

Applying genotypic principal component scores as latent phenotypes in genome-wide and epistatic analyses of soybean agronomic traits.

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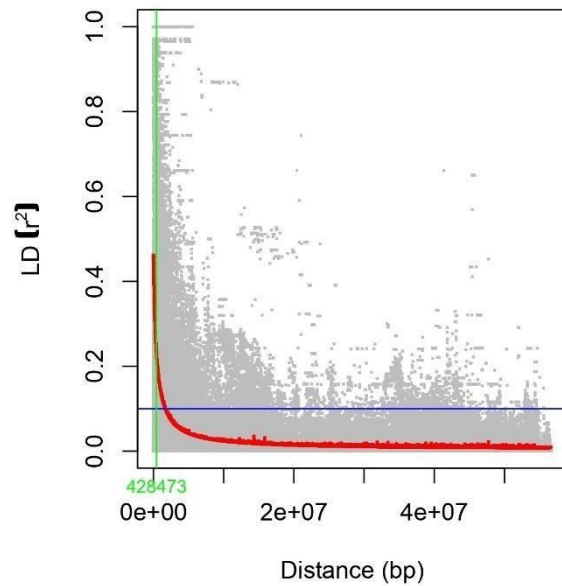
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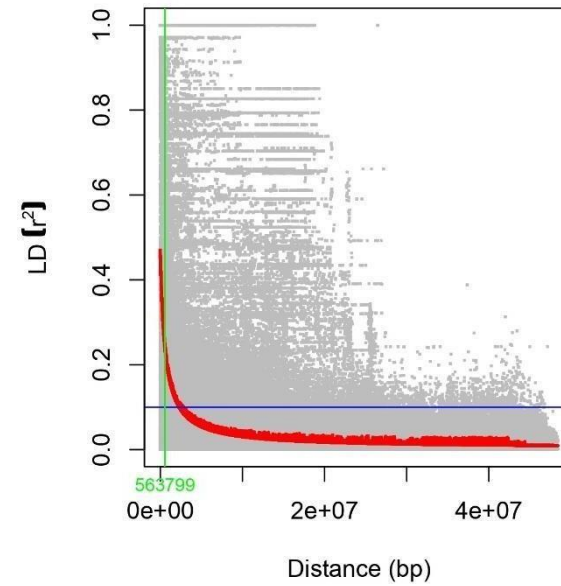
Elroy Cober, elroy.cober@agr.gc.ca

† co-first authors

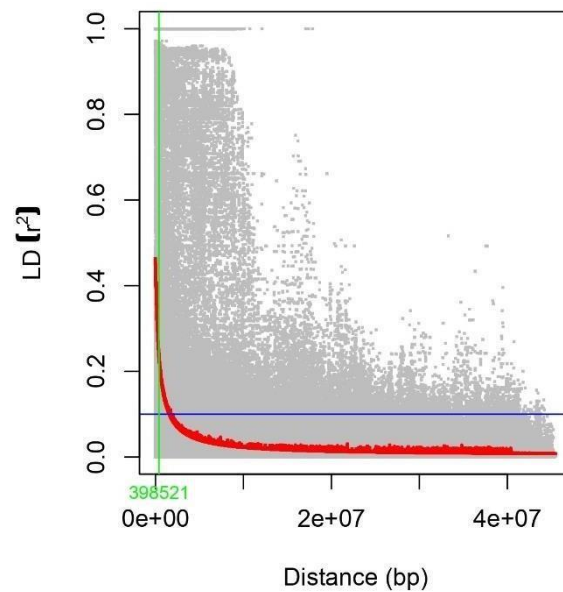
a. Gm 1



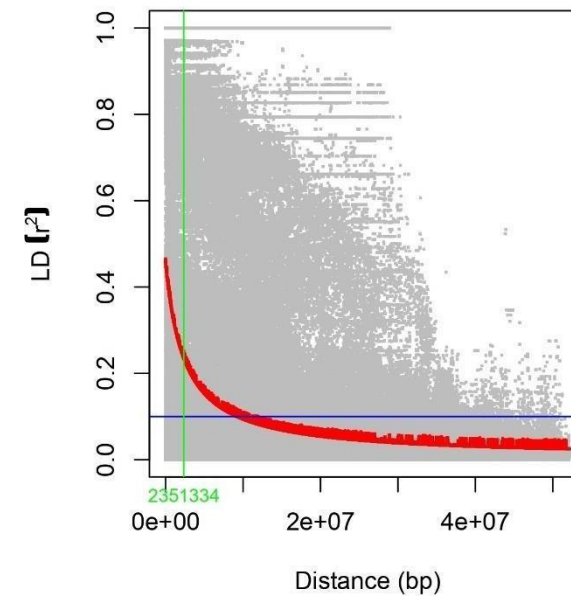
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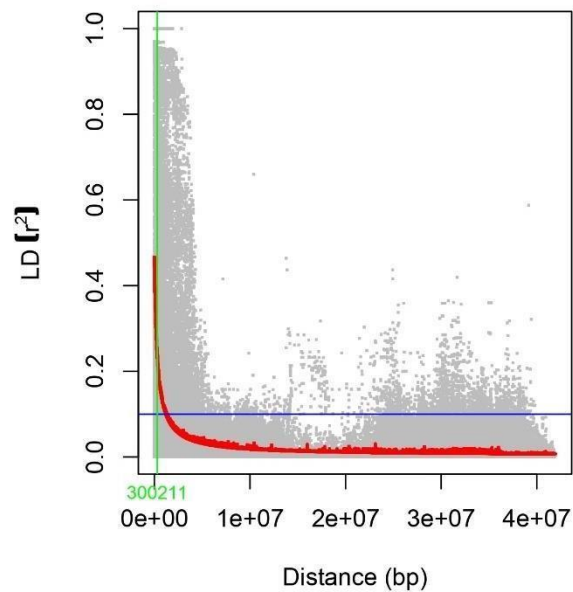
c. Gm 3



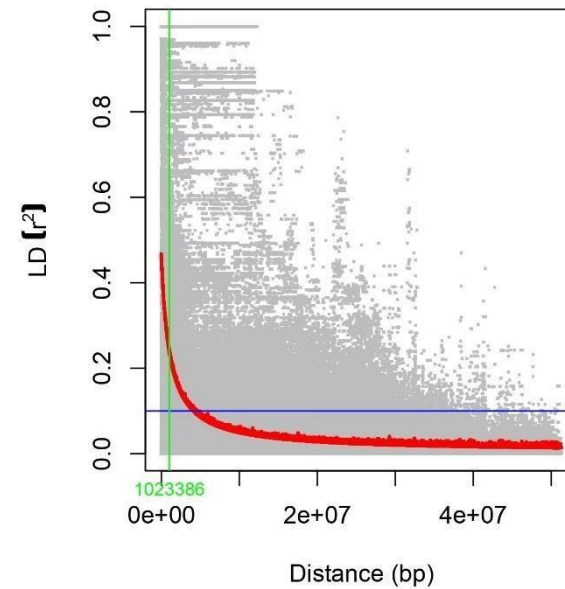
d. Gm 4



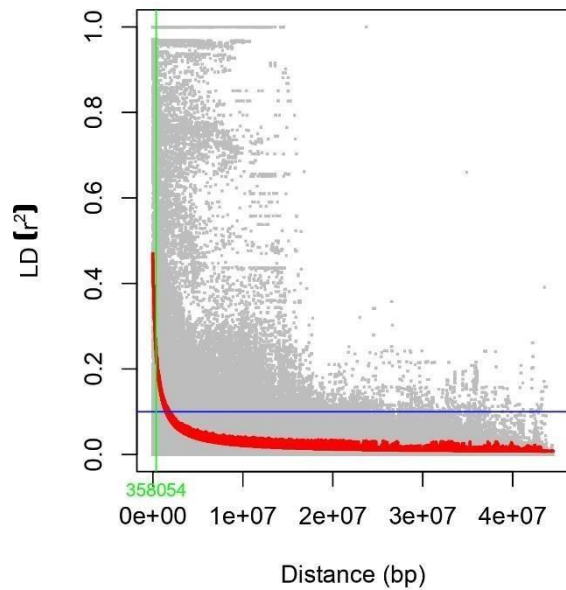
e. Gm 5



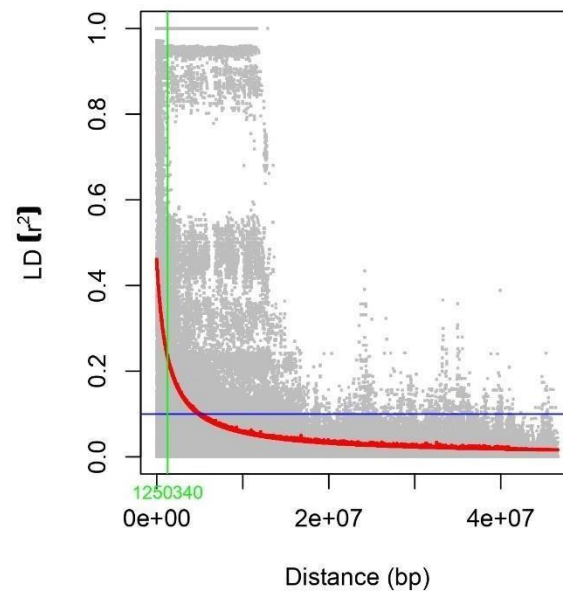
f. Gm 6



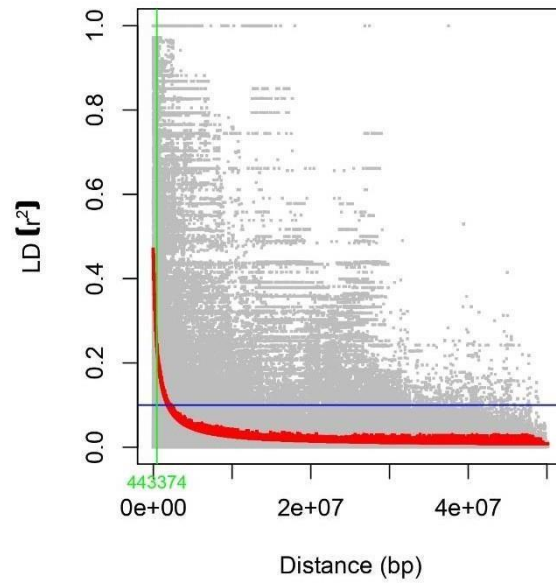
g. Gm 7



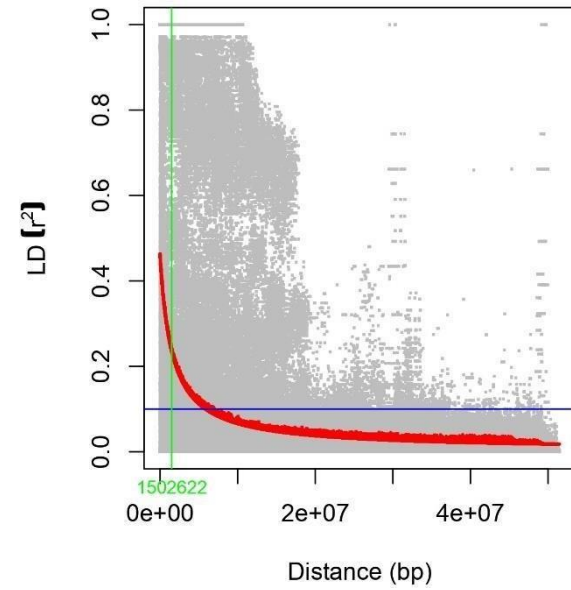
h. Gm 8



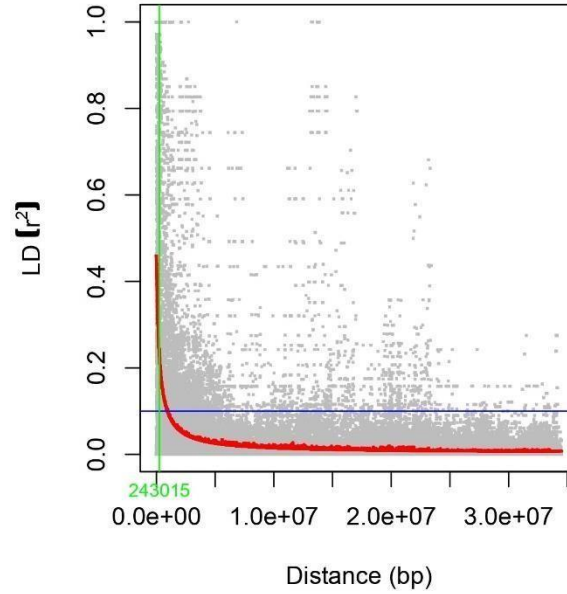
i. Gm 9



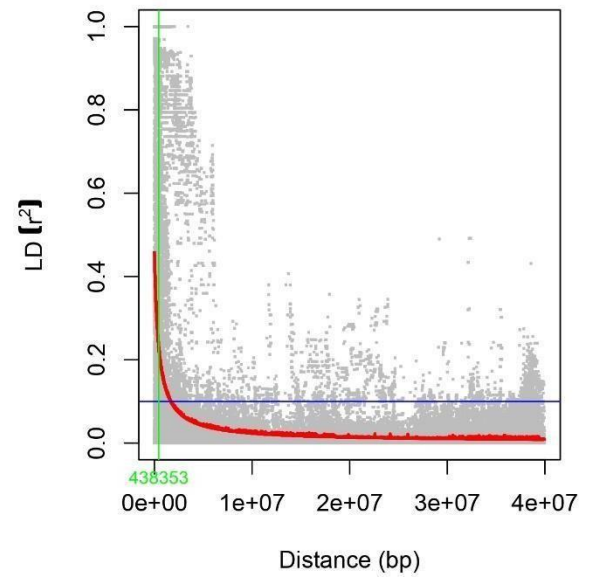
j. Gm 10



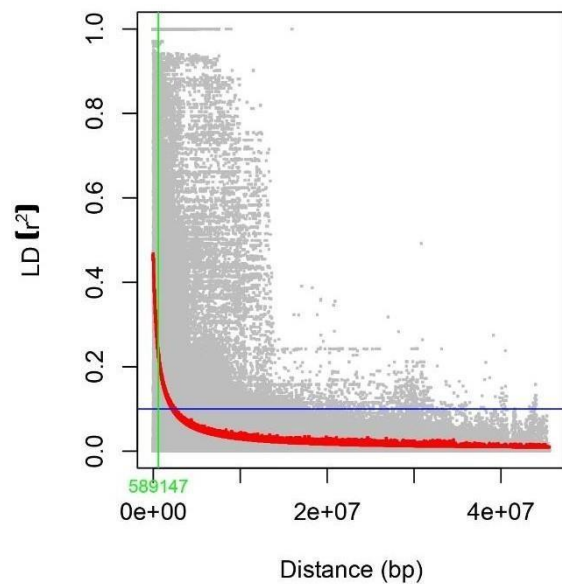
k. Gm 11



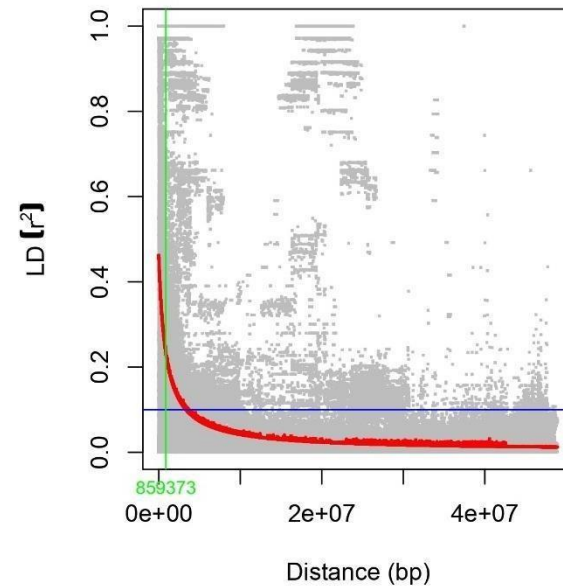
l. Gm 12



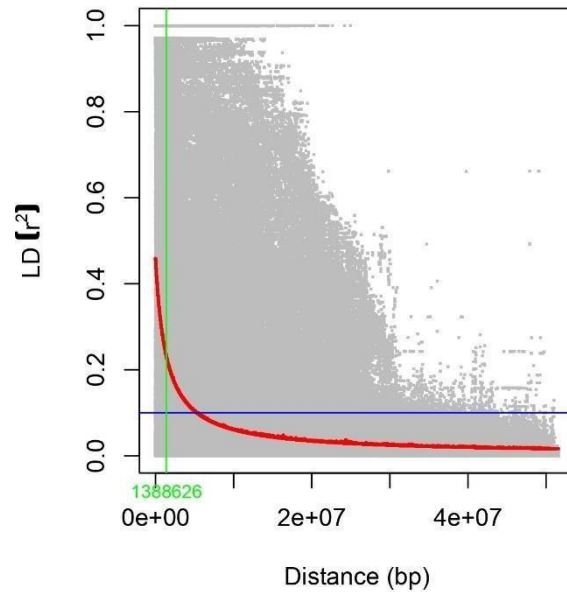
m. Gm 13



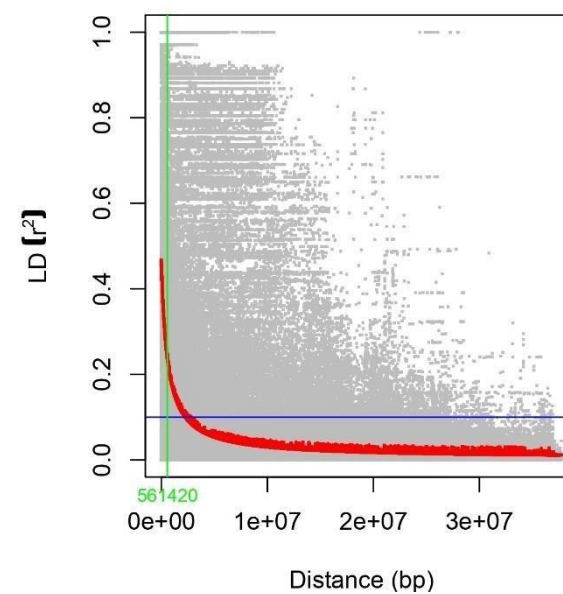
n. Gm 14



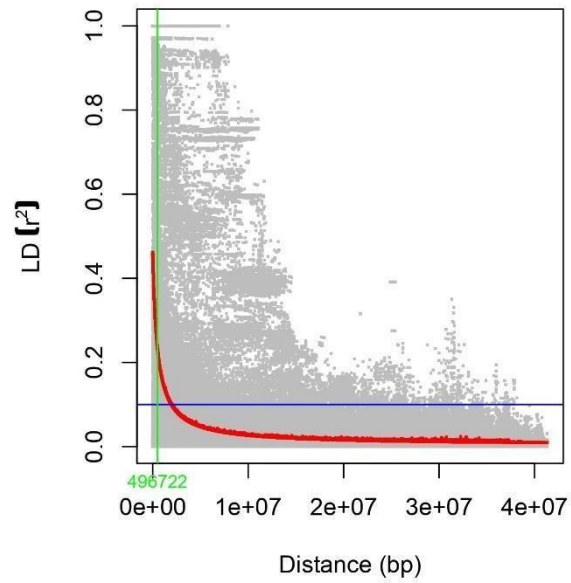
o. Gm 15



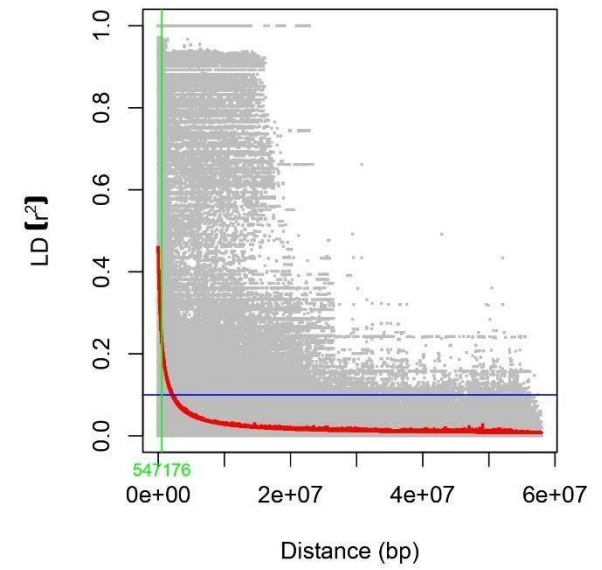
p. Gm 16



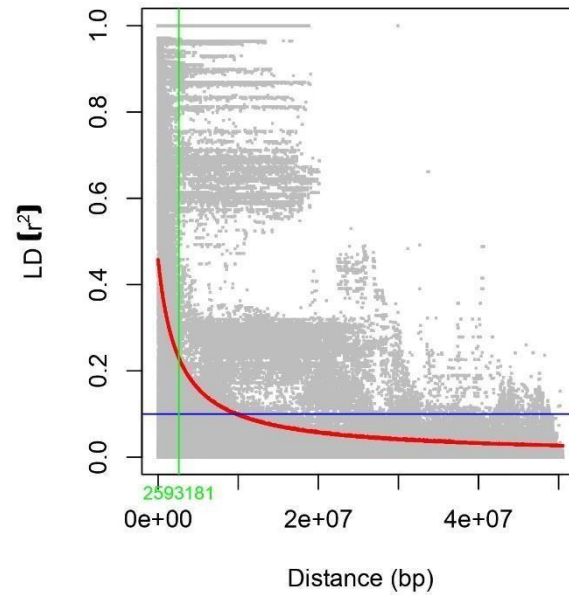
q. Gm 17



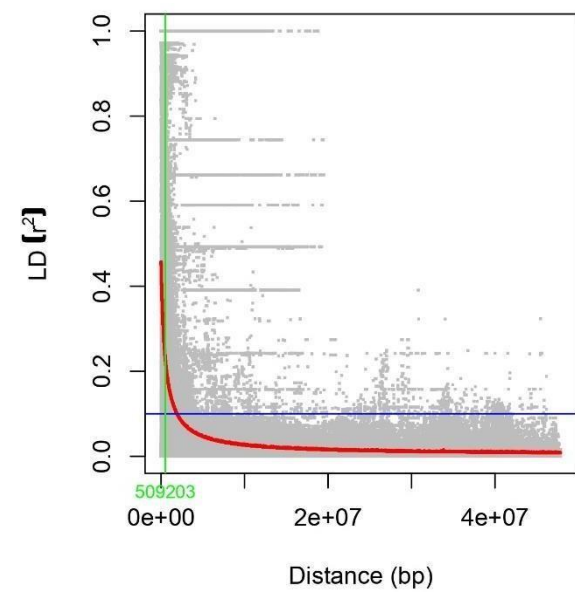
r. Gm 18



s. Gm 19



t. Gm 20



Supplementary Fig. S3 Linkage Disequilibrium plot of *G. max* chromosomes 1 – 20 (a – t respectively) showing linkage disequilibrium plotted against the distance between markers. Blue line indicated 0.1 LD, green line shows the half decay distance (HDD), and the red line shows the average LD as distance is increase