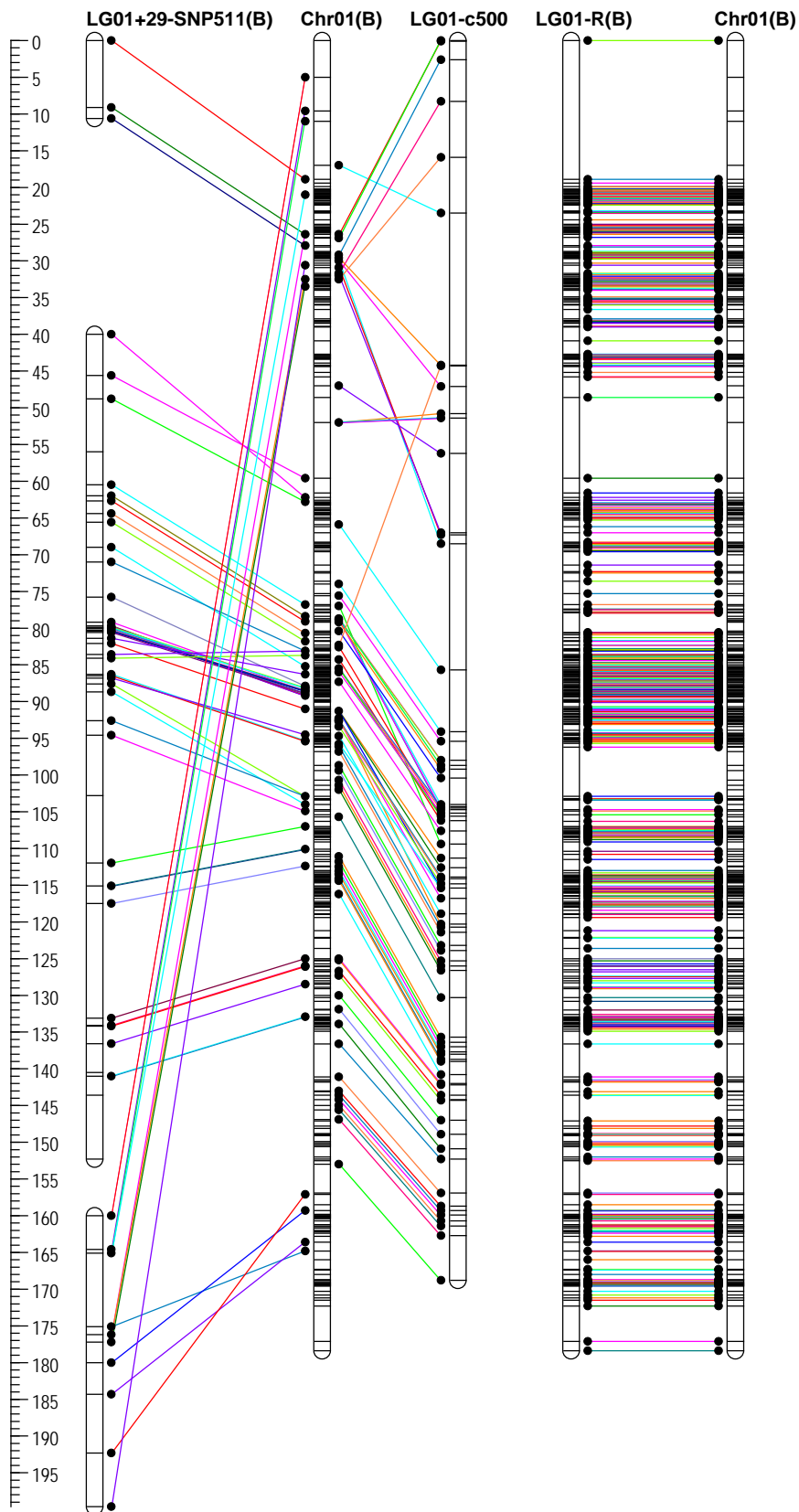
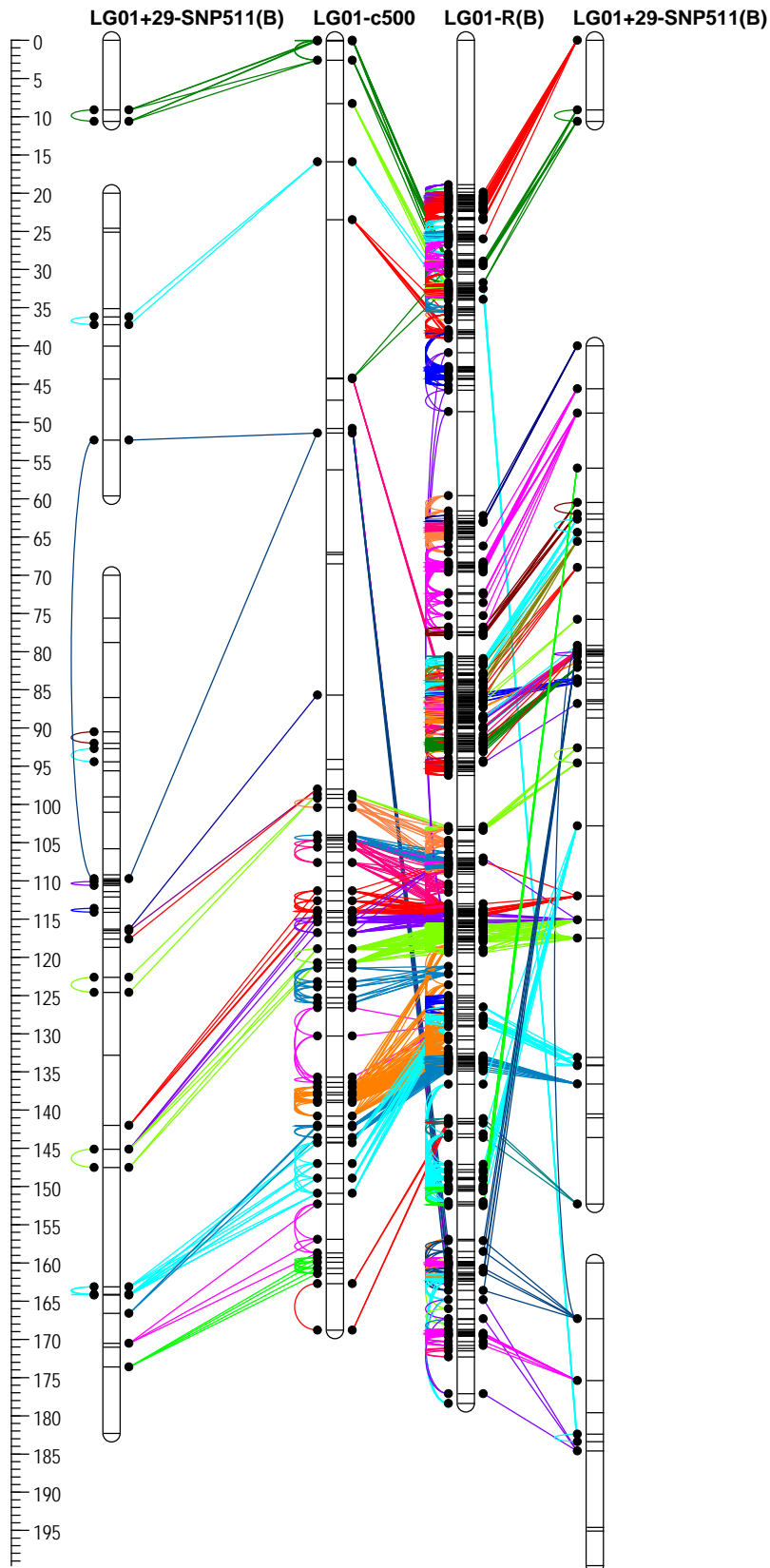


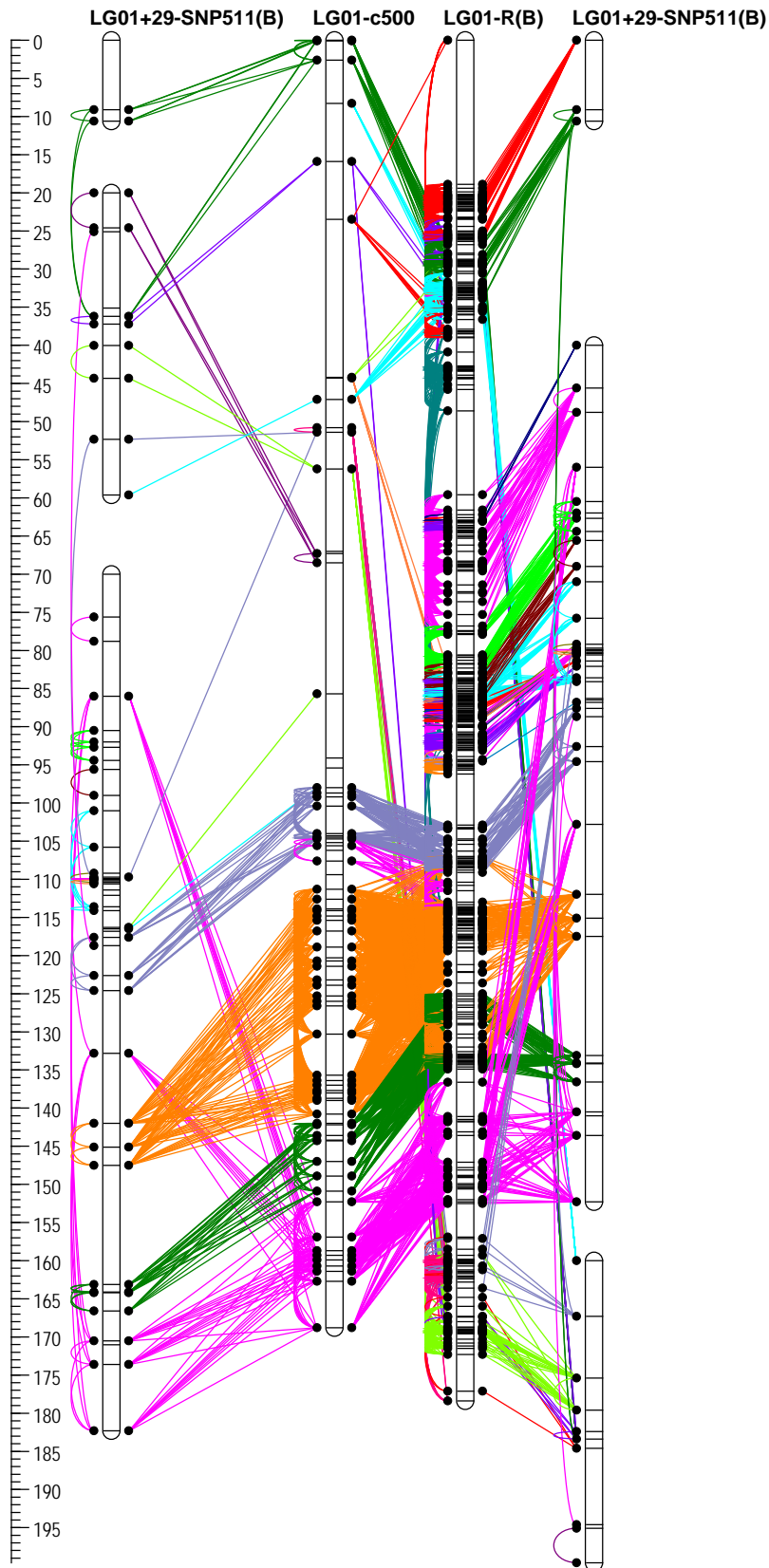
In the following pages, linkage group (LG) names containing “-SNP511” contain markers from the map reported by Maughan *et al.* (2012); LG names containing “-c500” contain markers from the Atlas × Carina Red population; and LG names containing “-R” contain RNA-Seq makers from the Kurmi × 0654 map. LGs from the integrated map are designated with “Chr” in the name.



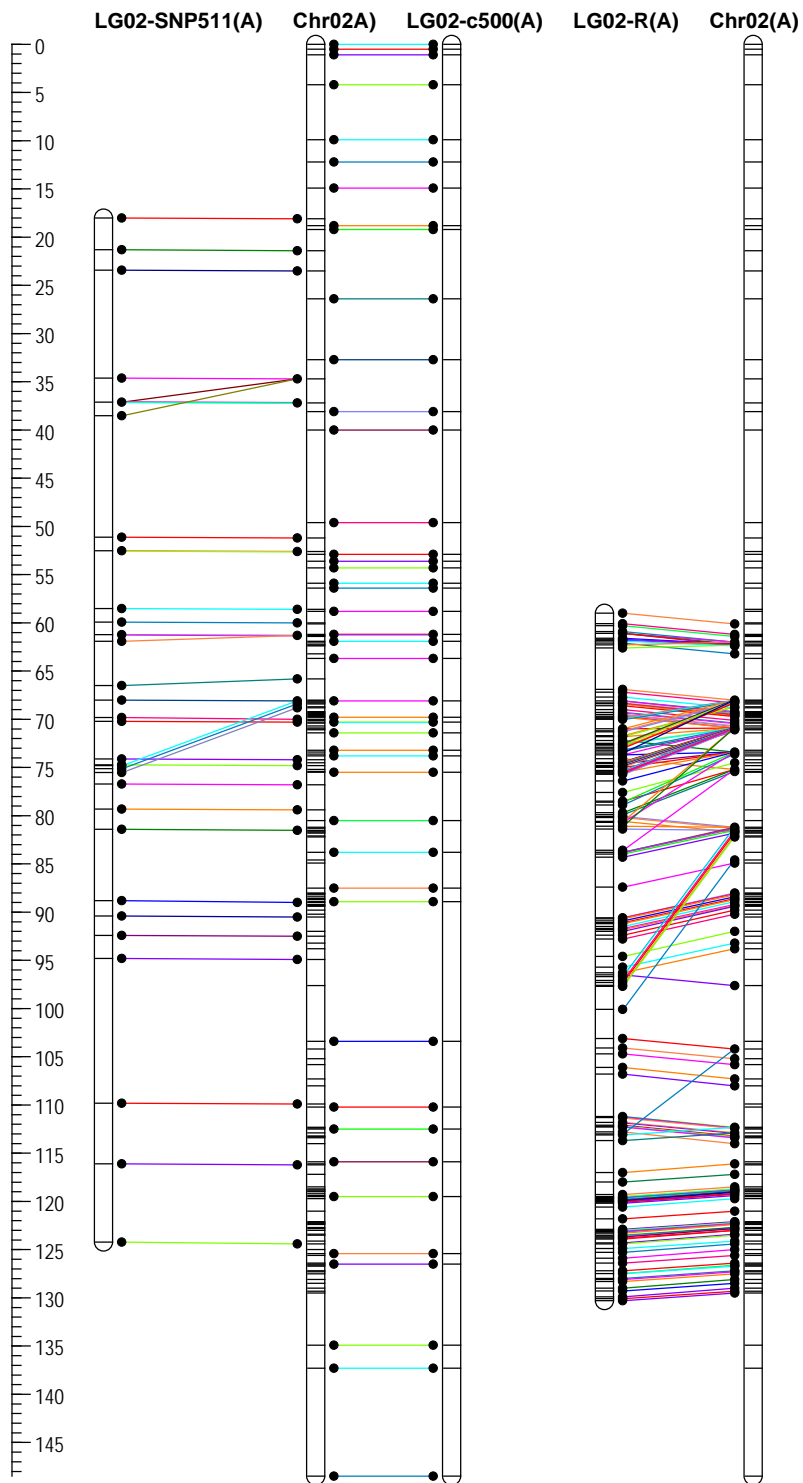
**Chr01:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



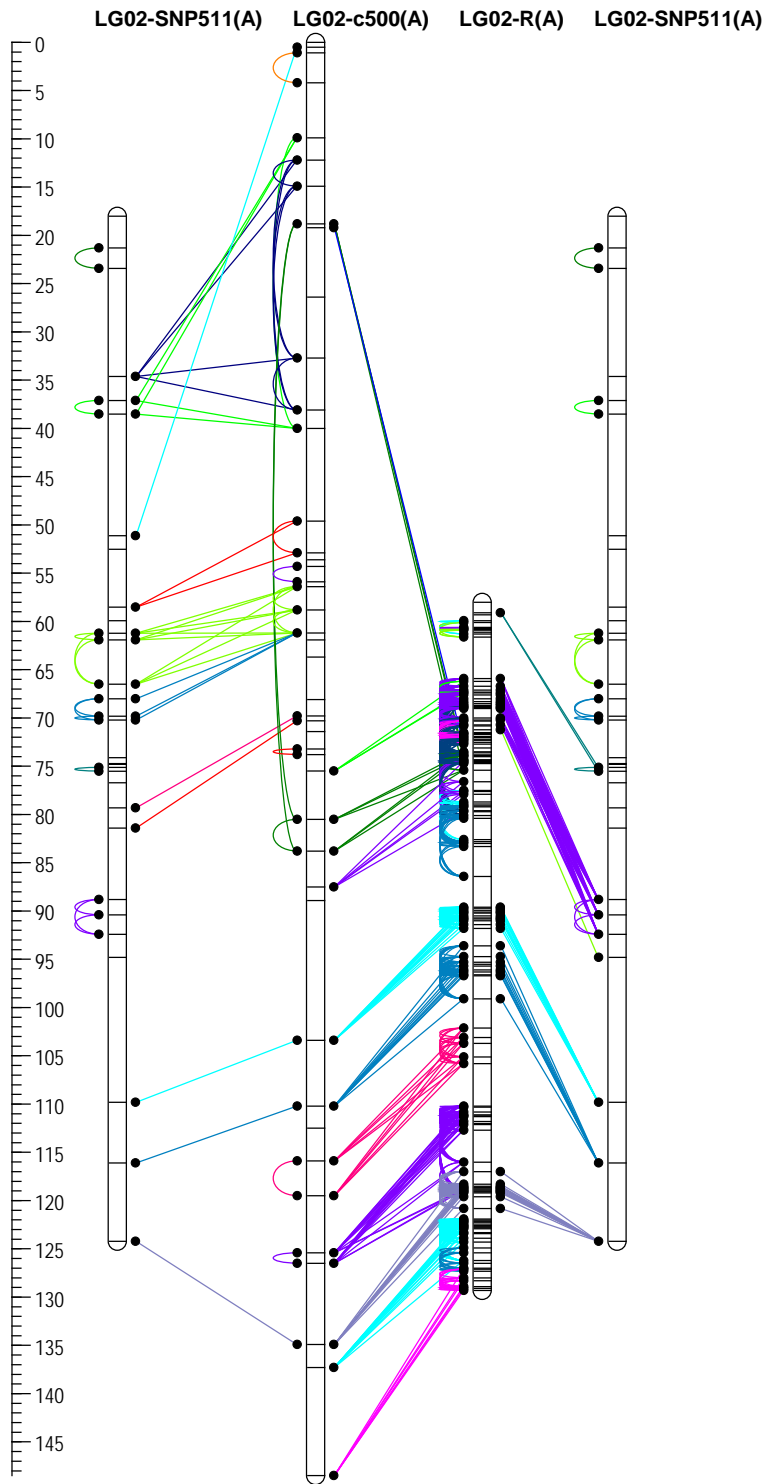
**Chr01:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.



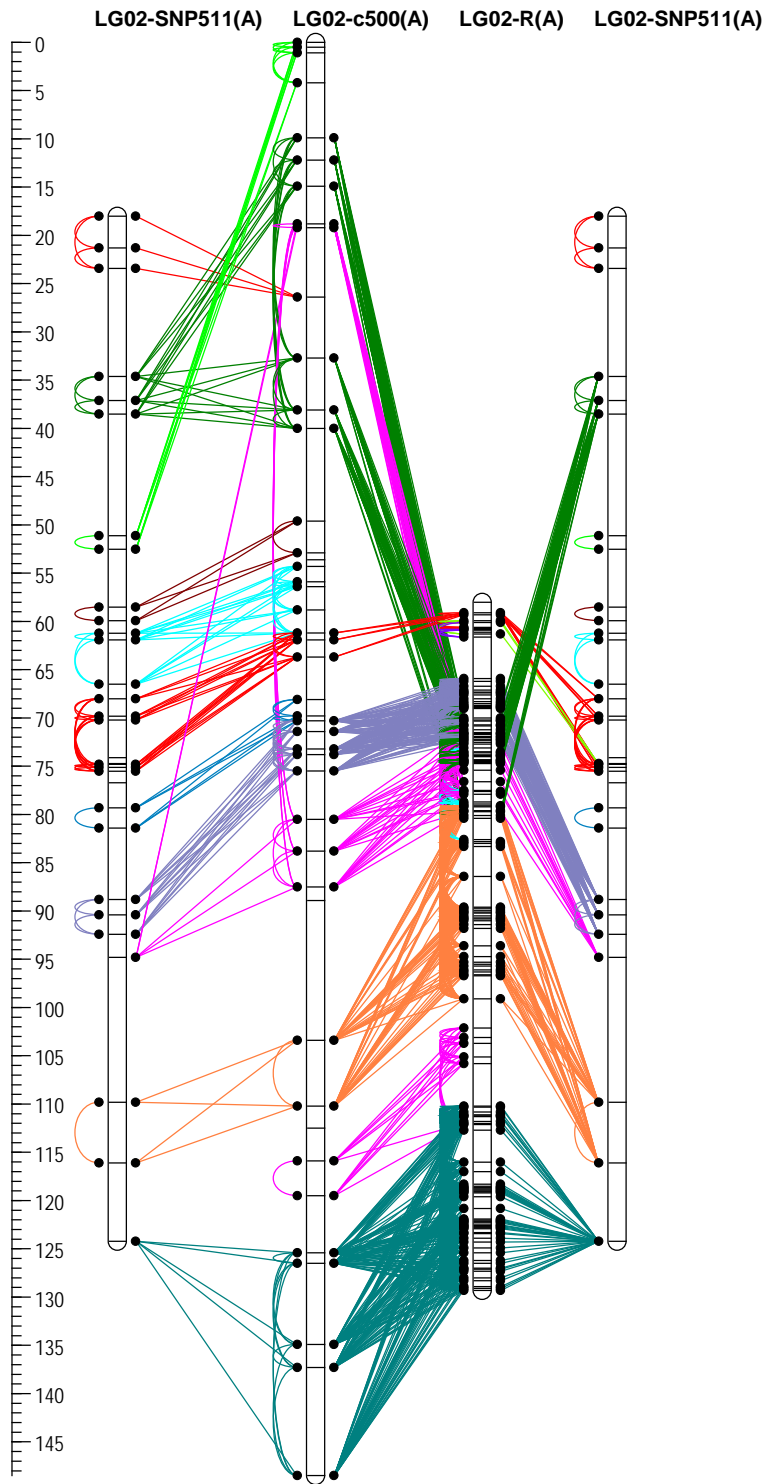
**Chr01:** Links between markers in the genetic maps of the three segregating populations within same scaffold of the assembly showing the concordance of order of scaffold positions (each scaffold has a separate color which color is used to indicated links within linkage groups with arcs of the same color as links between linkage groups).



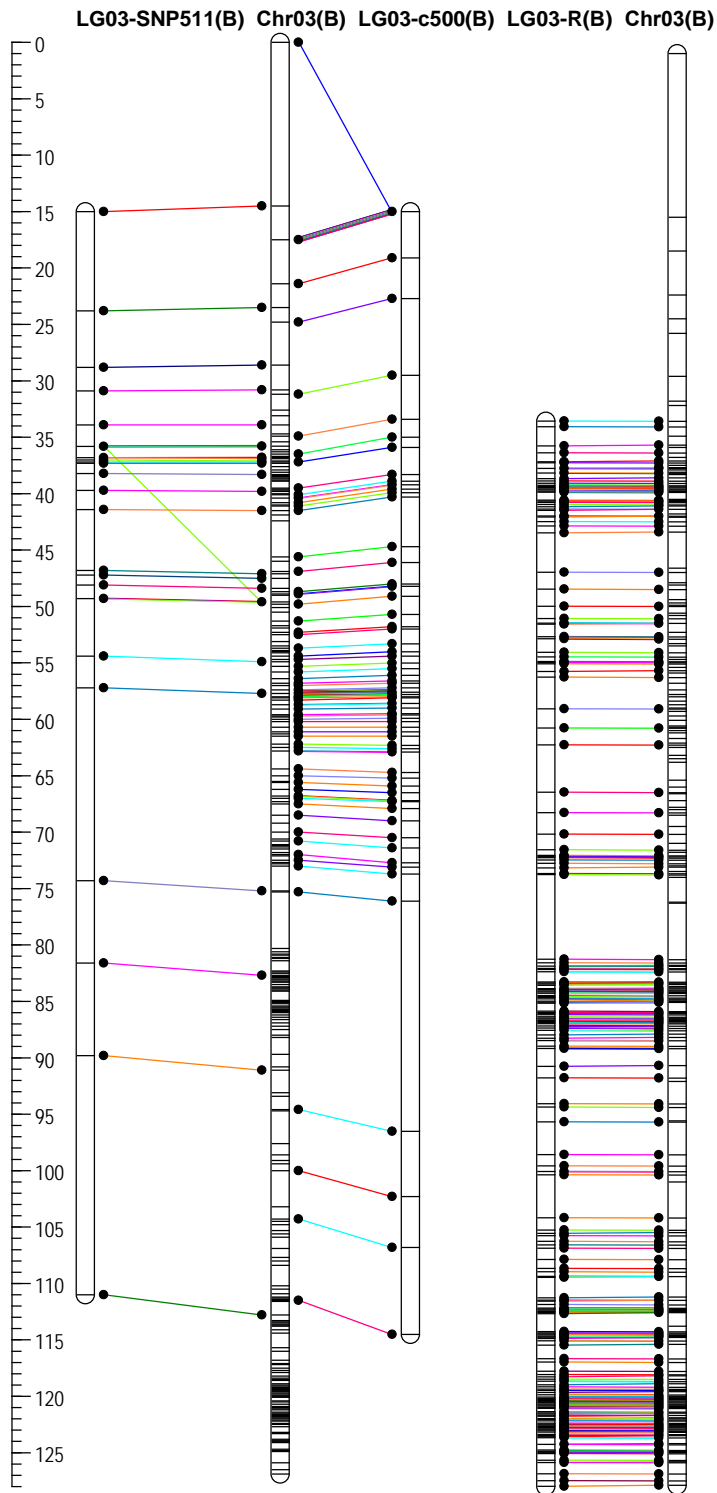
**Chr02:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



**Chr02:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.

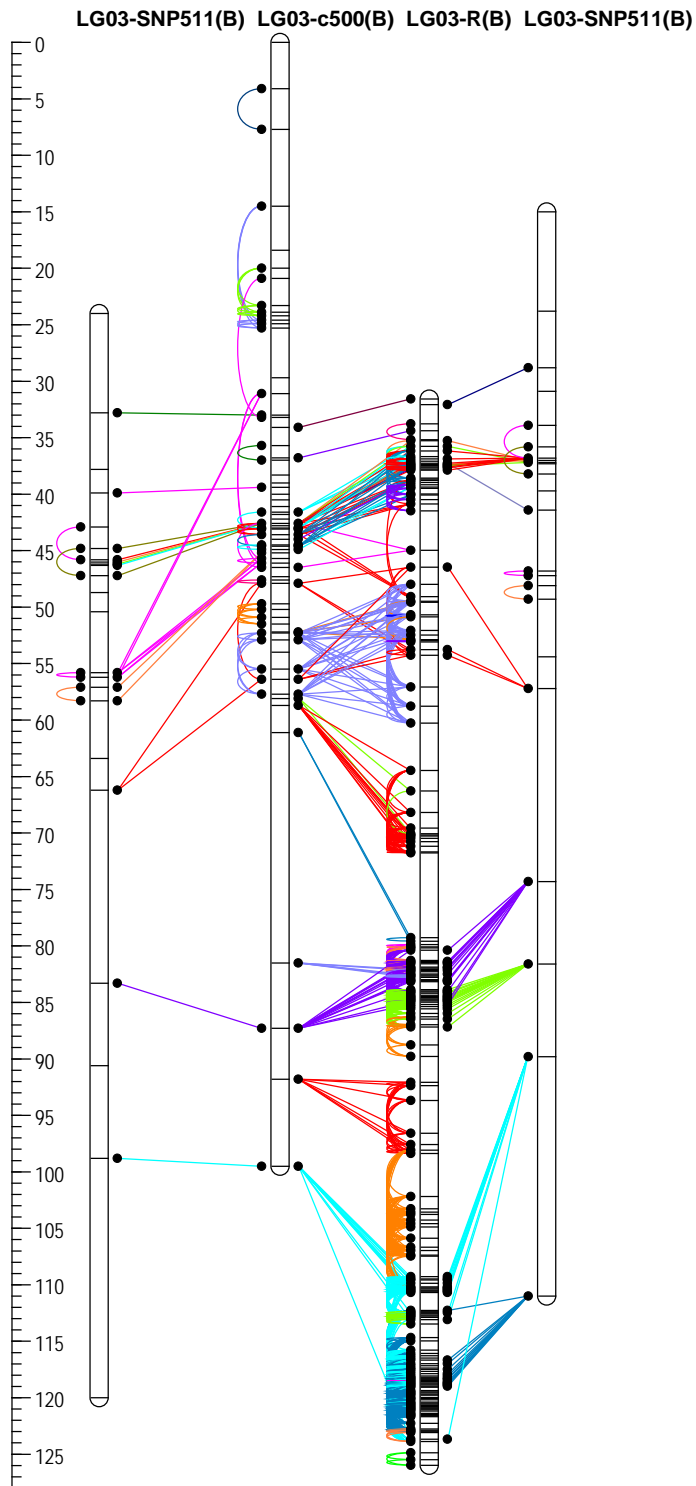


**Chr02:** Links between markers in the genetic maps of the three segregating populations within same scaffold of the assembly showing the concordance of order of scaffold positions (each scaffold has a separate color which color is used to indicated links within linkage groups with arcs of the same color as links between linkage groups).

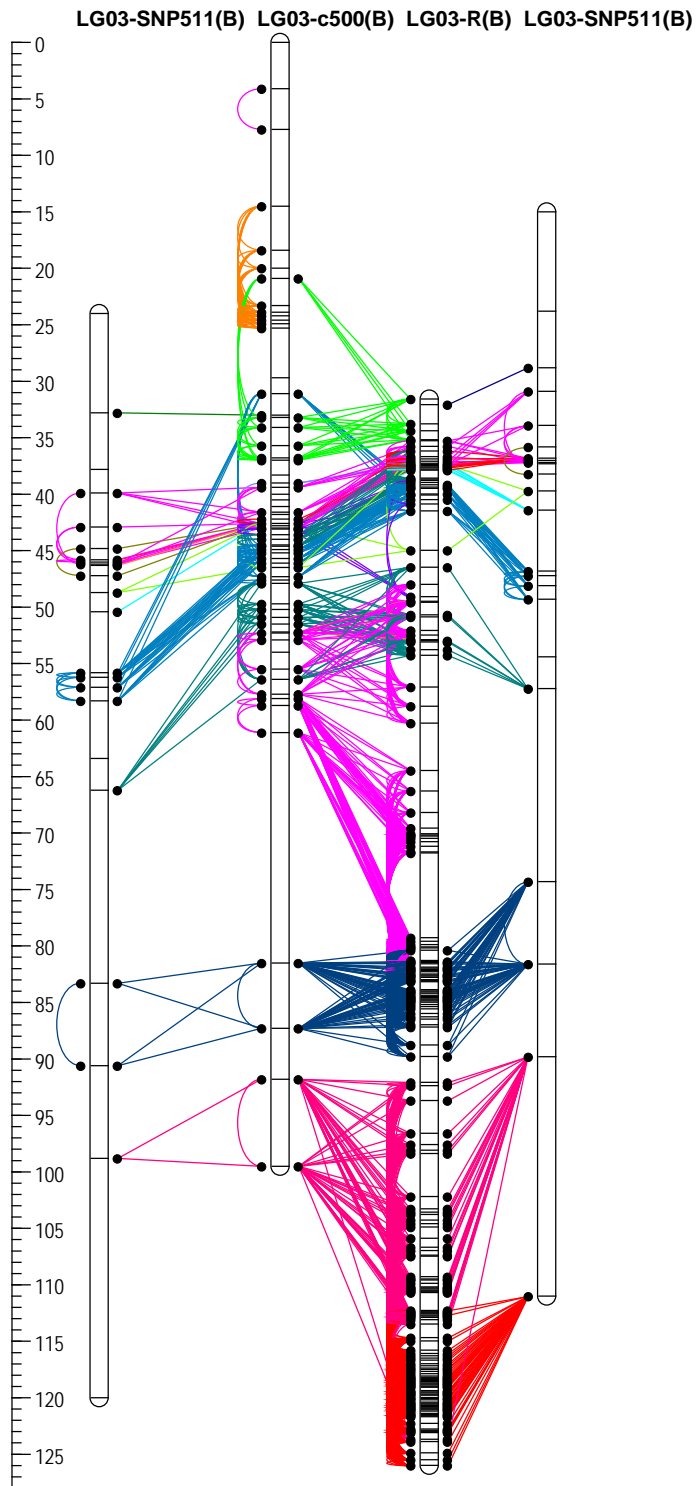


**Chr03:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.

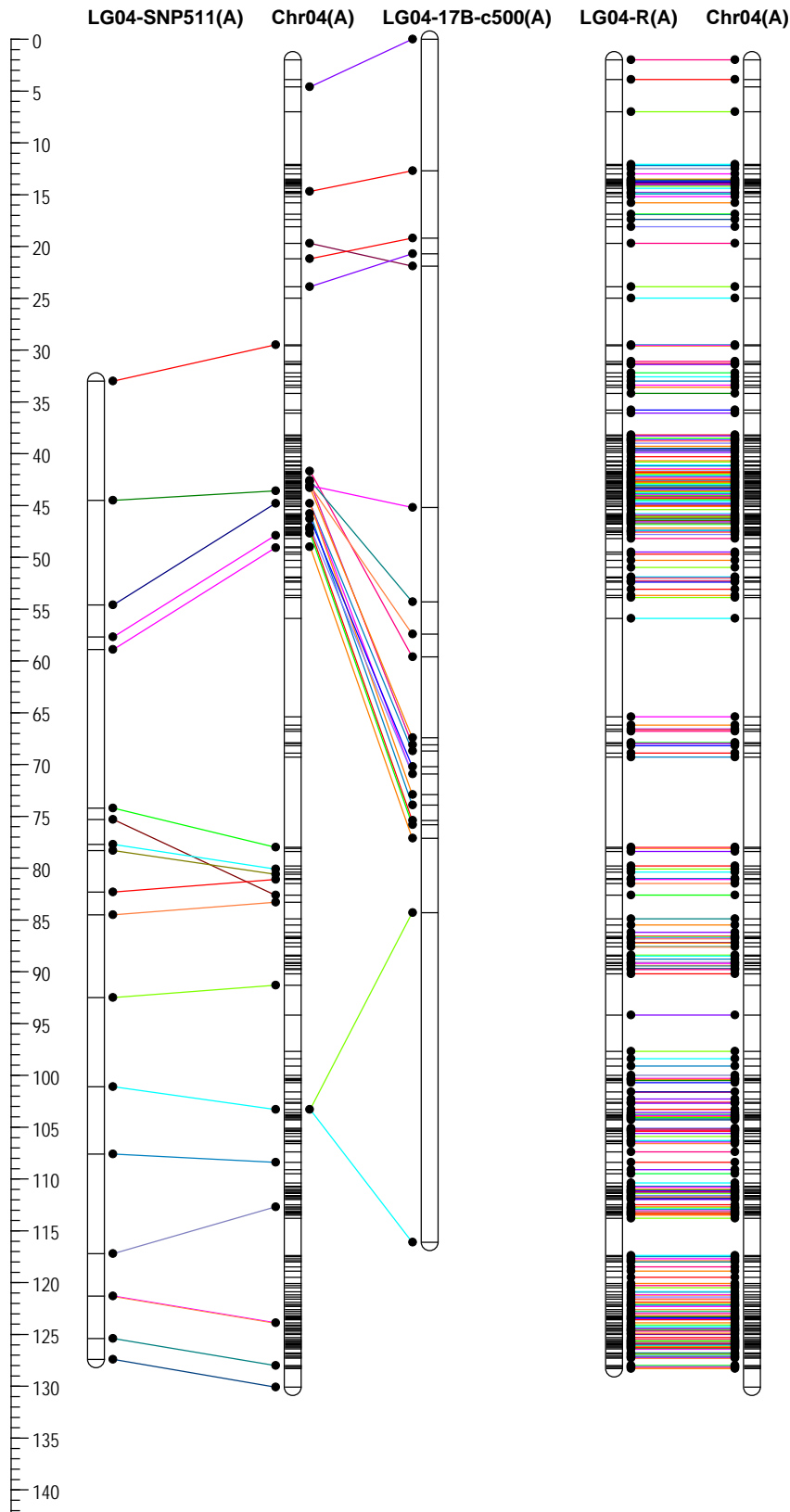




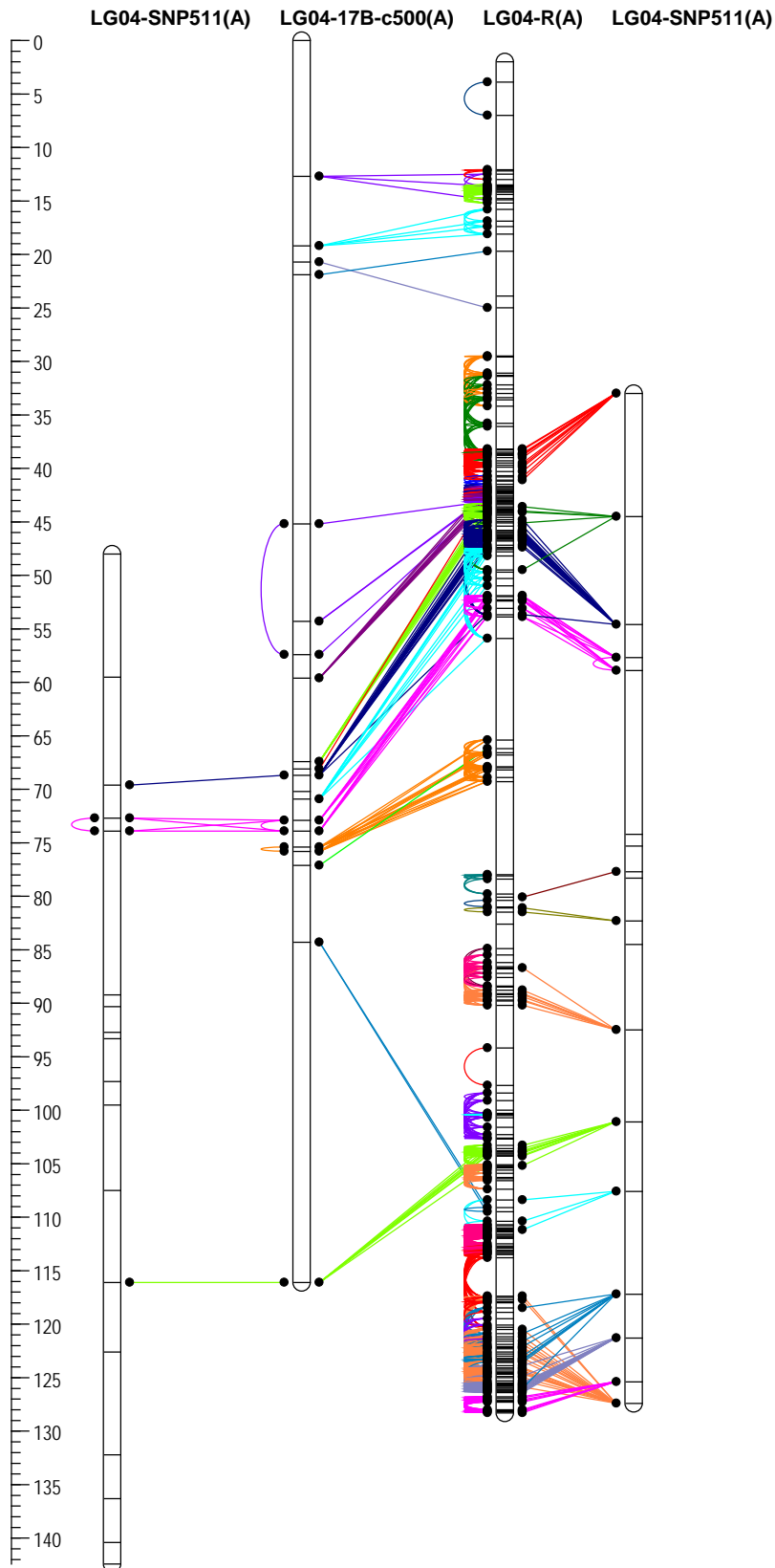
**Chr03:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.



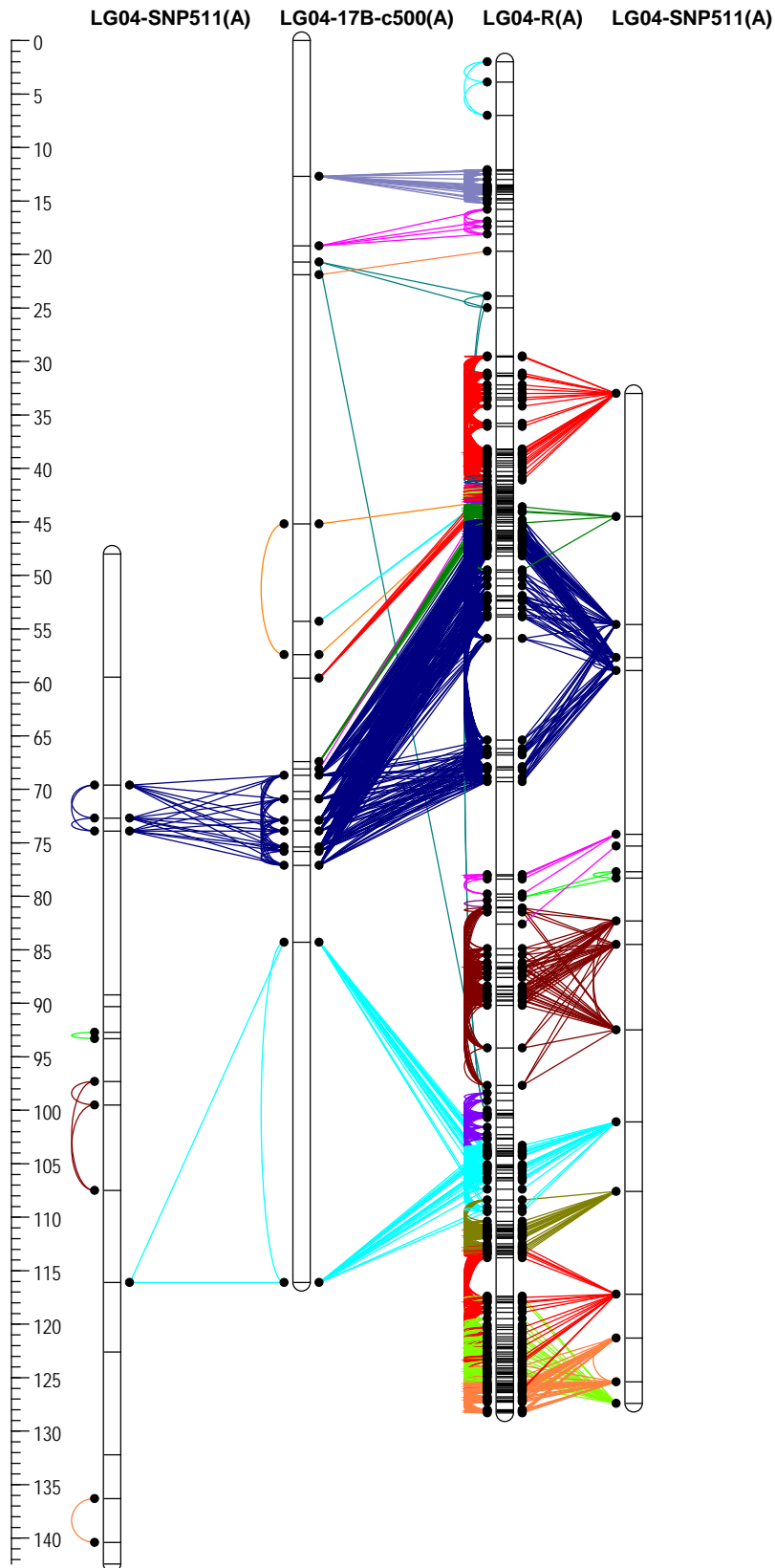
**Chr03:** Links between markers in the genetic maps of the three segregating populations within same scaffold of the assembly showing the concordance of order of scaffold positions (each scaffold has a separate color which color is used to indicated links within linkage groups with arcs of the same color as links between linkage groups).



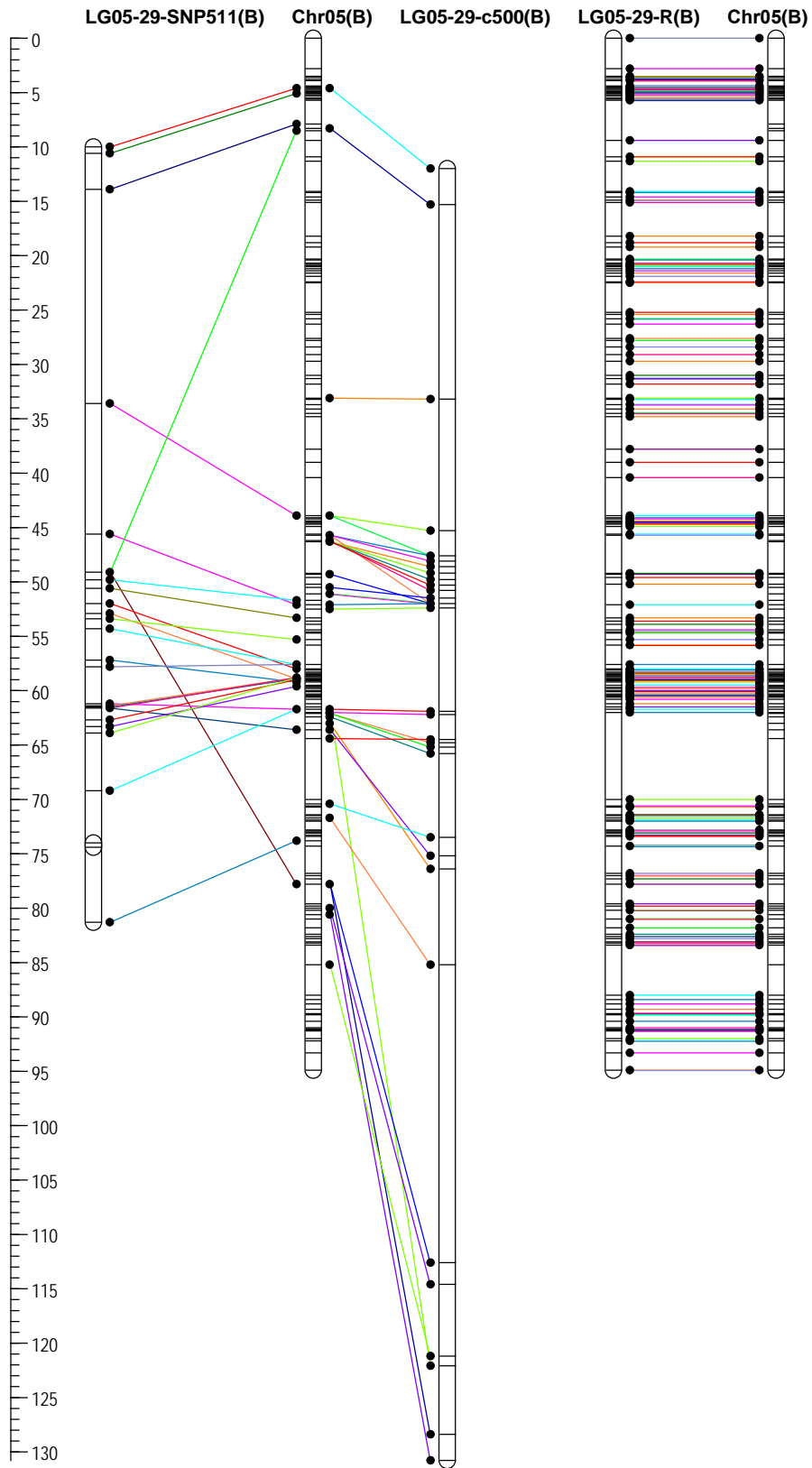
**Chr04:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



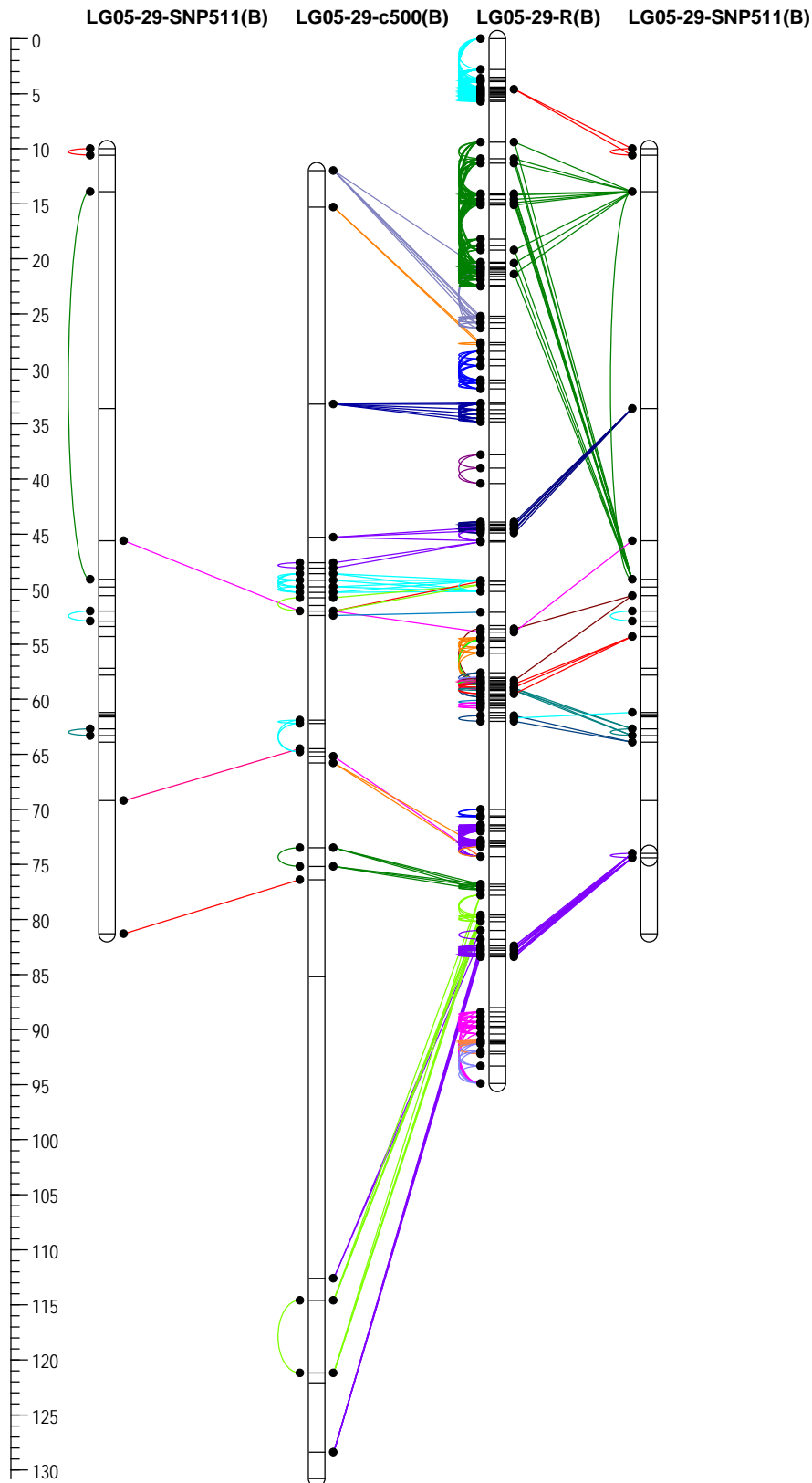
**Chr04:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.



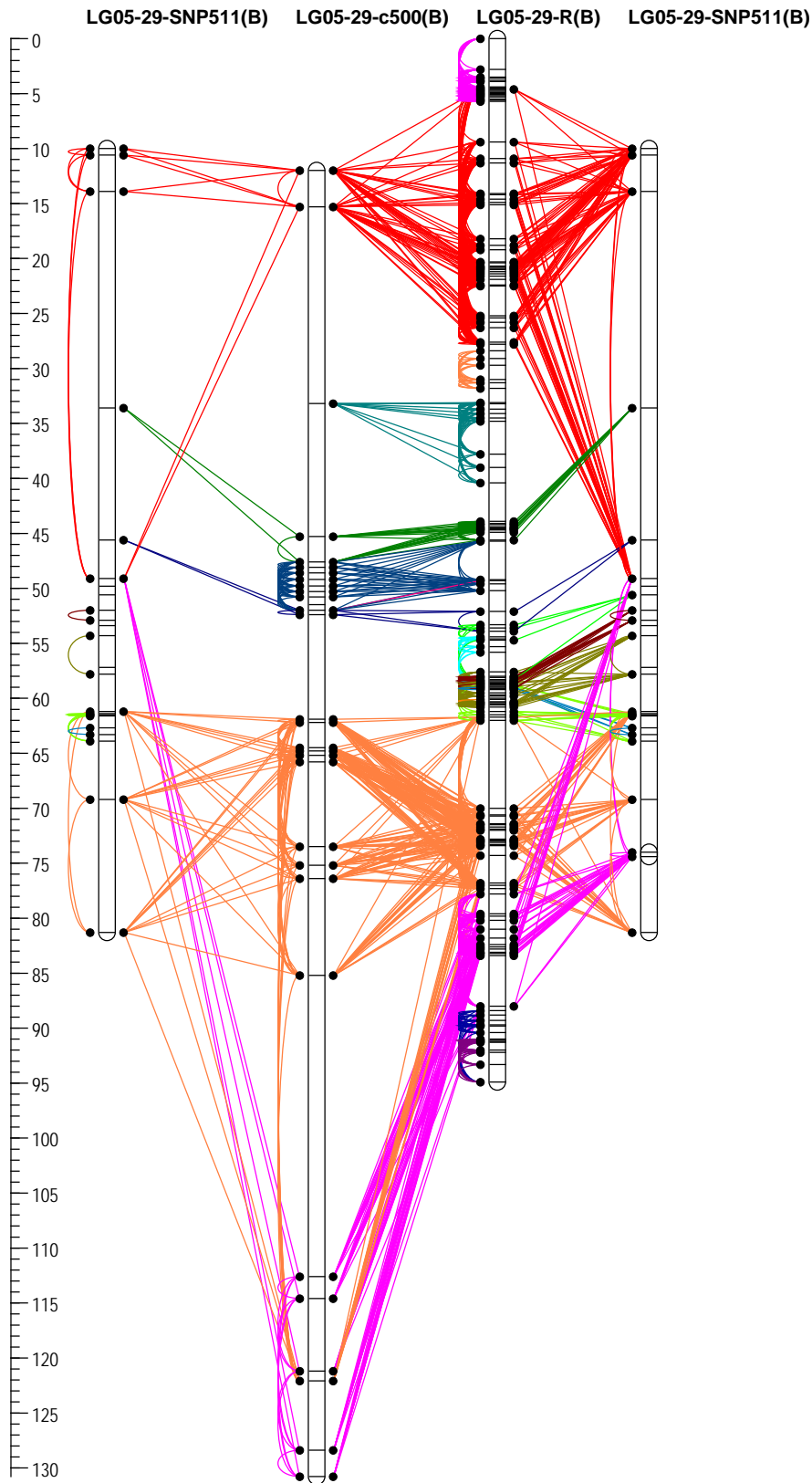
**Chr04:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mbase bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mbase bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.



**Chr05:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.

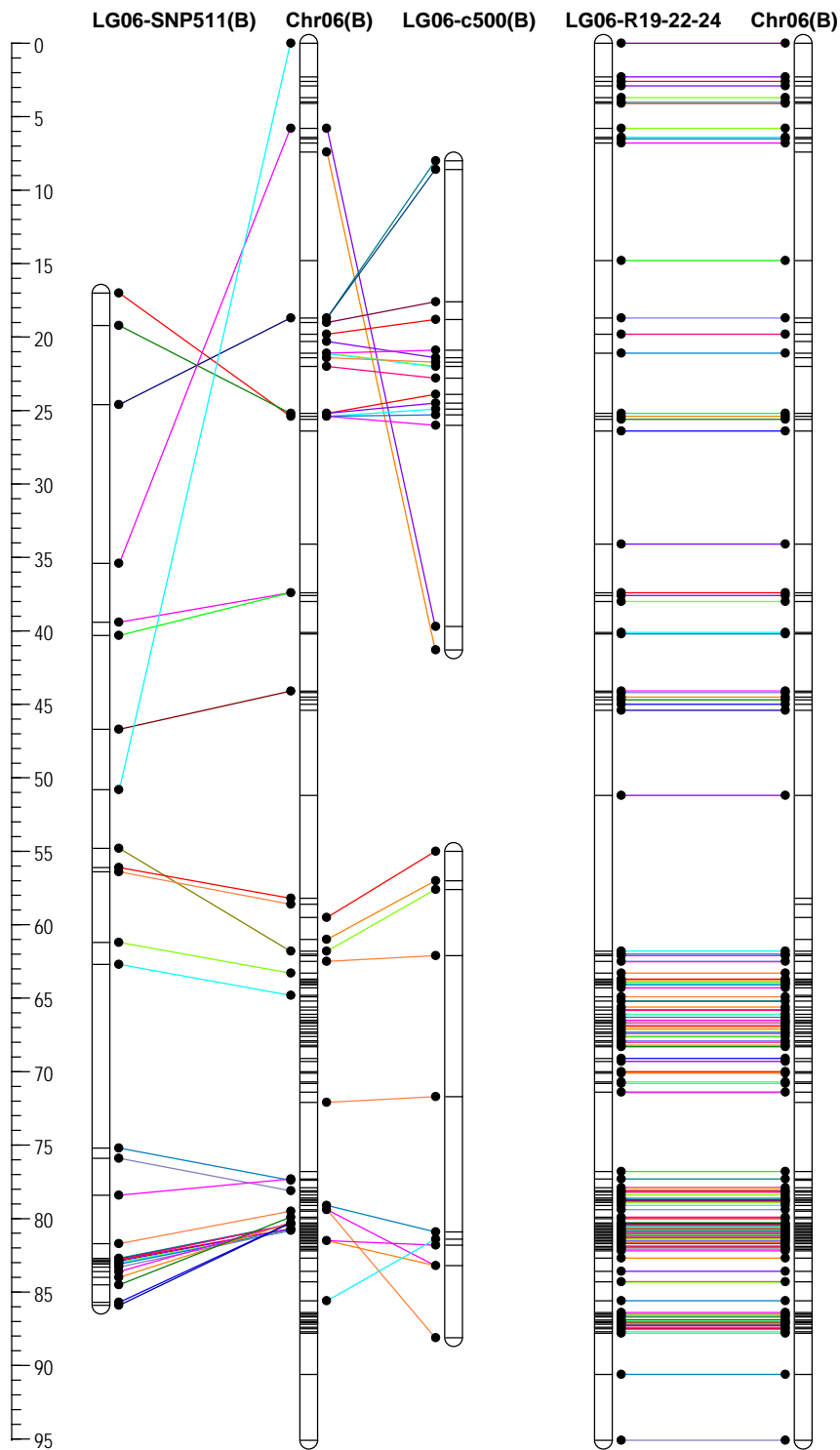


**Chr05:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.

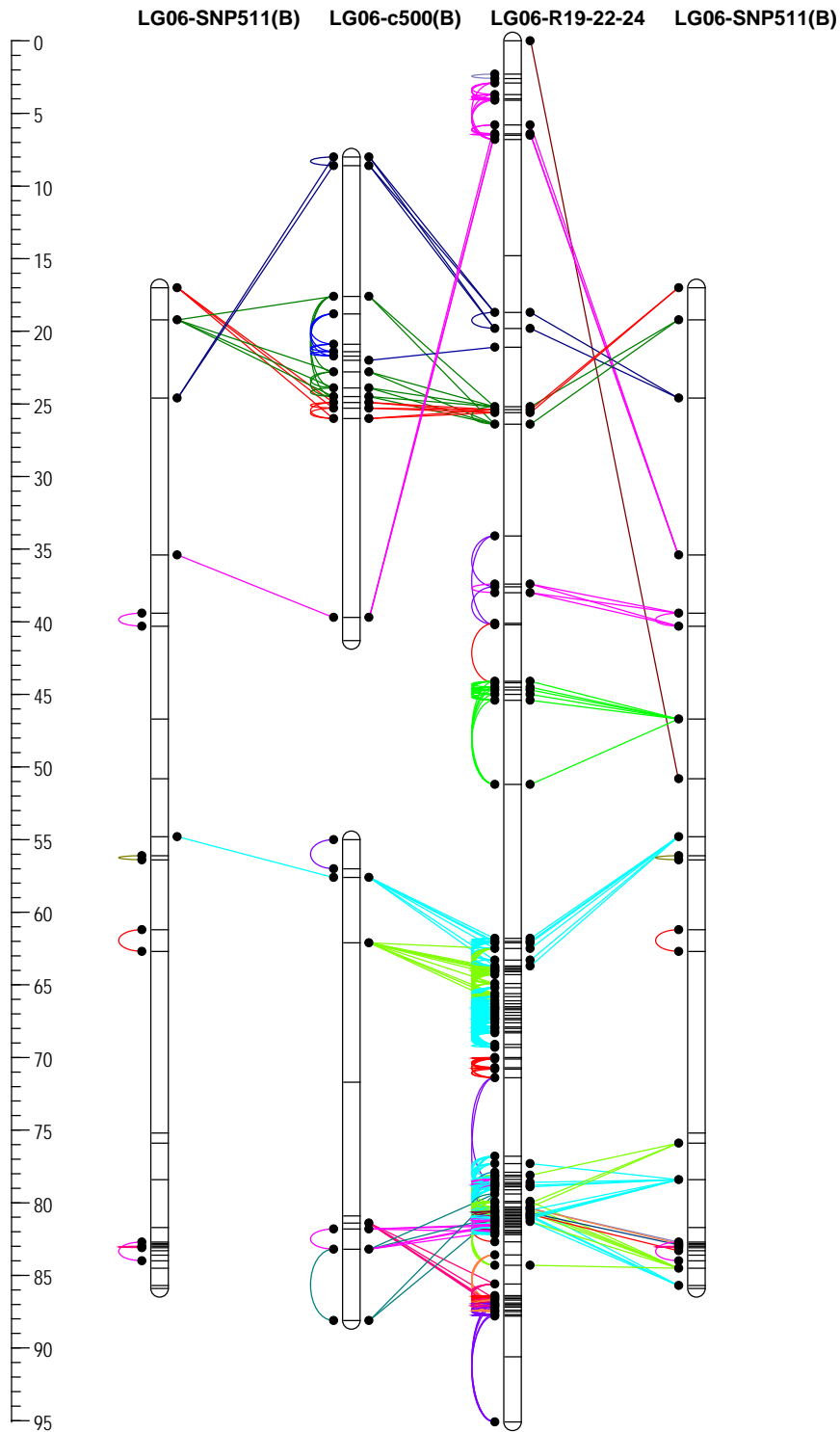


**Chr05:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mbase bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mbase bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.

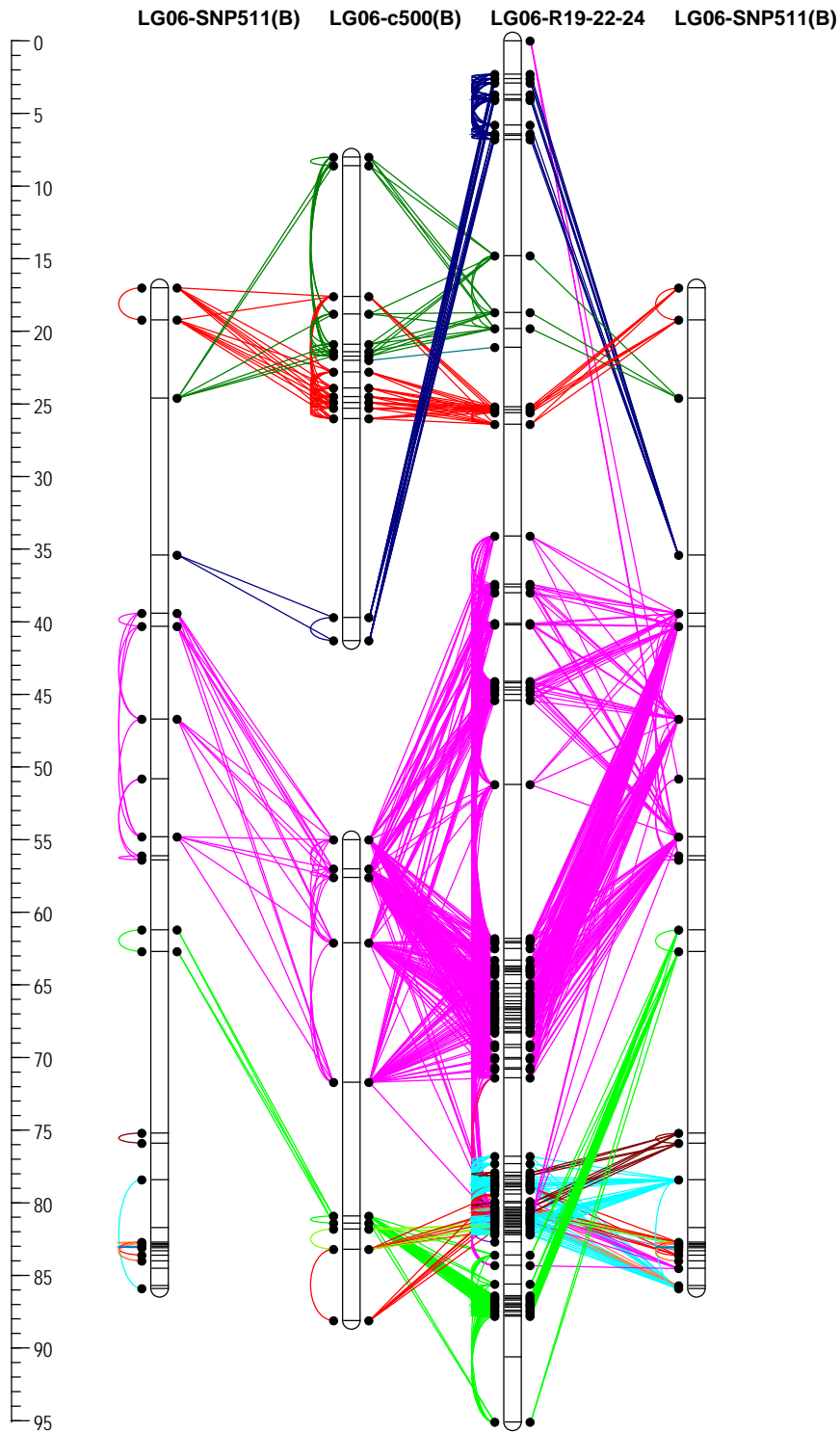




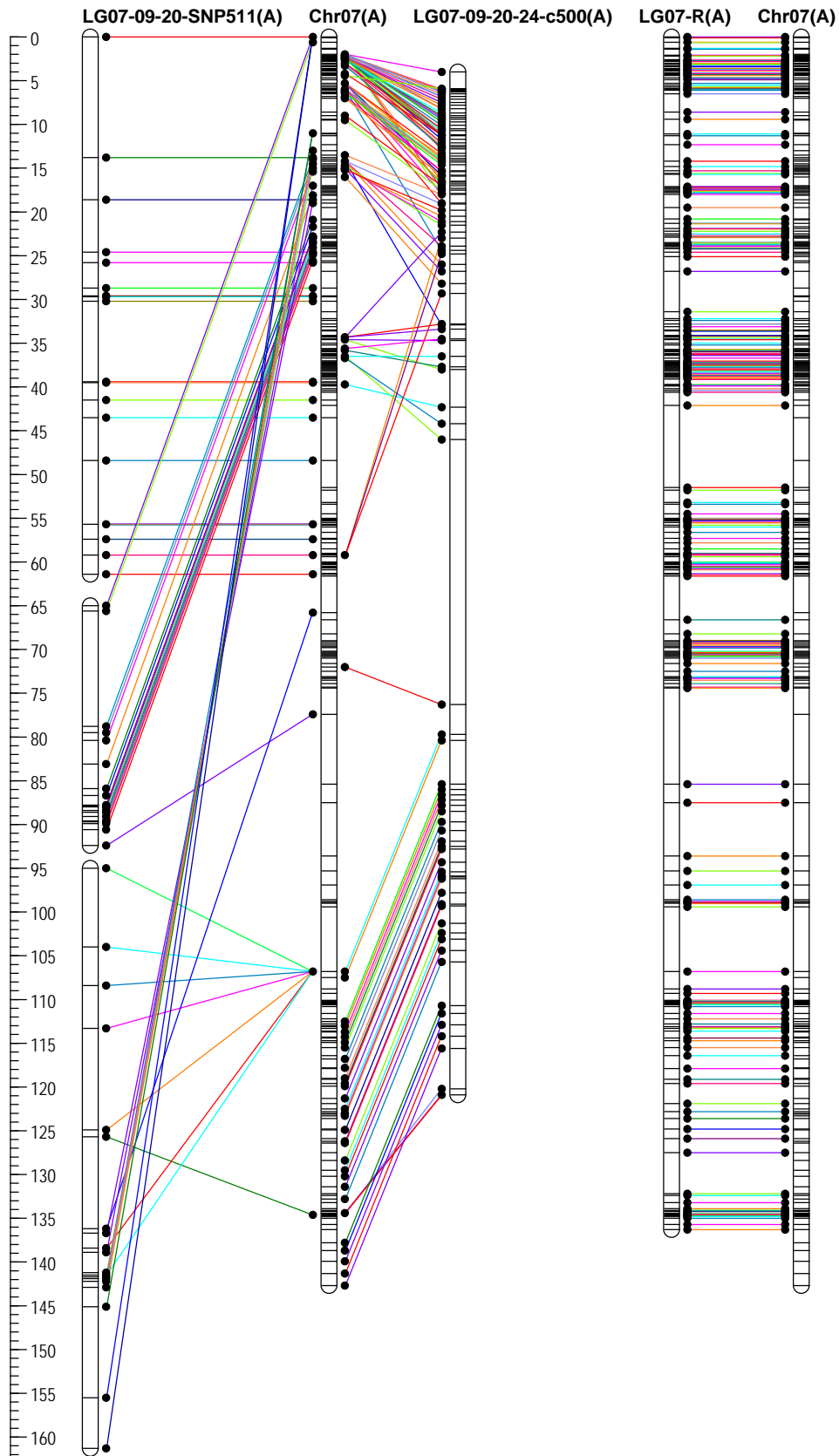
**Chr06:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



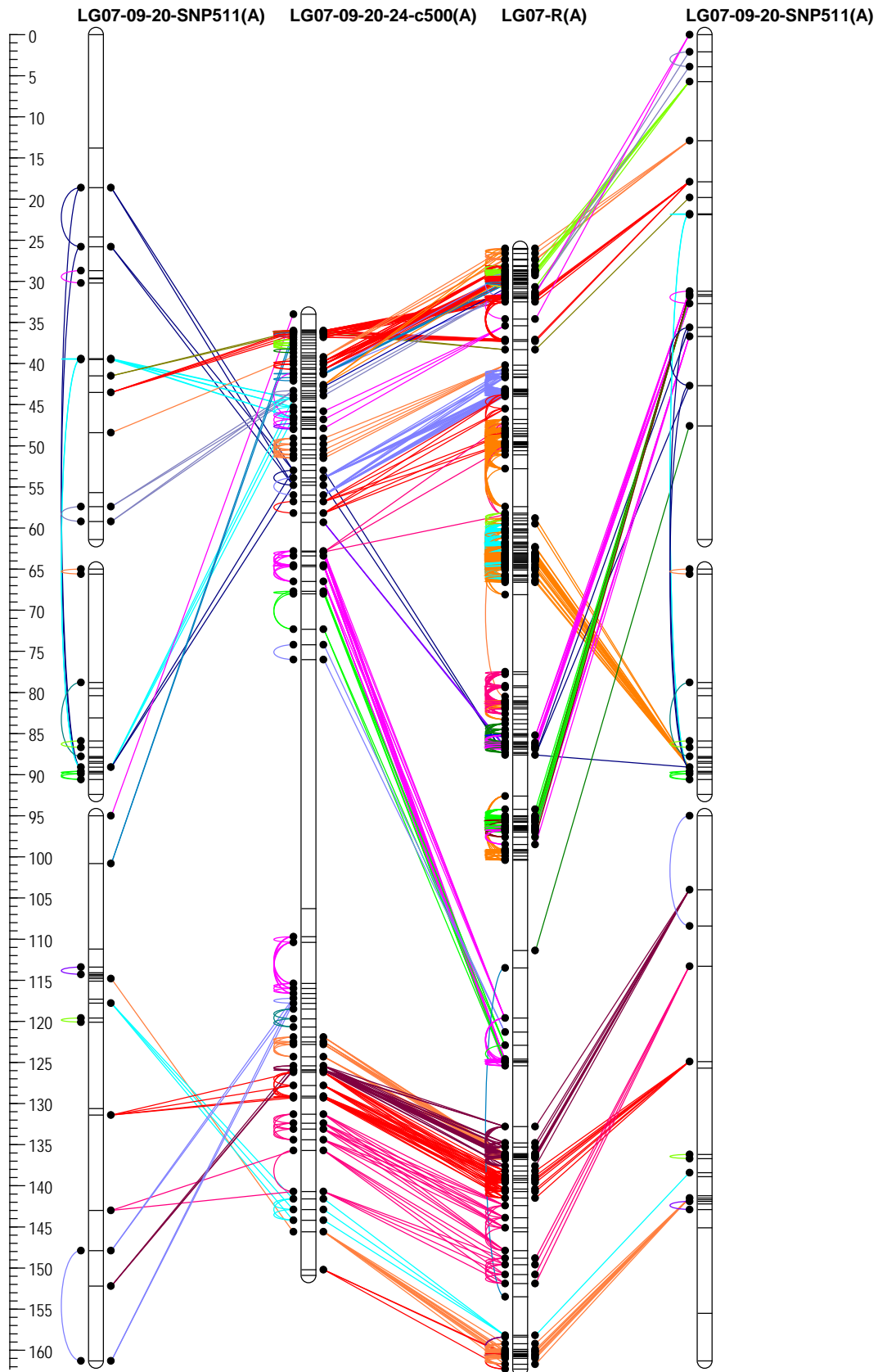
**Chr06:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.



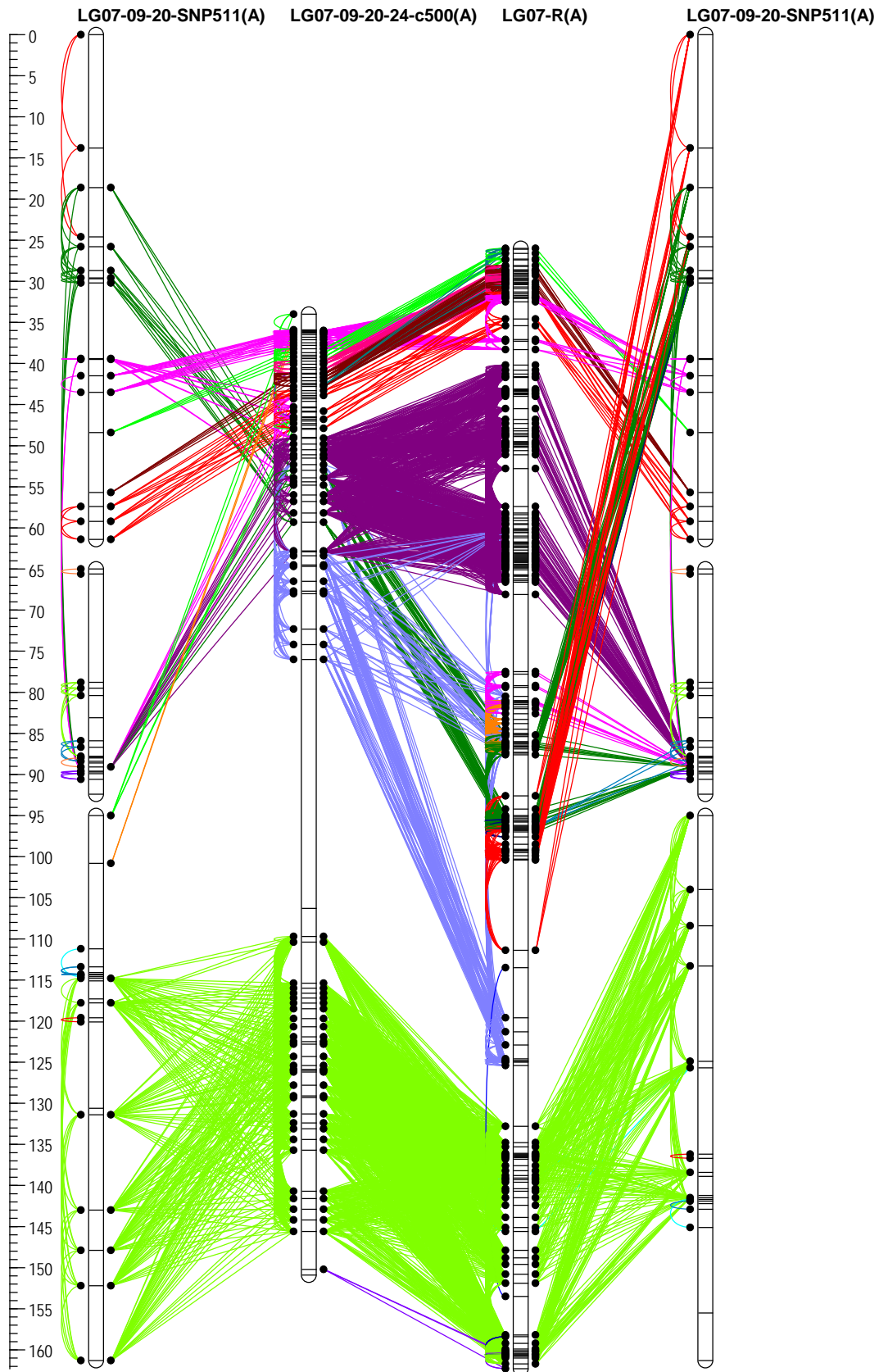
**Chr06:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mbase bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mbase bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.



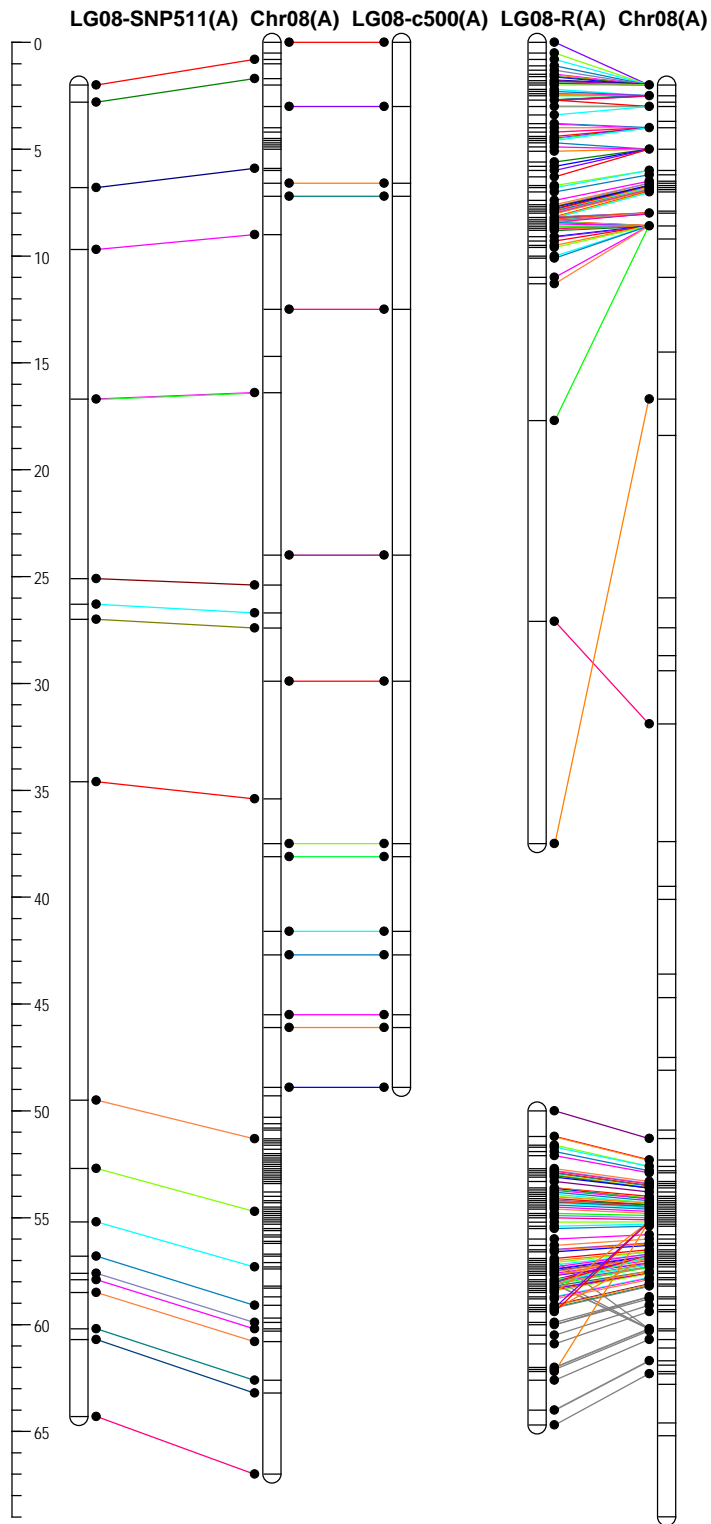
**Chr07:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



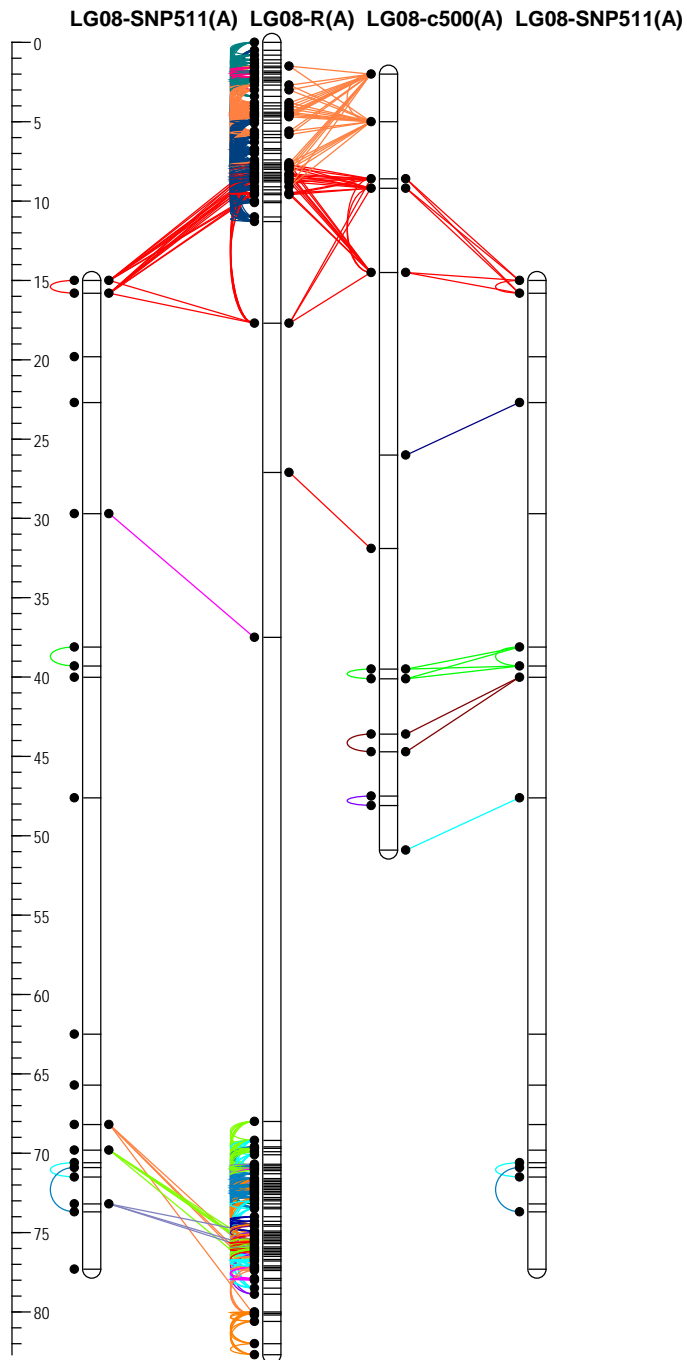
**Chr07:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.



**Chr07:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mbase bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mbase bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.

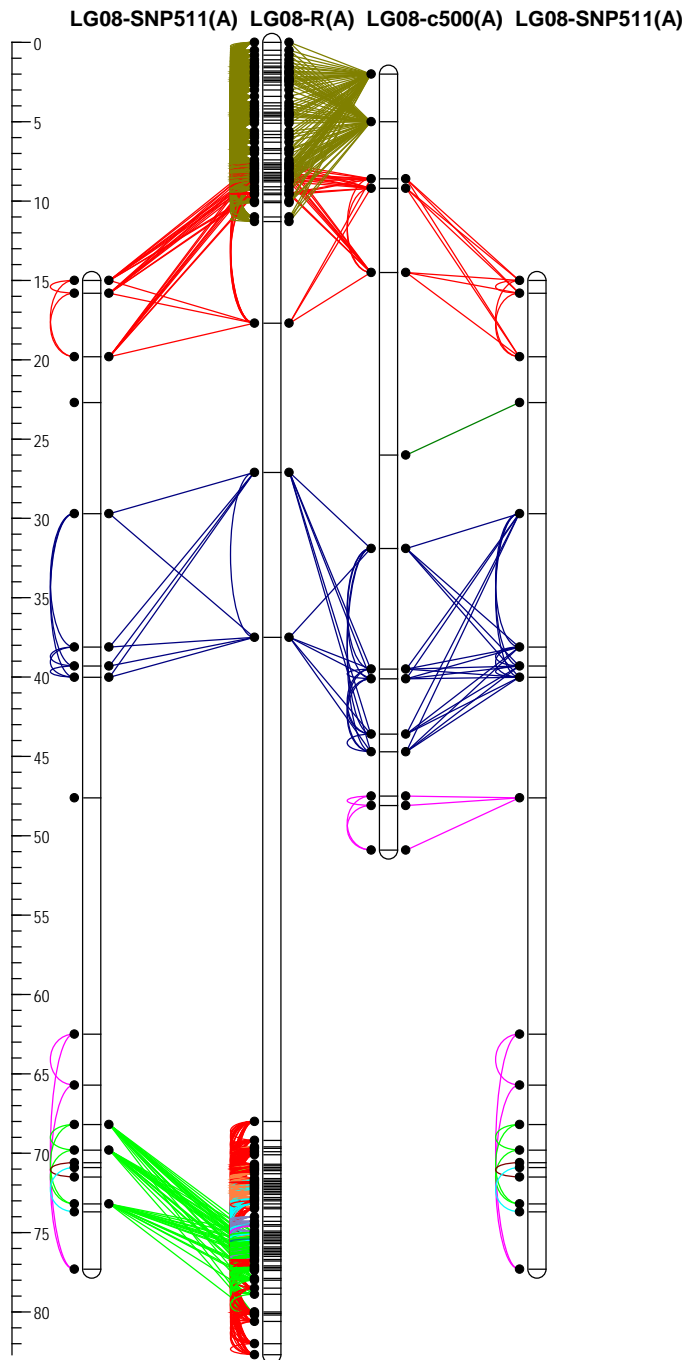


**Chr08:** Links at identity level between the genetic maps of the three segregating populations and the integrated map. Because the distance of the distal part of LG08-SNP511 in the RNAseq-map to the rest of the RNAseq-map is rather long (30 cM) and the SNP511 and c500-map have good concordance, for this Chr group, the c500-map was taken as reference for positions of anchor markers.

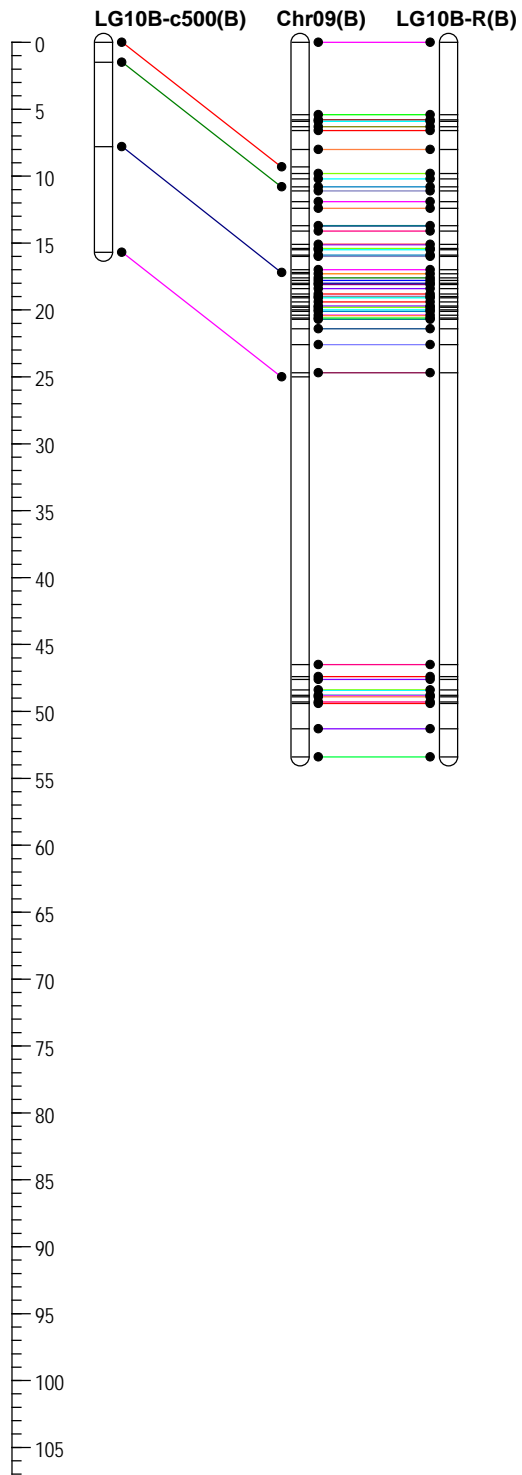


**Chr08:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.

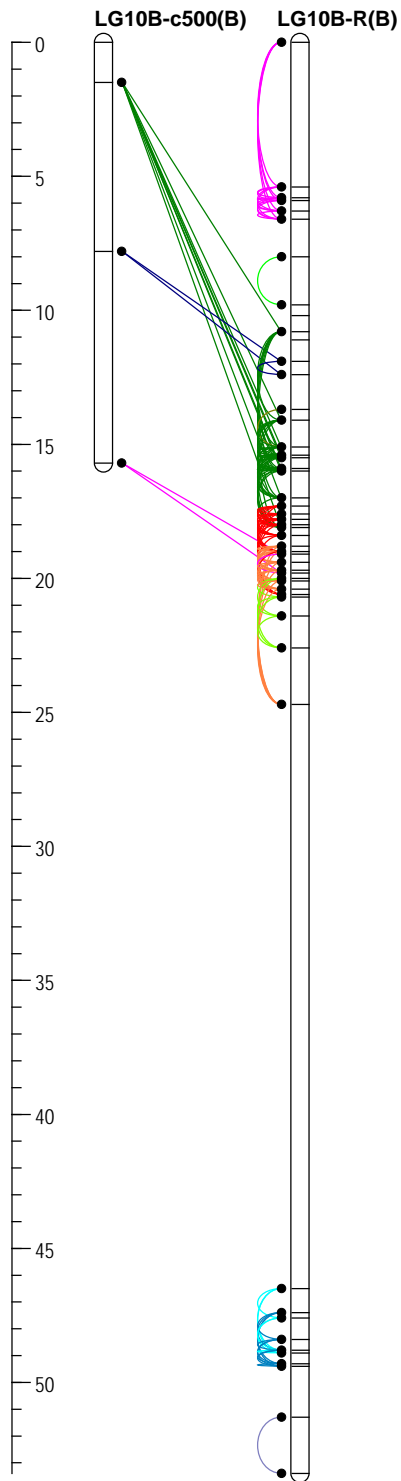




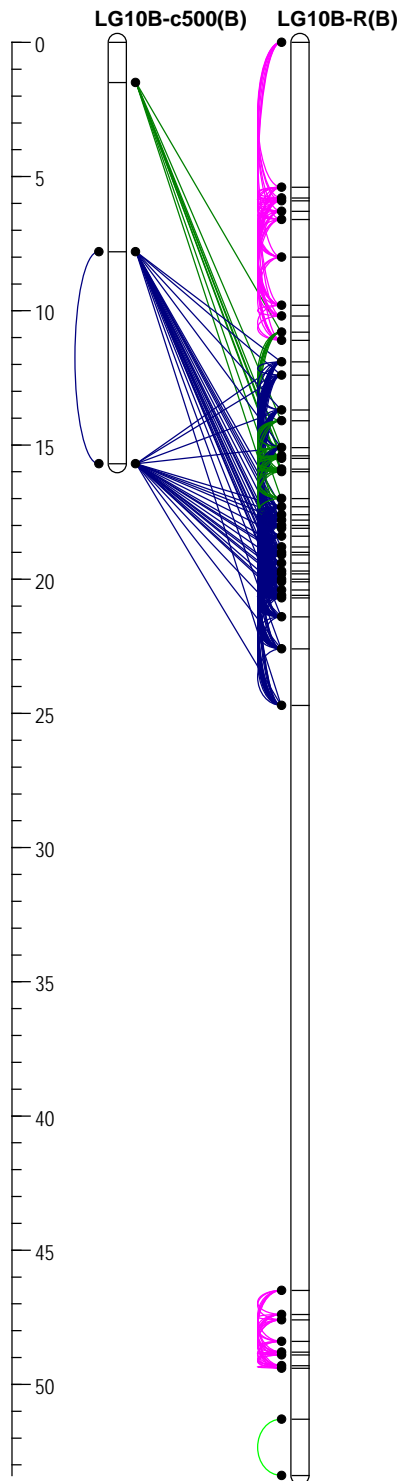
**Chr08:** Links between markers in the genetic maps of the three segregating populations within same scaffold of the assembly showing the concordance of order of scaffold positions (each scaffold has a separate color which color is used to indicated links within linkage groups with arcs of the same color as links between linkage groups).



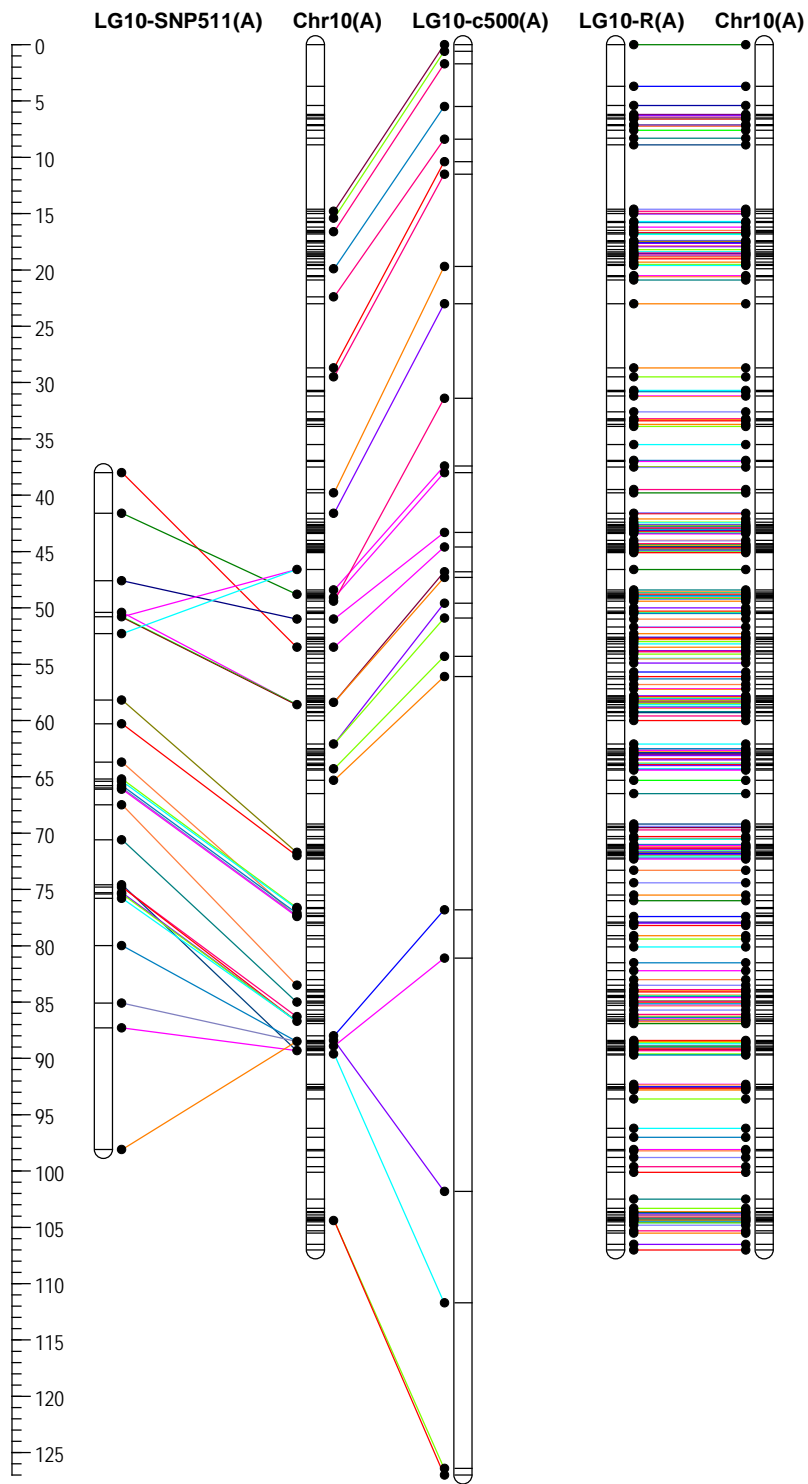
**Chr09:** Links at identity level between the genetic maps of the three segregating populations and the integrated map. No markers found in the SNP511 map on this Chr.



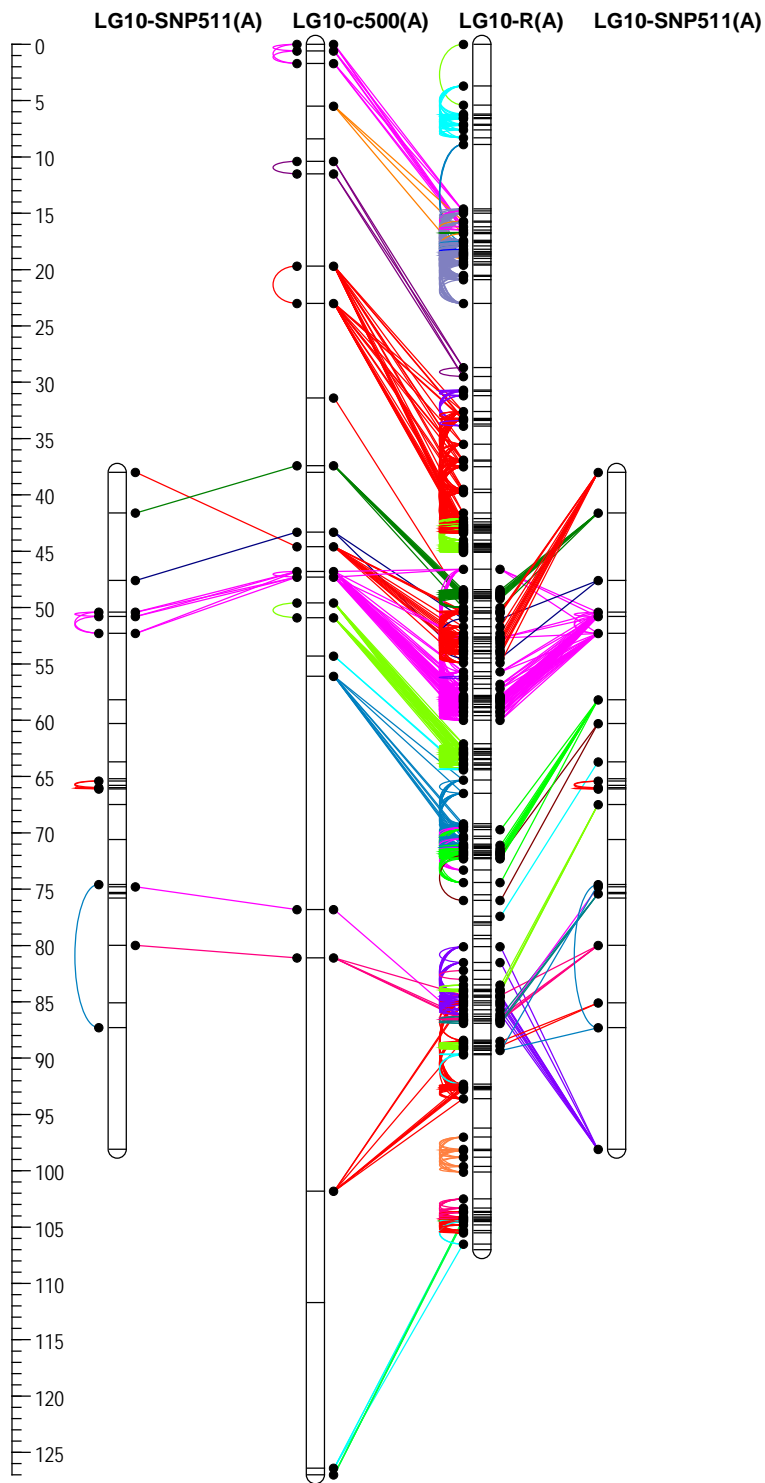
**Chr09:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.



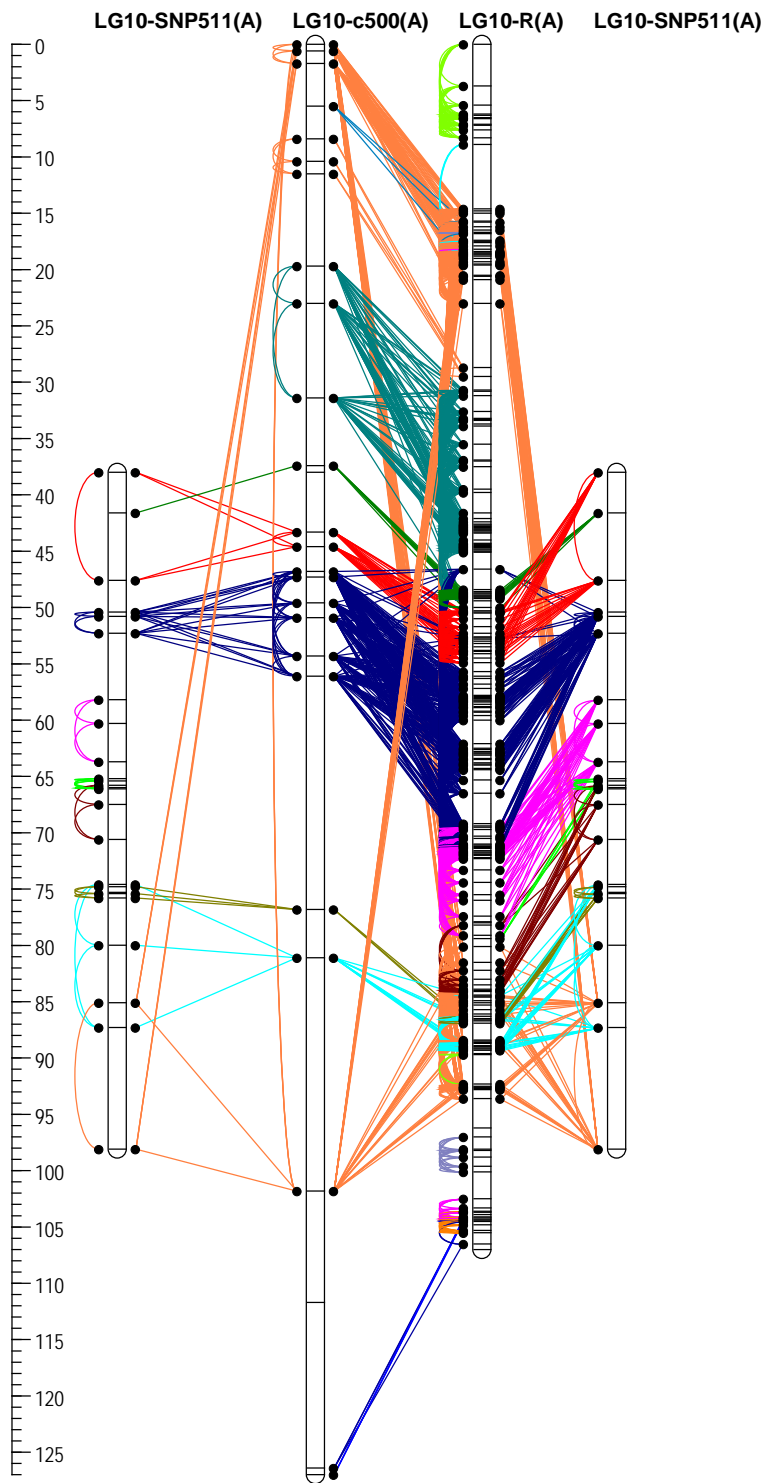
**Chr09:** Links between markers in the genetic maps of the three segregating populations within same scaffold of the assembly showing the concordance of order of scaffold positions (each scaffold has a separate color which color is used to indicated links within linkage groups with arcs of the same color as links between linkage groups). For comparison, the Chr10 (B-subgenome) has been shown next to the LG going into Chr09(B-subgenome). Only one marker links Chr10(A) with Chr09(subgenome B), and this was the reason for the initial naming of the LG in the Atlas x Carina Red cross (c500-map) and RNAseq-map as LG10B. Chr1.



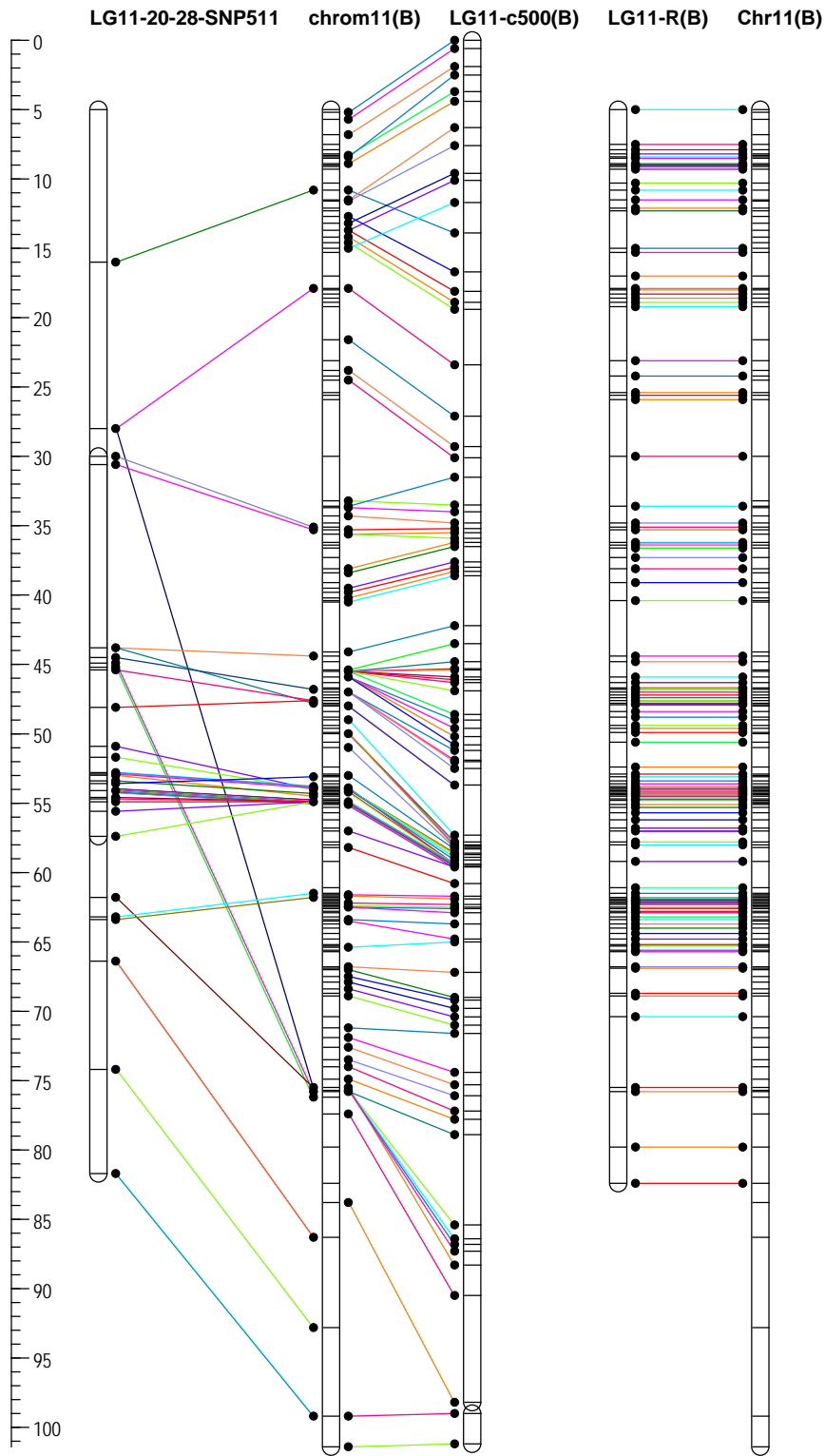
**Chr10:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



**Chr10:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions. Links of the same 1 Mb bin are linked within a linkage group with arcs of the same color and links between linkage groups use the same color.

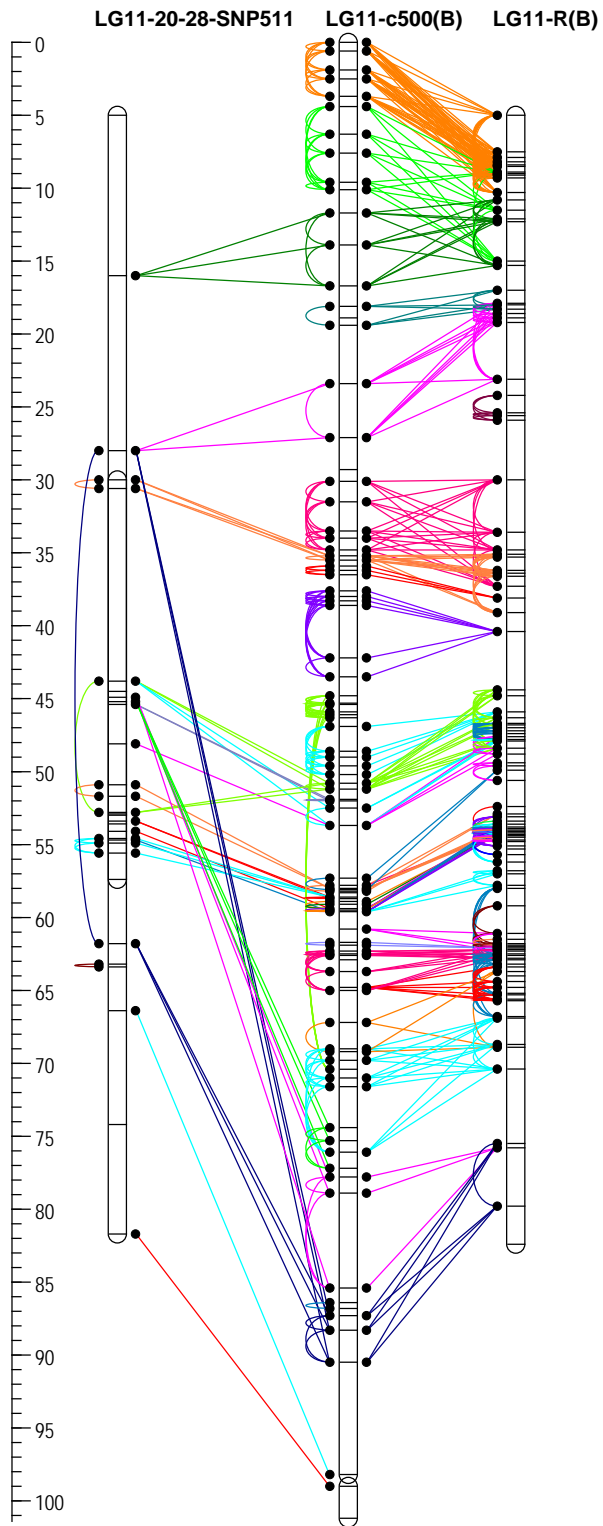


**Chr10:** Links between markers in the genetic maps of the three segregating populations within same scaffold of the assembly showing the concordance of order of scaffold positions (each scaffold has a separate color which color is used to indicated links within linkage groups with arcs of the same color as links between linkage groups).

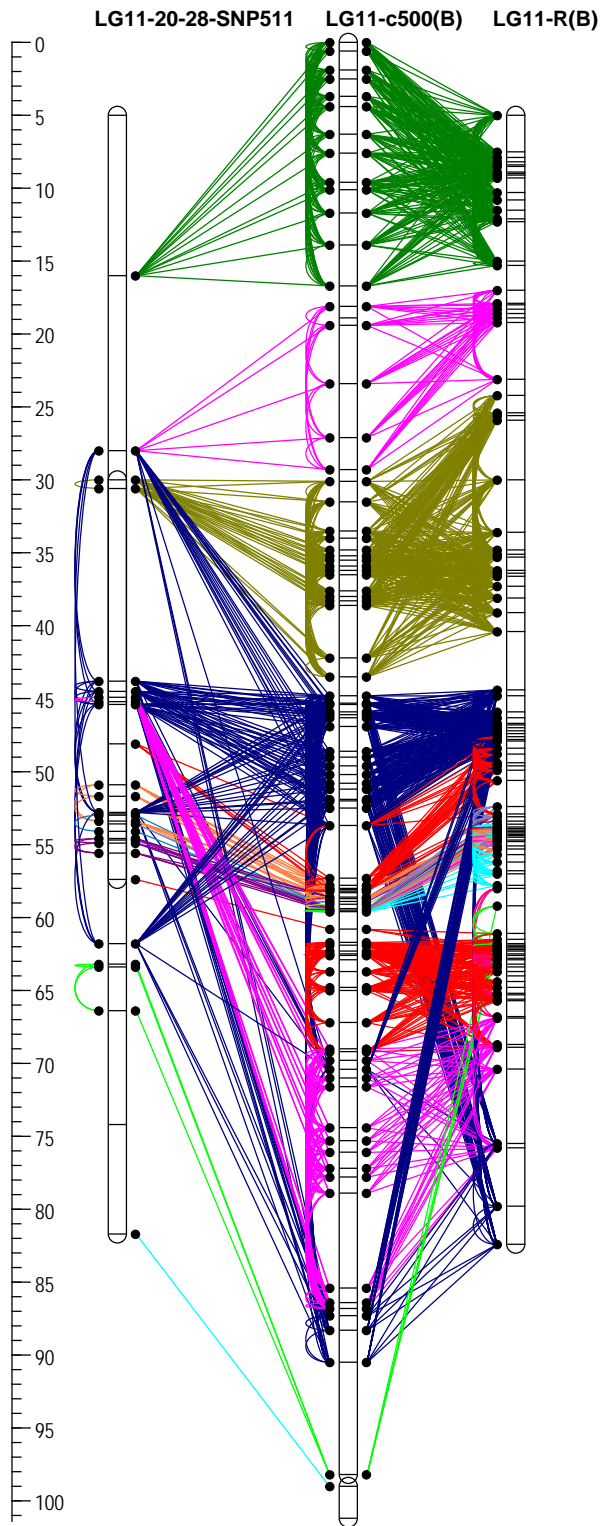


**Chr11**: Links at identity level between the genetic maps of the three segregating populations and the integrated map.

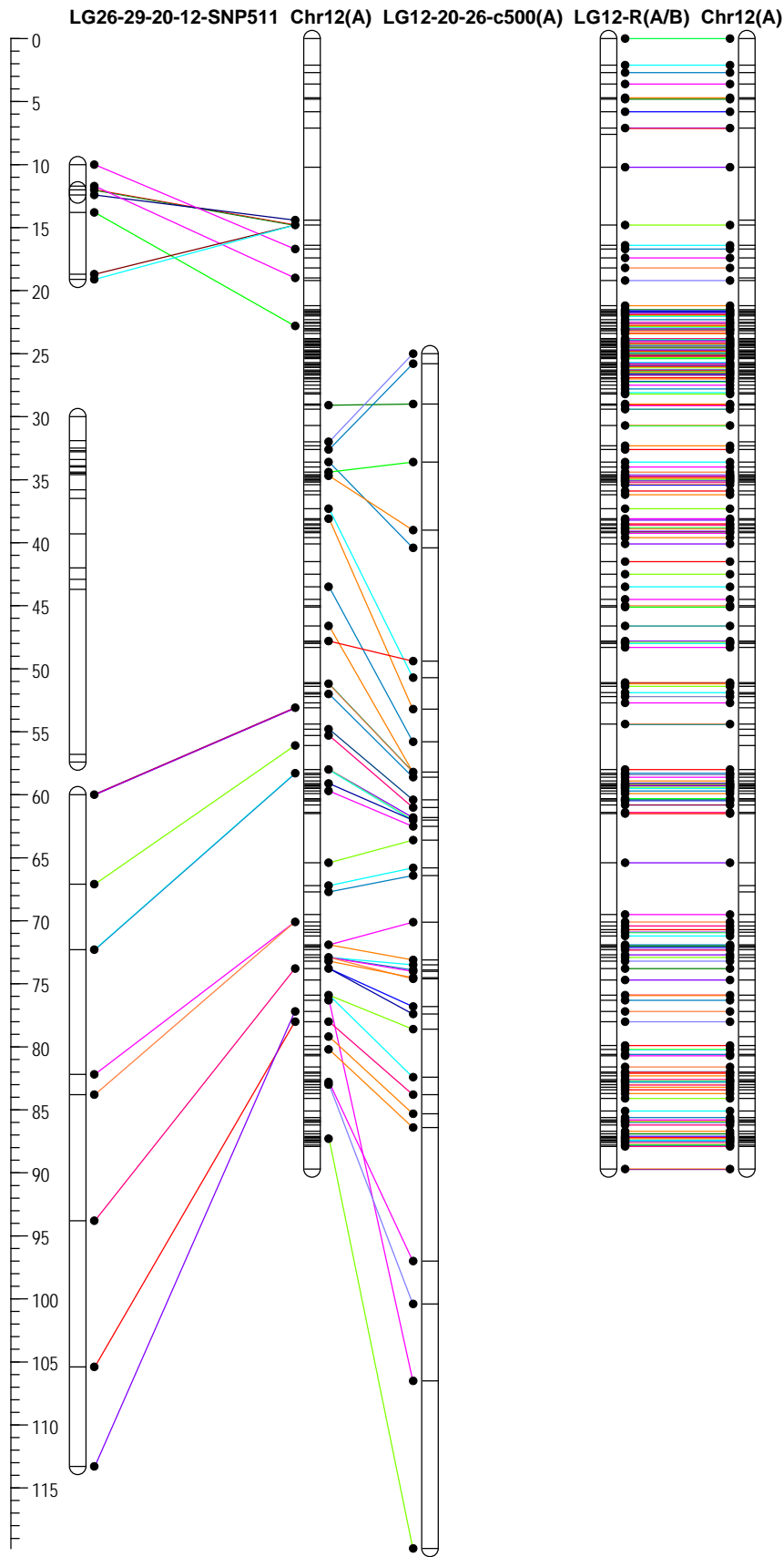




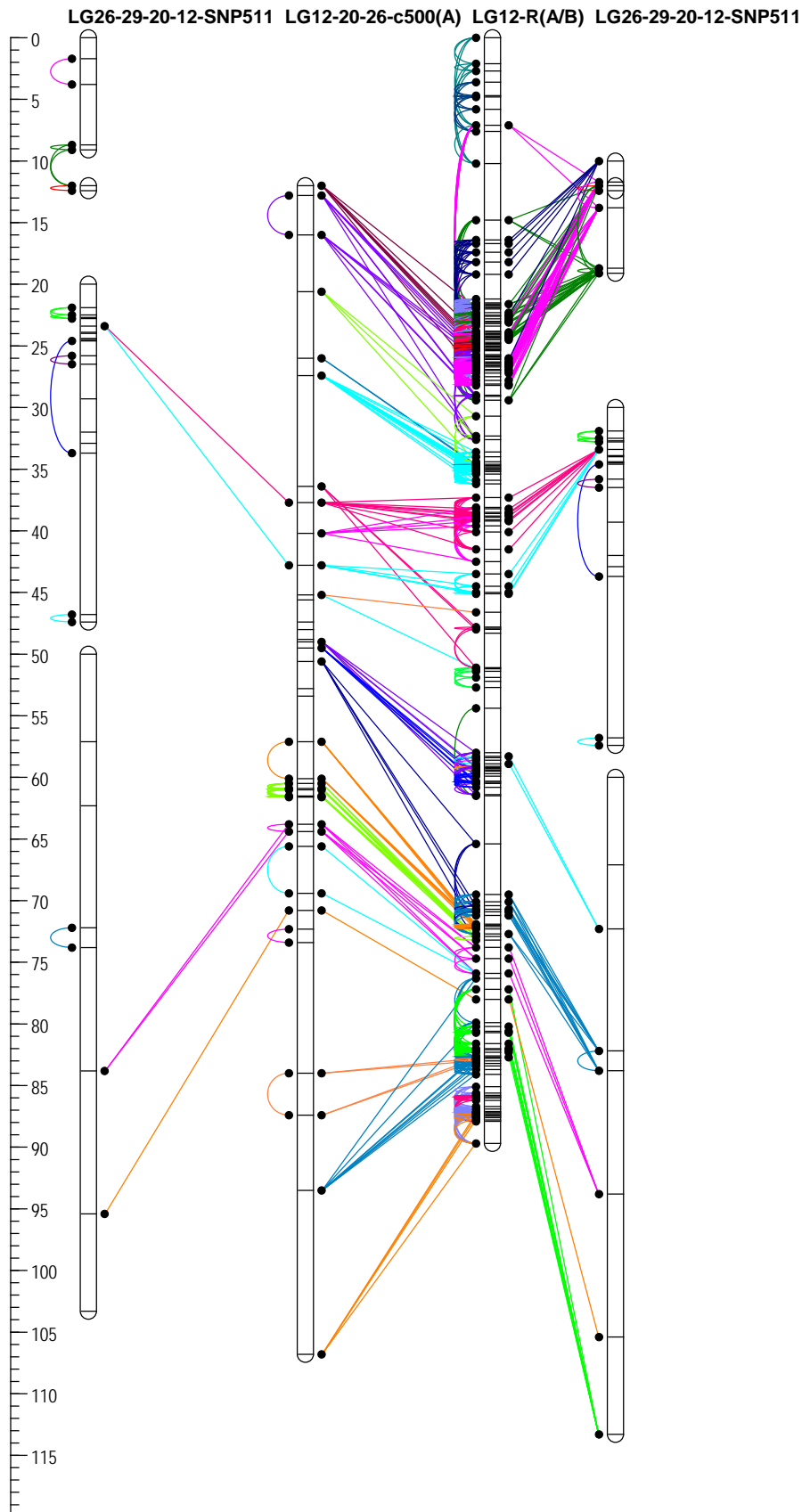
**Chr11:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions.



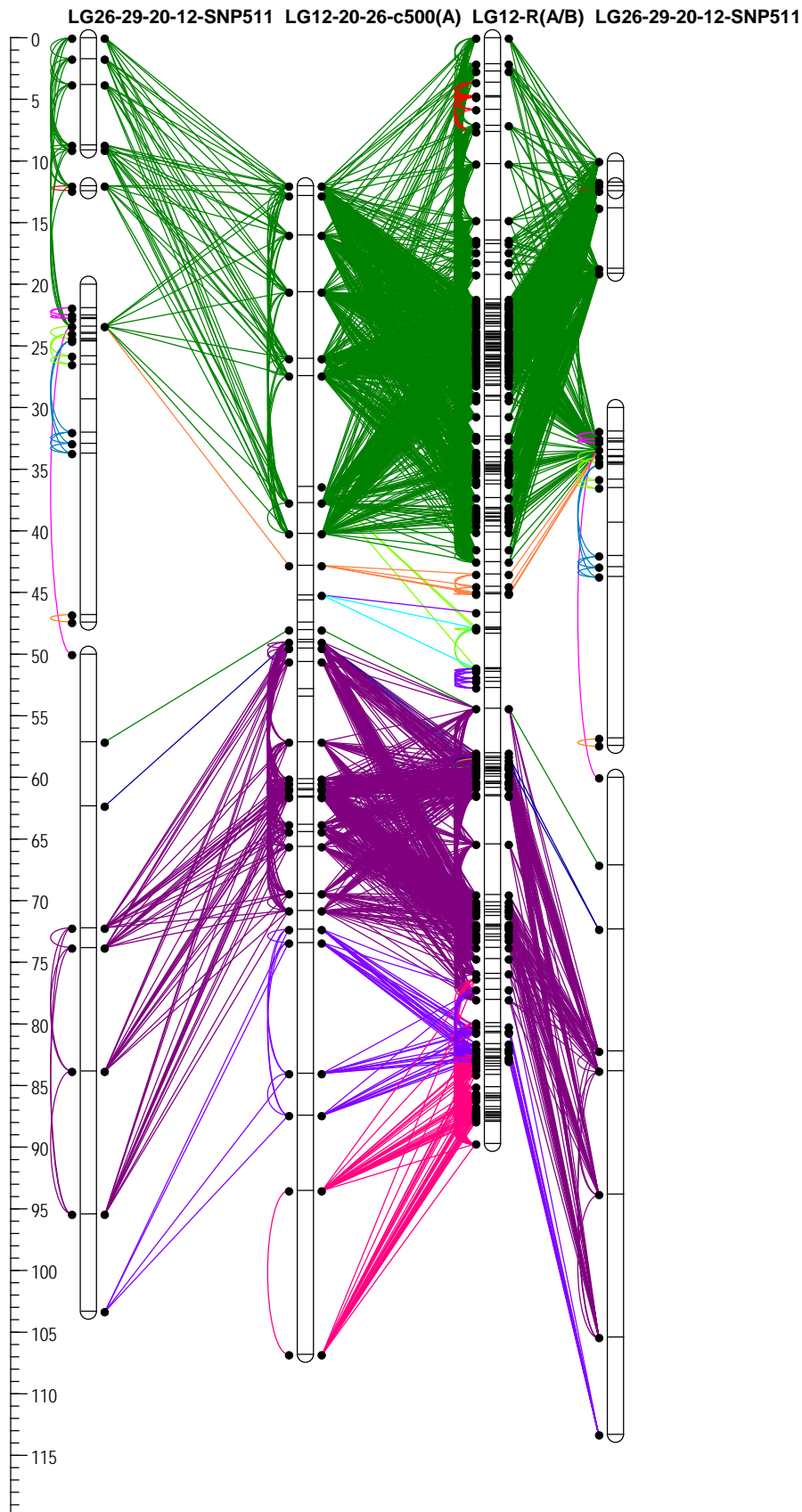
**Chr11:** Links between markers in the genetic maps of the three segregating populations within the scaffold of the assembly showing the concordance of order of scaffold positions.



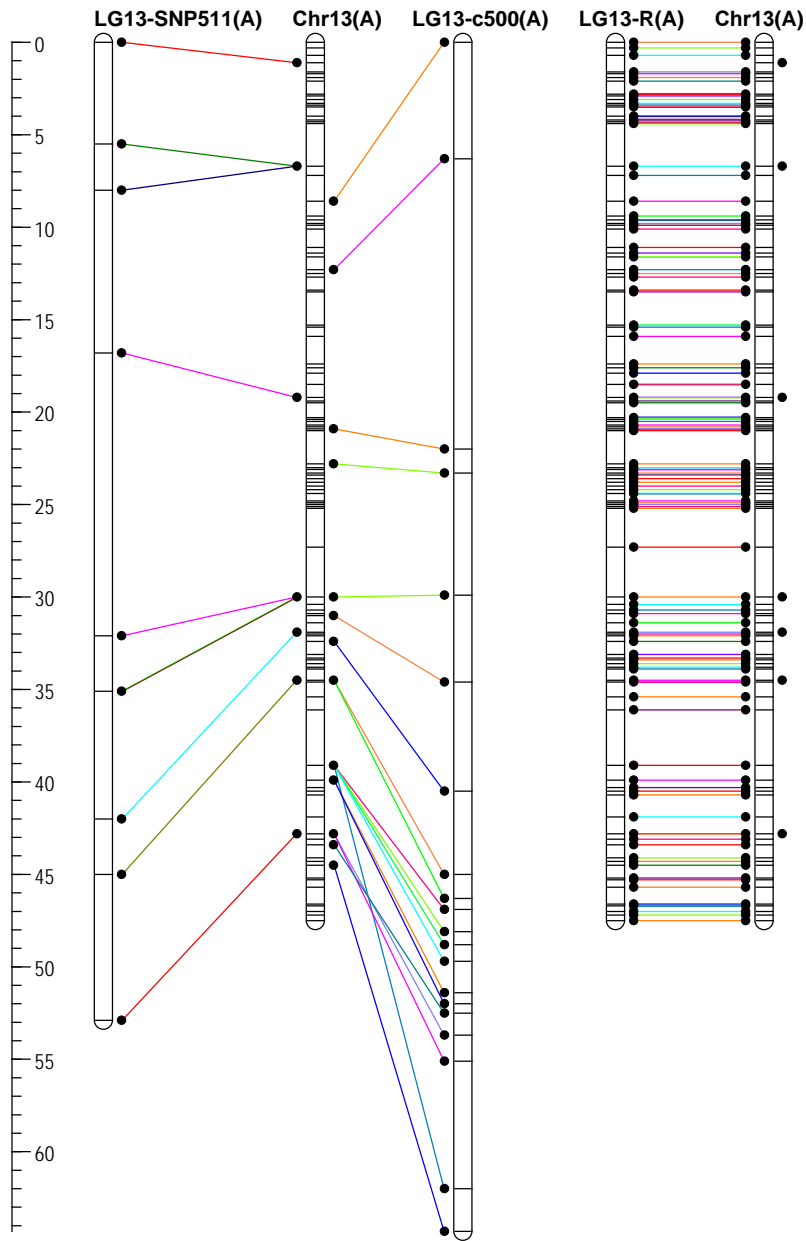
**Chr12:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



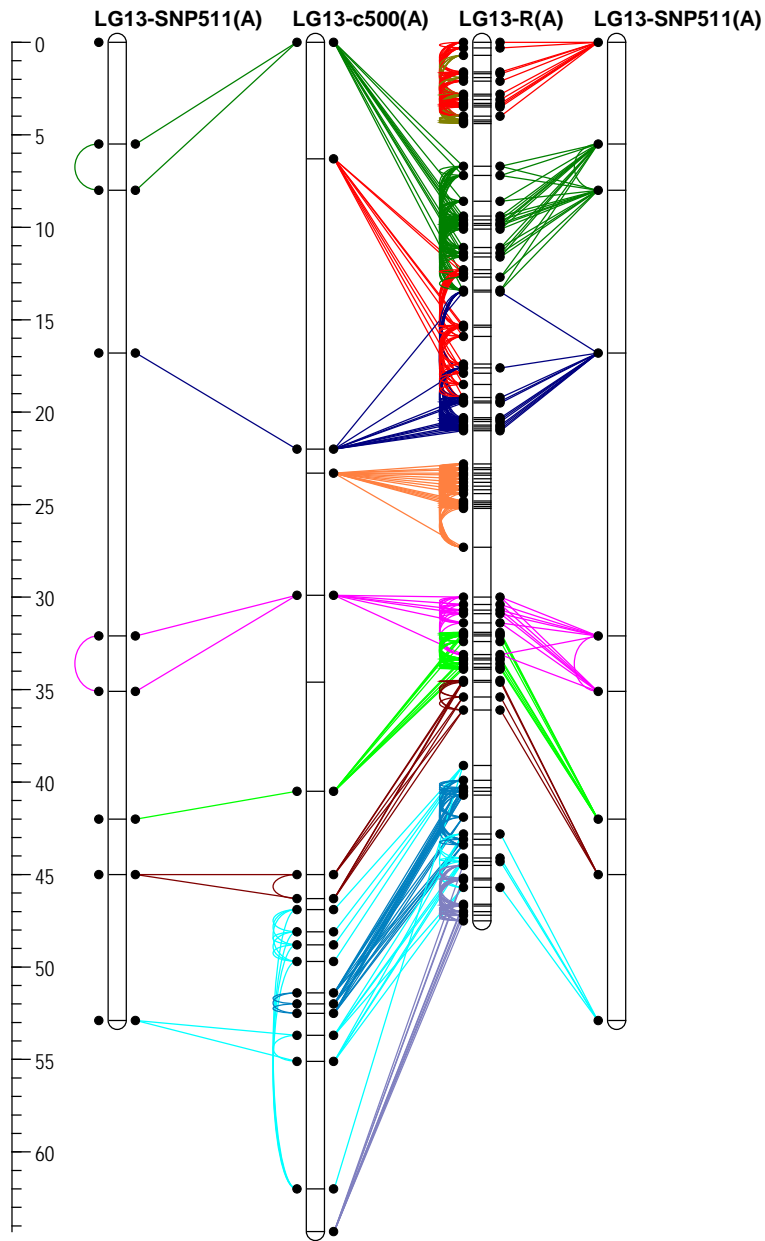
**Chr12:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions.



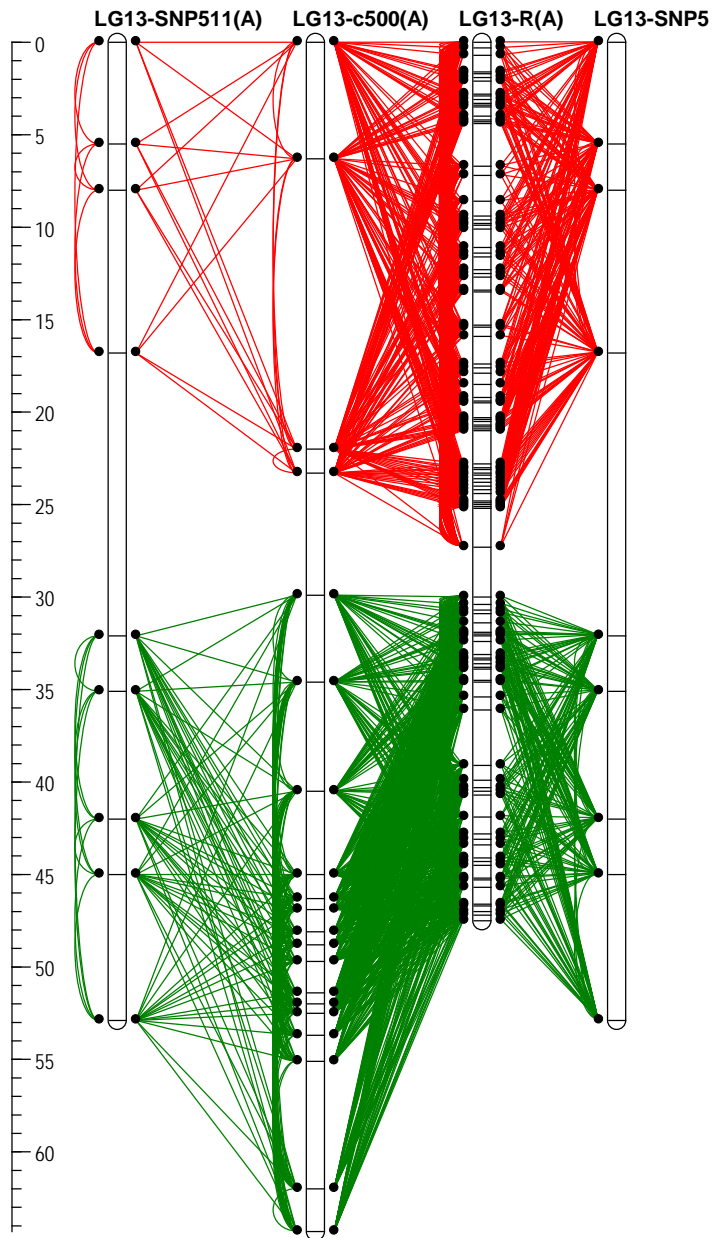
**Chr12:** Links between markers in the genetic maps of the three segregating populations within scaffolds of the assembly showing the concordance of order of scaffold positions.



**Chr13:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.

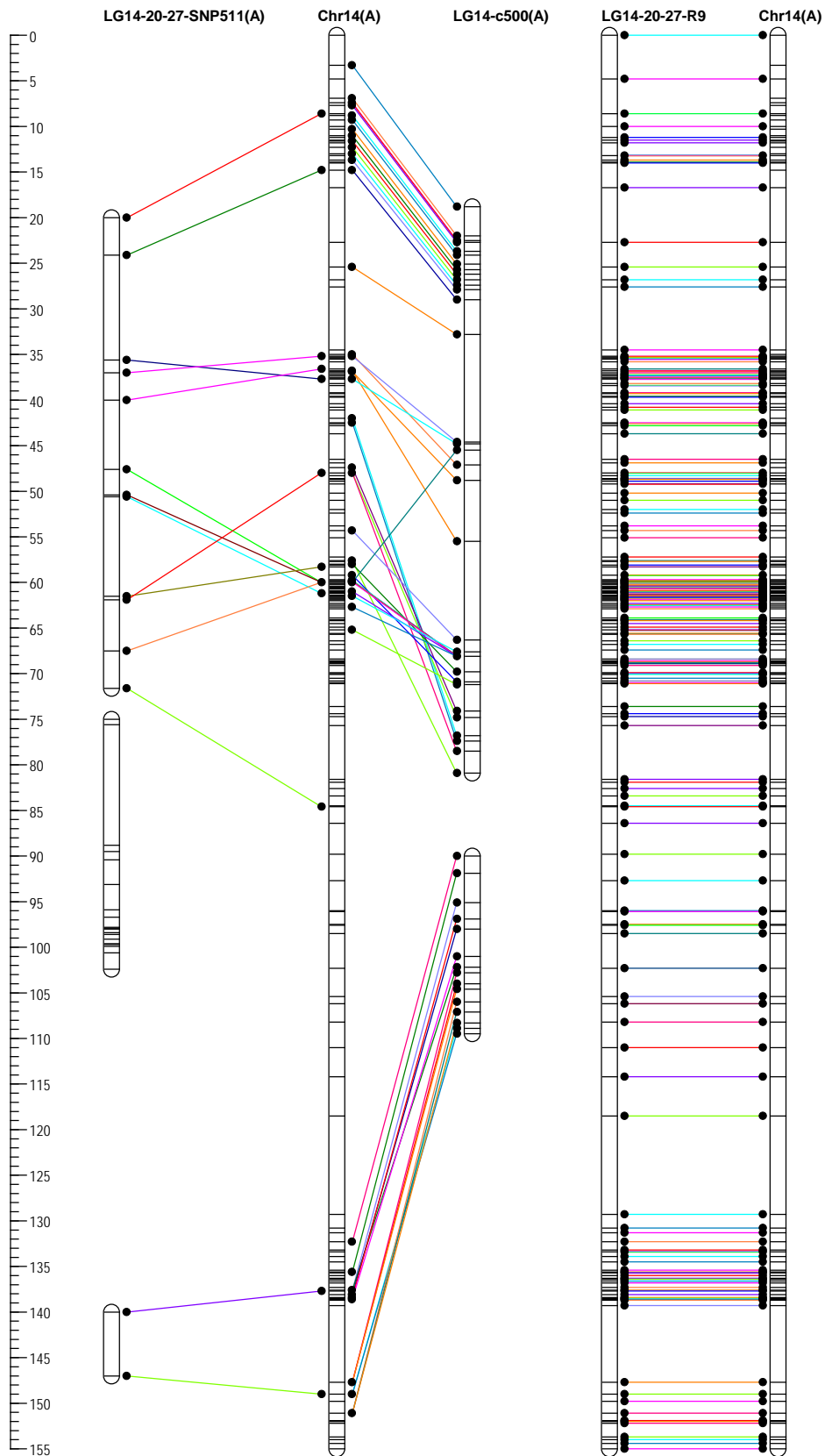


**Chr13:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions.

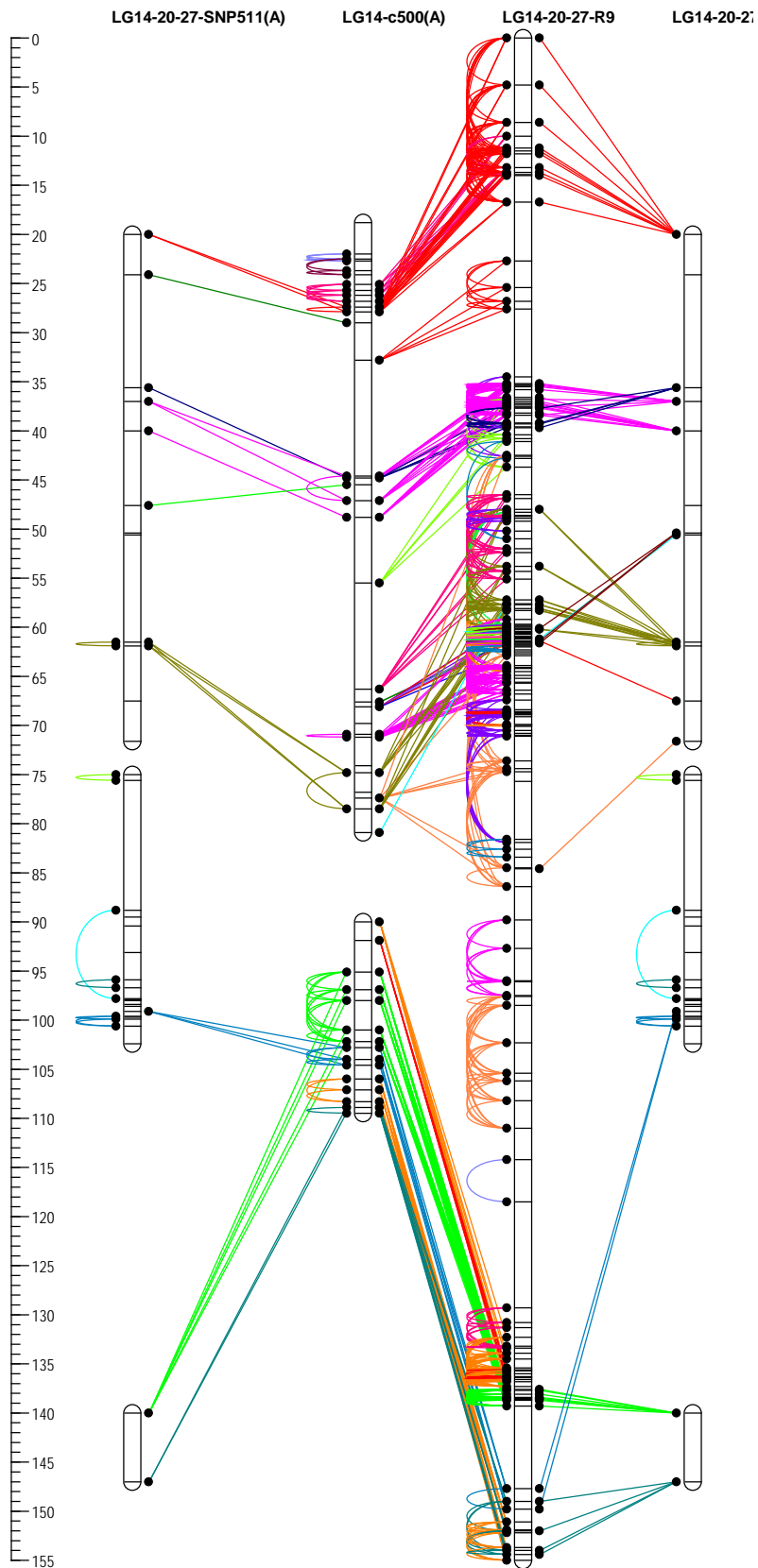


**Chr13:** Links between markers in the genetic maps of the three segregating populations within the scaffold of the assembly showing the concordance of order of scaffold positions. Distal end of LG13-R is located on LG8-SNP511; this might be a Chromosomal translocation. In the integrated map this has been placed in Chr08, because there is a link of this distal to LG08-R and also a strong link in LG8-SNP511.

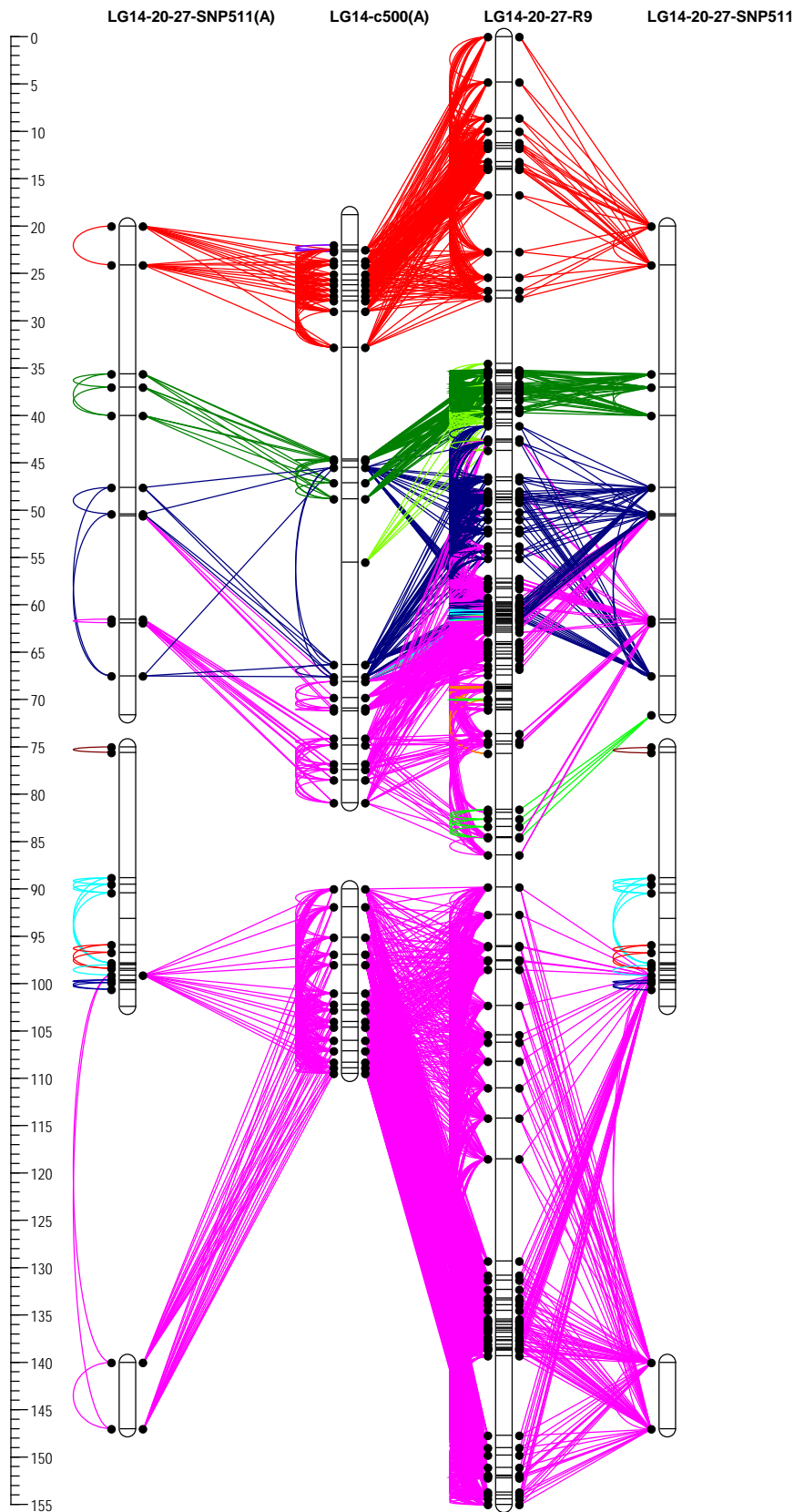




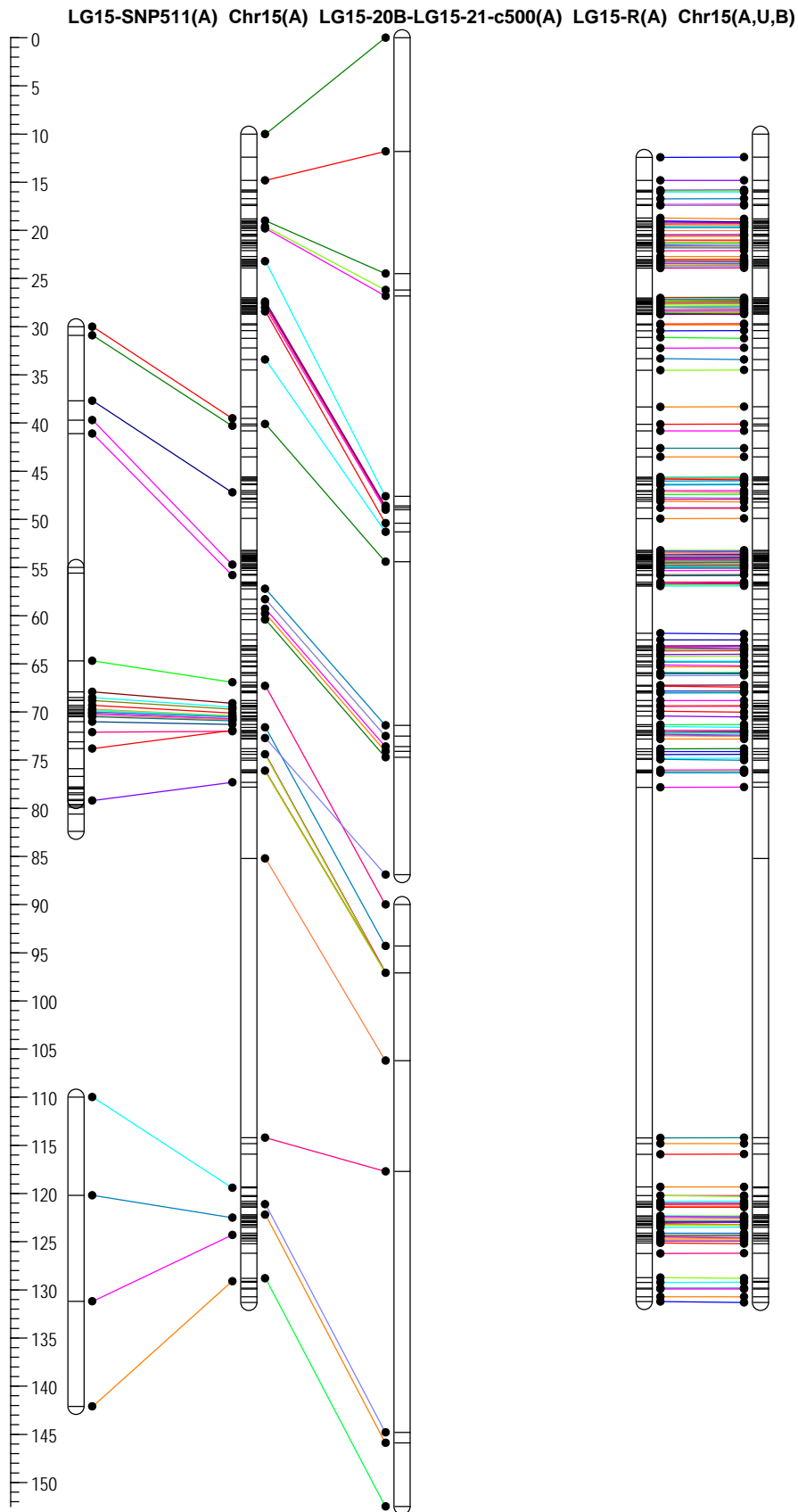
**Chr14:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



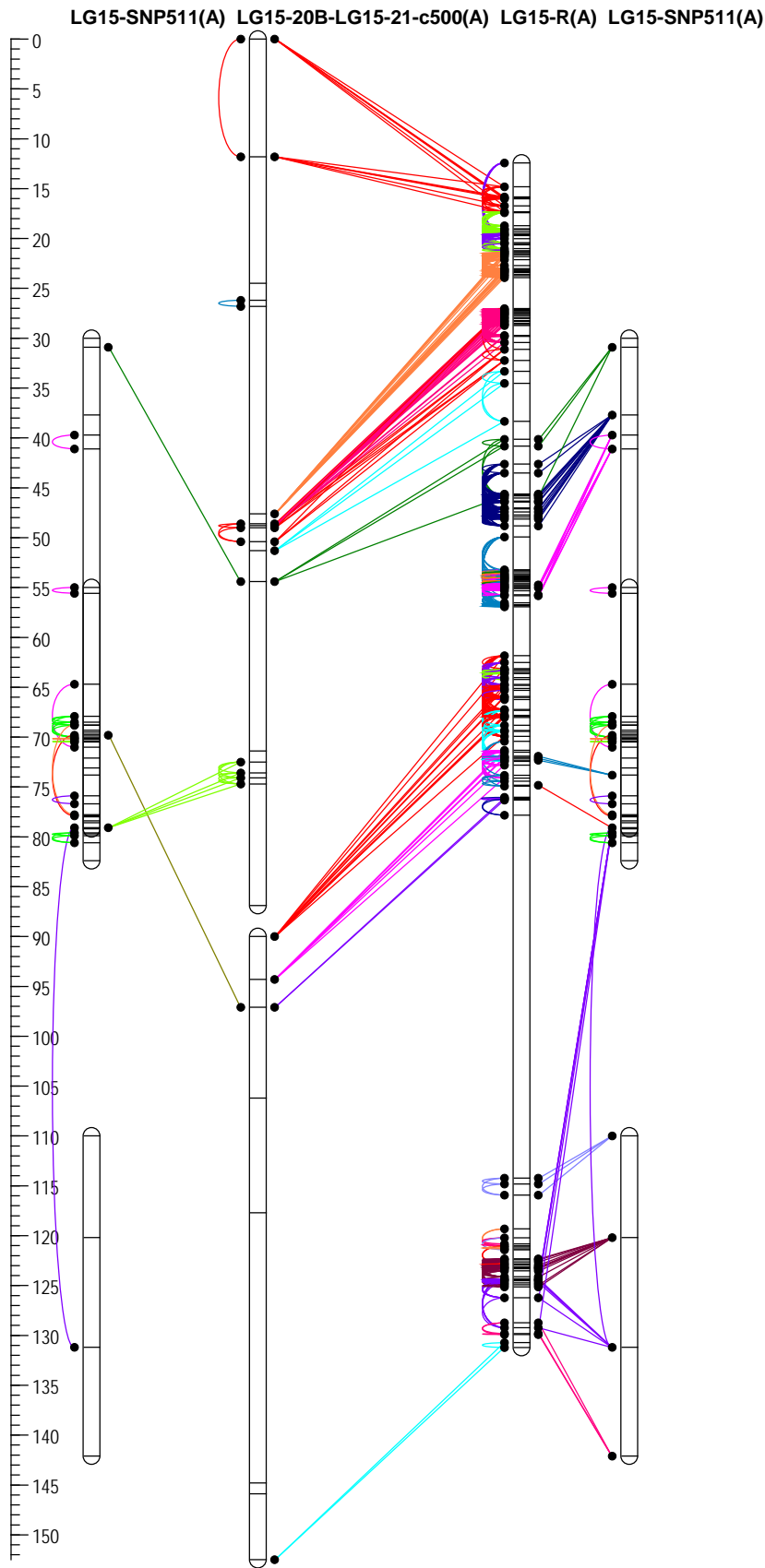
**Chr14:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions.



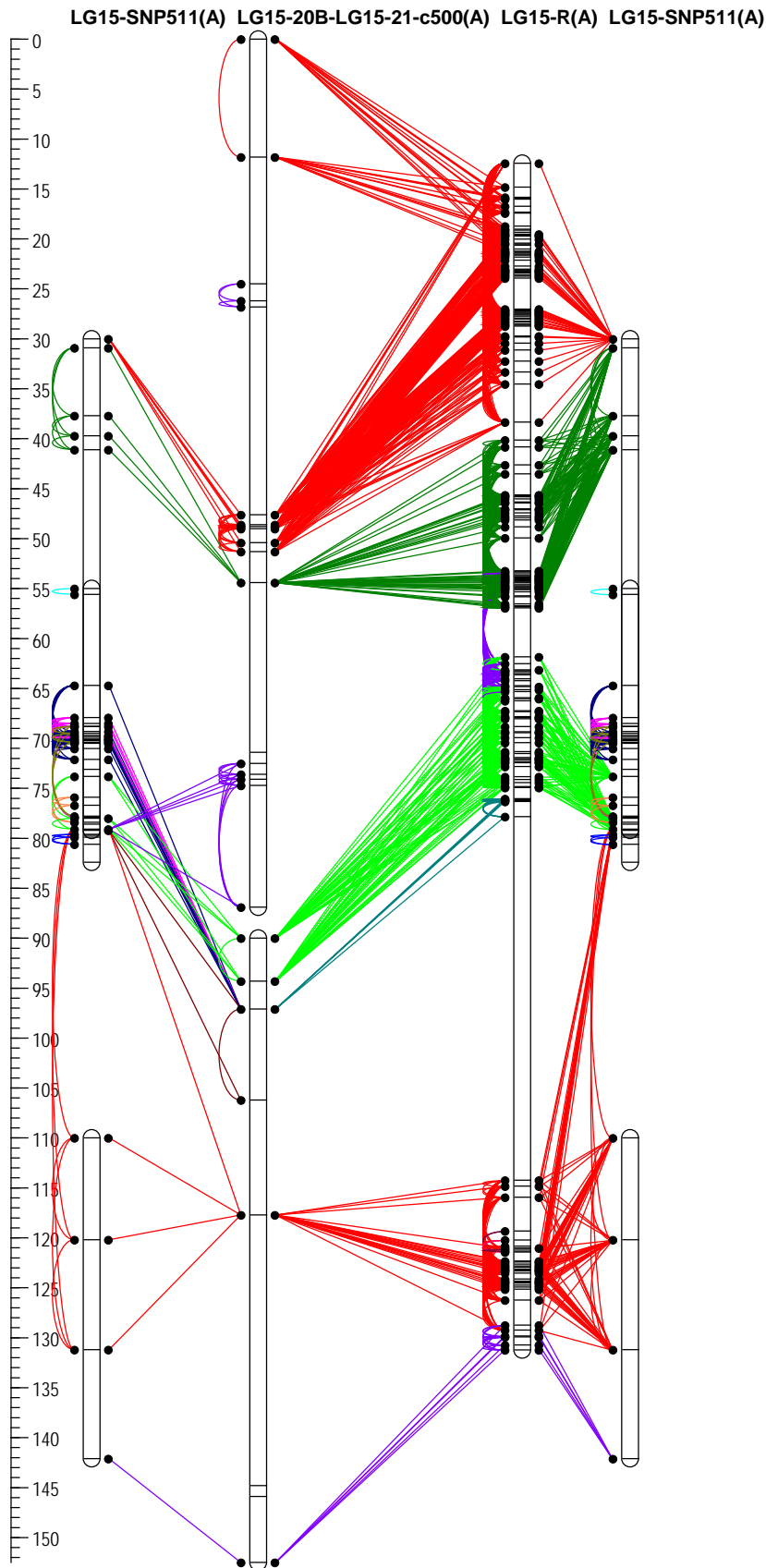
**Chr14:** Links between markers in the genetic maps of the three segregating populations within the scaffold of the assembly showing the concordance of order of scaffold positions.



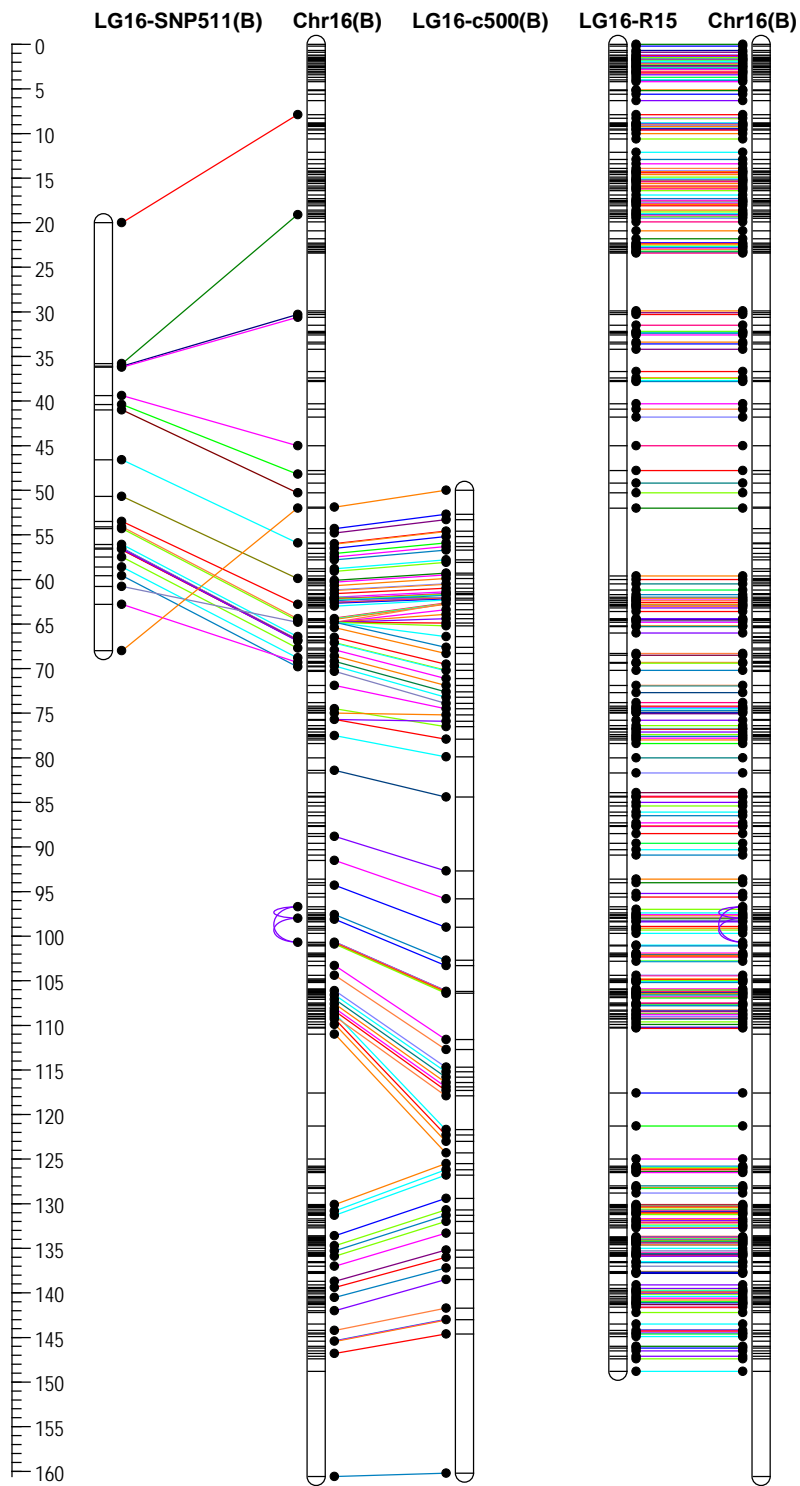
**Chr15:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



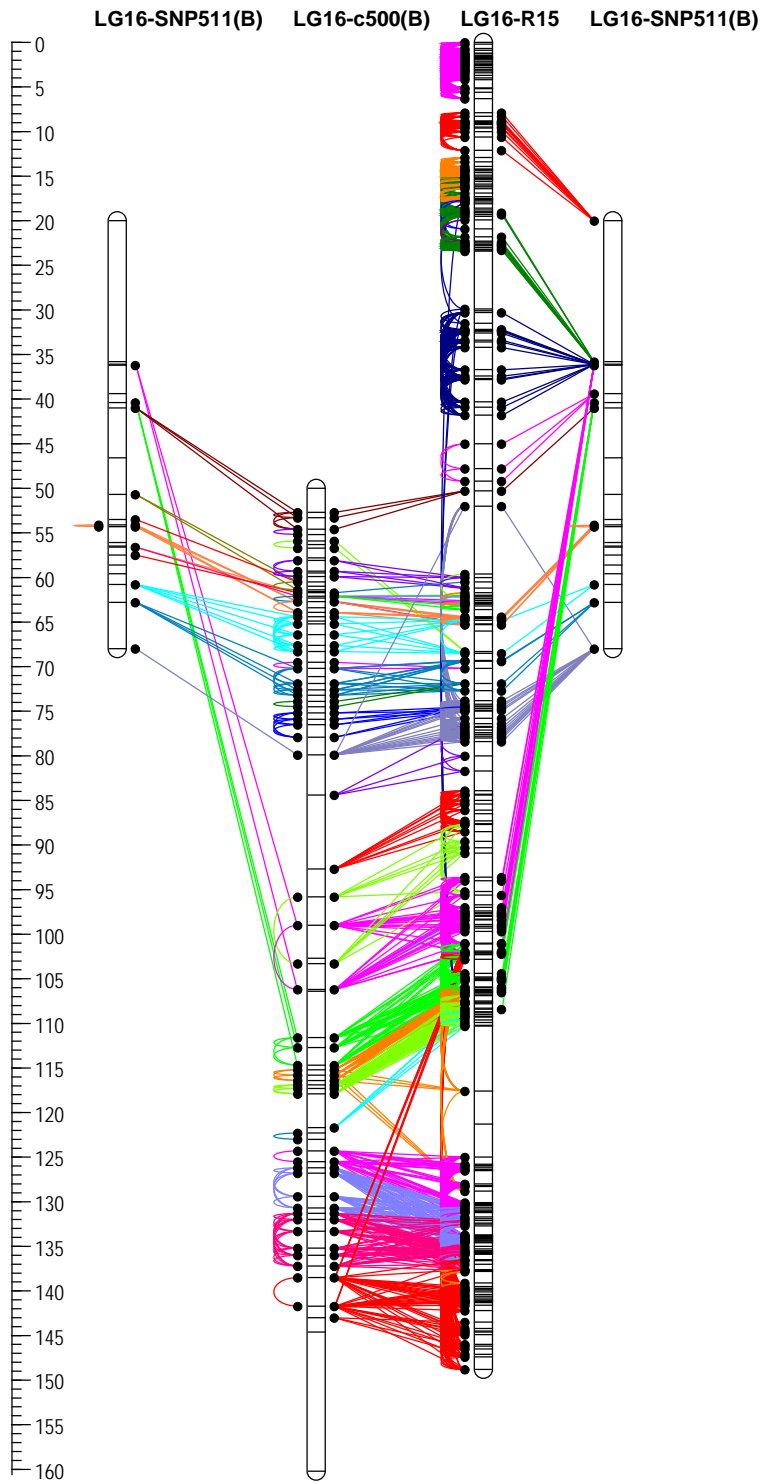
**Chr15:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions.



**Chr15:** Links between markers in the genetic maps of the three segregating populations within the scaffold of the assembly showing the concordance of order of scaffold positions.

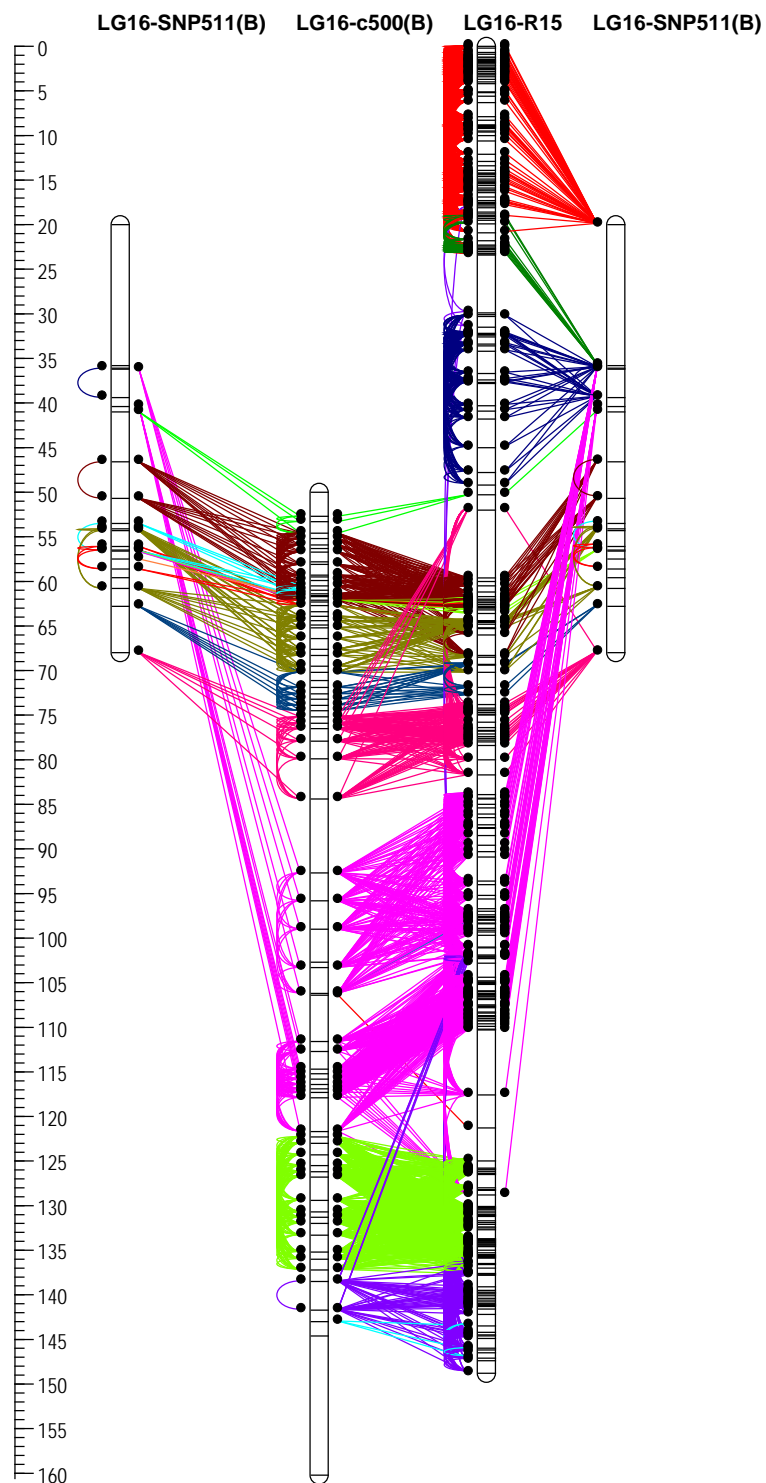


**Chr16:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.

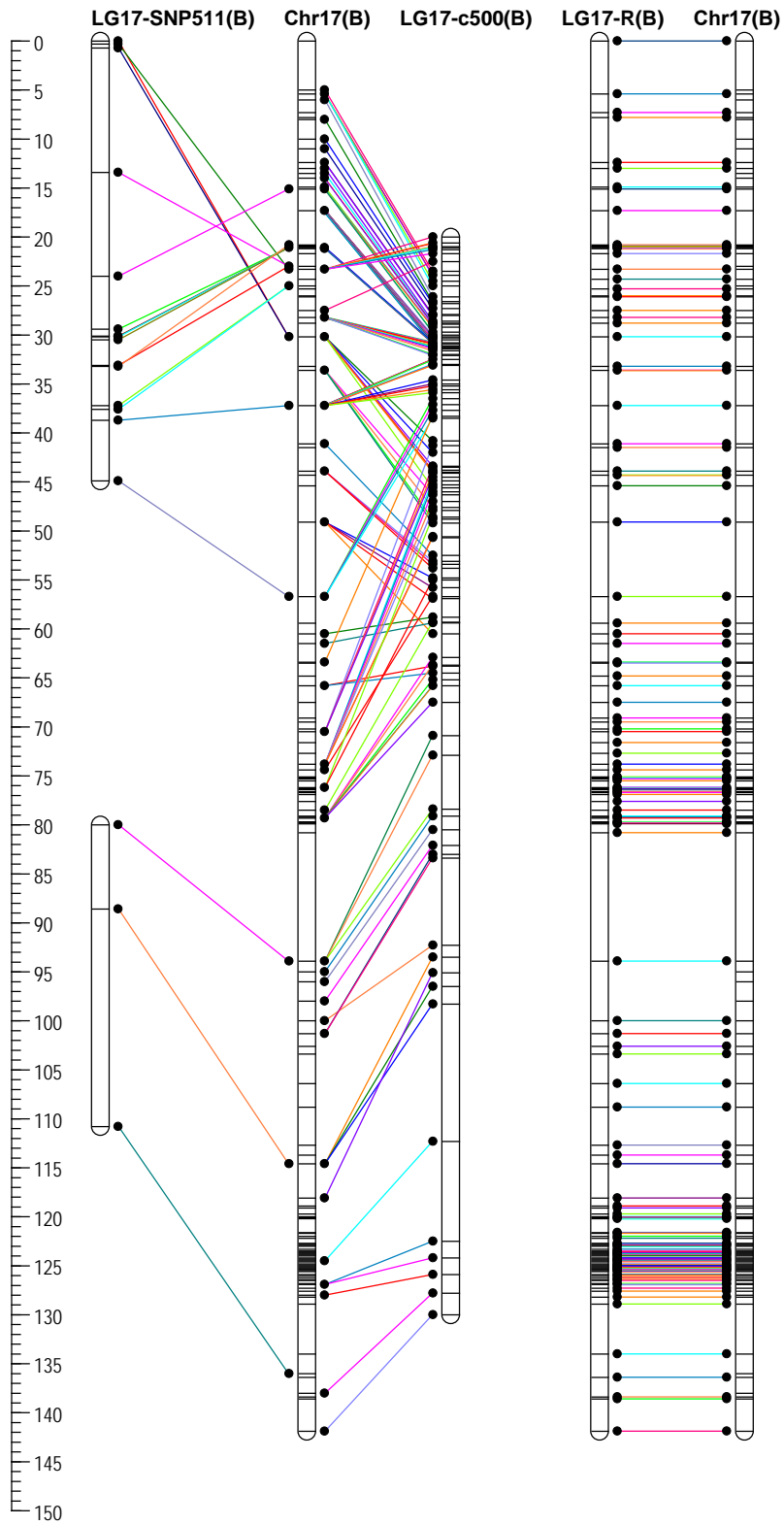


**Chr16:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions.

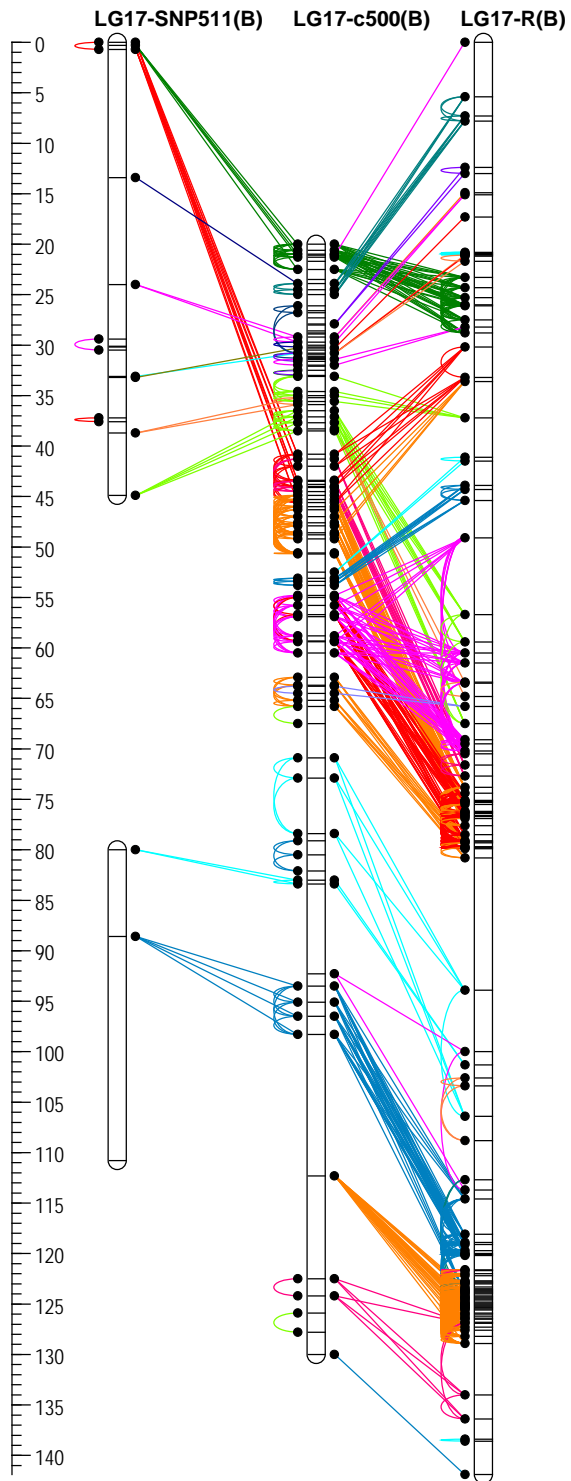




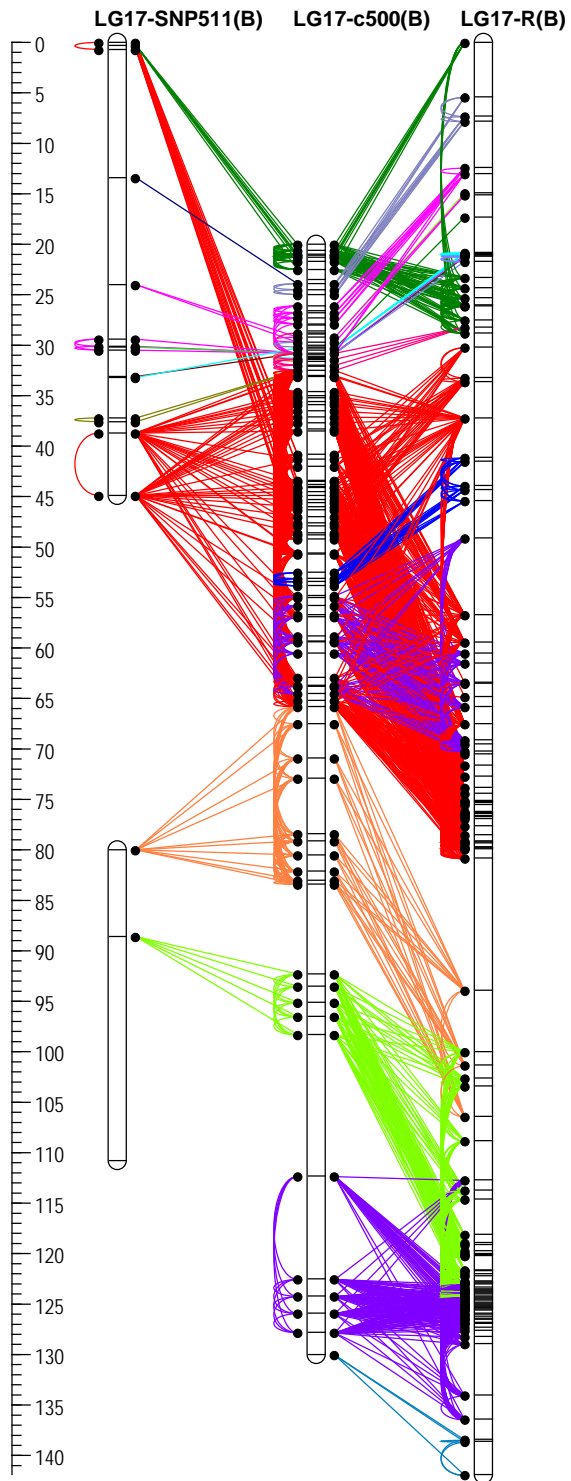
**Chr16:** Links between markers in the genetic maps of the three segregating populations within the scaffold of the assembly showing the concordance of order of scaffold positions.



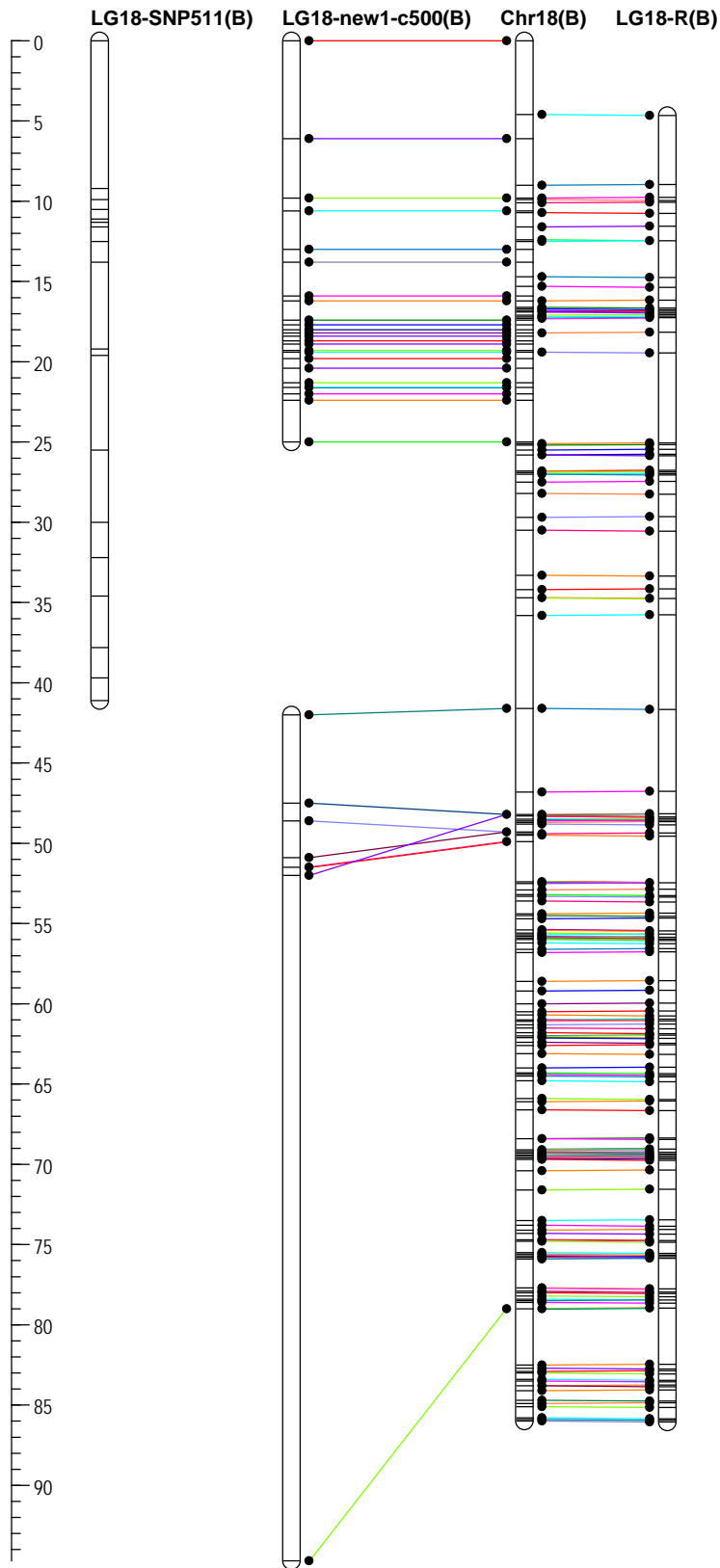
**Chr17:** Links at identity level between the genetic maps of the three segregating populations and the integrated map



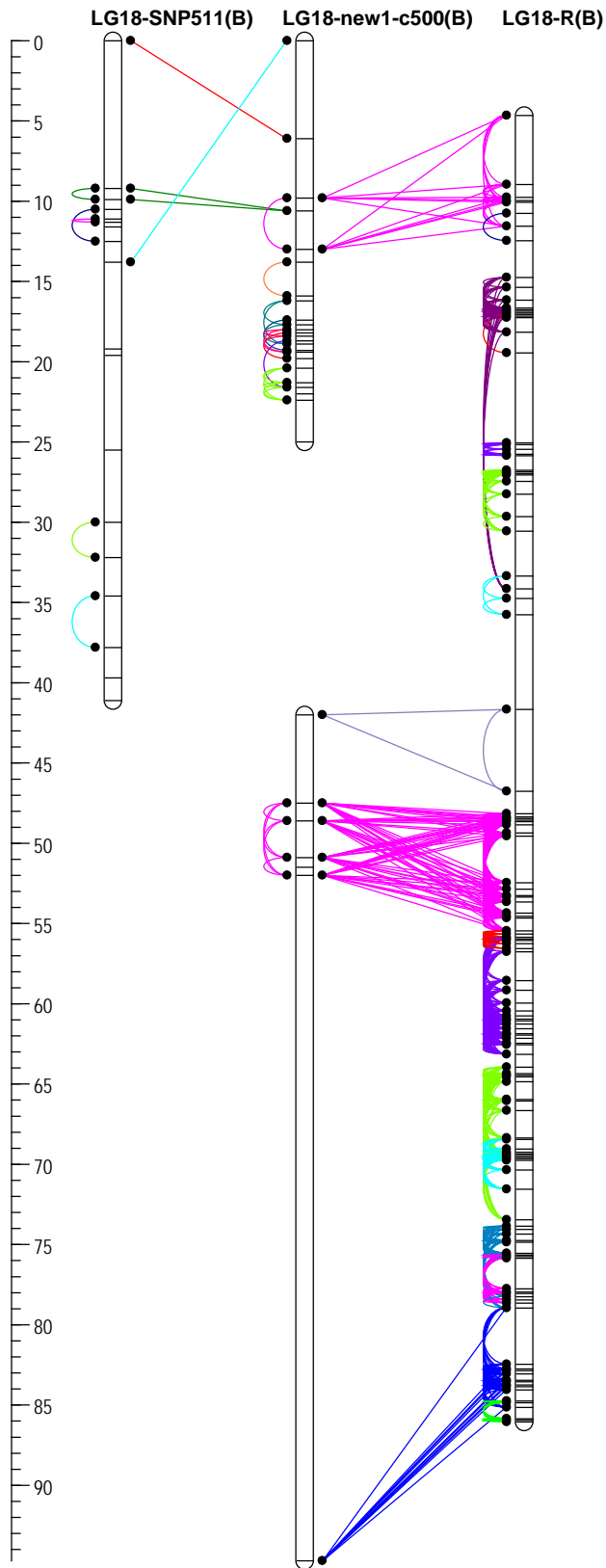
**Chr17:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions.



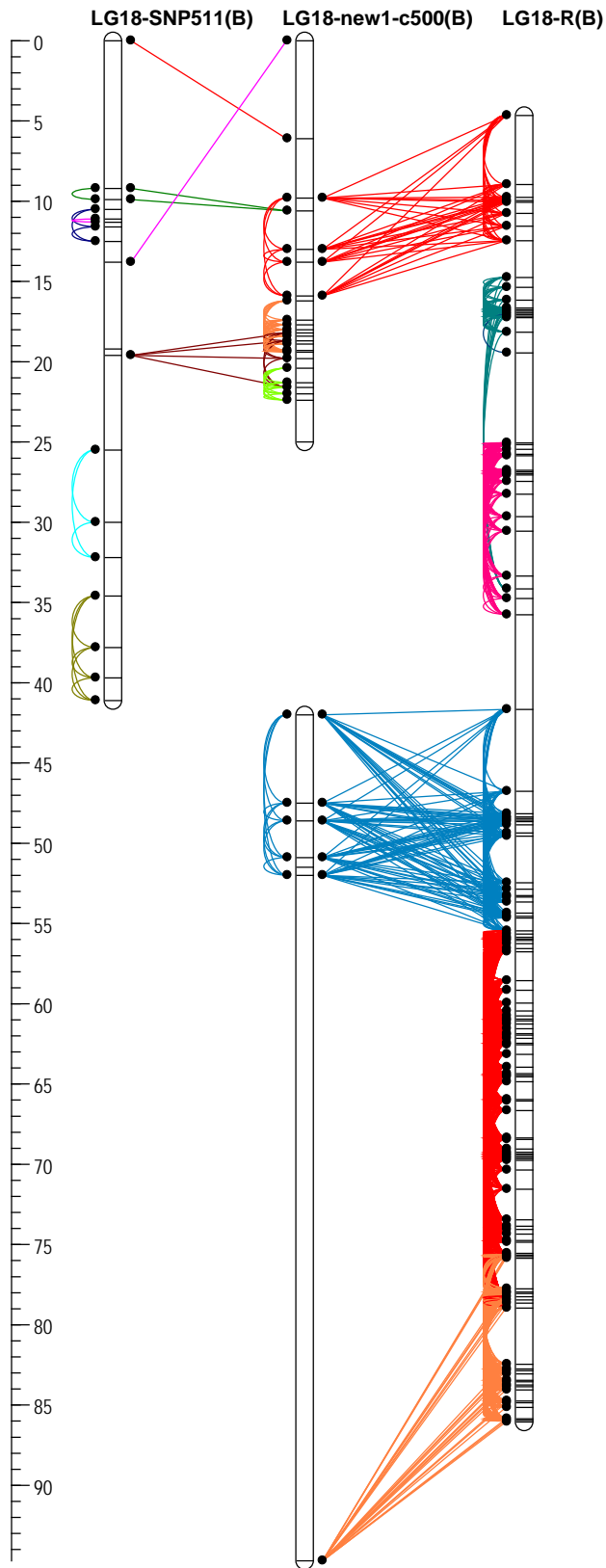
**Chr17:** Links between markers in the genetic maps of the three segregating populations within the scaffold of the assembly showing the concordance of order of scaffold positions.



**Chr18:** Links at identity level between the genetic maps of the three segregating populations and the integrated map.



**Chr18:** Links between markers in the genetic maps of the three segregating populations within the same 1 Mb bin (0-999,999 nt and so on) showing the concordance of order of marker positions.



**Chr18:** Links between markers in the genetic maps of the three segregating populations within the scaffold of the assembly showing the concordance of order of scaffold positions.