

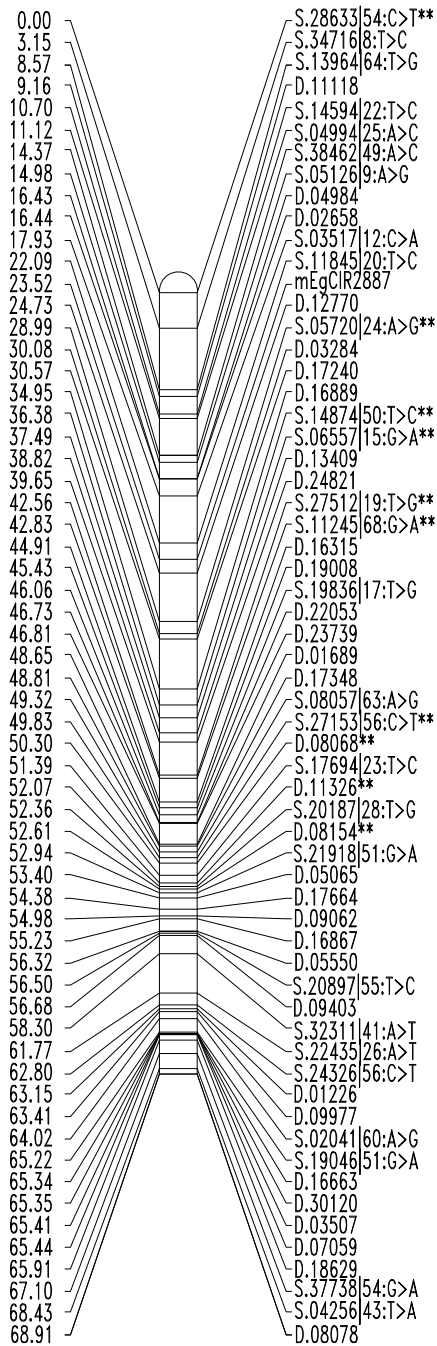
“High Density SNP and DArT-based Genetic Linkage Maps of Two Closely Related Oil Palm Populations”

Journal of Applied Genetics

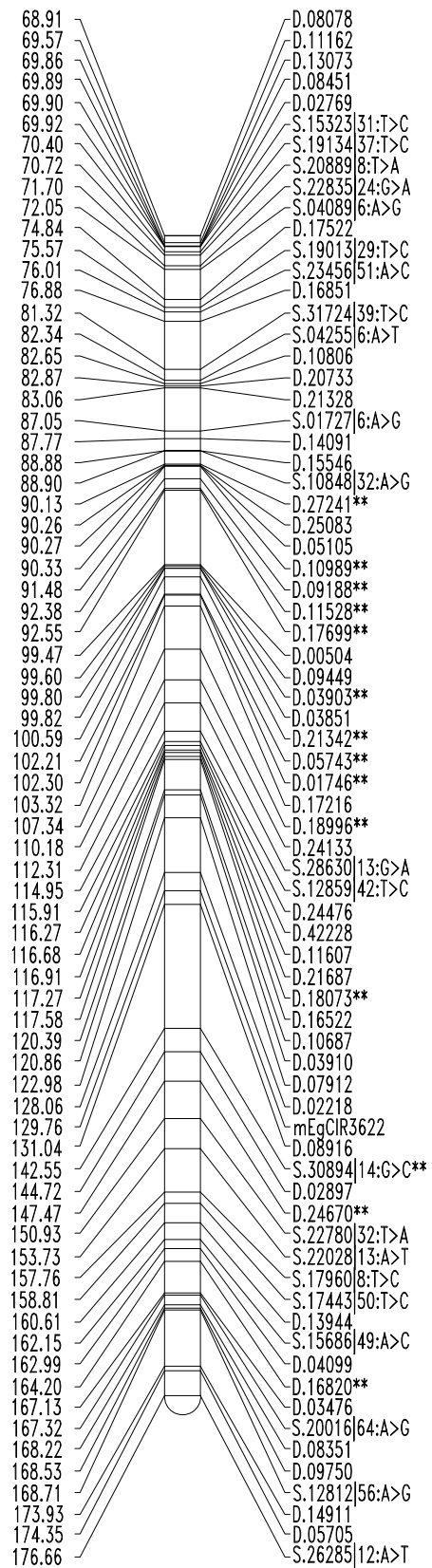
Siou Ting Gan, Wei Chee Wong, Choo Kien Wong, Aik Chin Soh, Andrzej Kilian, Eng-Ti Leslie Low, Festo Massawe and Sean Mayes

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Email address: ganst@aarsb.com.my

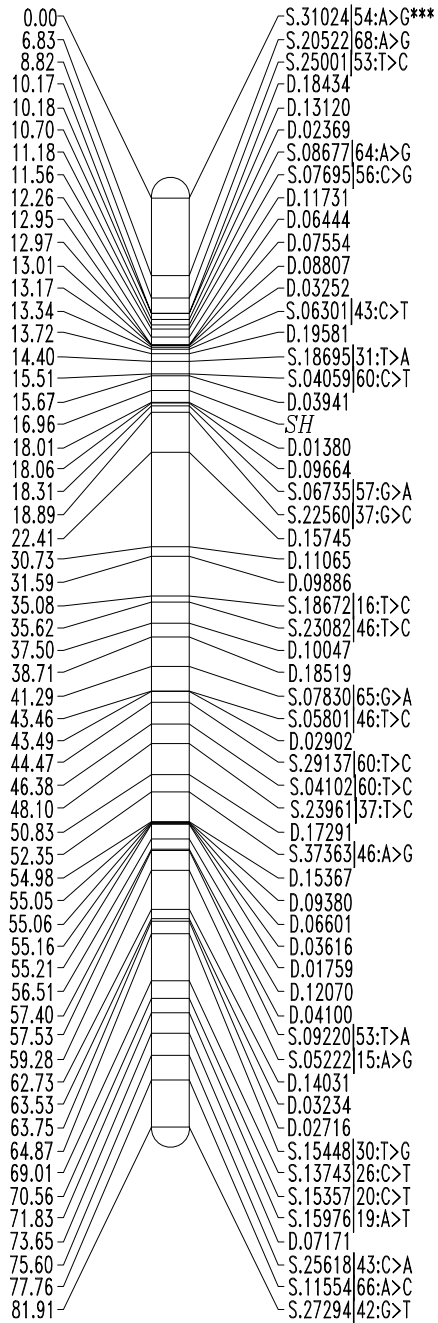
LG 1 (1)



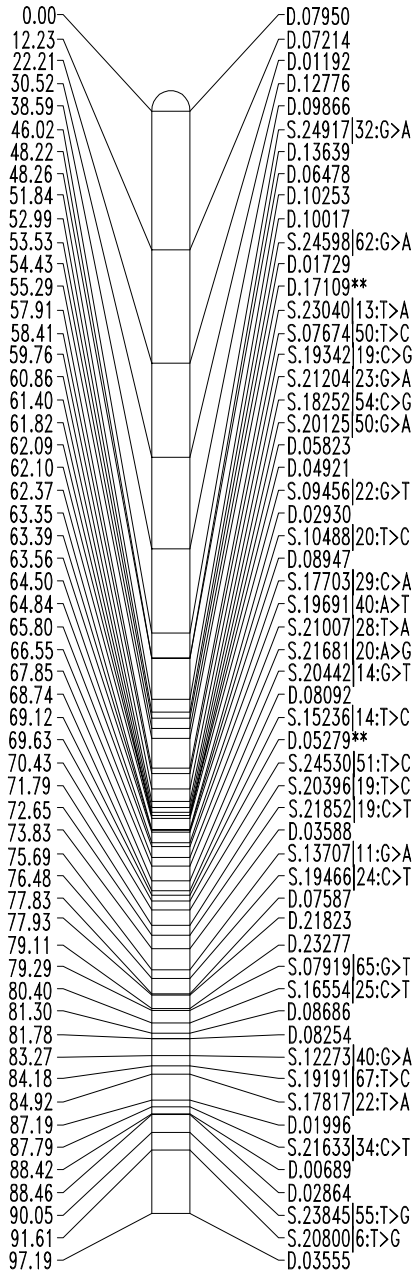
LG 1 (2)



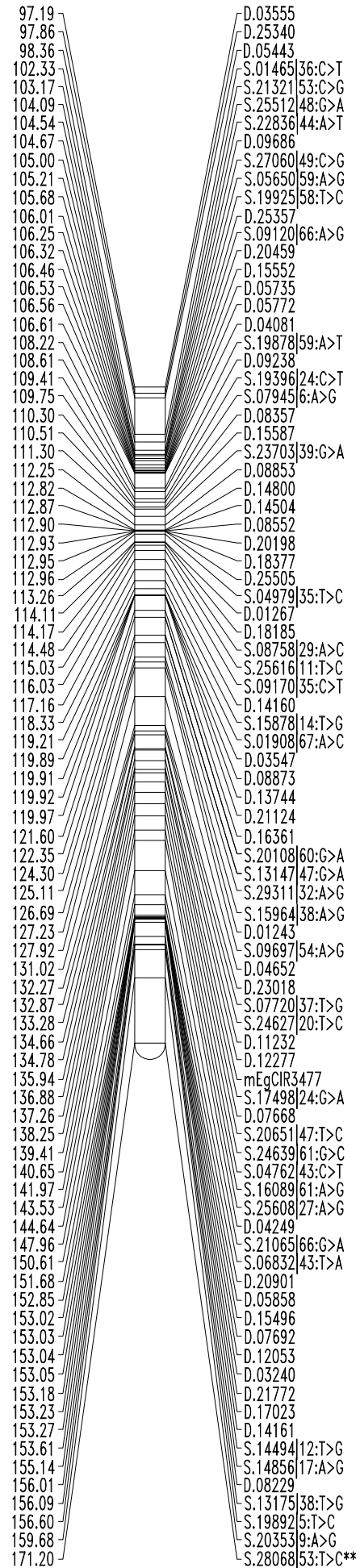
LG 2A



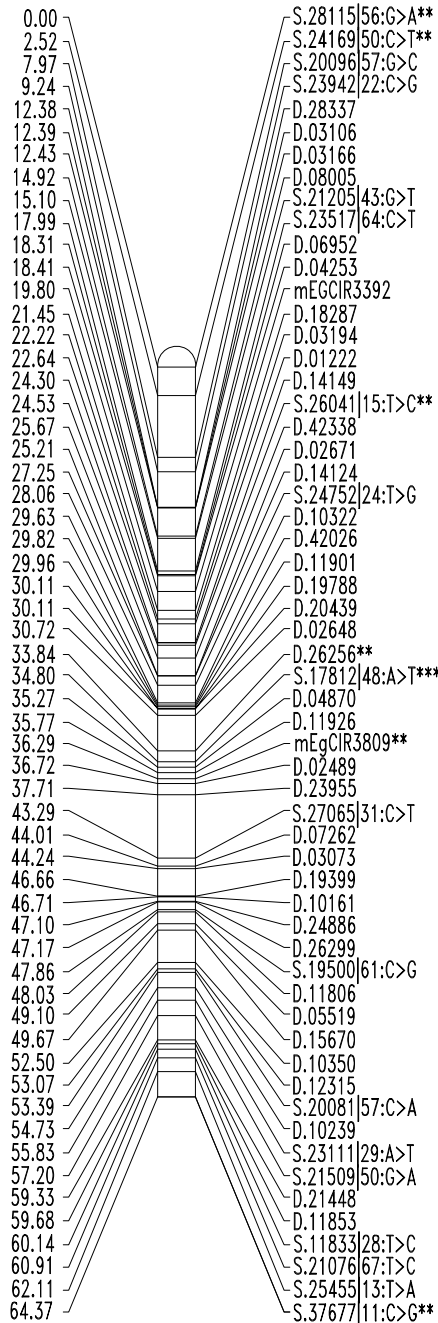
LG 2B (1)



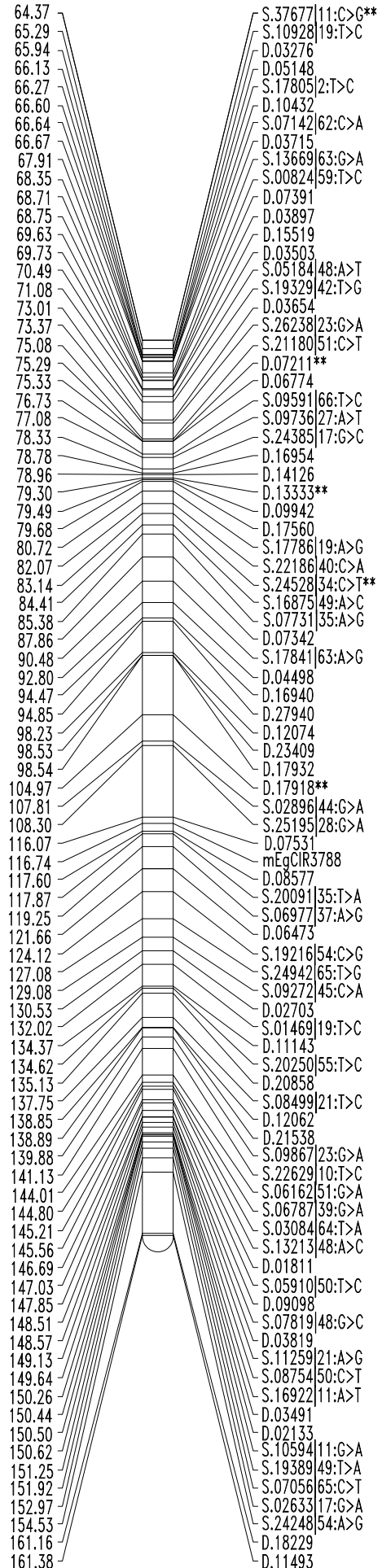
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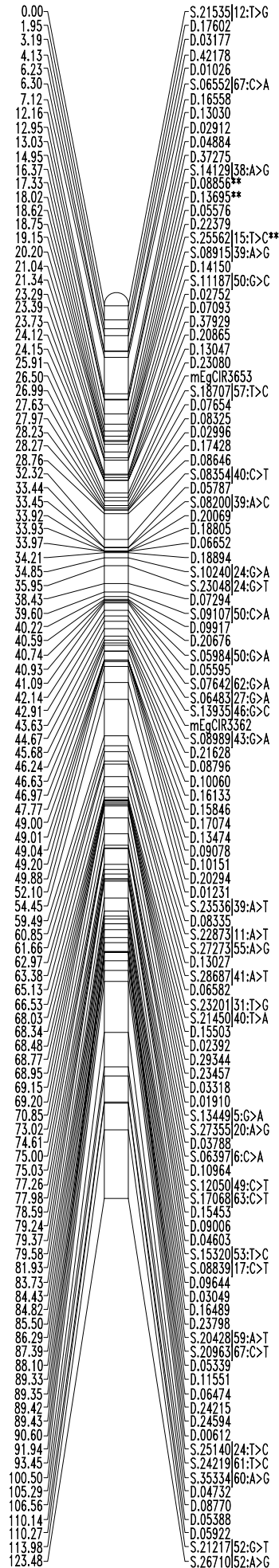
LG 3 (1)



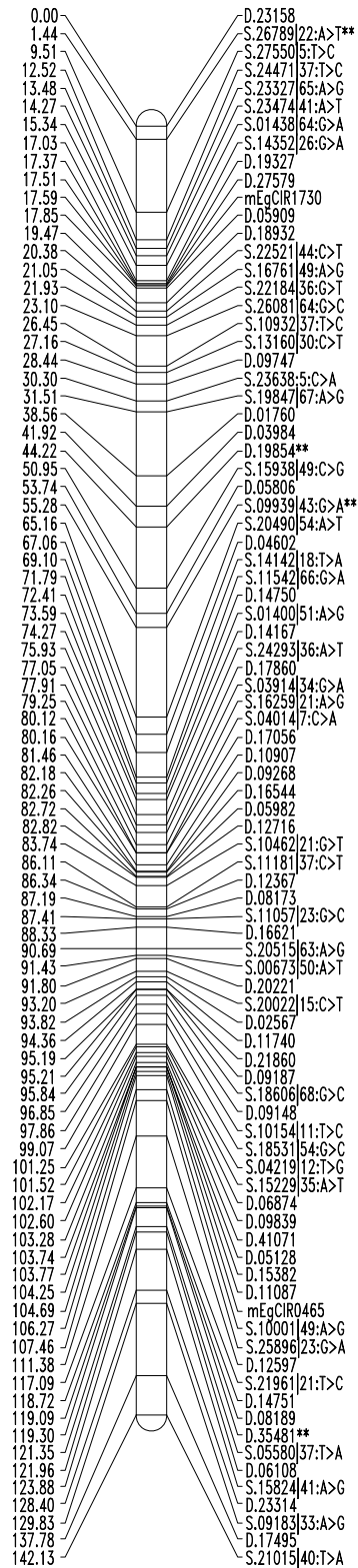
LG 3 (2)



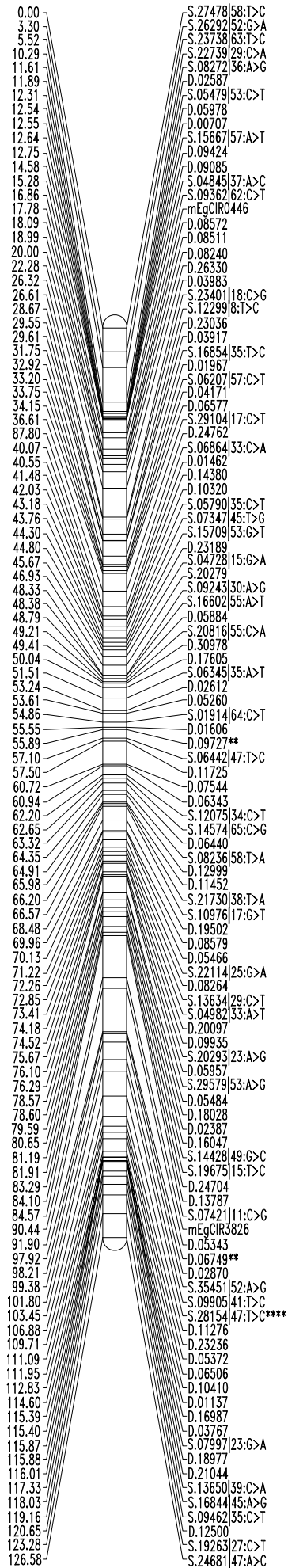
LG 4



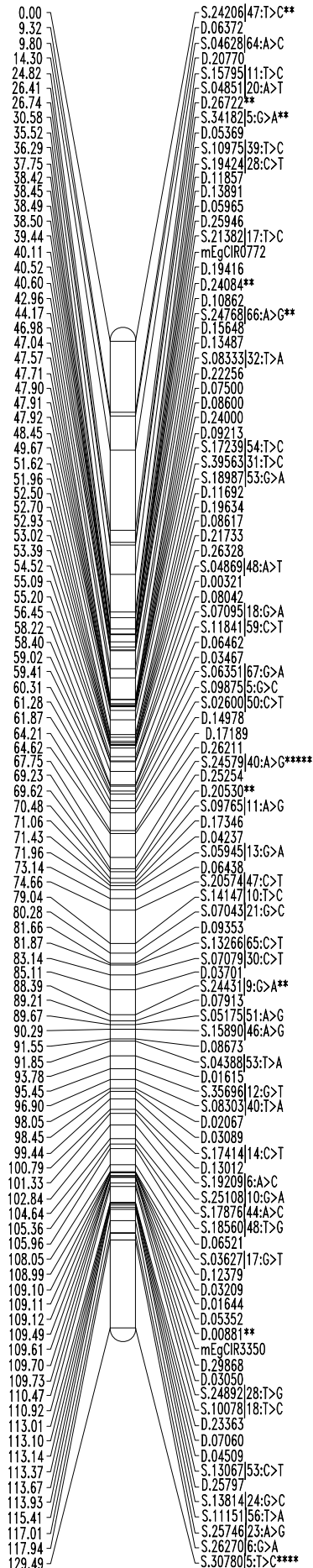
LG 5



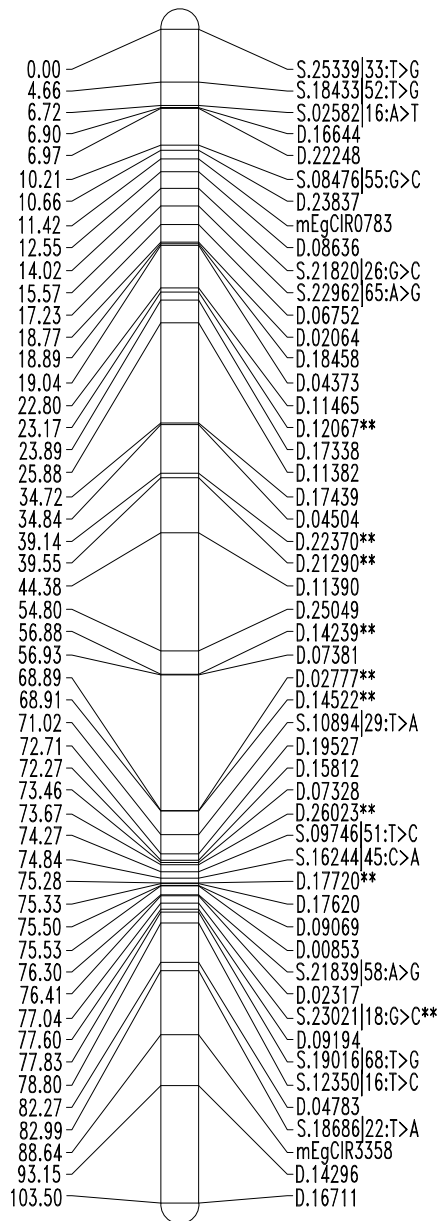
LG 6



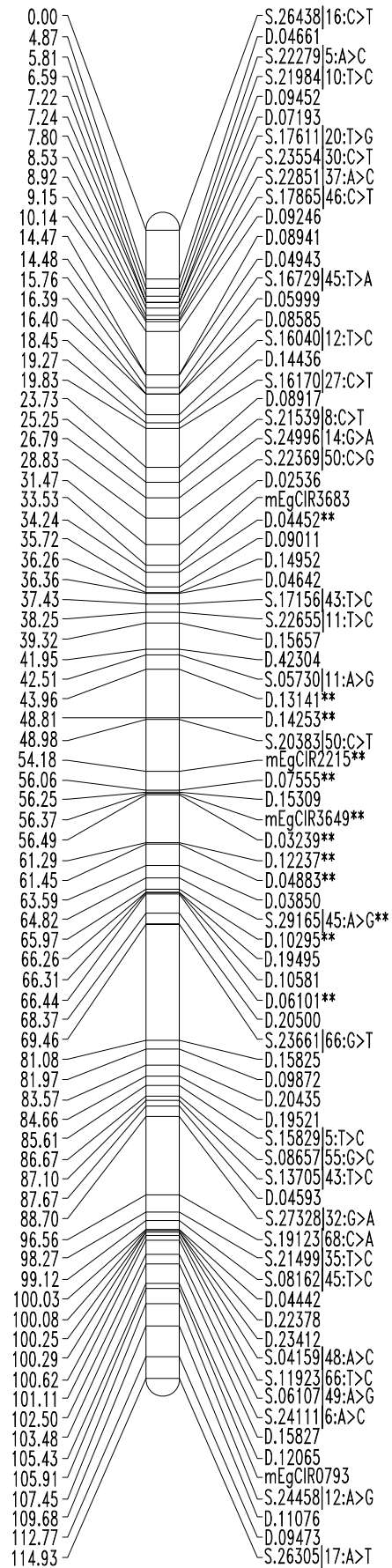
LG 11



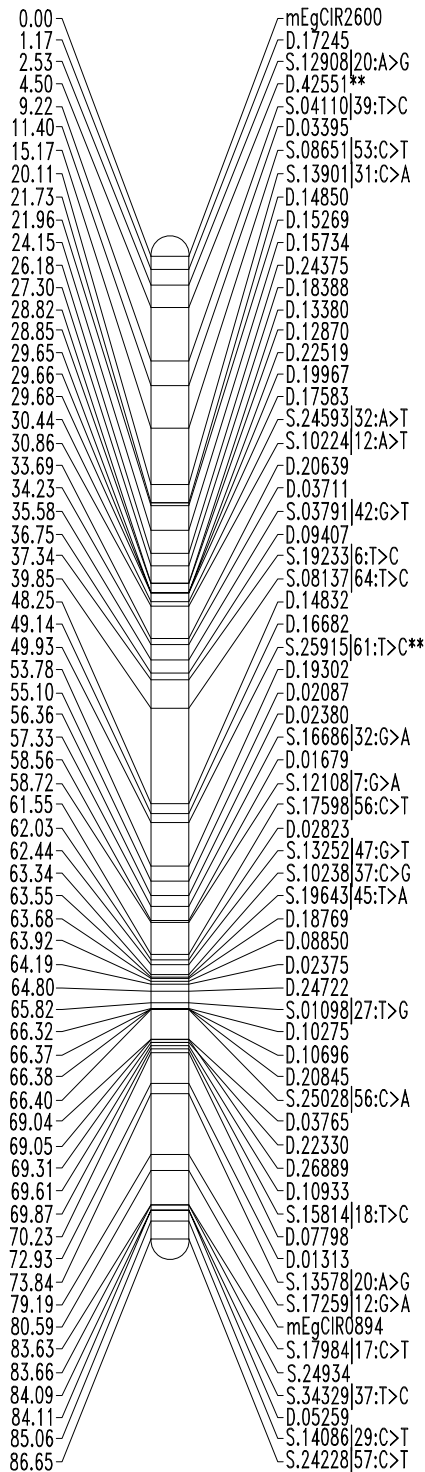
LG 7



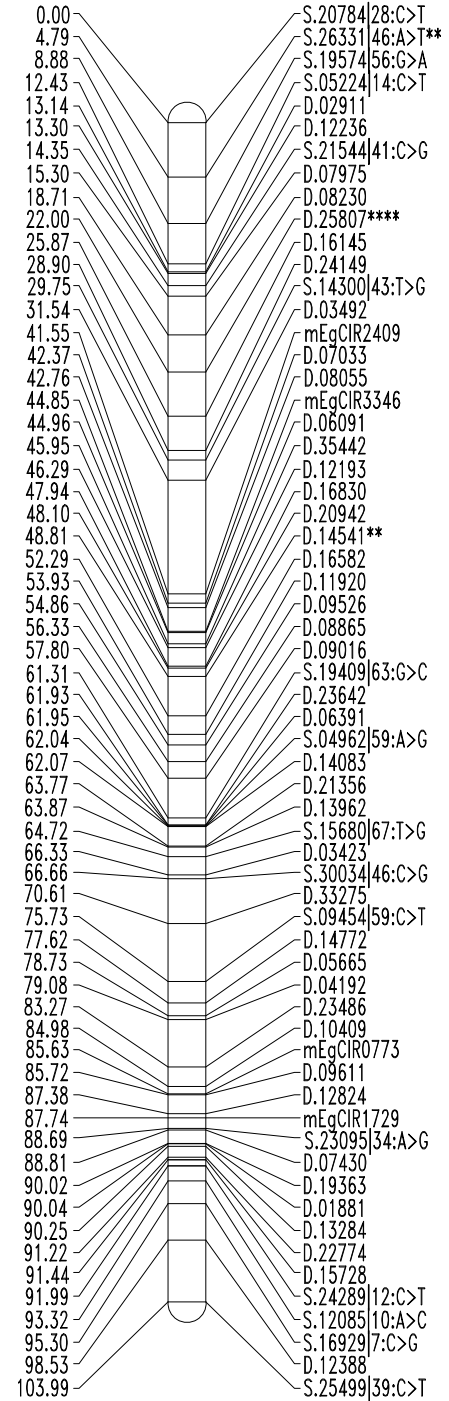
LG 8



LG 9

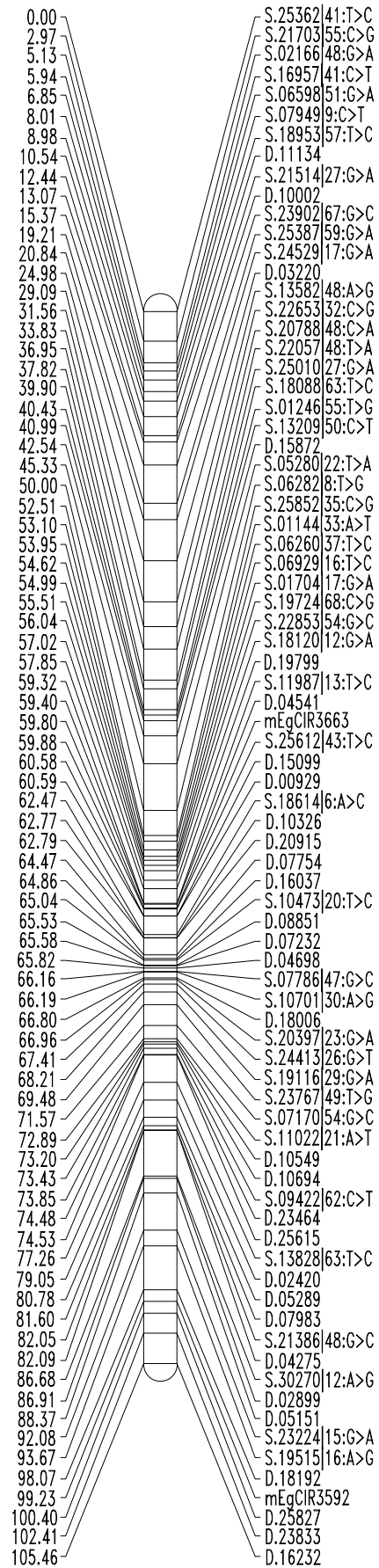
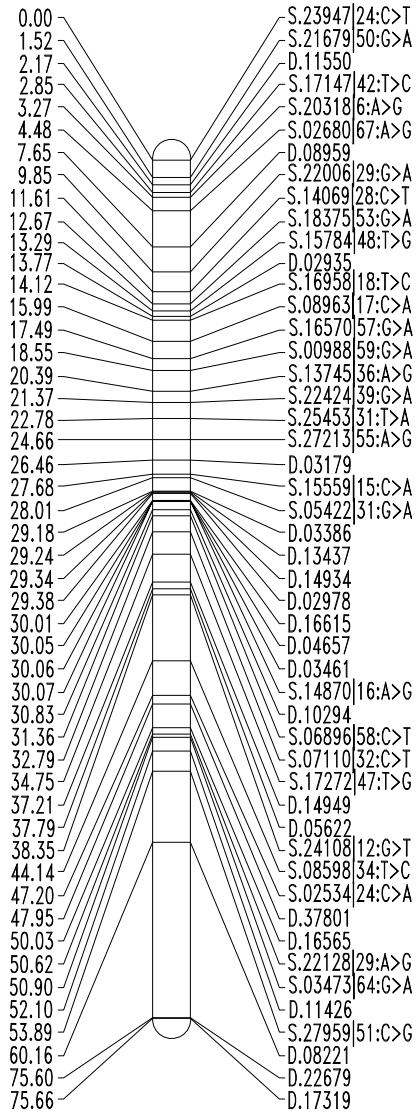


LG 10

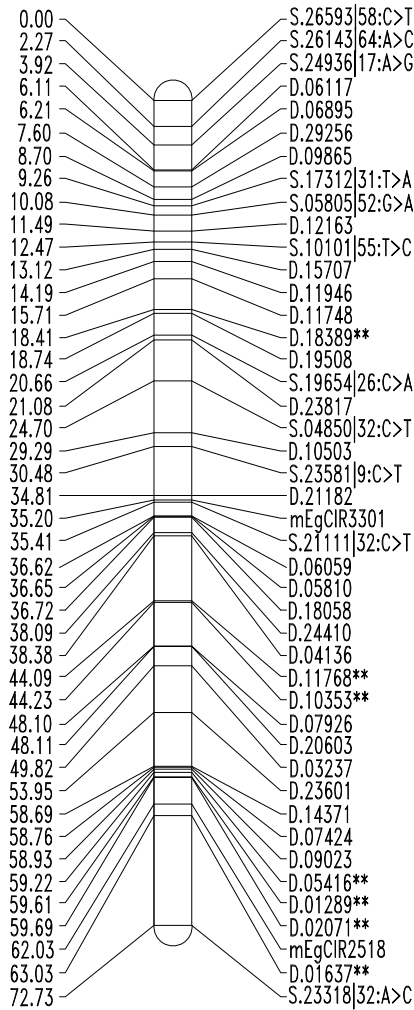


LG 13

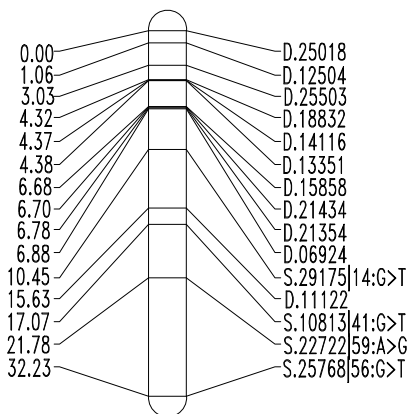
LG 12



LG 14



LG 16



LG 15

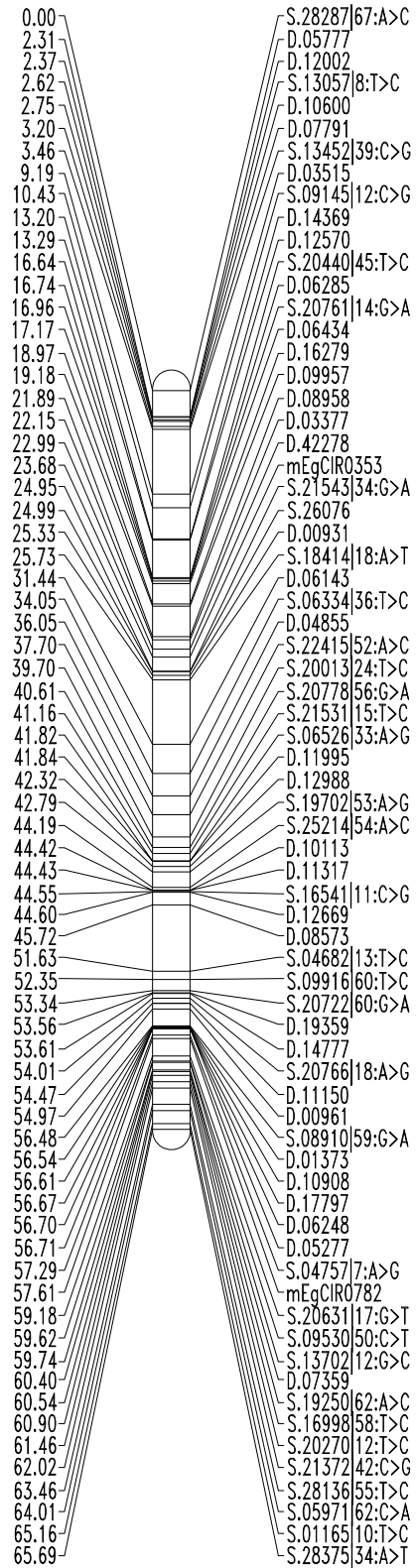


Fig. S1 Genetic linkage maps of the AA0768 population. The map consists of 1399 markers loci (32 SSR, 772 DArT, 594 SNP and *Sh* locus). Marker names are shown to the right of each LG, with map distances in centiMorgans (Haldane units) to the left. D: DArT marker, S: SNP marker, mEgCIR: *E. guineensis* SSR marker. *: Skewed markers at $P=0.1$, **: Skewed markers at $P=0.05$, ***: Skewed markers at $P=0.01$, ****: Skewed markers at $P=0.005$, *****: Skewed markers at $P=0.001$.