Final map construction (TX)

1. Construct map with ASMAP (**F2Asmap\_TX\_sex\_linked\_plus\_biggest\_100\_scaffolds\_final.R**)
2. Use **Colocalized\_marker\_positions\_final.R** to connect colocalized markers with LG and CM positions. 579 markers on the linkage group are included in bins of colocalized markers, and a total of 8839 markers are placed.
3. Check small linkage groups (under 40 markers - TX: 1,2,4,6,9,12) for unique scaffolds. 22 scaffolds were unique to small LGs (17 on LG 4, 1 on LG 6, 4 on LG11). We prioritized including the small sex-linked scaffolds.
   1. Merging unique scaffolds to correct linkage groups.
      1. XXX scaffold was shared between LG 4 and LG 10; the remaining XXX were unique to LG 4. The single marker from a shared scaffold was from scaffold 17040 on the sex chromosome; XXX of the remaining XXX were known to be sex-linked based on [the list Felix sent me]. These markers from LG 4 were added to the sex chromosome as follows: the LG designation was changed from LG4 to LG10 and the difference between the genetic position of the marker from 17040 of LG 4 and the markers from 17040 on LG 10 was added to the genetic position of all the markers on LG 4. 17040 is situated in an area of low recombination on LG 10 (6 markers, spanning 4117396 bp, are all at the same genetic position, and the bp position of the marker from LG 4 was nested within them).
      2. Scaffold 15769 was unique to LG 6. The sole marker from that small (178591) bp scaffold was at the same genetic position on LG 6 as 3 markers from scaffold 17265, which was split in an intercalated manner between LG 5 and LG 6. The marker from scaffold 15769 was therefore assigned the same genetic position the marker on LG 6 scaffold 17265 which was physically nearest (823634 bp) to the markers in the same genetic position on LG 5.
      3. Scaffolds 292, 3947, 14219, and 16321 were unique to LG 11, which is largely collinear with LG7. All were in largely non-recombining regions. Scaffolds 292, 3947, and 14219 were reassigned the LG7 genetic position of a marker from another scaffold at the same genetic position as a physically nearby marker on the same scaffold in LG11. As 16321 was uniquely positioned on LG11, it was discarded rather than estimating the position relative to adjacent markers.
4. Remove small linkage groups.
5. Chromonomer used on edited map.

Final map construction (NC)

1. Construct map with ASMAP (**"D:\Dropbox\Dropbox\Professional\University\_of\_Toronto\Genomics\HiCSNPs\TranscriptomeLinkageMap\ASMAP\NC\_transcriptome\F2\_style\_NC\_map\_clean\_biggest100\_5-28.csv"**)
2. Use **Colocalized\_marker\_positions\_final.R** to connect colocalized markers with LG and CM positions. 503 markers on the linkage group are included in bins of colocalized markers, and a total of 5853 markers are placed.
3. Check small linkage groups (under 100 uniquely placed markers - NC: 2,3,4,5,6,8,11) for unique scaffolds. 12 scaffolds were unique to small LGs (2 on LG 3, 23 on LG 5, 5 on LG 9). We prioritized including the small sex-linked scaffolds.
   1. Merging unique scaffolds to correct linkage groups.
      1. LG 11 is collinear with a section of the sex chromosome. 20 scaffolds were shared between LG 5 and the sex chromosome; 5 were unique to LG 5. All scaffolds unique to LG 5 were known to be sex-linked. Markers from scaffolds unique to LG 5 were added to the sex chromosome as follows: the LG designation was changed from LG5 to LG10 and their CM position was reassigned based on the difference between the genetic position of the marker from LG10 closest to the closest marker on a shared scaffold.  
         Scaffold 17270 – nearest markers on shared scaffolds are over 500,000bp away, omitted.   
         Scaffold 17271, 17272, 4250, 6377 all at the same block of suppressed recombination, and positioned based on   
         17040-HRSCAF-21160 4007915 L.11 25.24465047  
         17040-HRSCAF-21160 4008573 L.10 50.79511513  
         All four entirely contained in the same large non-recombining region of L.11.   
          and the markers from XX on LG XX was added to the genetic position of all the markers on LG XX. XX is situated in an area of low recombination on LG XX (XX markers, spanning XXbp, are all at the same genetic position, and the bp position of the marker from LG 4 was nested within them).
4. Remove small linkage groups.
5. Chromonomer used on edited map, with TX .agp (i.e., scaffolds positioned relative to the TX linkage map) to identify inversions and rearrangements.