Break assembly at all N gaps and reassemble based on chromatin contacts

**High Quality Orientation: increases from 84 to 91.3%**

- Final pseudo chromosome assembly:
  - Contigs: 915
  - Total length: 405.3 Mb
  - N50 contigs: 24.1 Mb
  - L50 scaffolds: 3
  - N50 scaffolds: 3048
  - N50 config: 404,432

**Rescaffolding Call back statistics**
- Cluster recall: 99.9%
- Order recall (HQ)**: 94.1%
- Orientation recall (HQ): 94.9%

**Comparison of the clustering, ordering and orientation of clusters from the 1st N50 assembly to the final PGA assembly:**
- % of predicted chromosome length:
  - N50 contigs: 93% of predicted chromosome length
  - N50 scaffolds: 92% of predicted chromosome length

**How complete are the pseudo chromosomes?**

- Number of Bionano physical maps and total aligned length for each assembly:

<table>
<thead>
<tr>
<th>Assembly</th>
<th>Total (Univ)</th>
<th>Total (Ori)</th>
<th>Total (Order)</th>
<th>Total (Orientation)</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>3.41 Gb</td>
<td>2.88 Gb</td>
<td>2.71 Gb</td>
<td>2.64 Gb</td>
</tr>
</tbody>
</table>

**Validation—Genotyping by Sequencing**

- Bi-parental recombinant introgression population (n=96 RILs)

**Sub-genome Identification**

- Partial Chr10 fusion chromosome

**Bionano Genome Map Validation**

- A 17x coverage Bionano Genomics physical map was assembled into 427 physical maps and compared to the different sequence assemblies.

**Utility: Linkage mapping of betalain locus**

- Hamblin et al. (2012 & 2013)

- Sub-genome Synteny

- Dahl et al. 2014

- Think about A. cruentas (2n=34)

- a19 is the basic chromosome number for the family — So how do you go to 2n=32?

**Sub-genome Synteny**

- Genes within the betalain gene family vary in chromosome numbers. Including genes with 20, 18, 16, 13, 11, and 9 chromosomes. Chromosome synteny is shown in Figure 3.