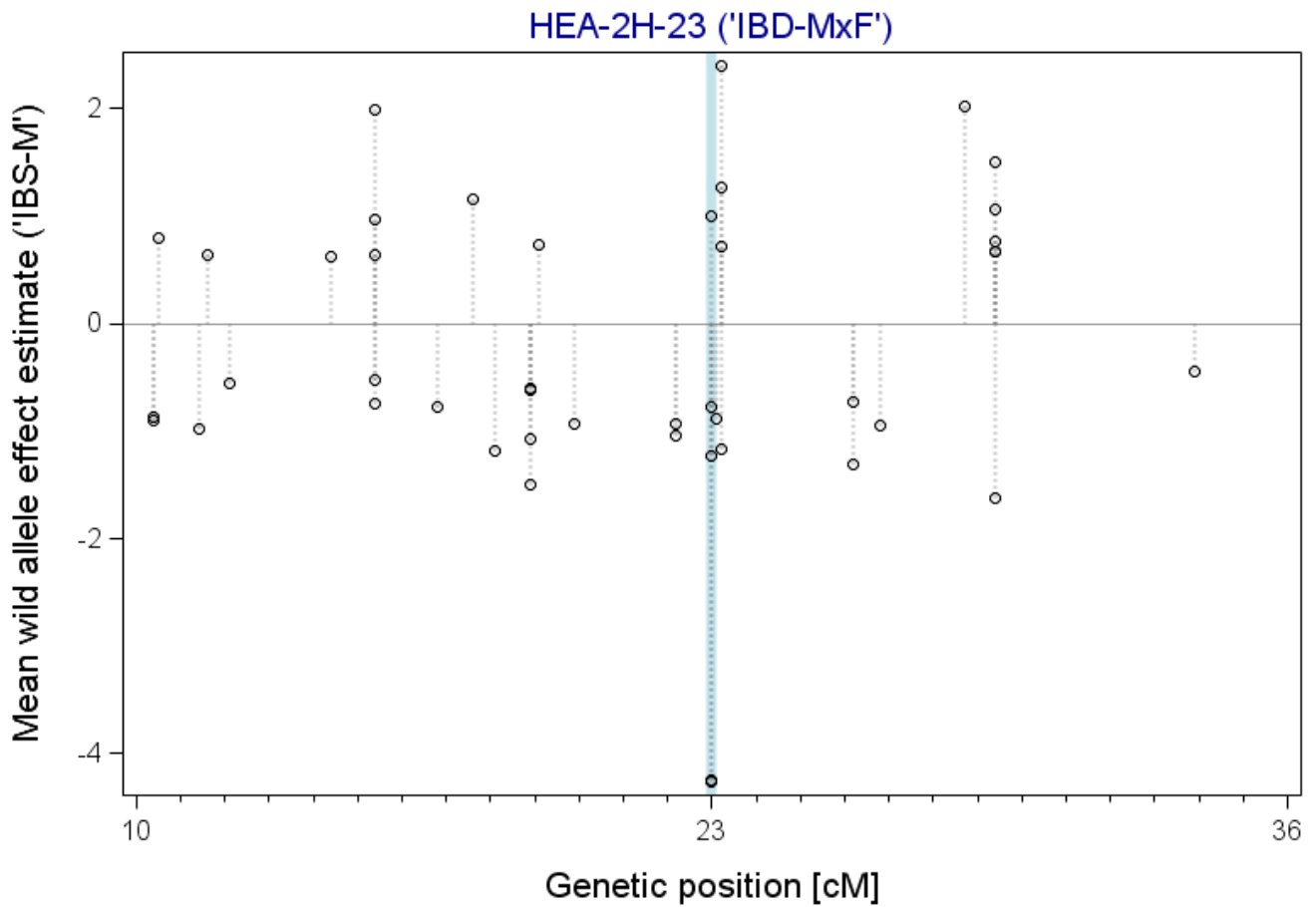
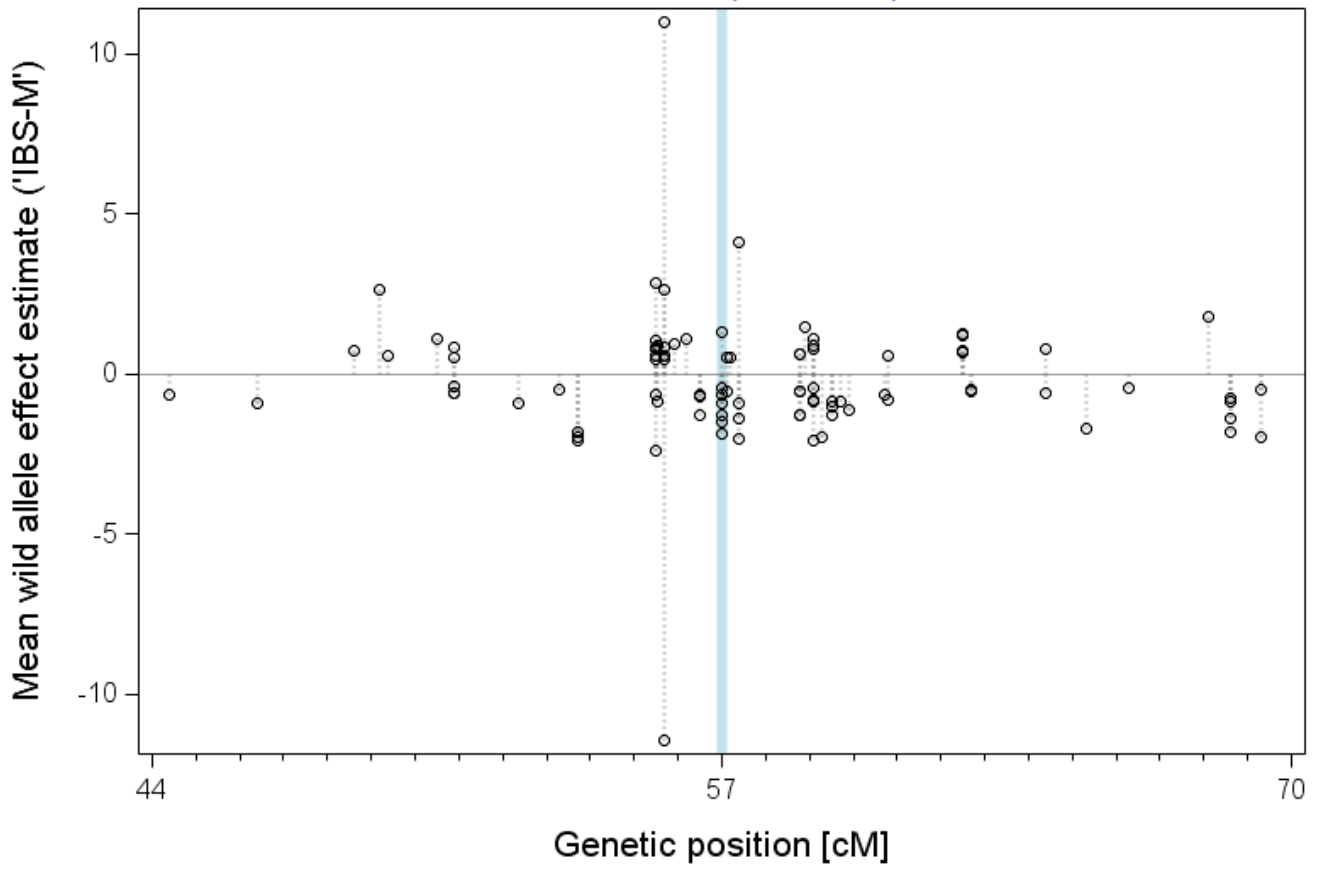


**Figure S3) Graphs depicting all significant marker effects obtained from model 'IBS-M' in the major QTL regions of HEB-25.**

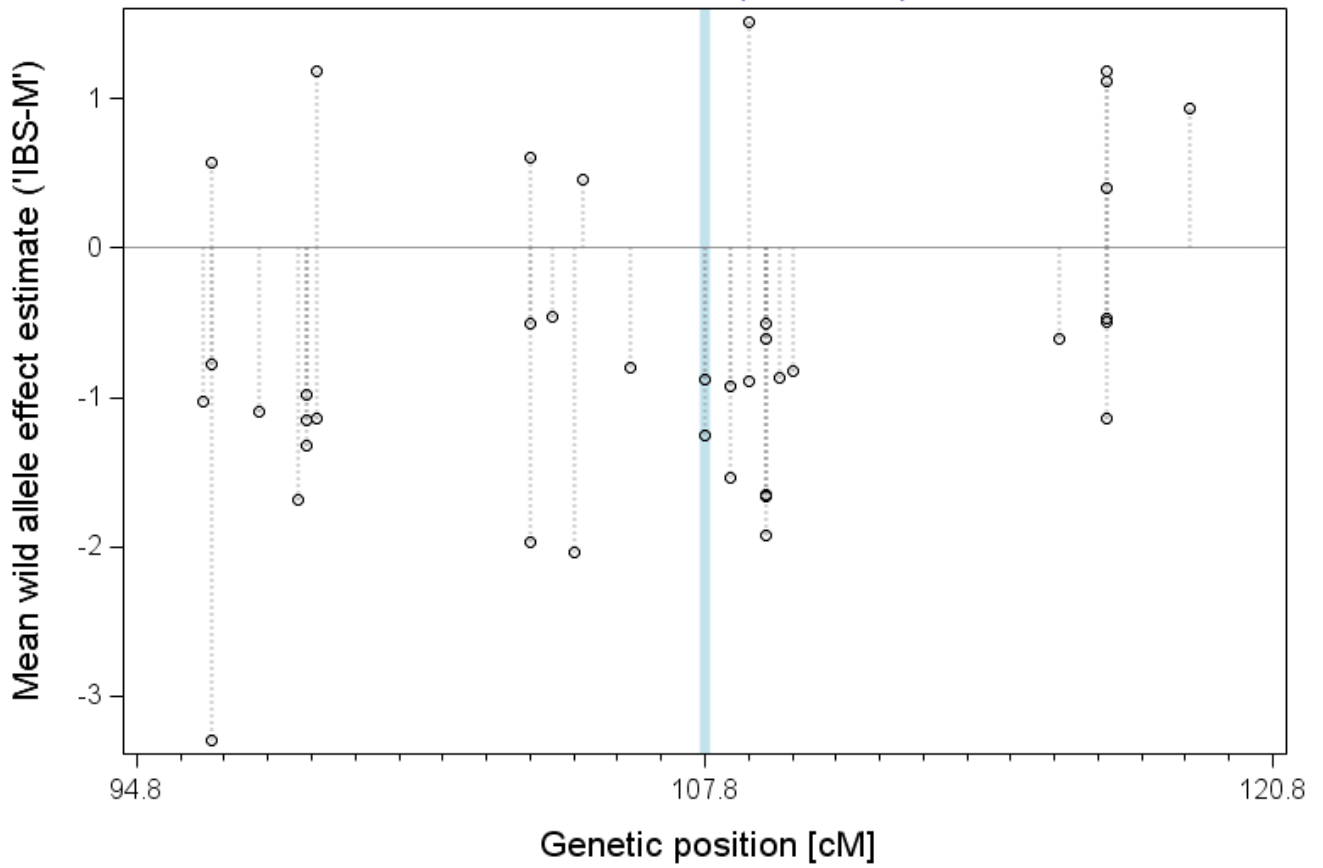


The presented interval spans 26 cM within the QTL position detected by model 'IBD-MxF' (indicated by a light blue background) in its centre. Each dot represents the mean wild effect estimate of a marker detected in 100 cross-validation runs of model 'IBS-M'. Those effects were first multiplied by the parental marker genotypes. Then, the obtained products were summed up to obtain parent-specific effects of the respective QTL (so-called cumulation method).

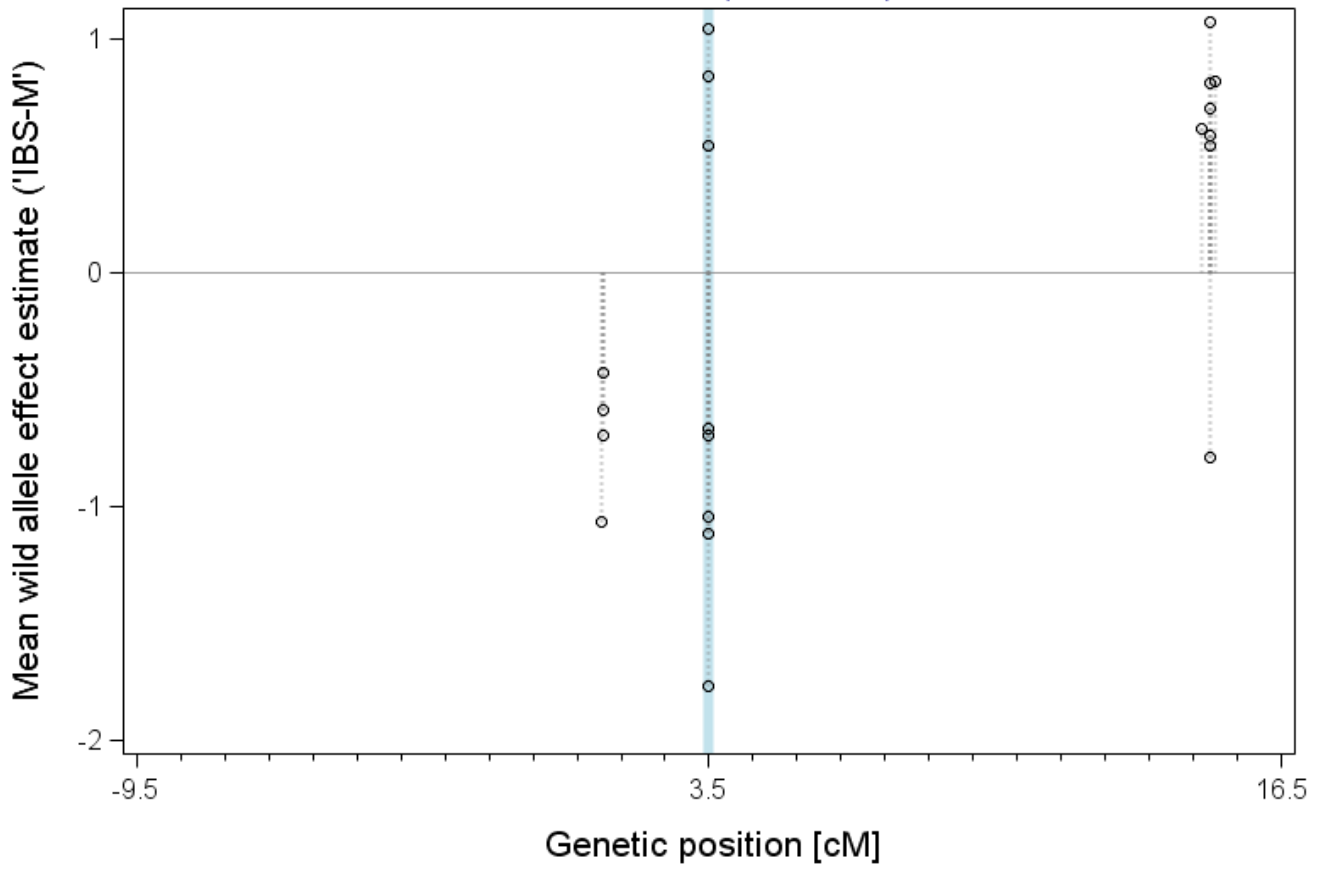
HEA-2H-57 ('IBD-MxF')



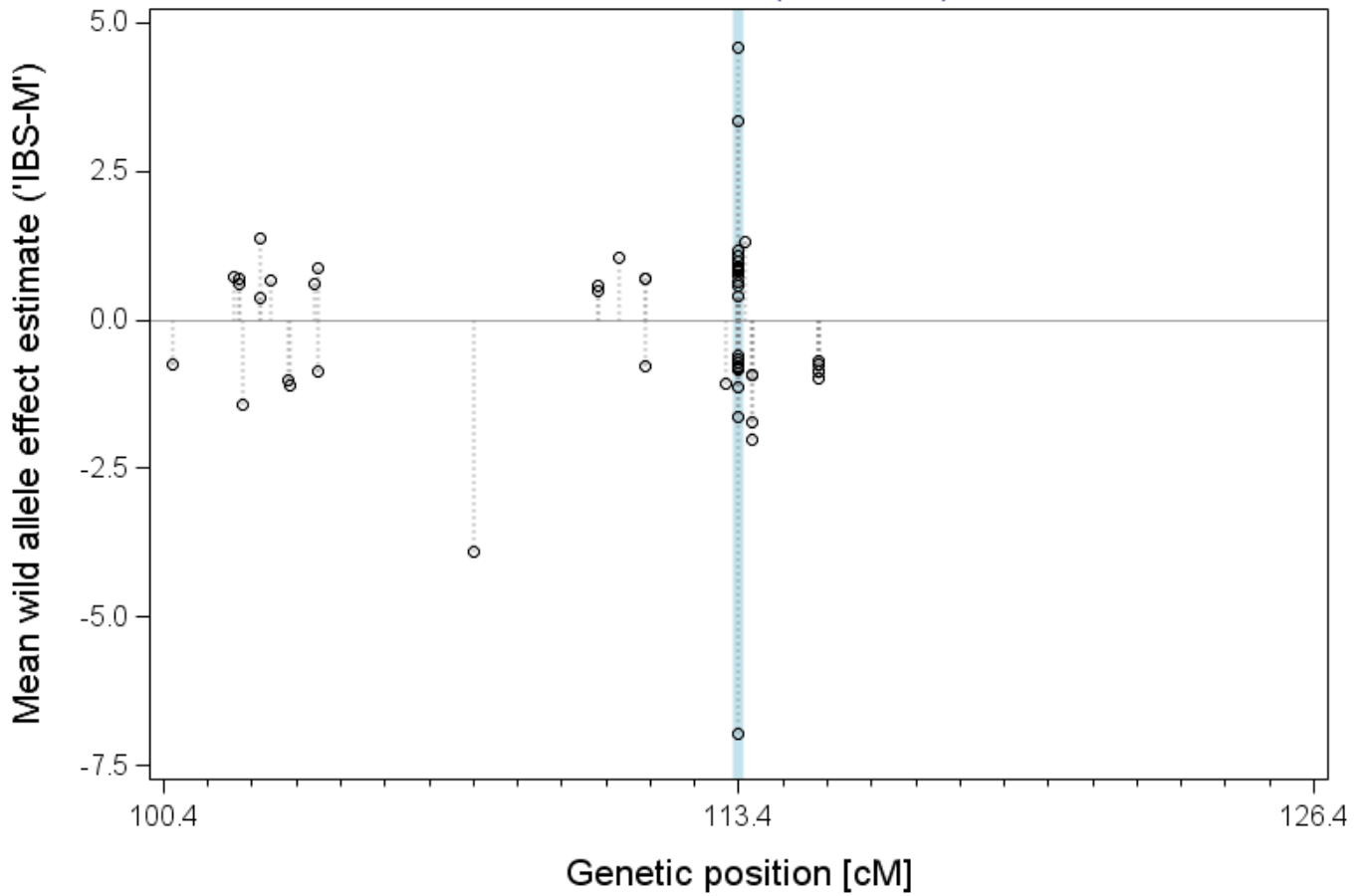
HEA-3H-107.8 ('IBD-MxF')



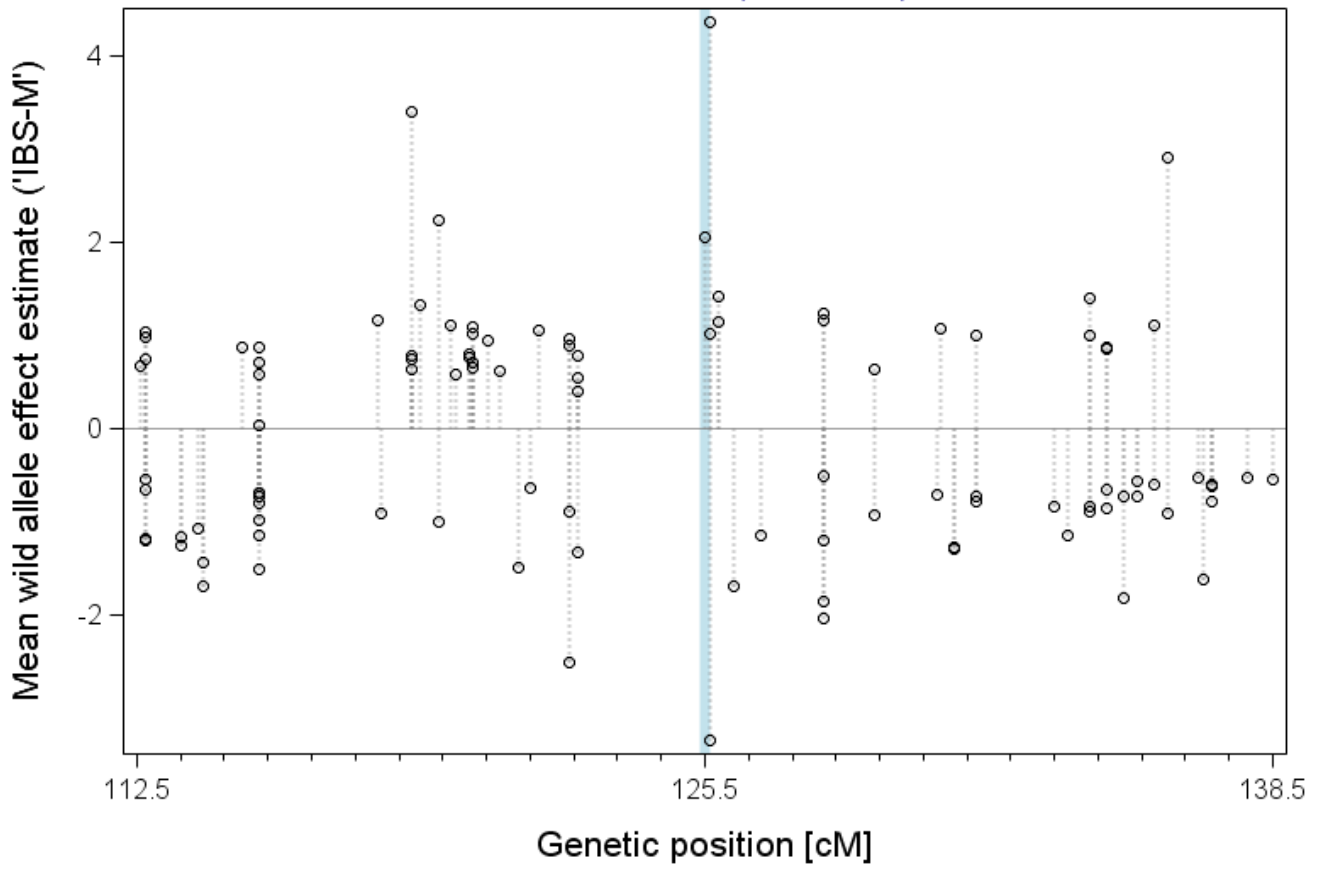
HEA-4H-3.5 ('IBD-MxF')



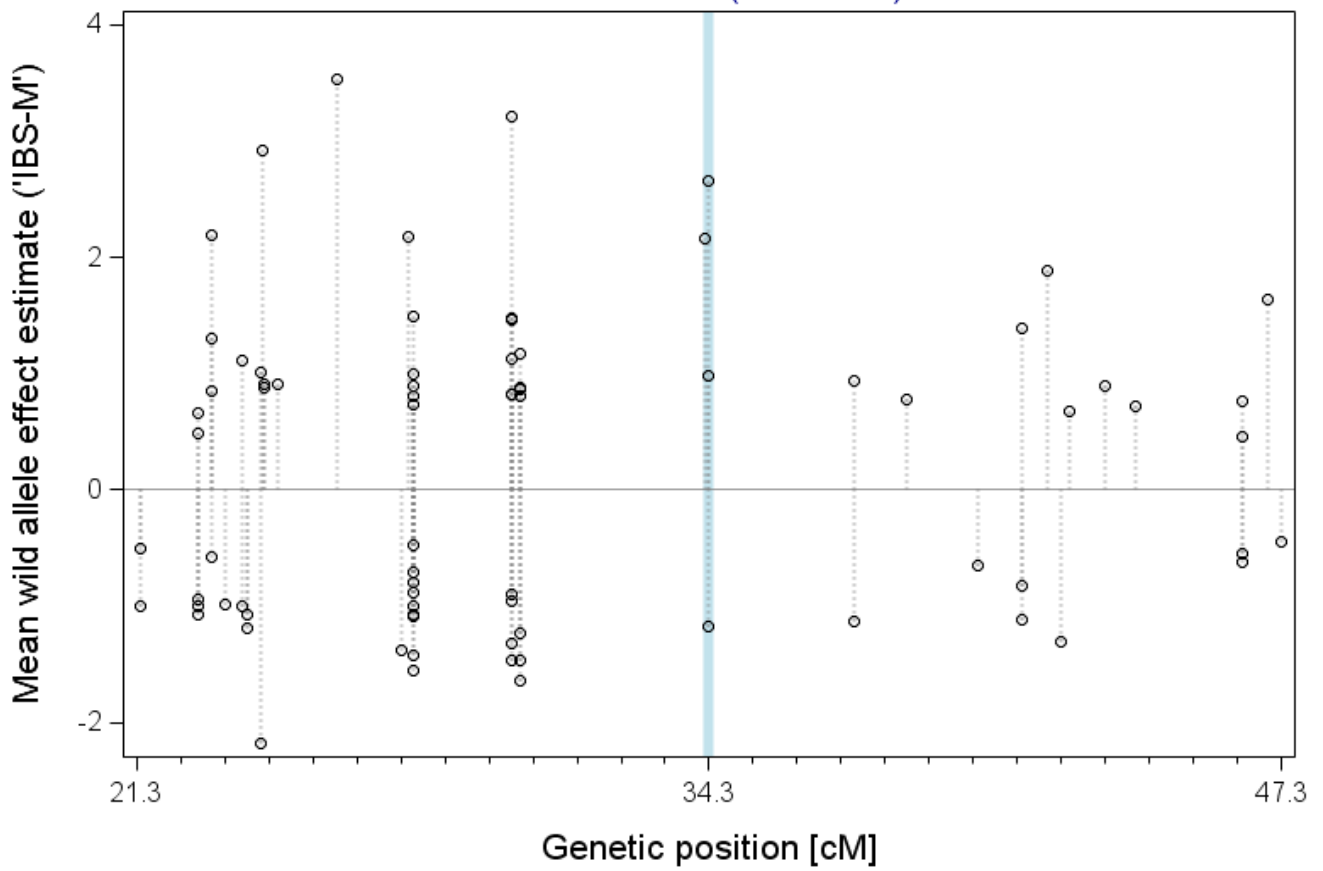
HEA-4H-113.4 ('IBD-MxF')



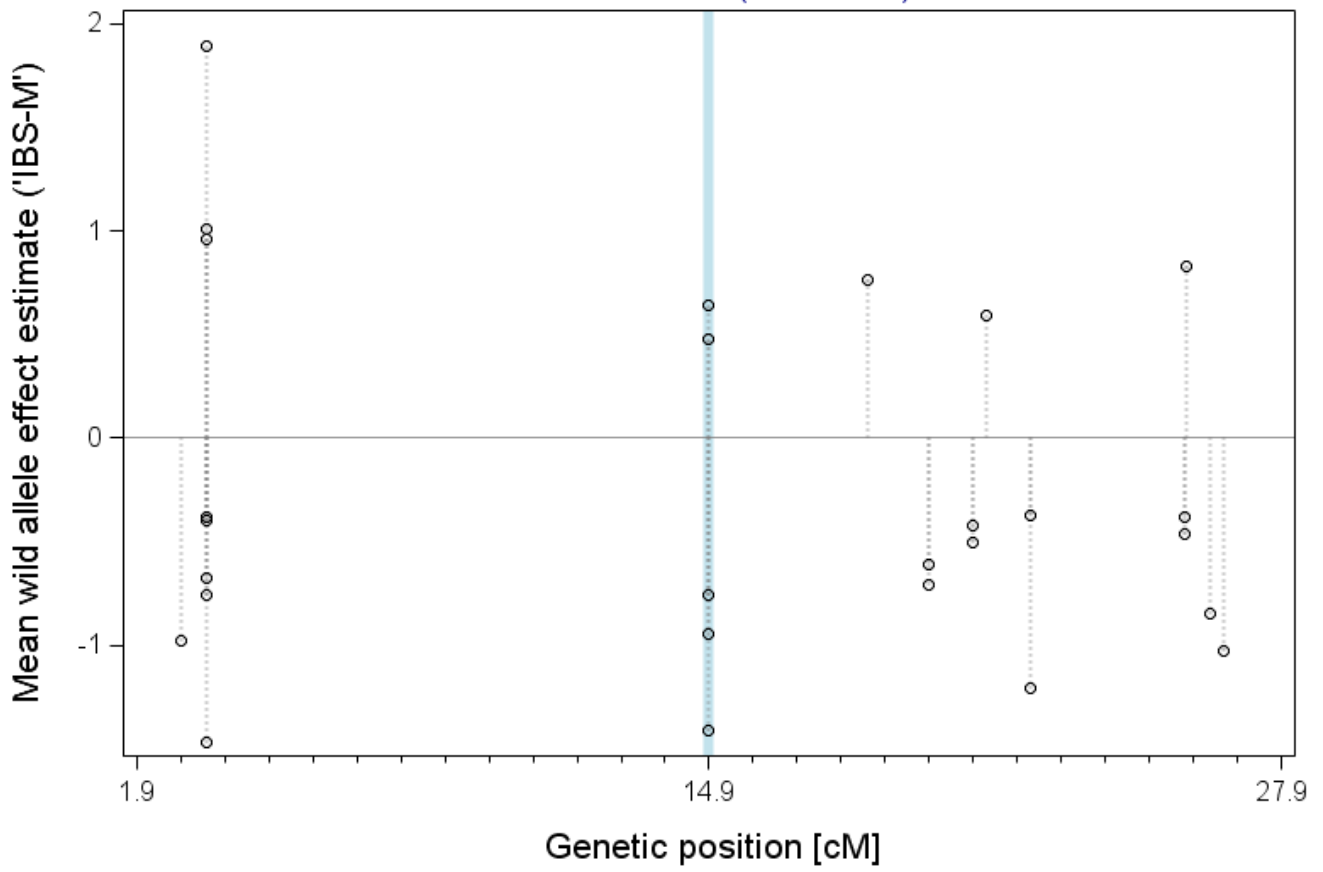
HEA-5H-125.5 ('IBD-MxF')



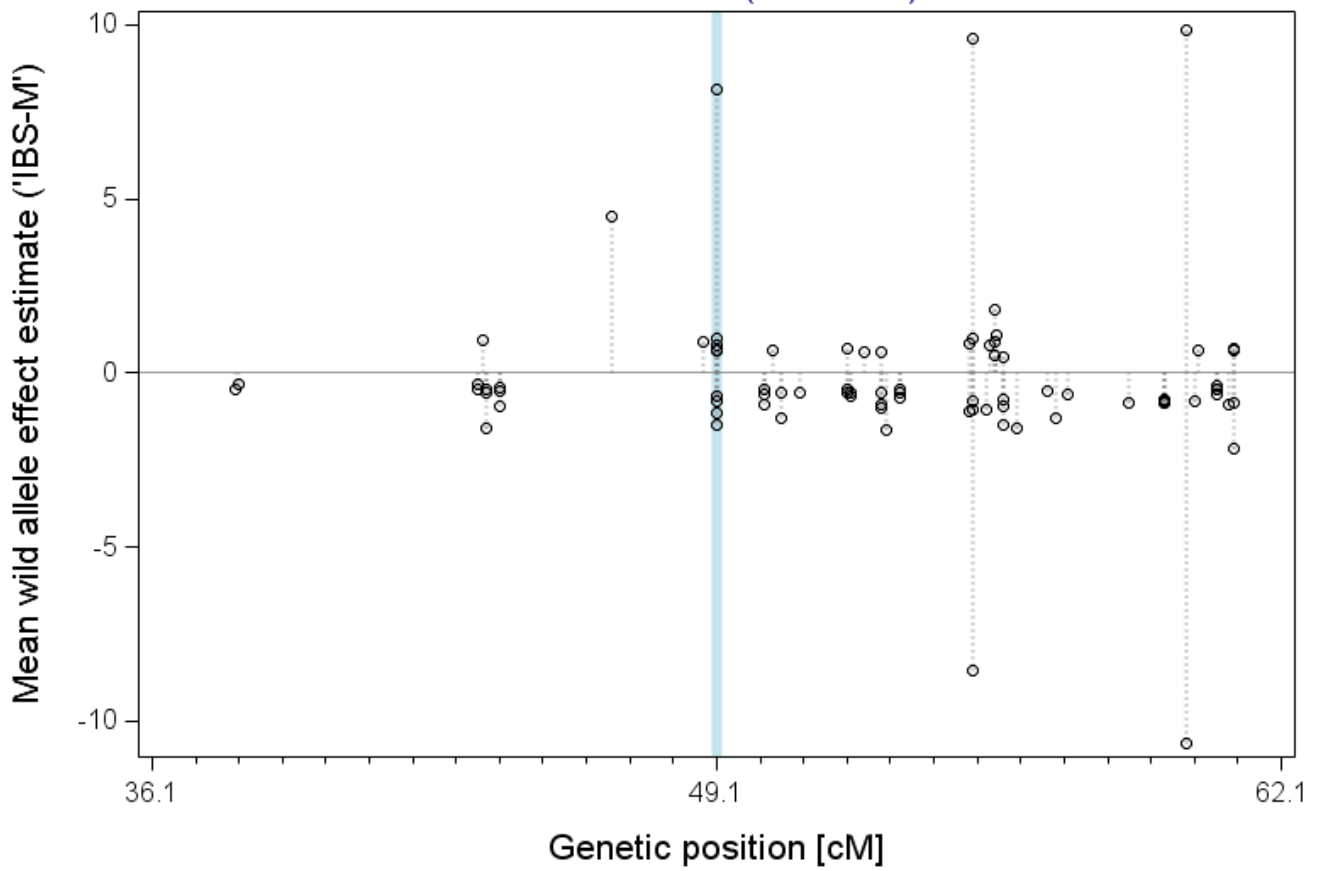
HEA-7H-34.3 ('IBD-MxF')

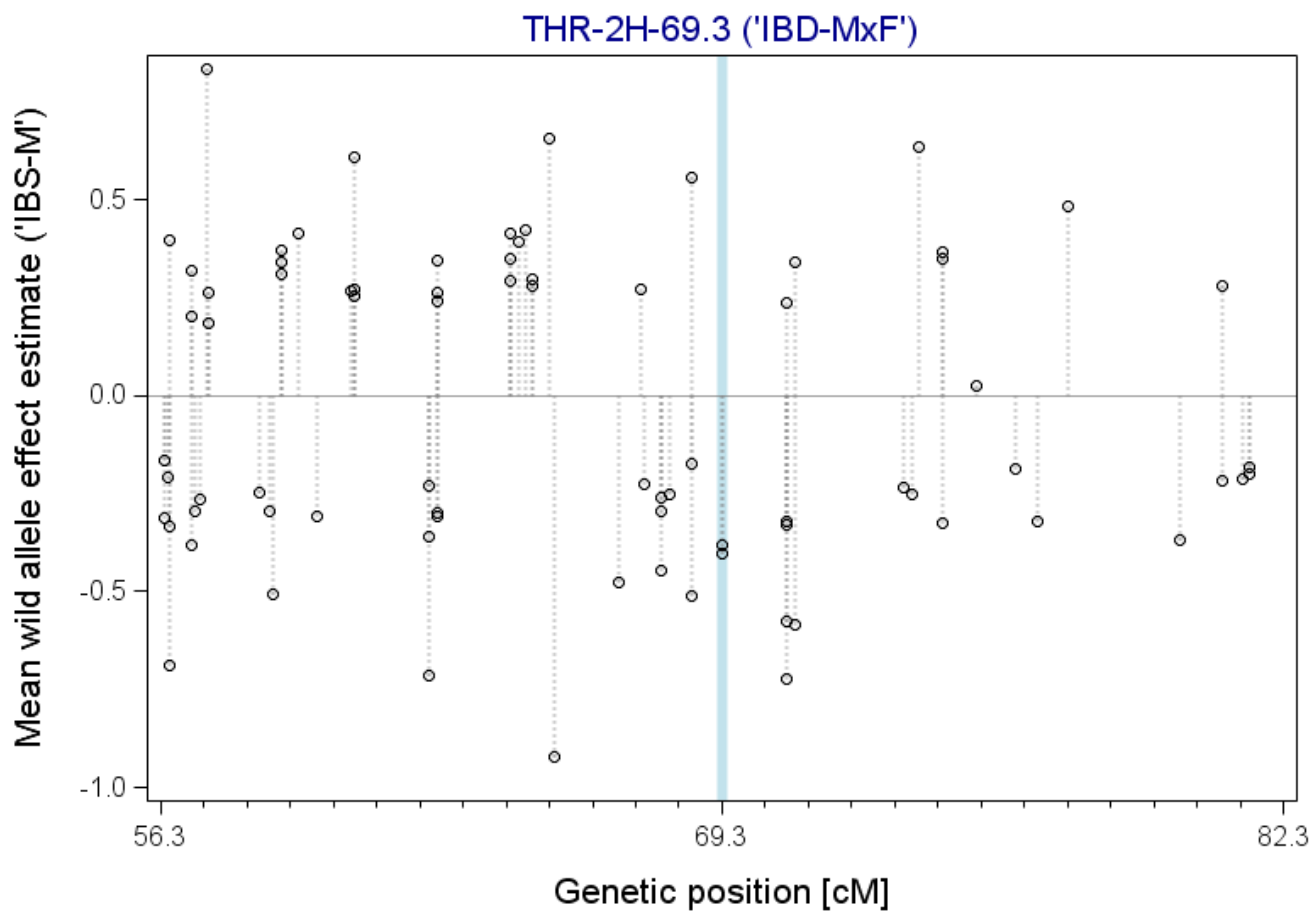
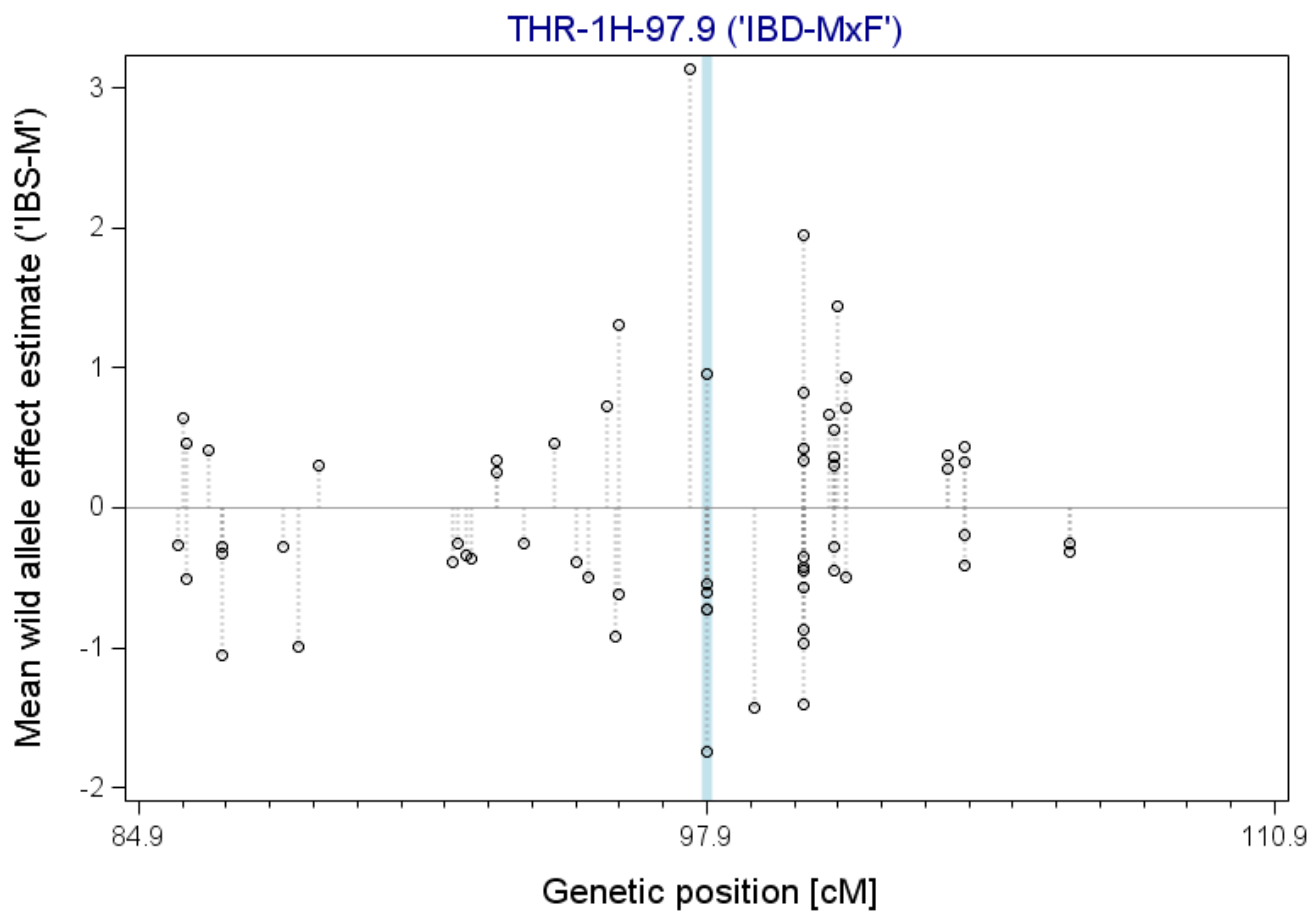


TGW-4H-14.9 ('IBD-MxF')



TGW-6H-49.1 ('IBD-MxF')





GrCol-1H-116.8 ('IBD-MxF')

