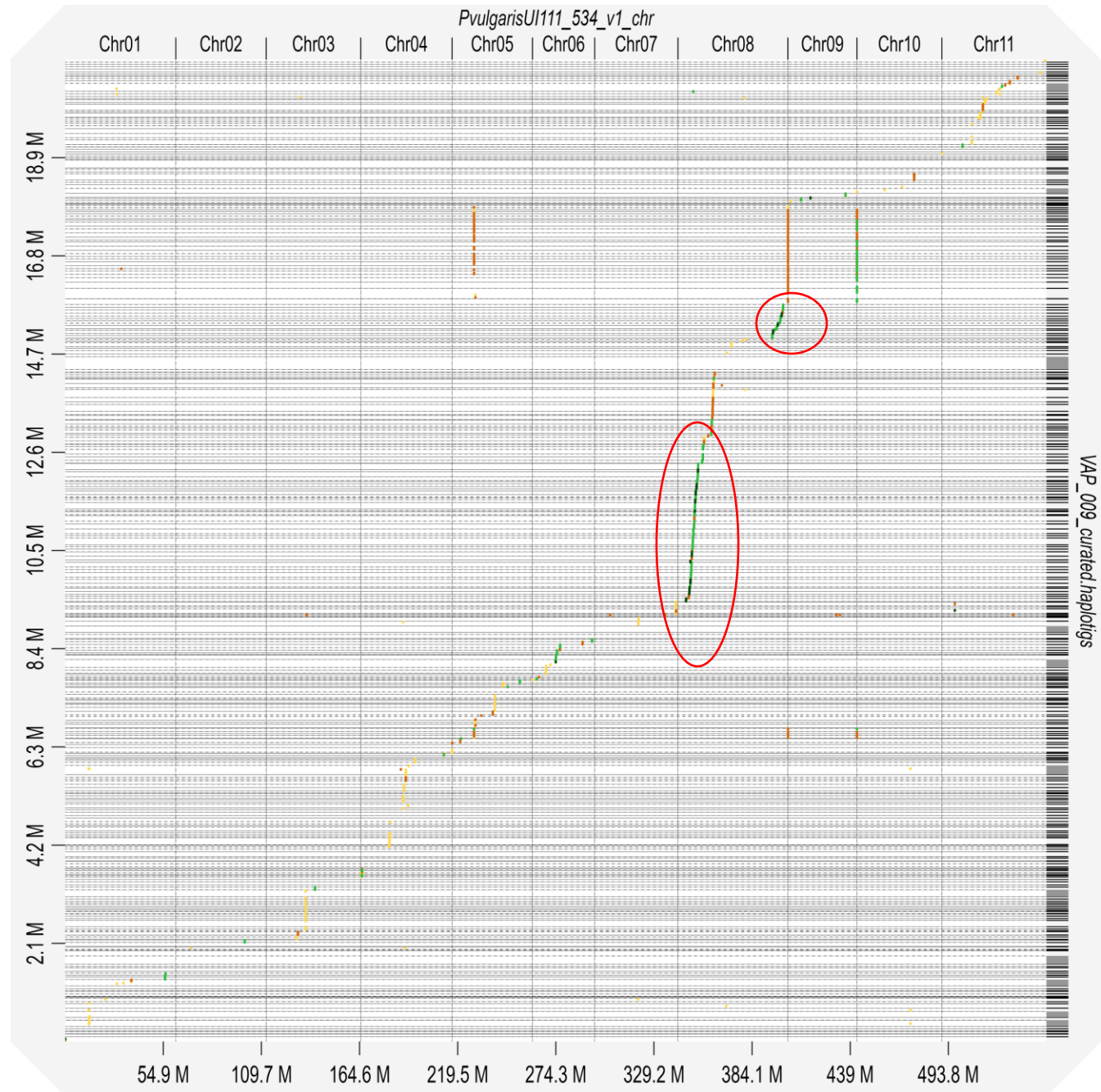
# Collinearity with UI-111 (Durango)



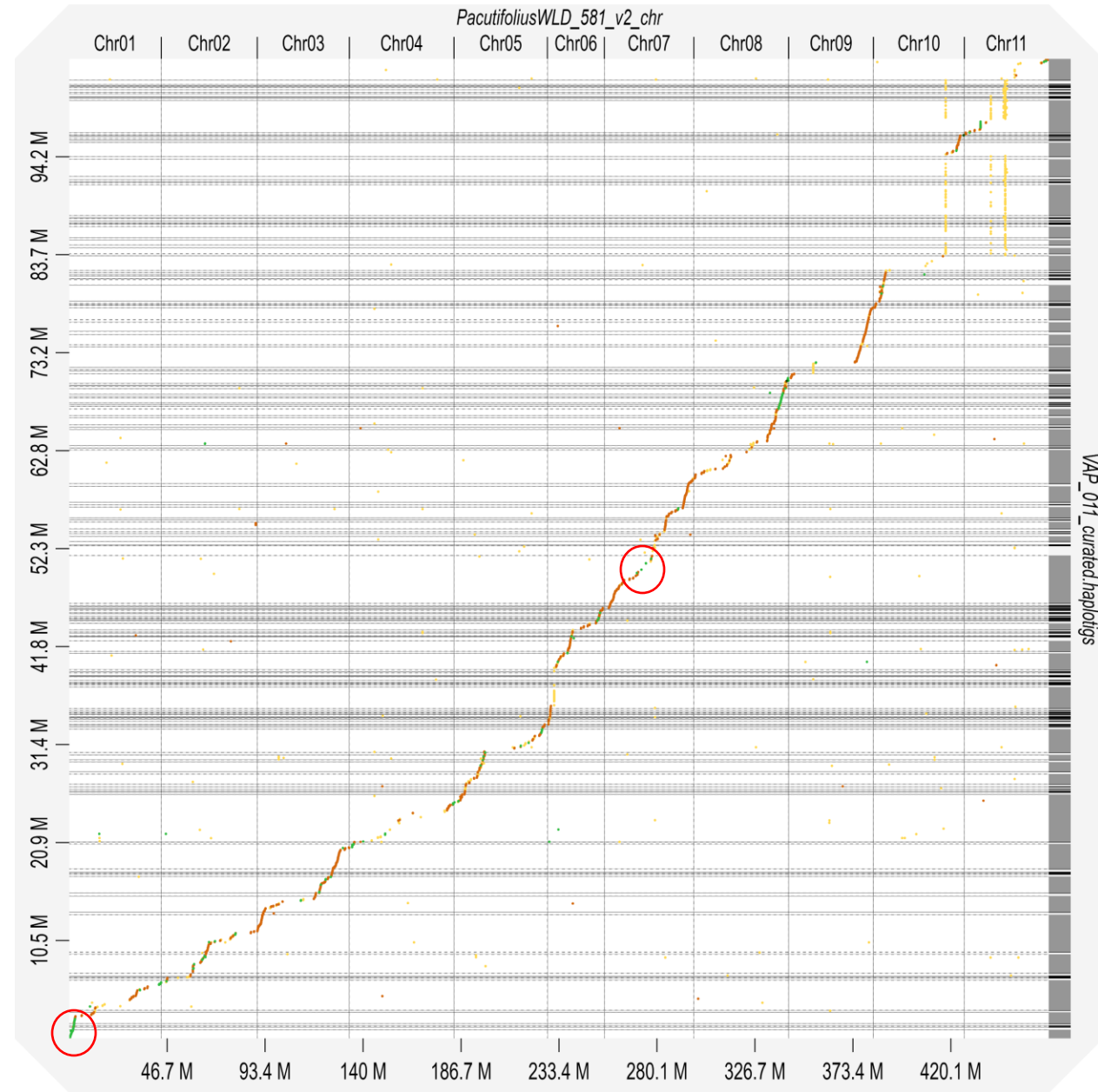
# Collinearity with WLD\_581 (wild tepary)



# Haplotigs VAP\_009



# Haplotigs VAP\_011





# INB 841

- Selected originally under drought
- Expressed resistance to wilting under intense mid-season drought
- May have rapid pod elongation
- Heat tolerance
- Resistance to wilting
- Uniform and stable maturity
- Higher number of seeds per pod



(JD Lobaton, CIAT)



# CGIAR Research Program on Grain Legumes

## Our Strategy

### CGIAR Research Programs

- Agriculture for Nutrition and Health
- Aquatic Agricultural Systems
- Climate Change, Agriculture and Food Security (CCAFS)
- Dryland Cereals
- Dryland Systems
- Forests, Trees and Agroforestry
- Grain Legumes

### PARTNERS:

- CIAT
- Ethiopian Institute of Agricultural Research (EIAR), Ethiopia
- Brazilian Agricultural Research Corporation (EMBRAPA)
- General Directorate of

Environment



NGSEP team @NGSEP · 6 h  
 At the Colombian Bioinformatics Congress  
 #CCBCOL3



Alliance



International Center for Tropical Agriculture  
Since 1967 Science to cultivate change

# Thanks



Bioversity International and the International Center for Tropical Agriculture (CIAT) are CGIAR Research Centers.  
CGIAR is a global research partnership for a food-secure future.