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.
Chromosome 7: 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 RNAsec-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.