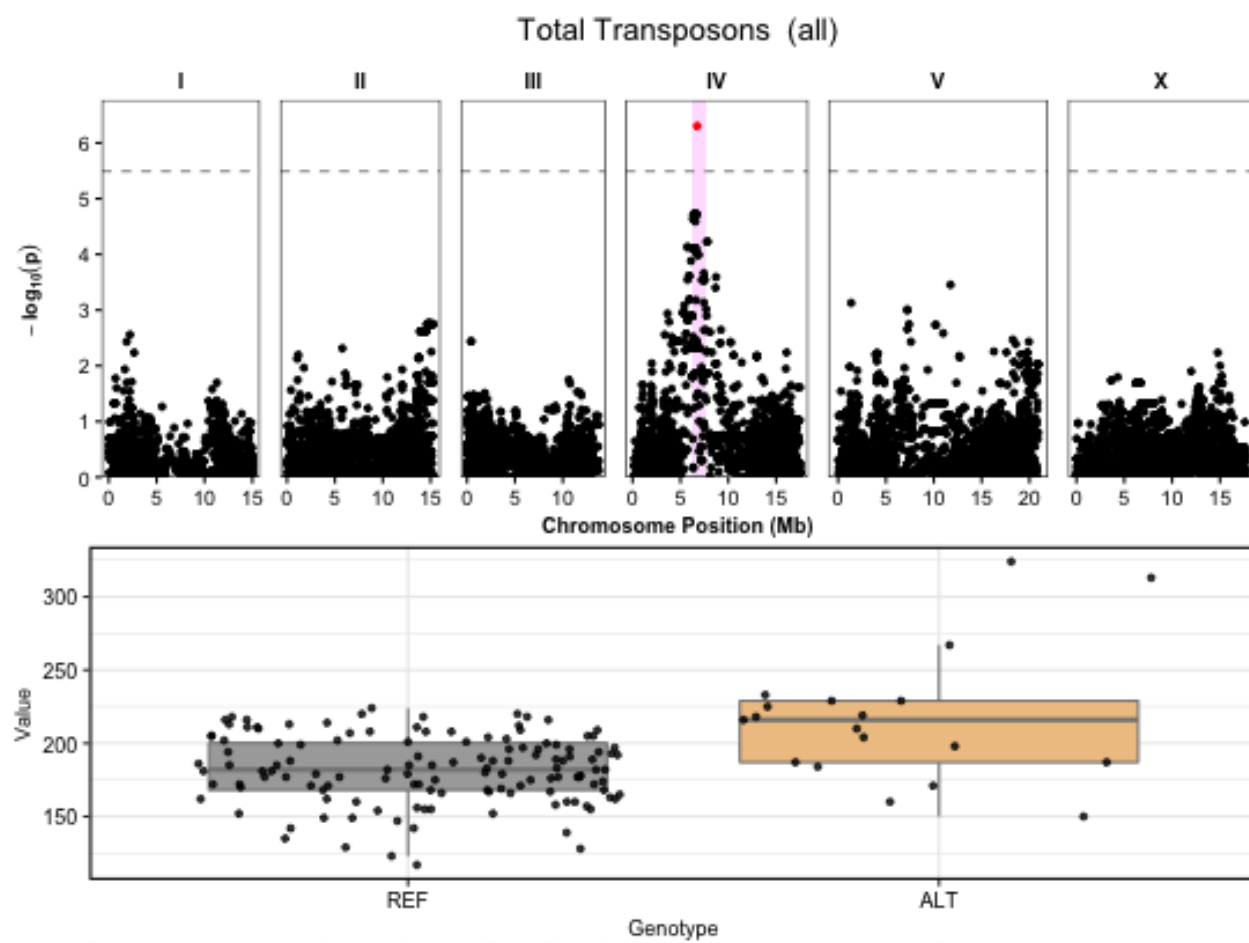
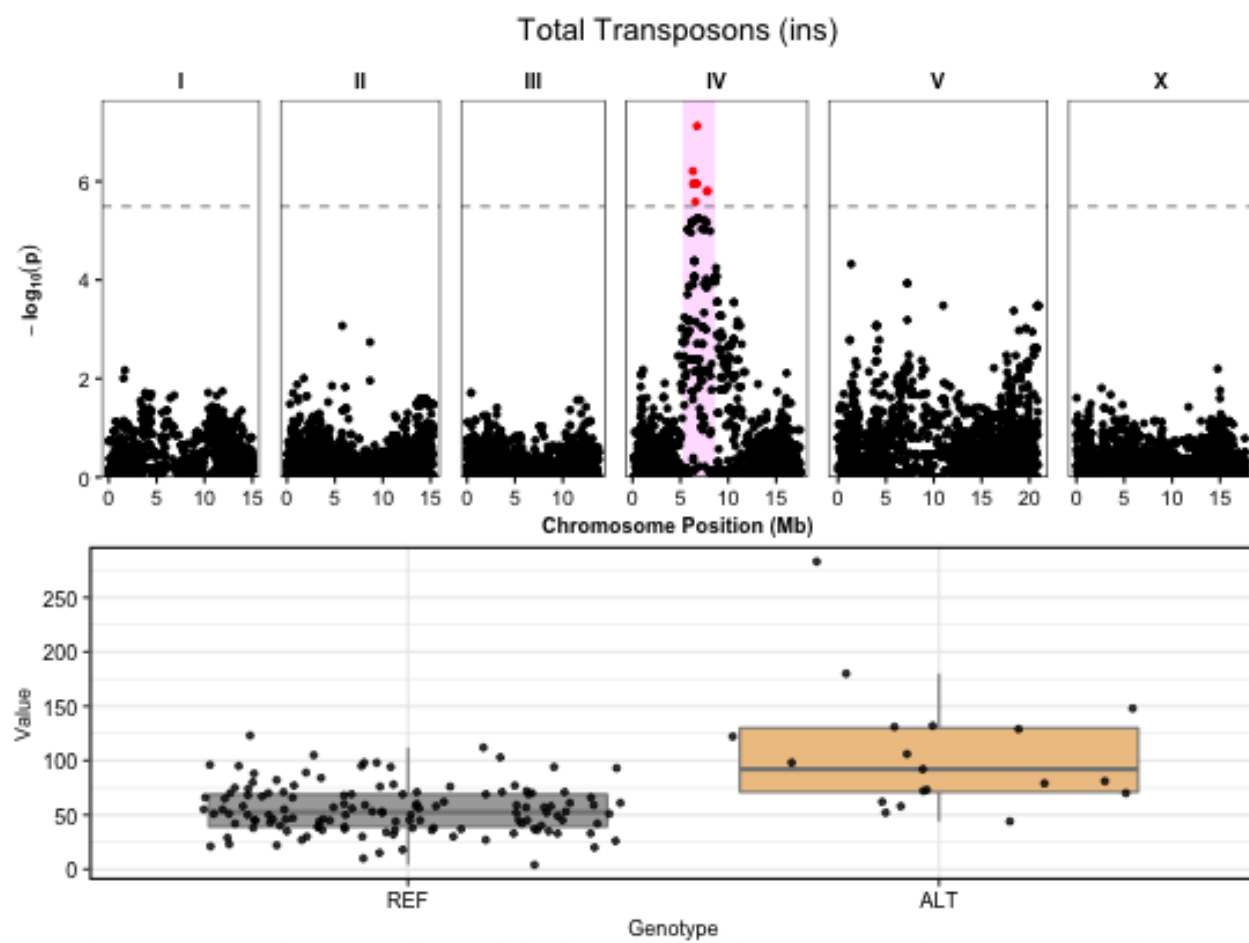
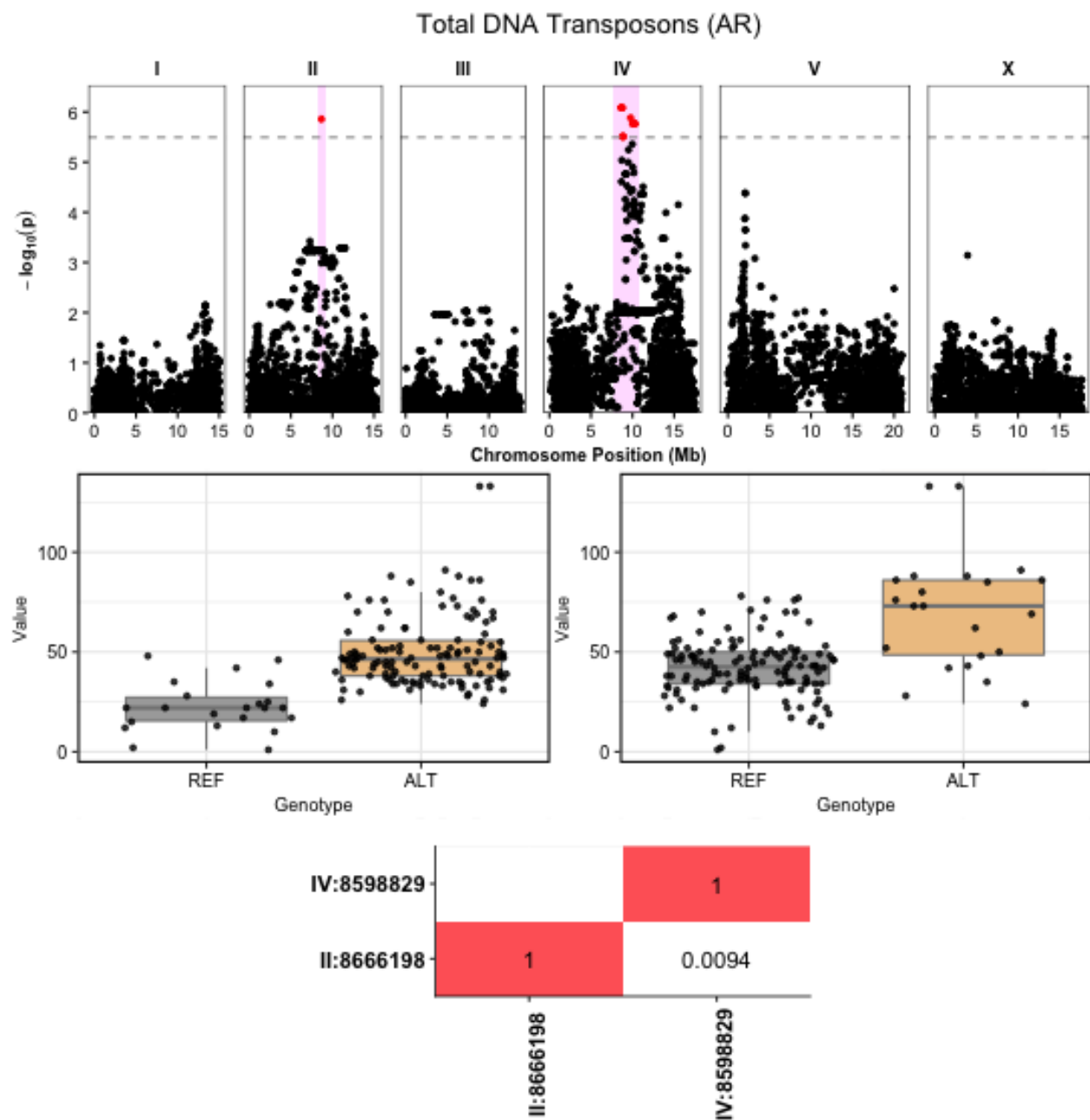


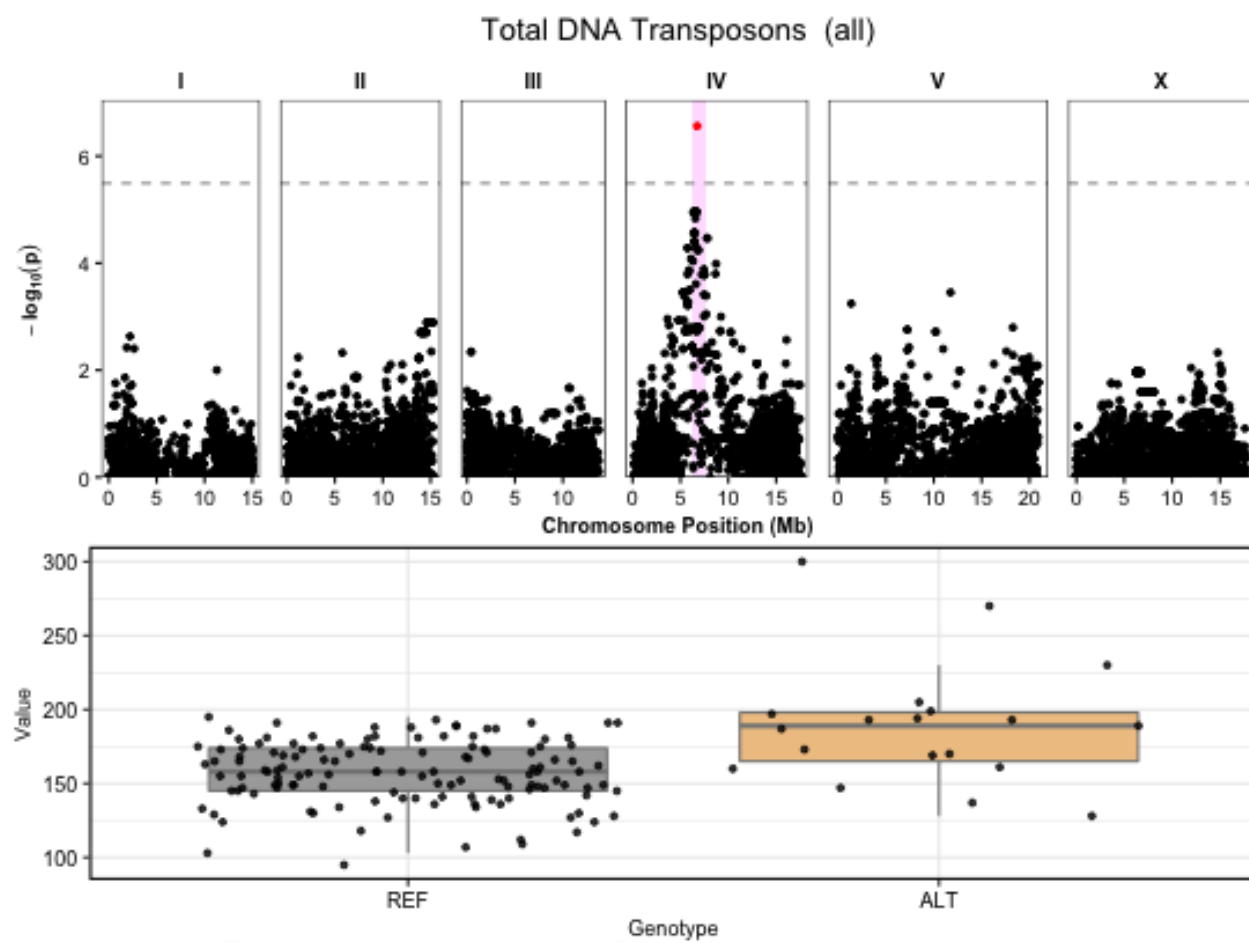
Supplemental Figure S9. Manhattan plots and boxplot phenotype-by-genotype splits for total TE counts of all transposons. The top plots are Manhattan plots of GWA mappings with the significance threshold indicated by the dotted gray line. SNVs that are above the Bonferroni threshold are shown in red and SNVs that are below the significance threshold or do not pass our heuristic filters (see Methods) are shown in black. Confidence intervals are represented by the pink bars, and the x-axis indicates base positions with ticks every 5 Mb. The middle plots show the phenotype values for the TE count traits on the y-axis split by the genotype (reference or alternative allele) on the x-axis. The bottom plots display measures of linkage disequilibrium between the peak SNVs for each significant QTL.

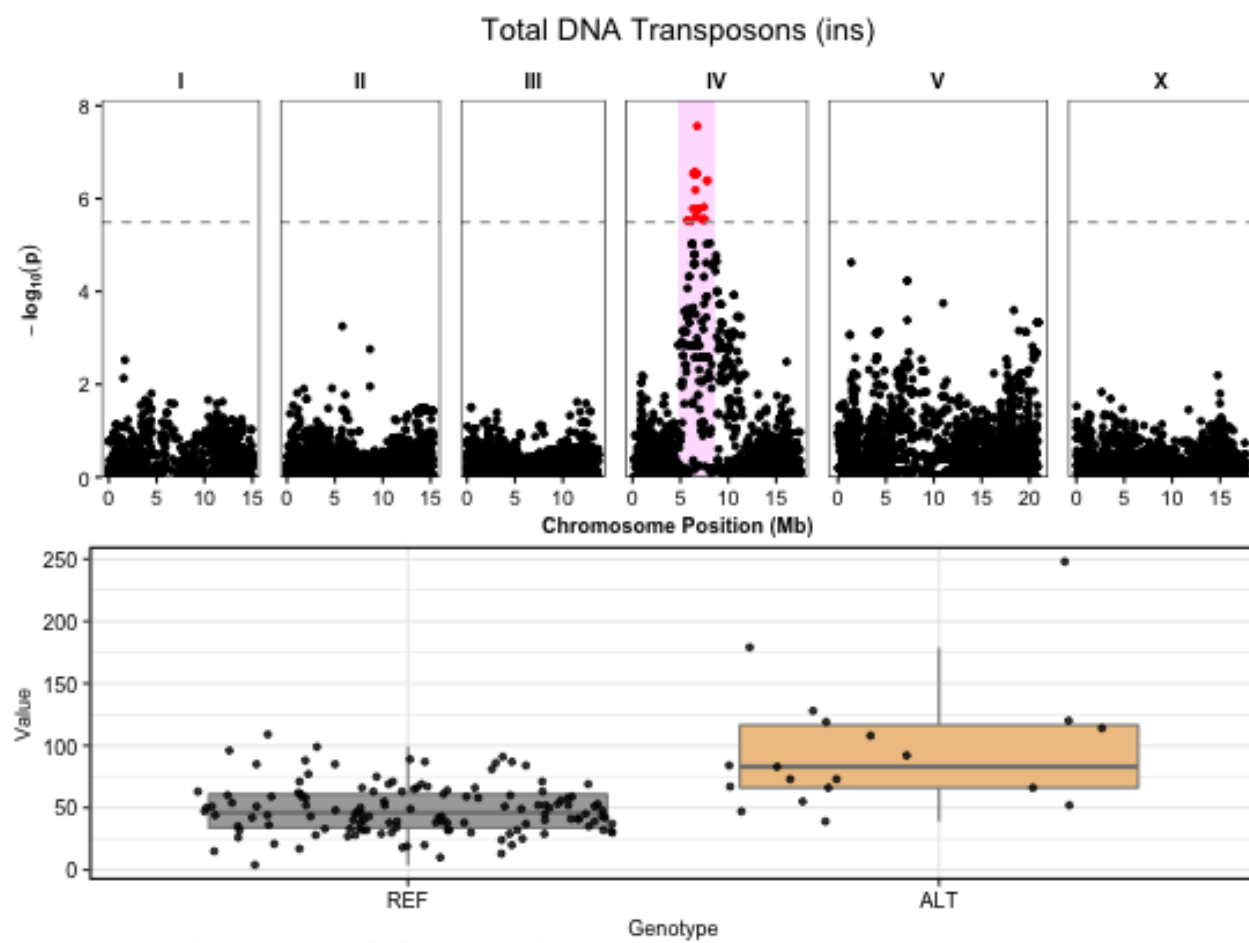


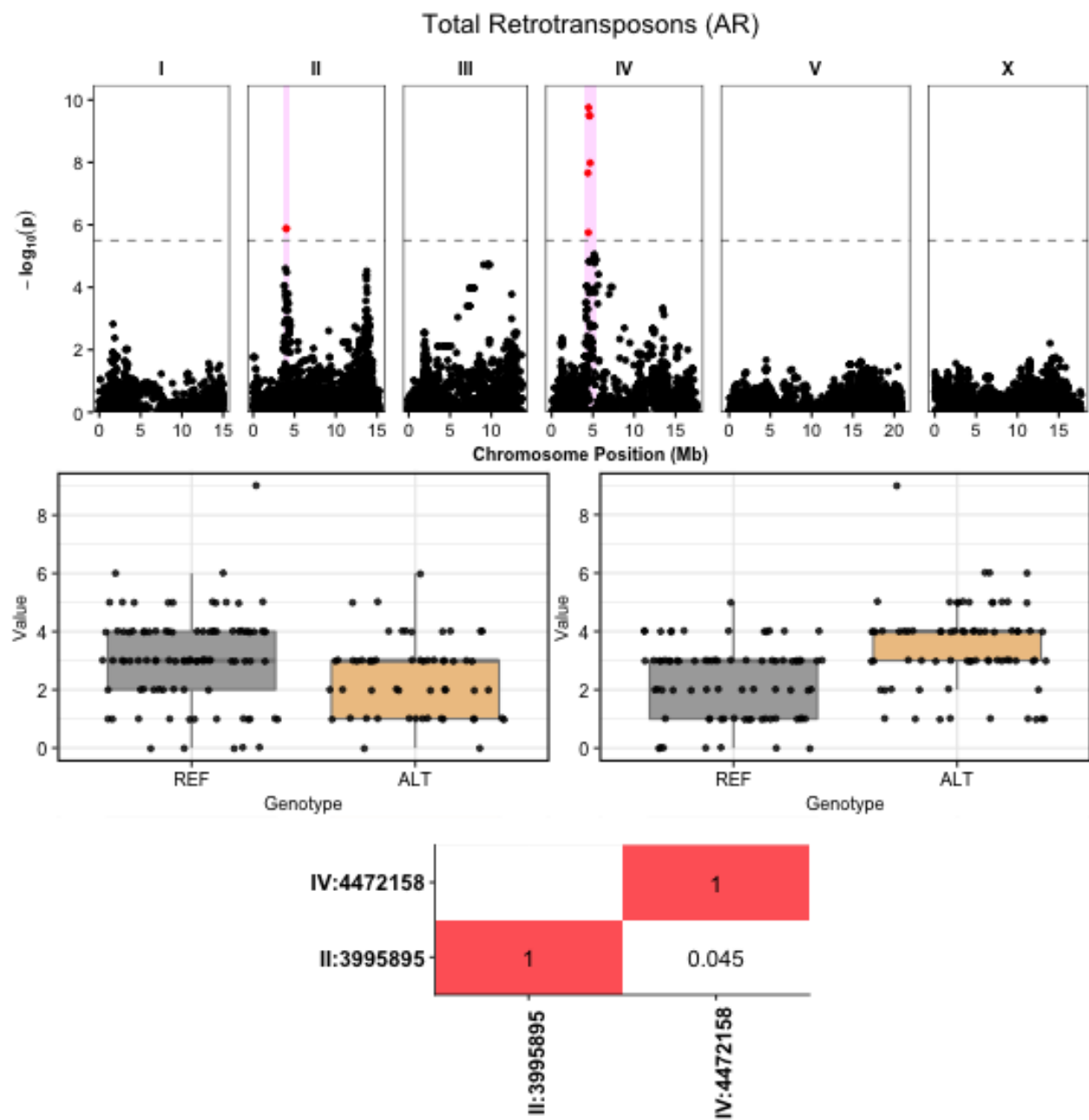


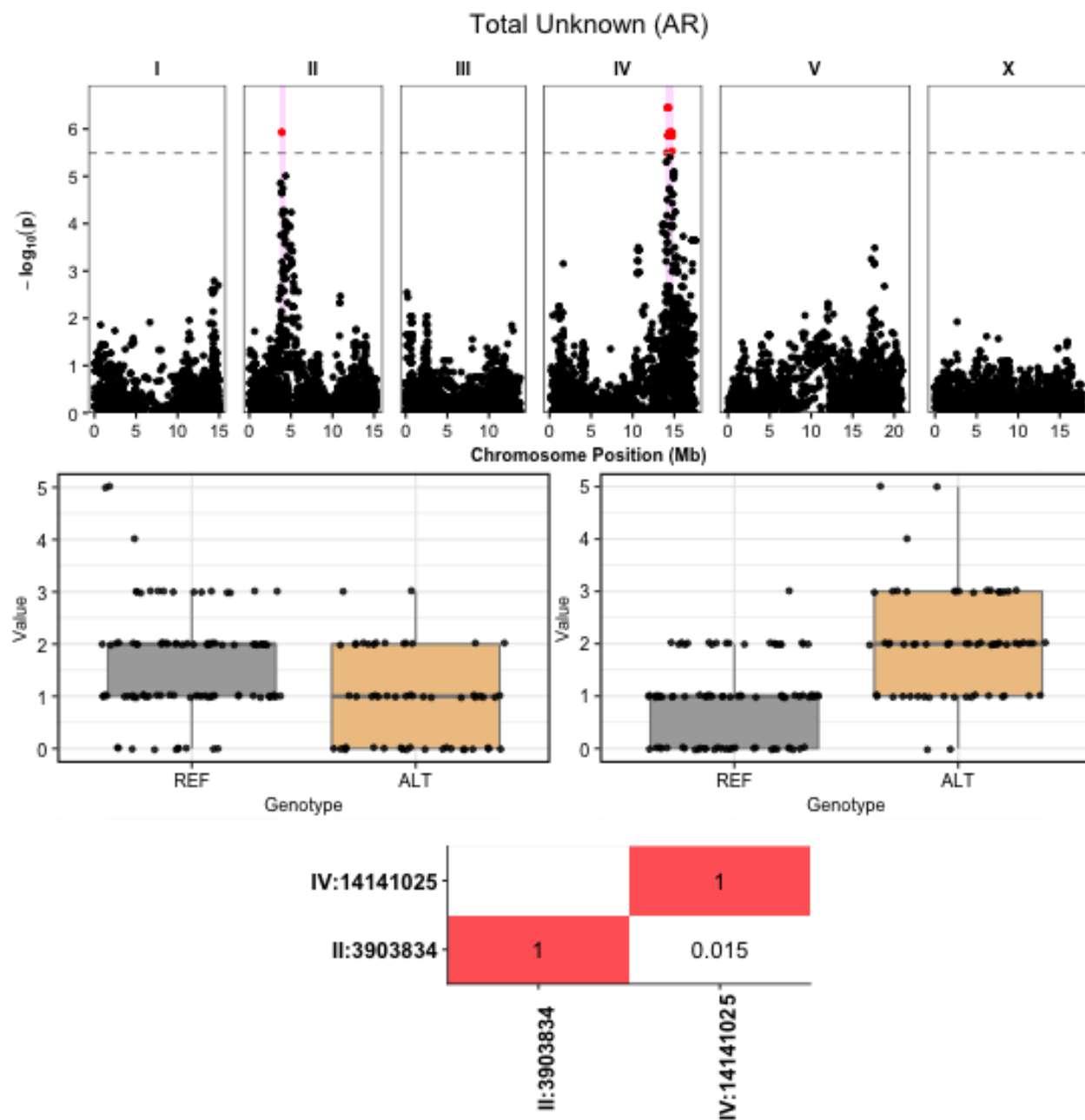
Supplemental Figure S9. Manhattan plots and boxplot phenotype-by-genotype splits for TE type counts of DNA transposons, retrotransposons, and transposons of unknown classification. The top plots are Manhattan plots of GWA mappings with the significance threshold indicated by the dotted gray line. SNVs that are above the Bonferroni threshold are shown in red and SNVs that are below the significance threshold or do not pass our heuristic filters (see Methods) are shown in black. Confidence intervals are represented by the pink bars, and the x-axis indicates base positions with ticks every 5 Mb. The middle plots show the phenotype values for the TE count traits on the y-axis split by the genotype (reference or alternative allele) on the x-axis. The bottom plots display measures of linkage disequilibrium between the peak SNVs for each significant QTL.





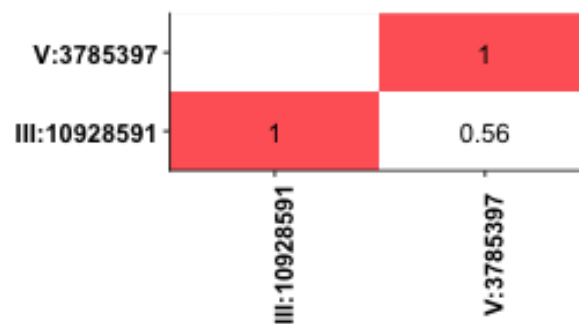
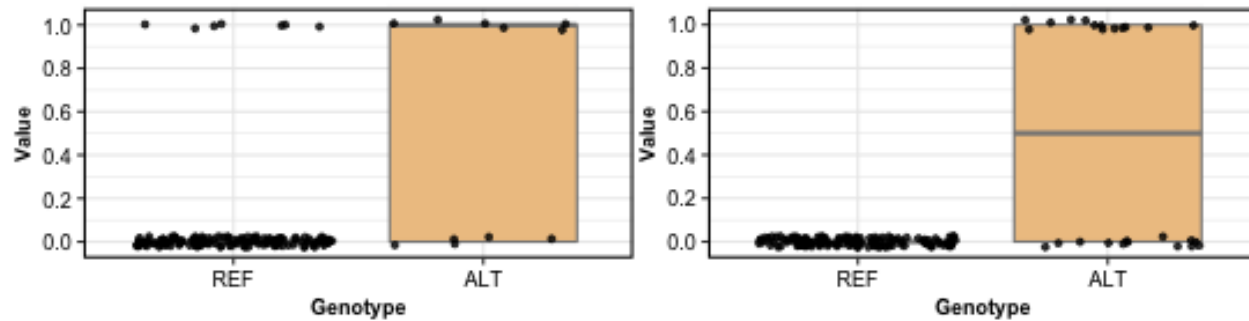
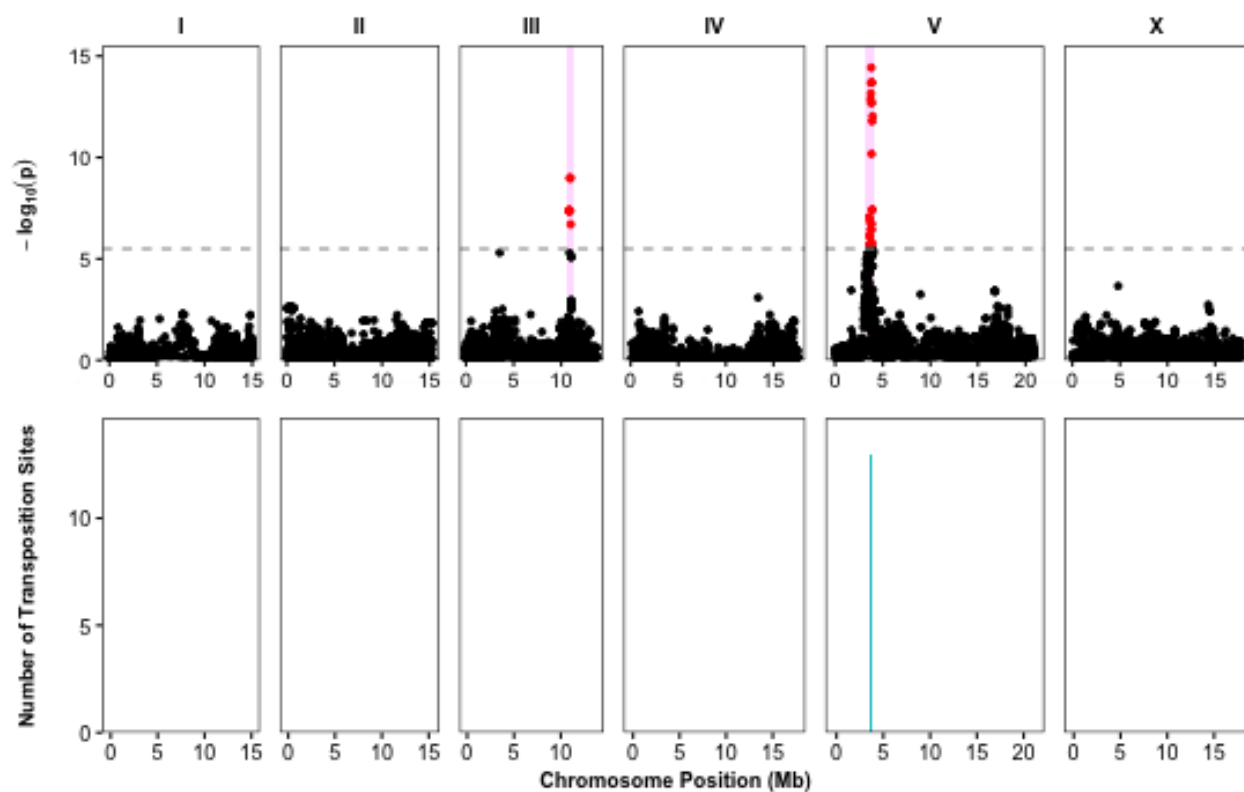




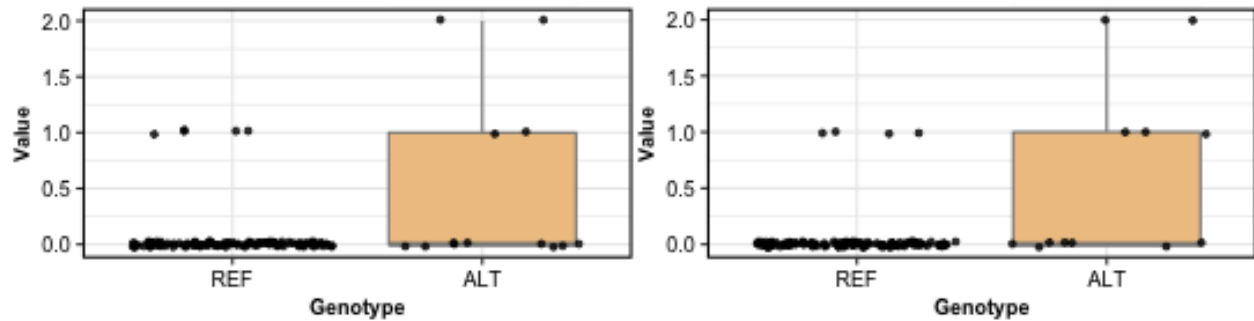
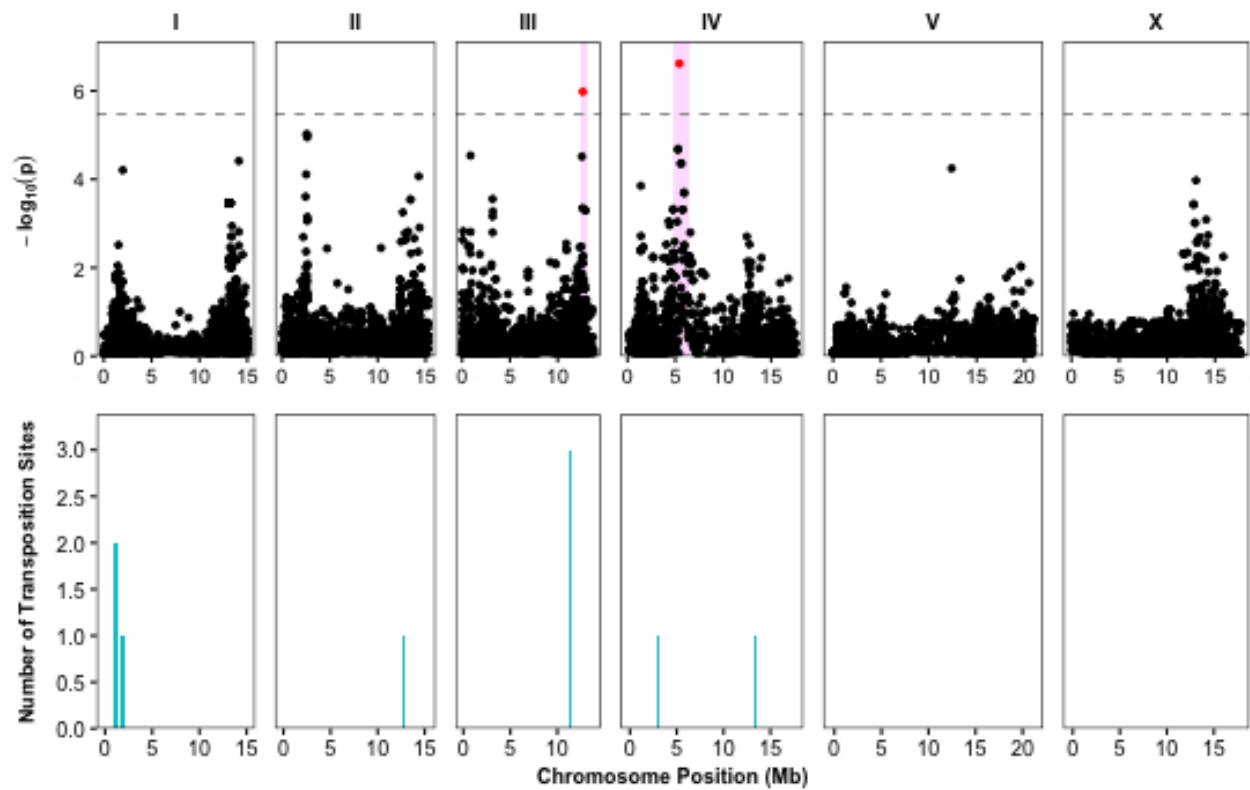


Supplemental Figure S9. Manhattan plots, position map, and boxplot phenotype-by-genotype splits for each transposon family with a significant QTL. The top plots are Manhattan plots of GWA mappings with the significance threshold indicated by the dotted gray line. SNVs that are above the Bonferroni threshold are shown in red and SNVs that are below the significance threshold or do not pass our heuristic filters (see Methods) are shown in black. Confidence intervals are represented by the pink bars, and the x-axis indicates base positions with ticks every 5 Mb. The second plot shows the genomic positions of the transposon that was mapped with the total number of active reference and insertion calls from all the strains displayed in orange and blue, respectively. The third set of plots shows the phenotype values for the TE count traits on the y-axis split by the genotype (reference or alternative allele) on the x-axis. The bottom plots display measures of linkage disequilibrium between the peak SNVs for each significant QTL.

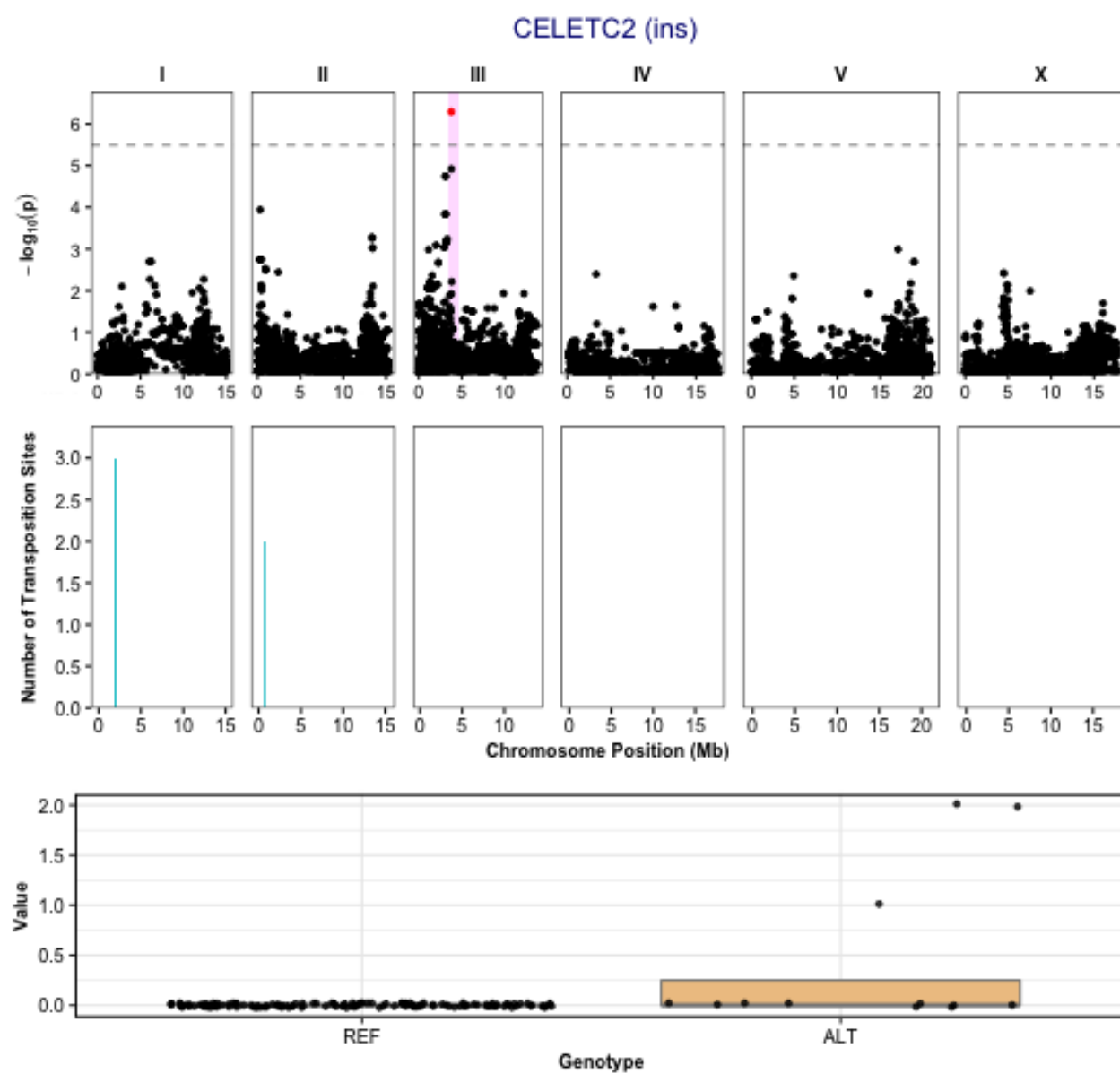
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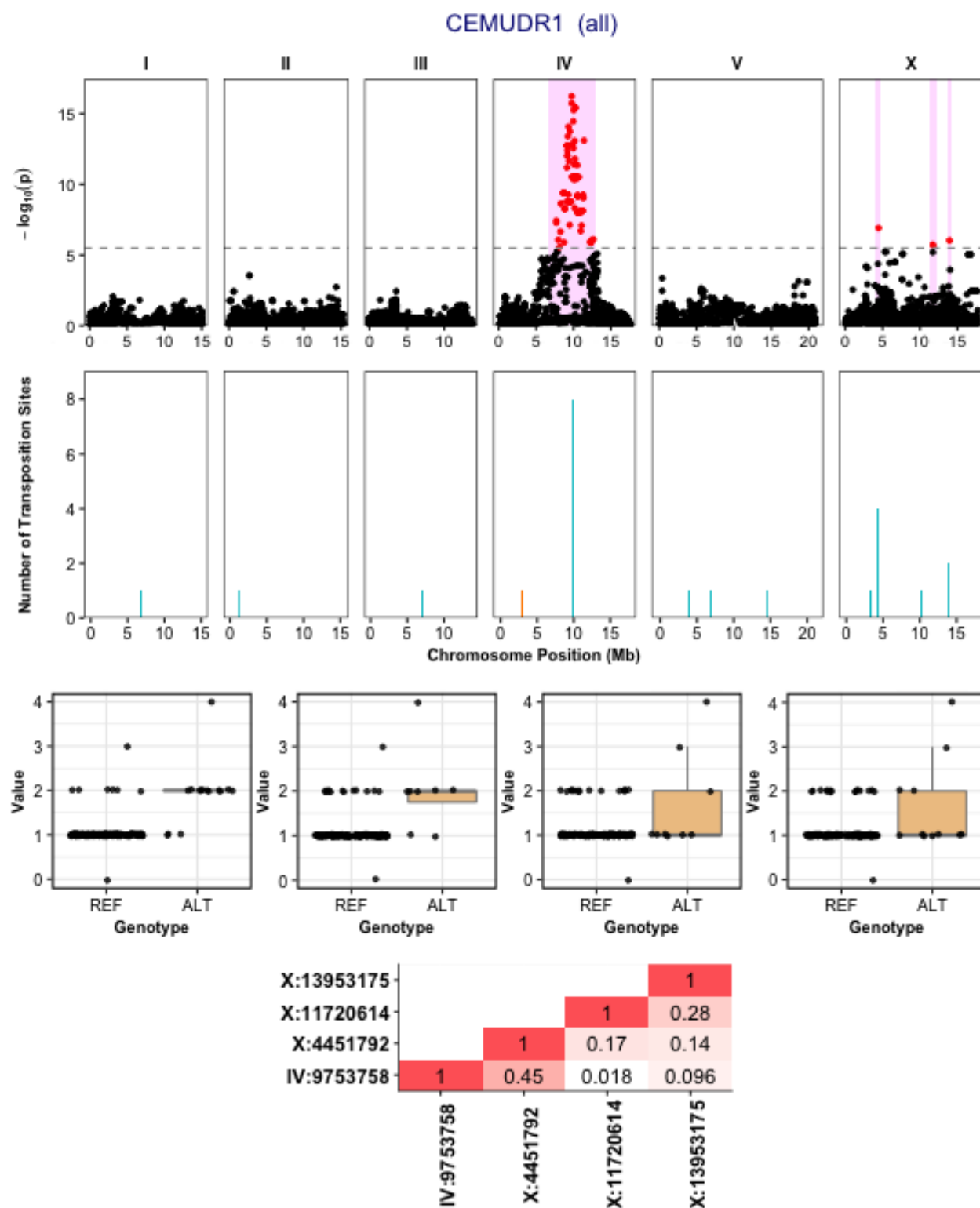


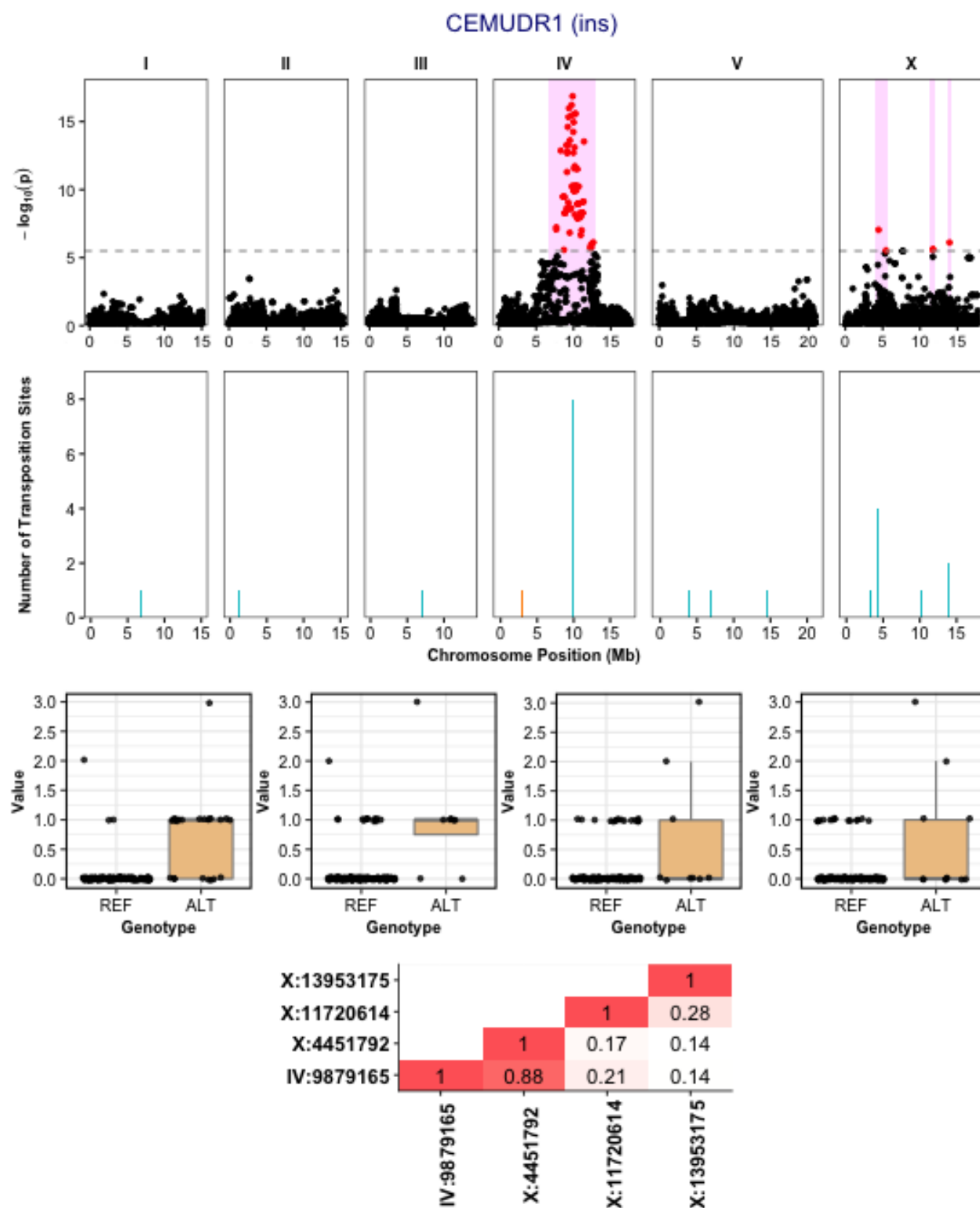
CELE42 (ins)

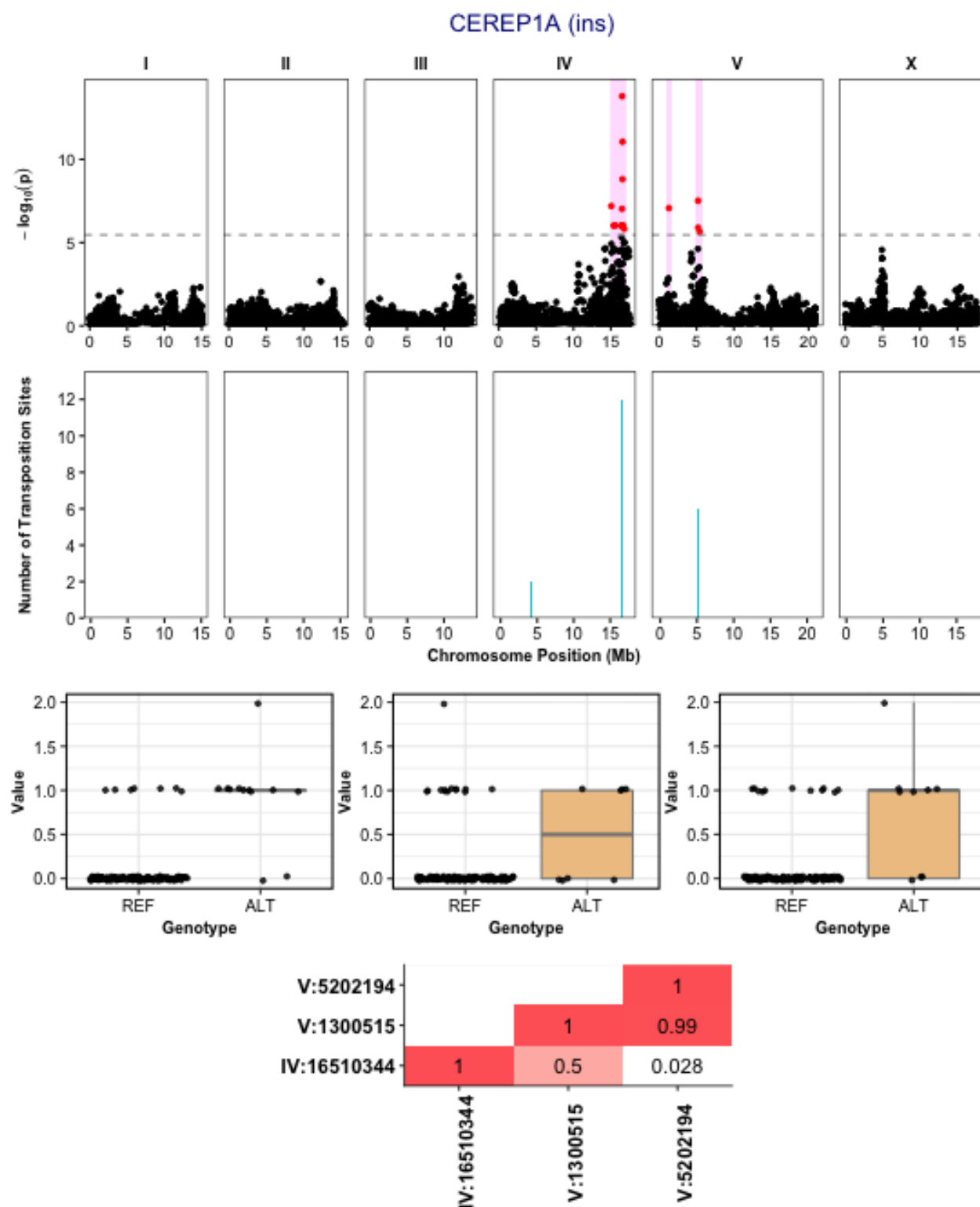


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III:12613203	1	0.21
	III:12613203	IV:5409635

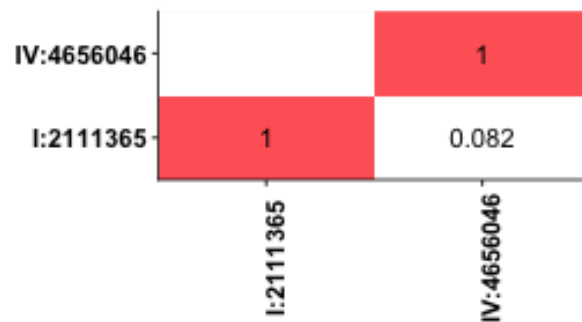
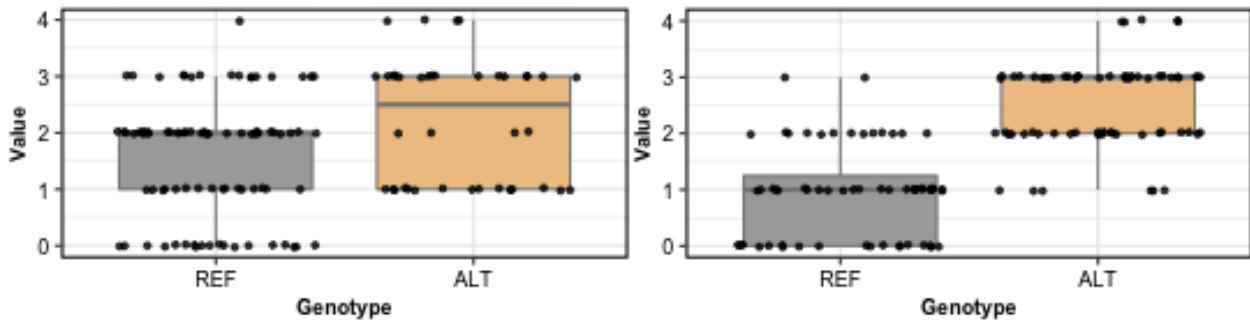
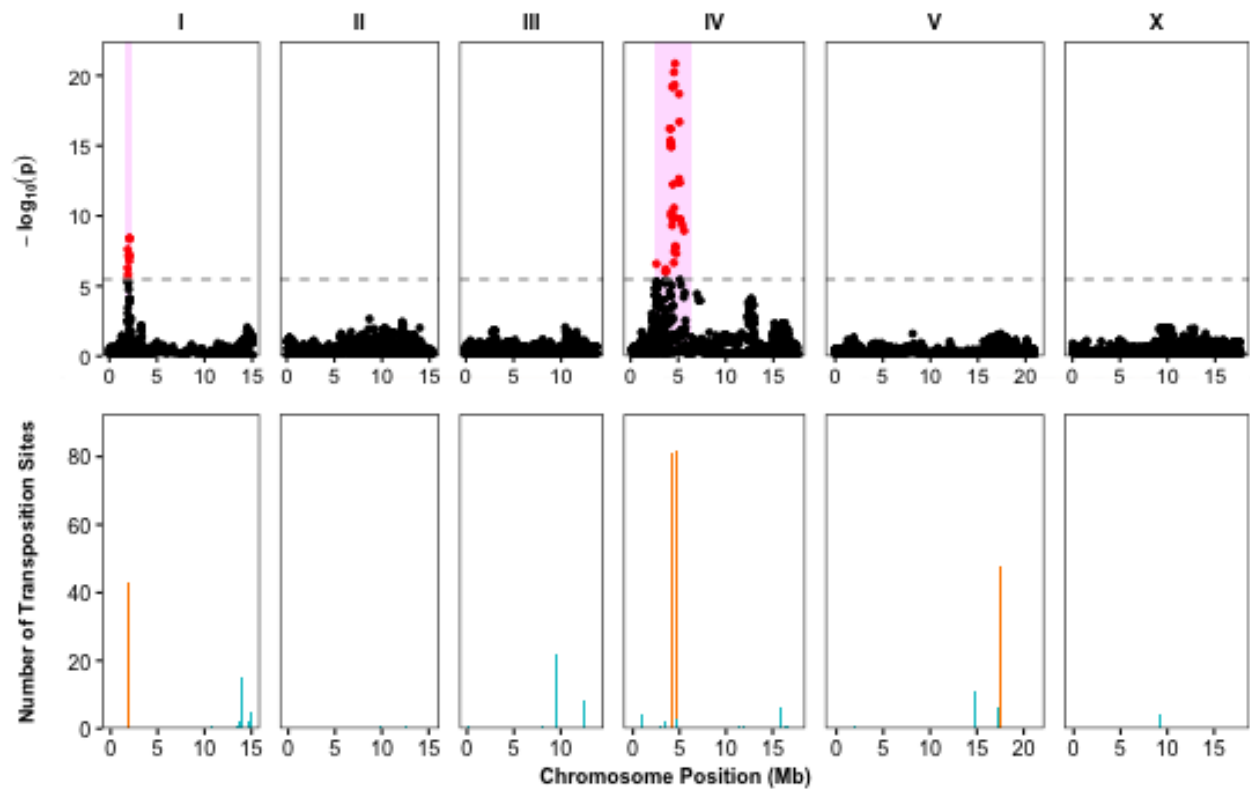




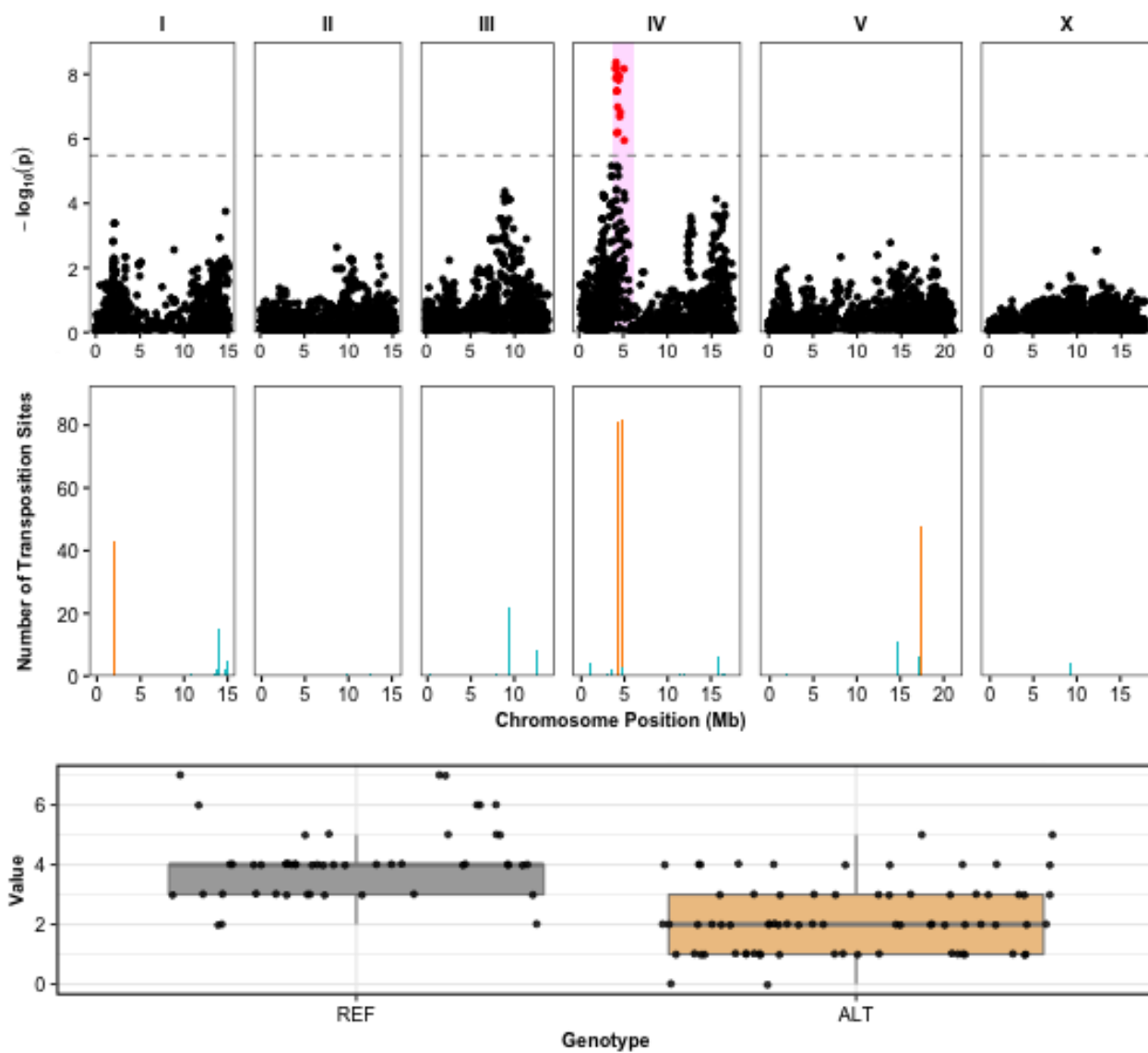




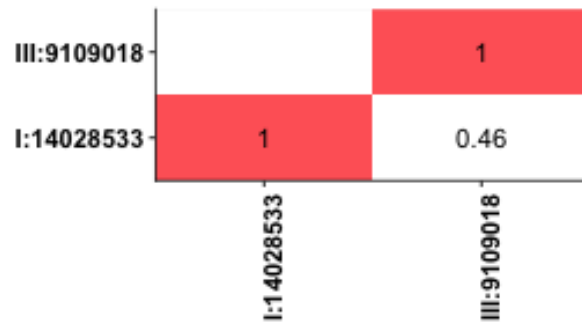
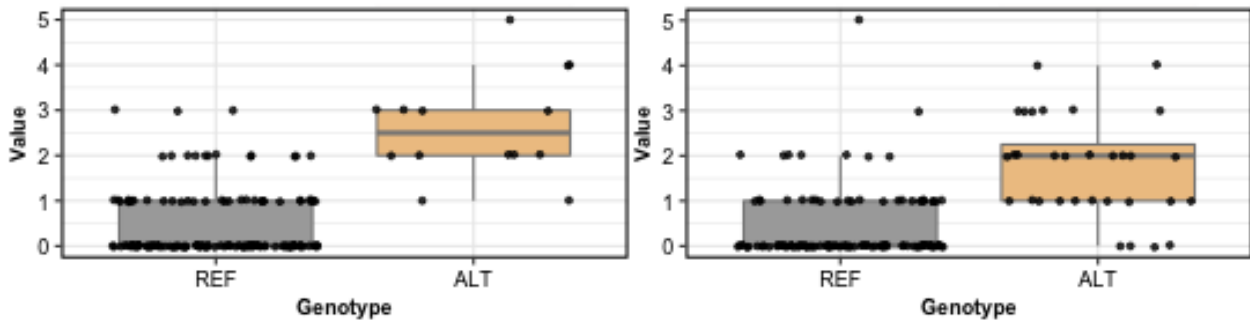
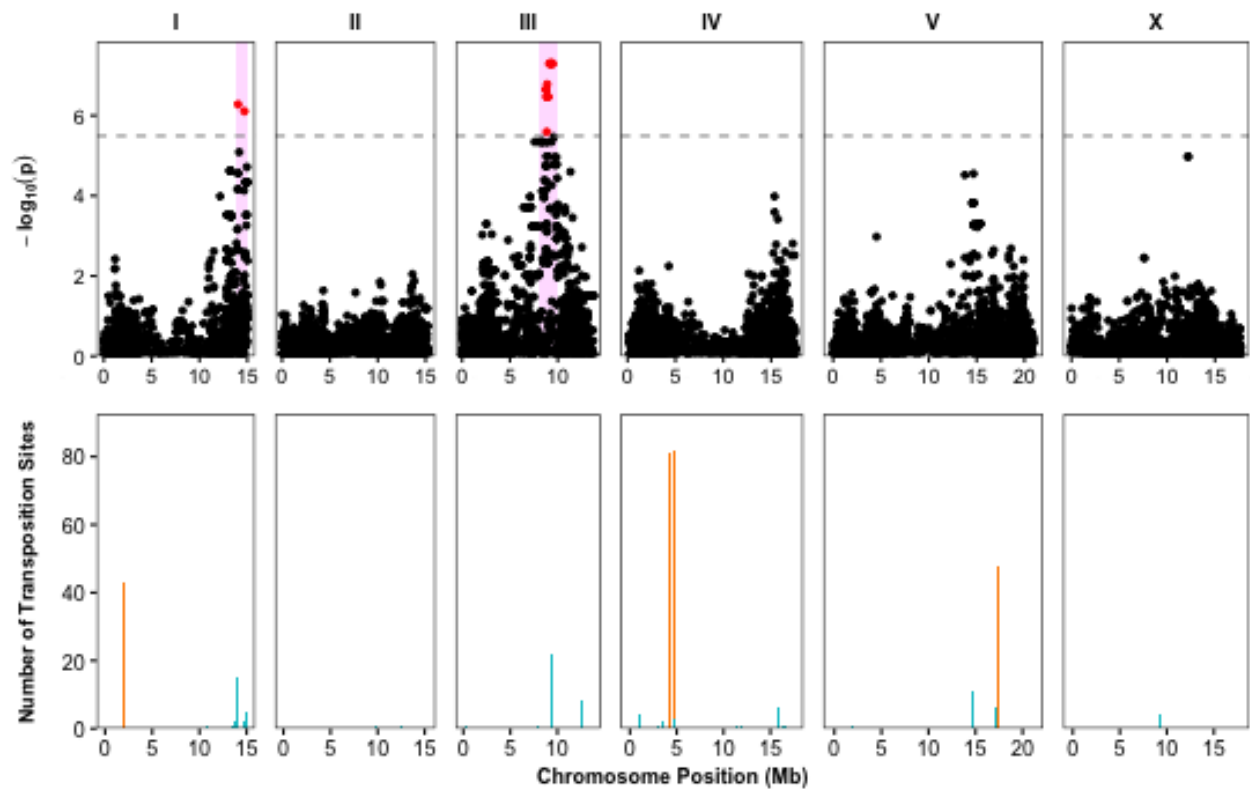
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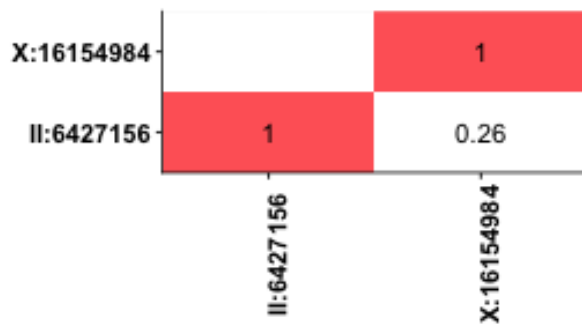
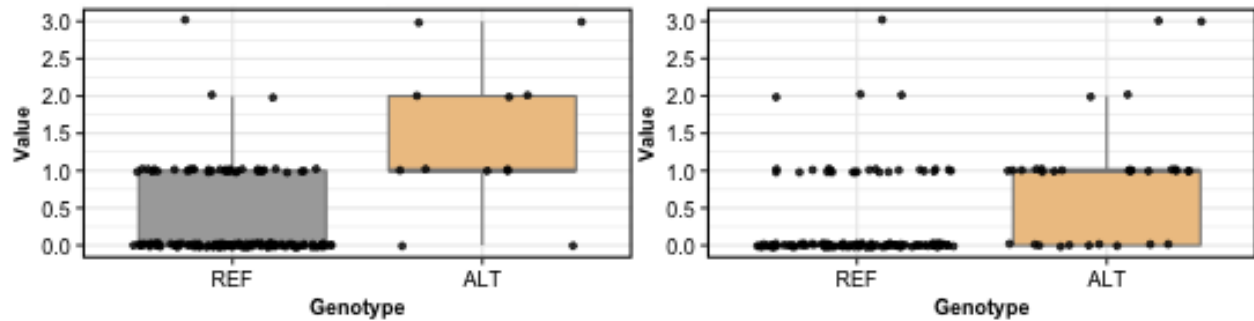
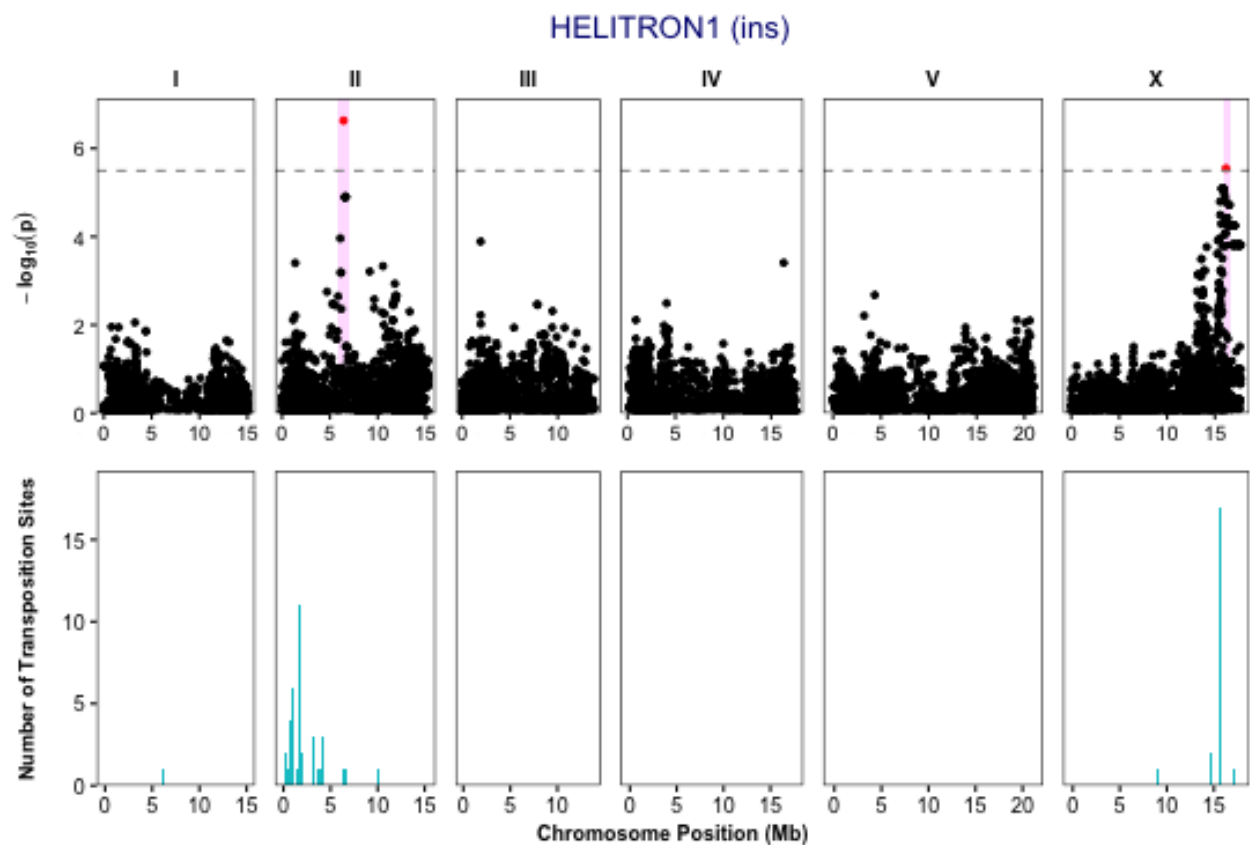


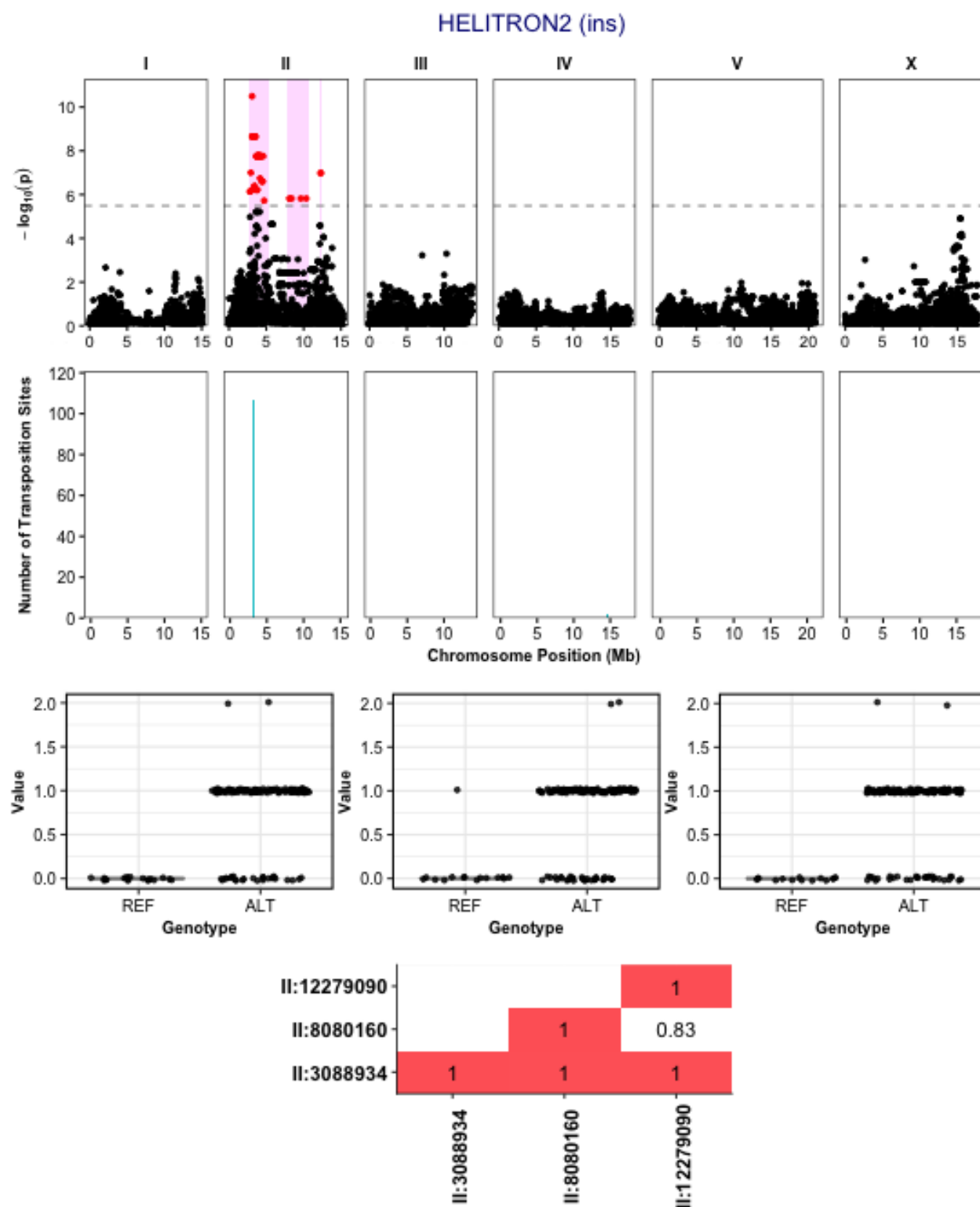
Chapaev-1 (all)

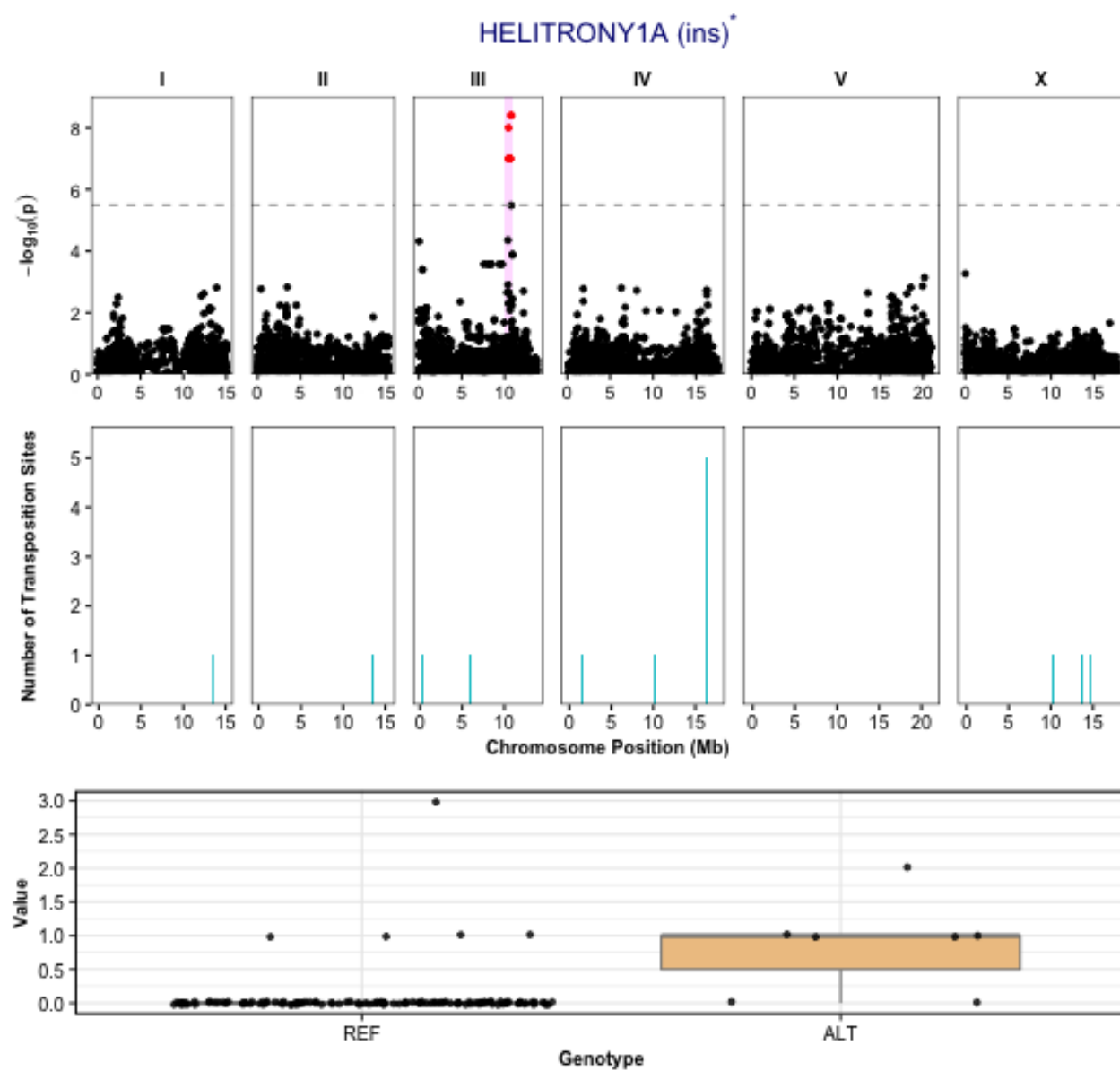


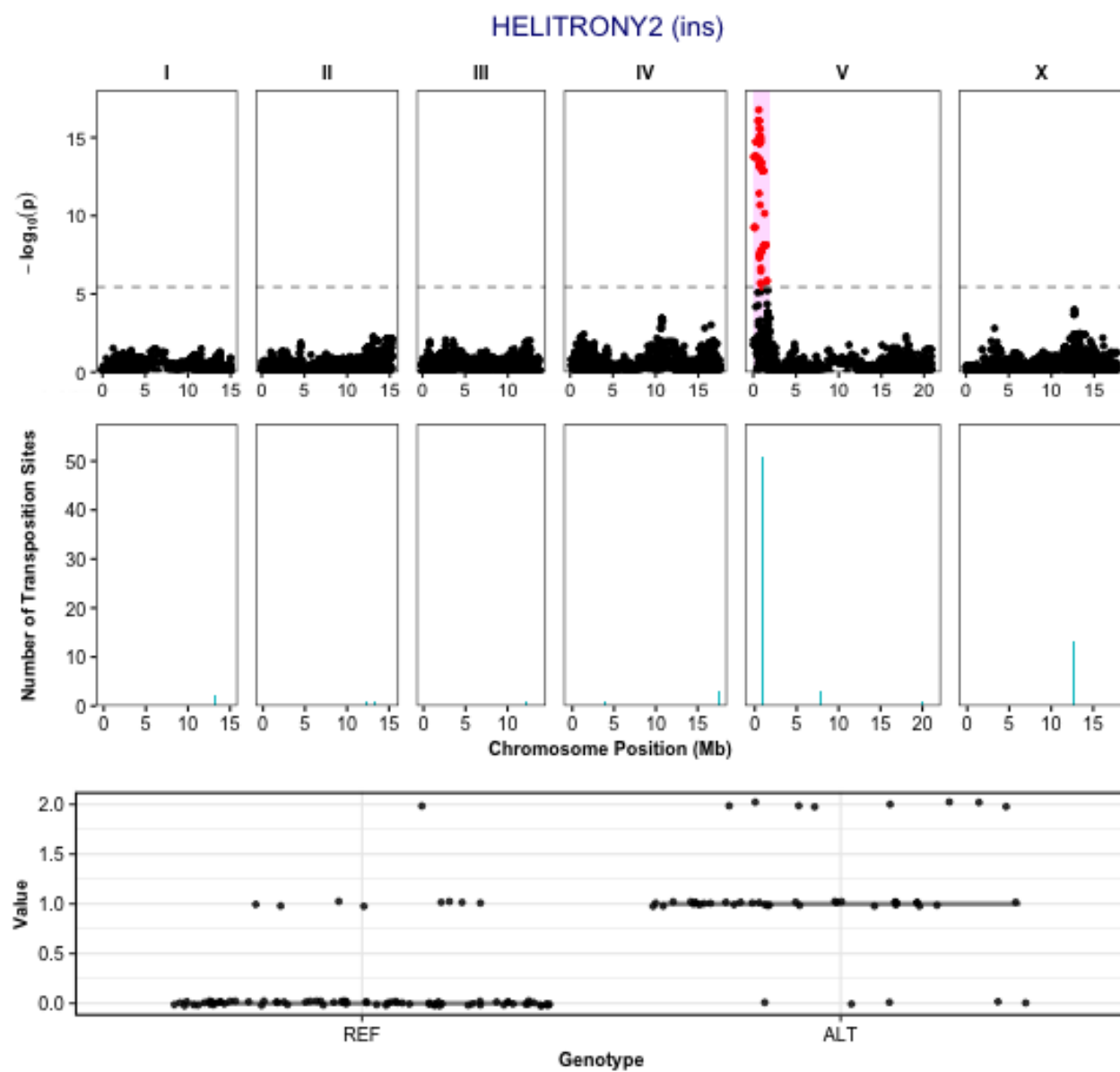
Chapaev-1 (ins)

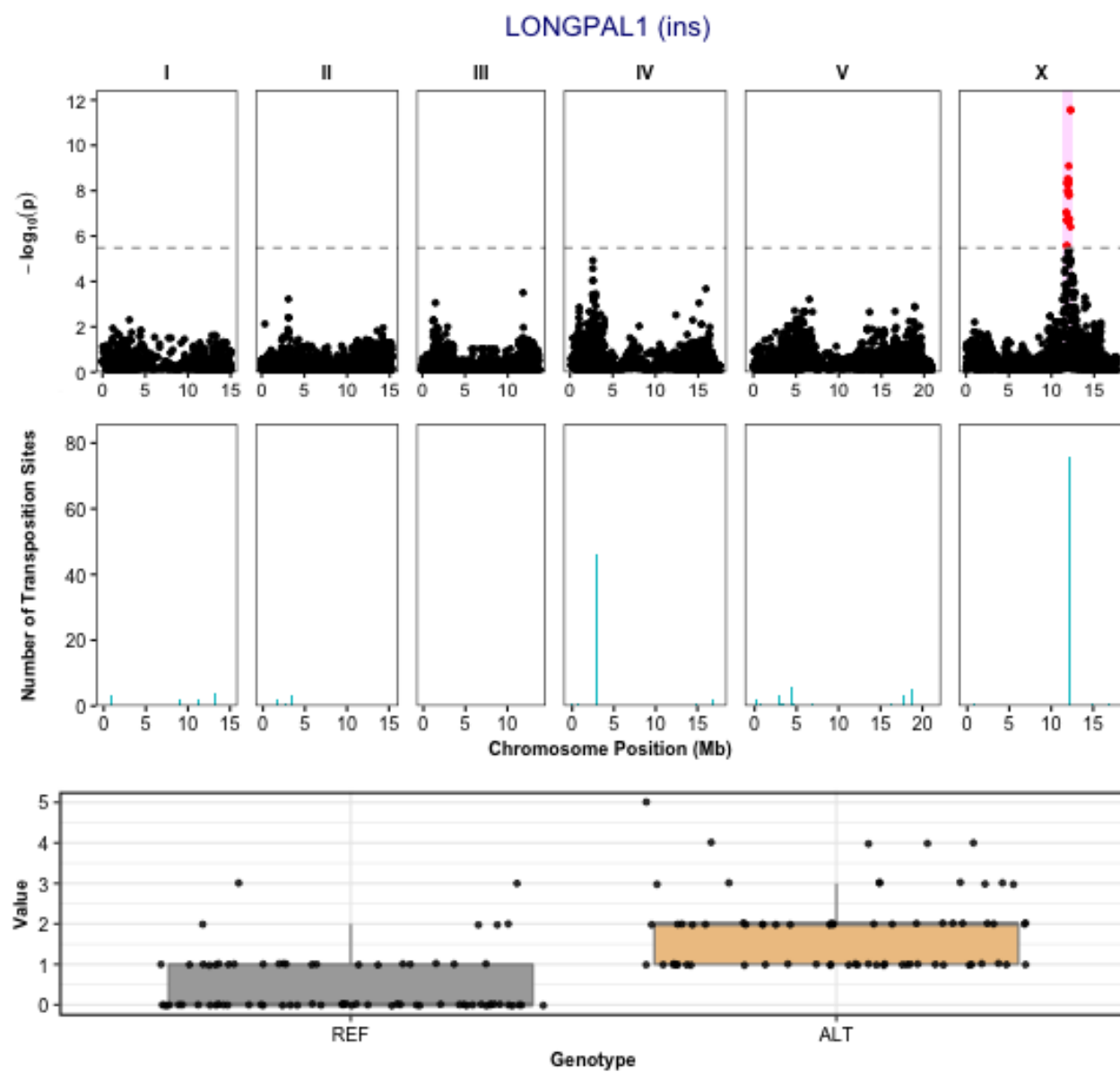


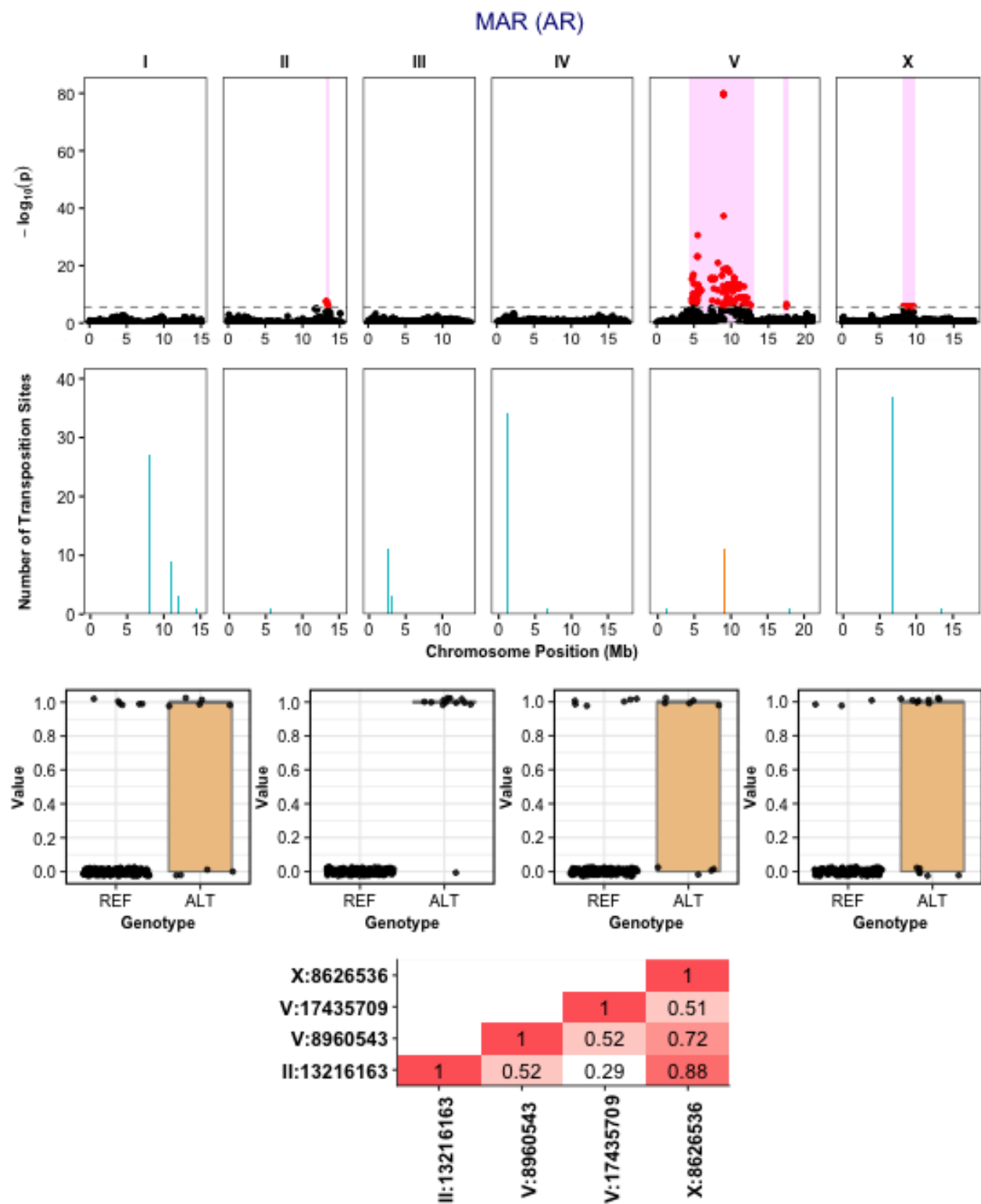




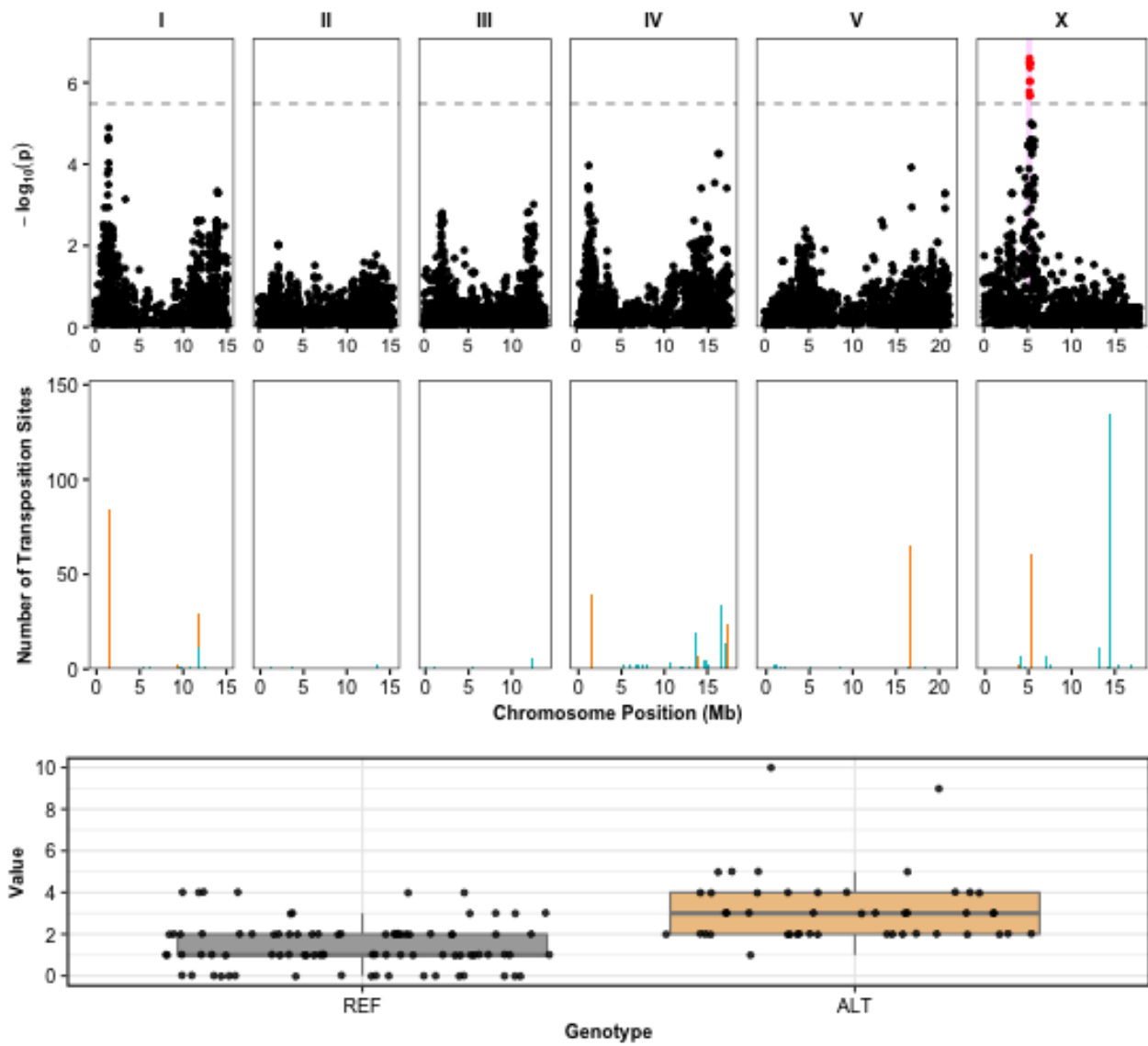




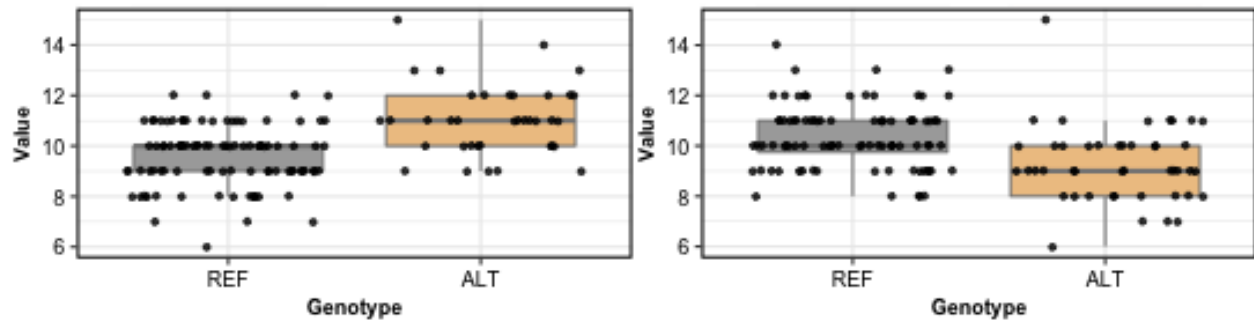
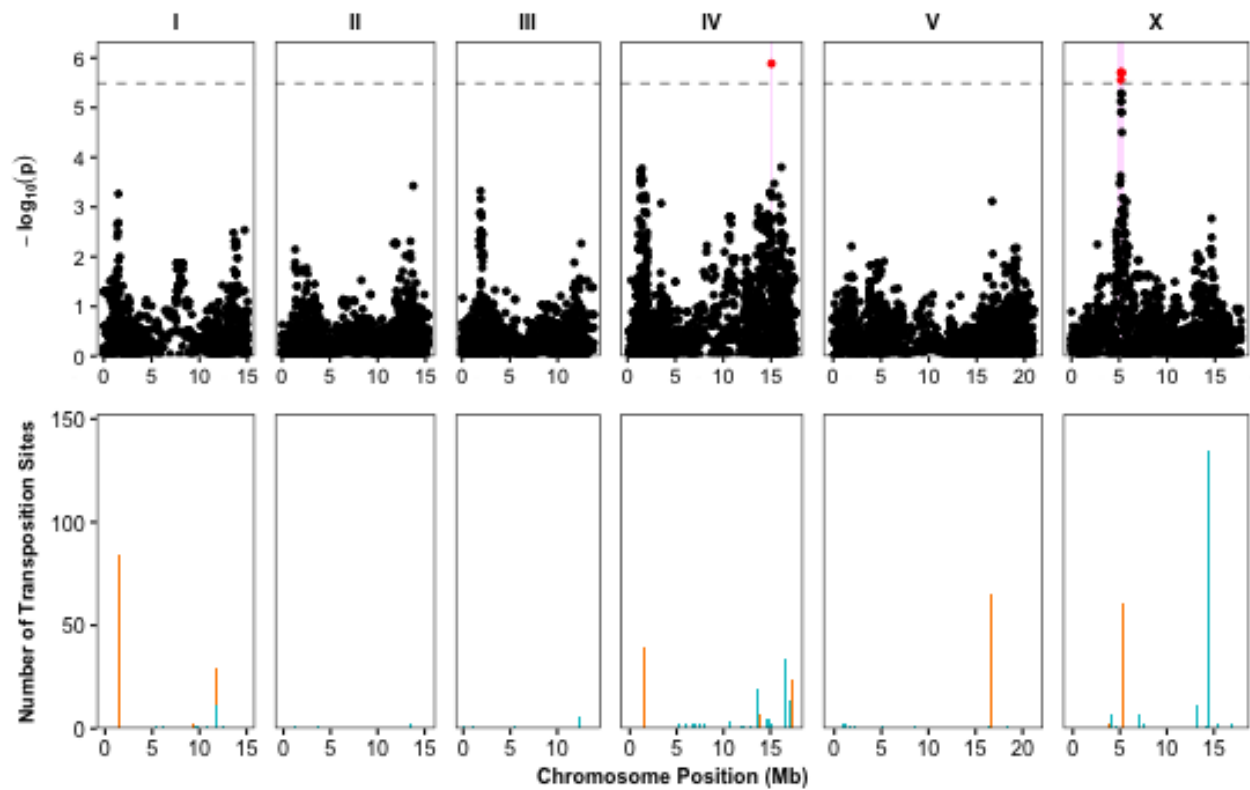




MARINCE1 (AR)

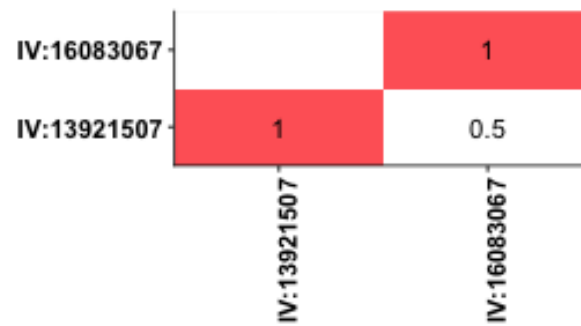
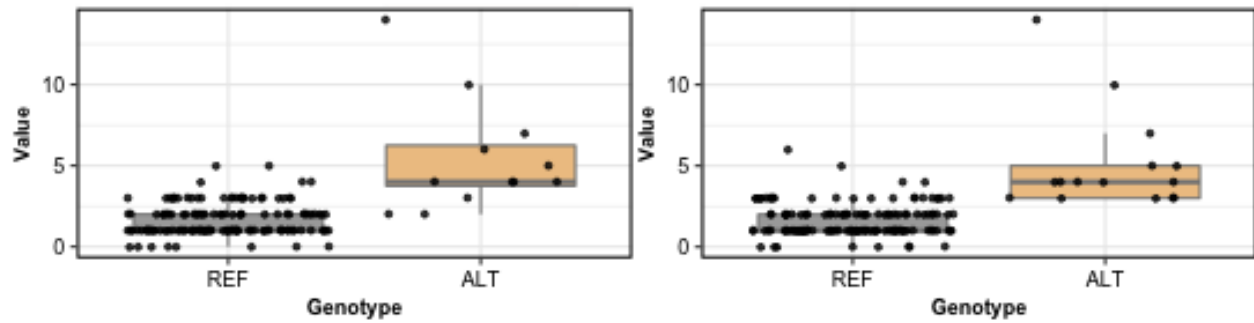
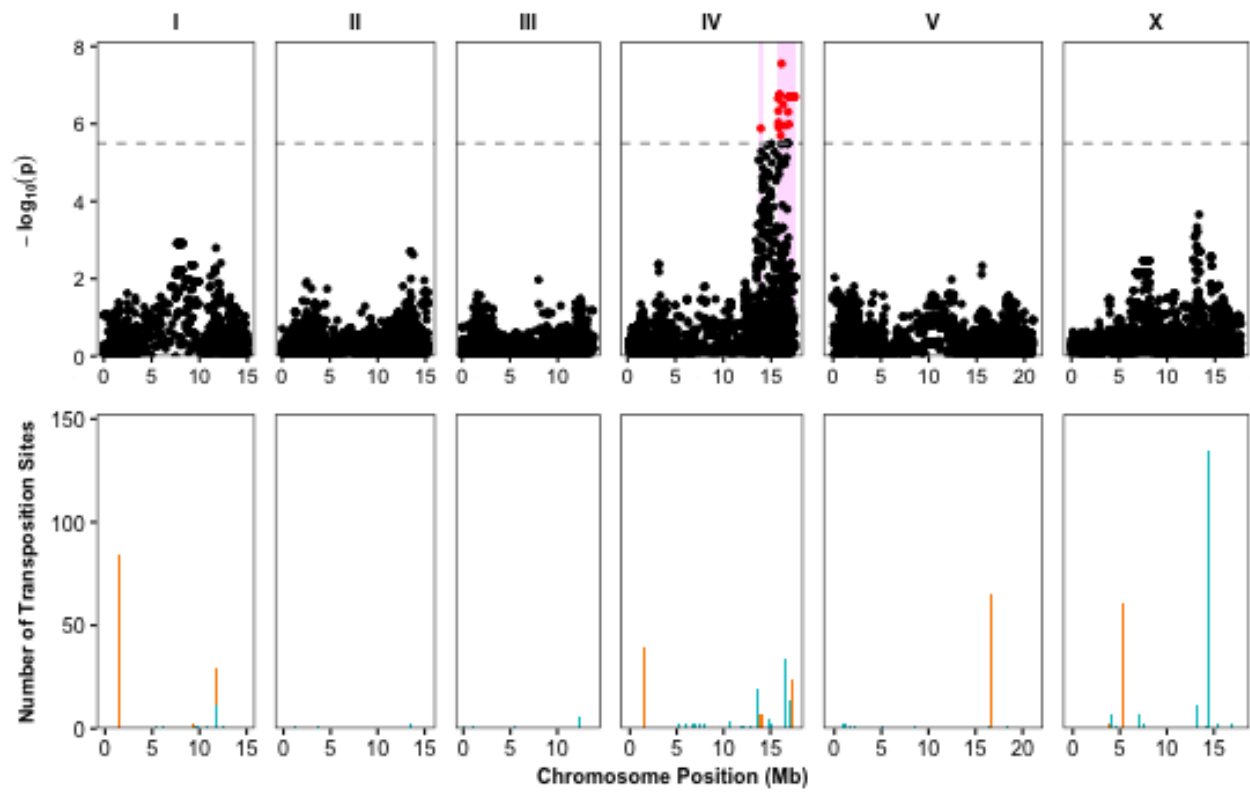


MARINCE1 (all)

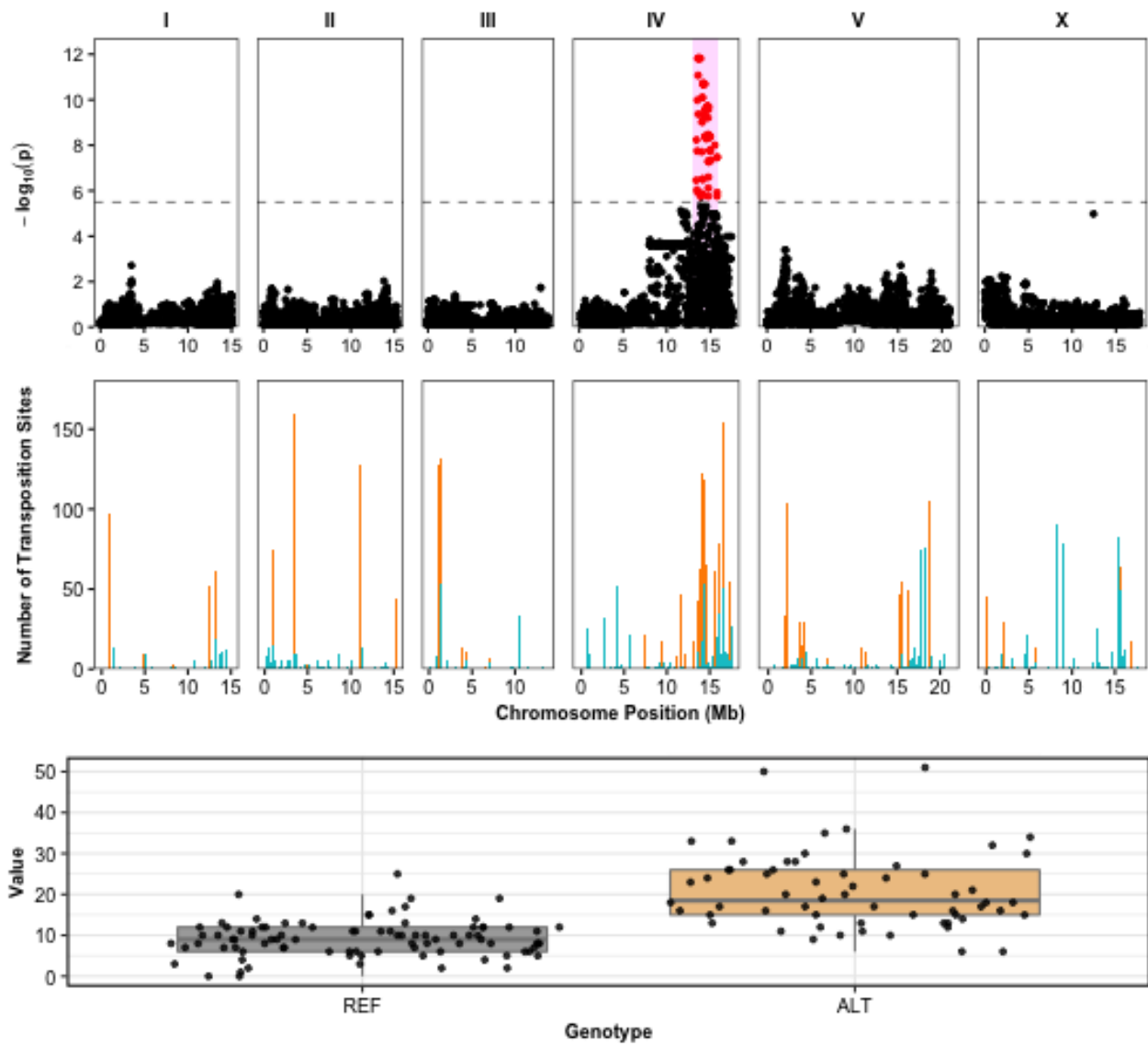


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IV:15044238	1	0.15
	IV:15044238	X:5193340

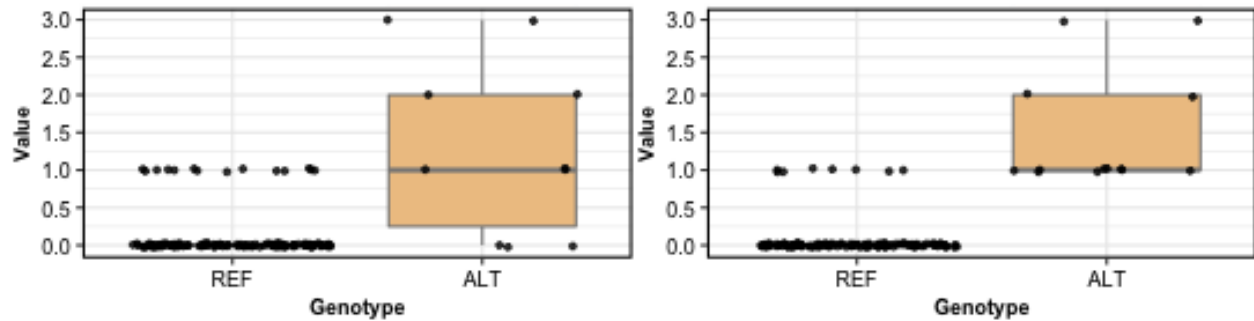
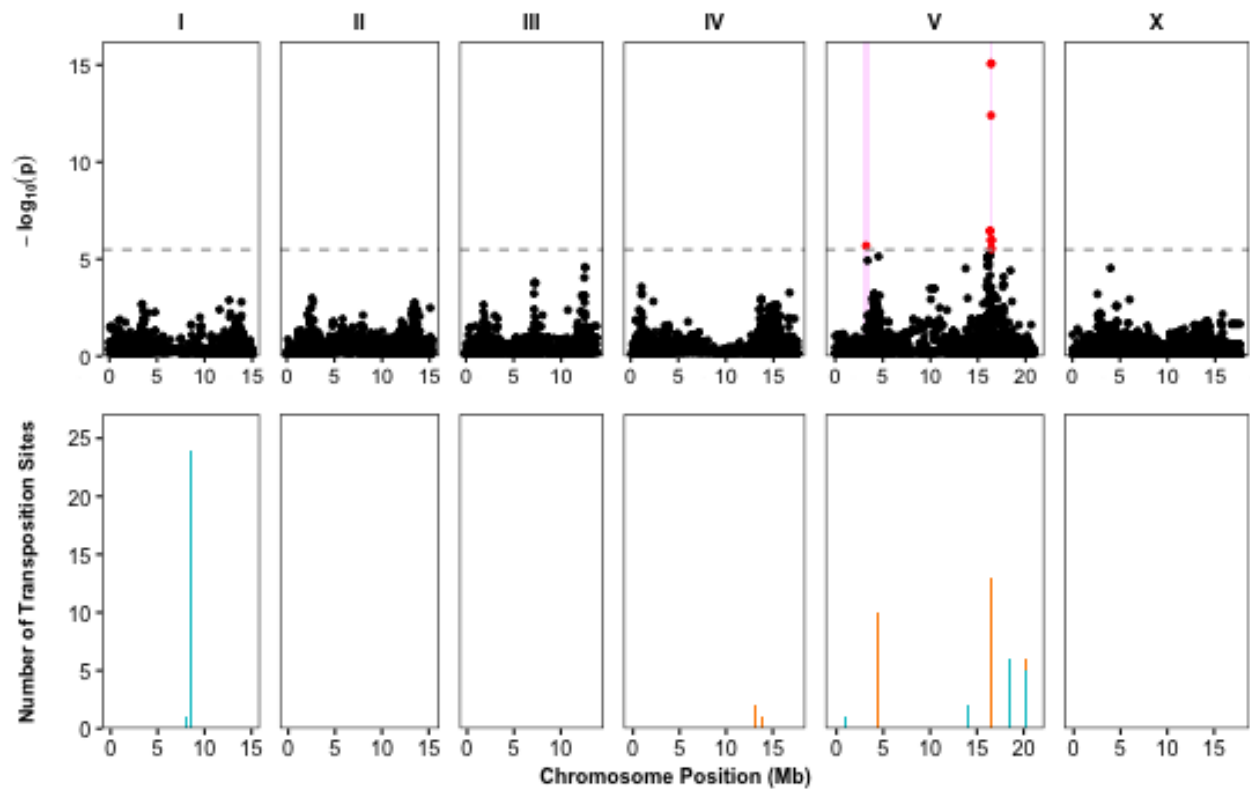
MARINCE1 (ins)



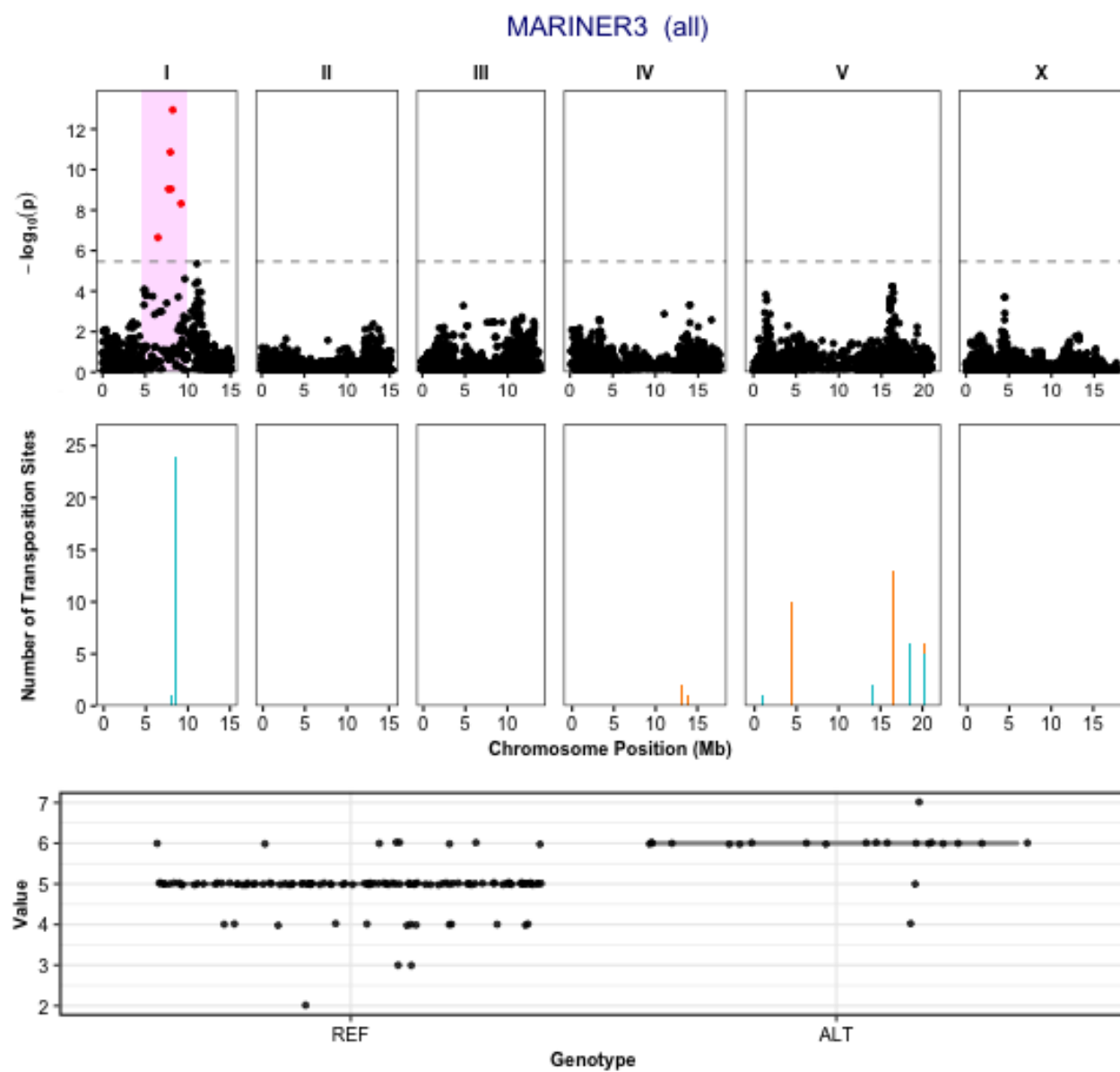
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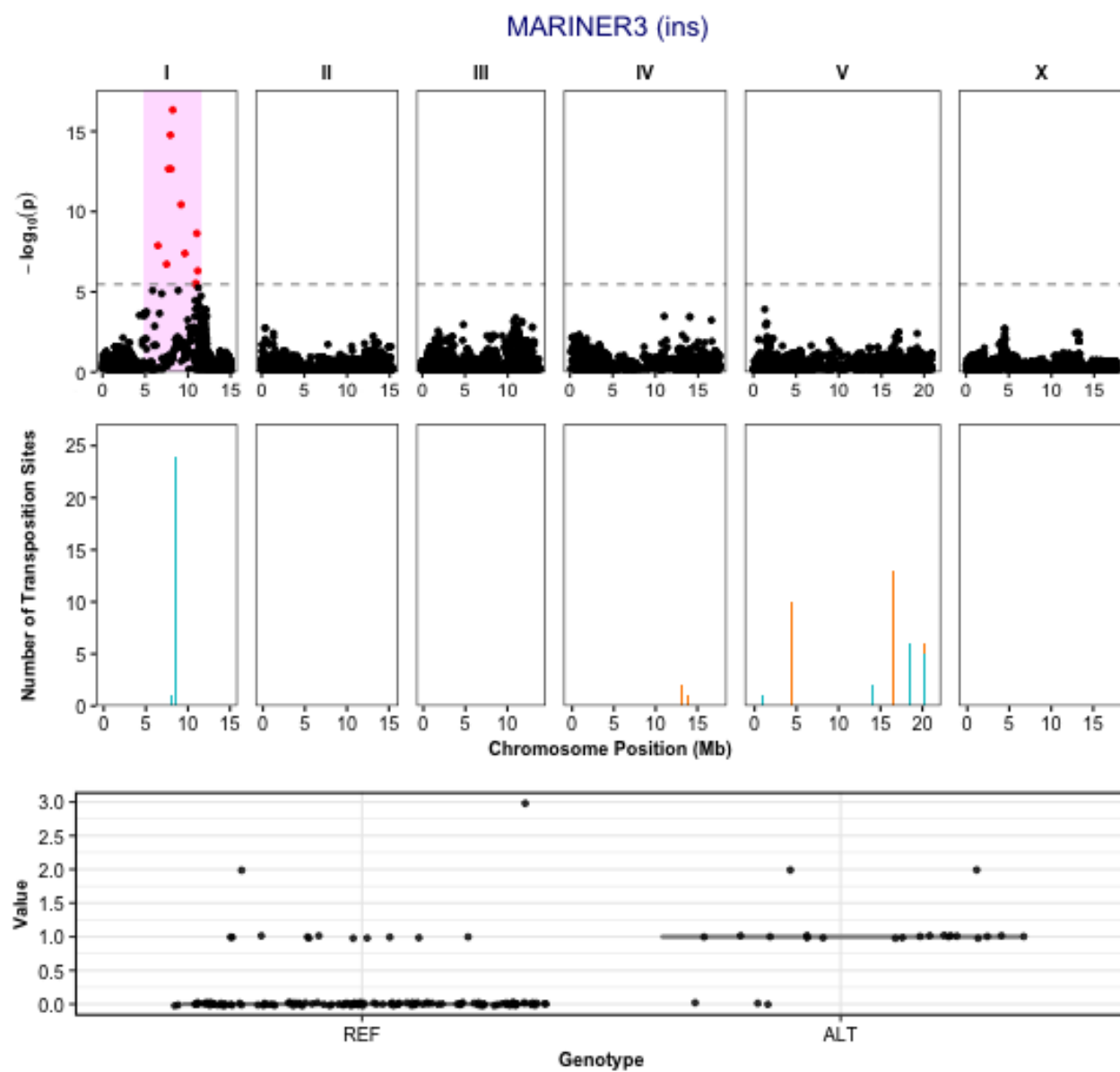


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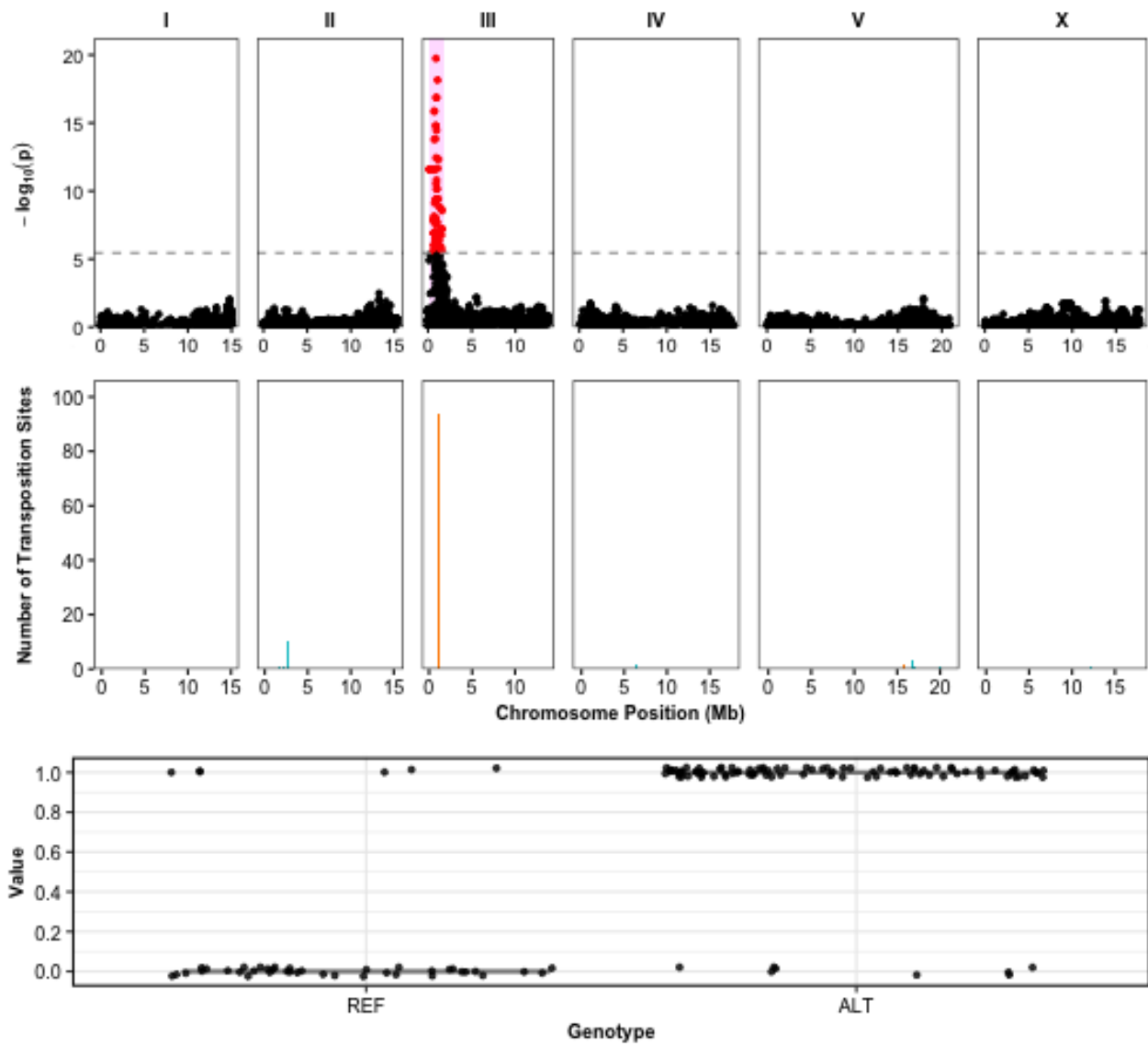


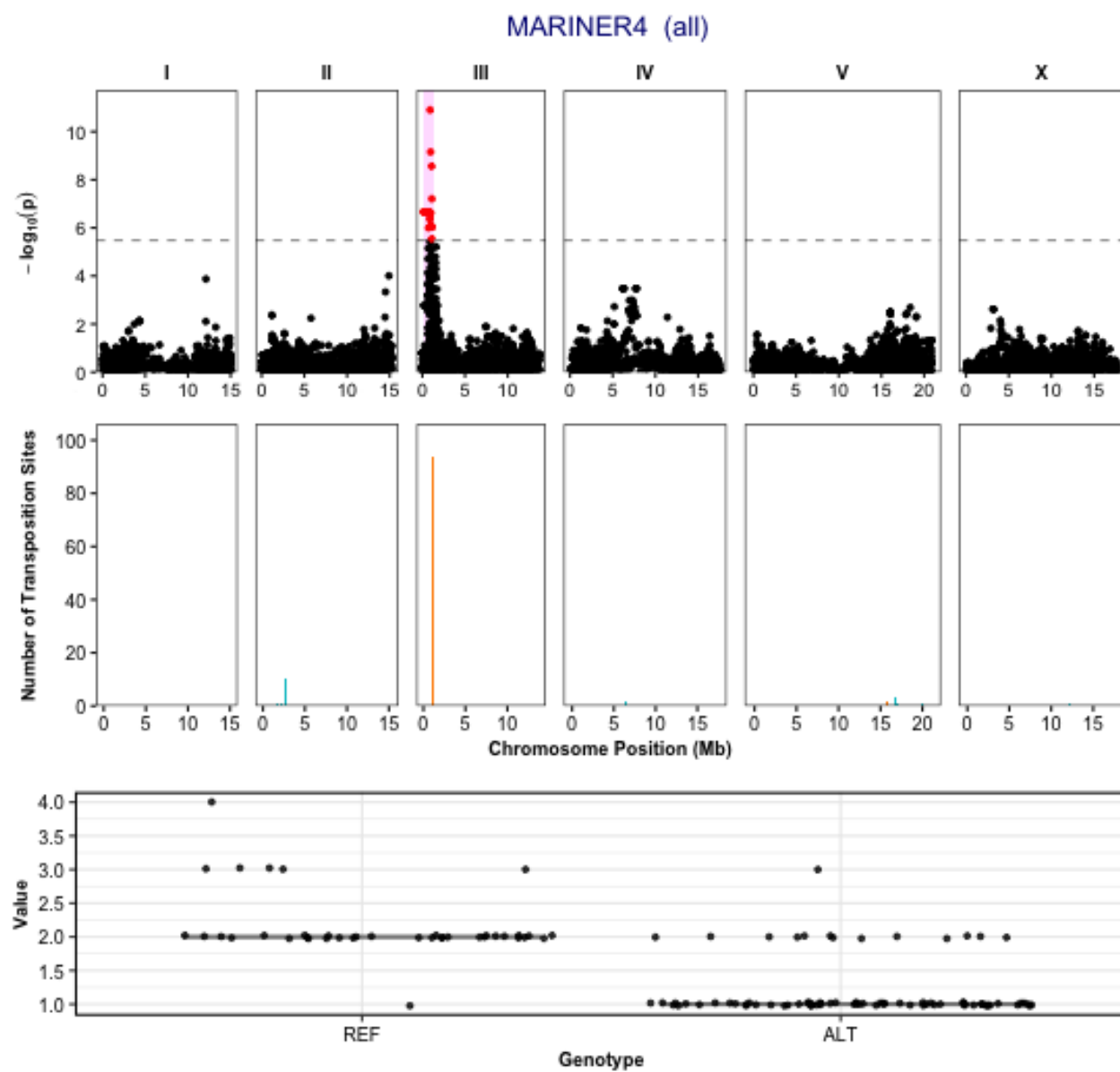
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V:3242075	1	0.51
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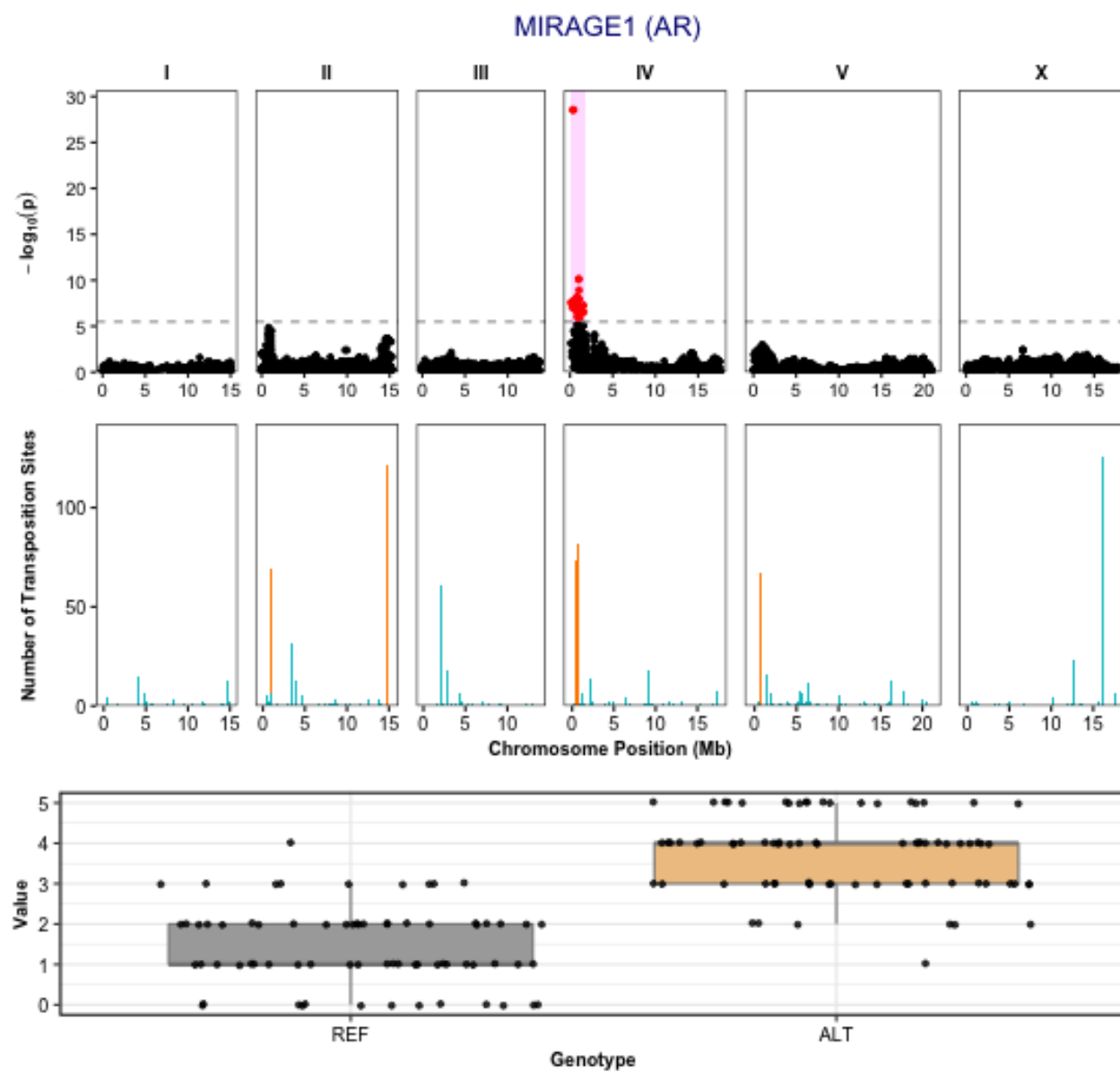




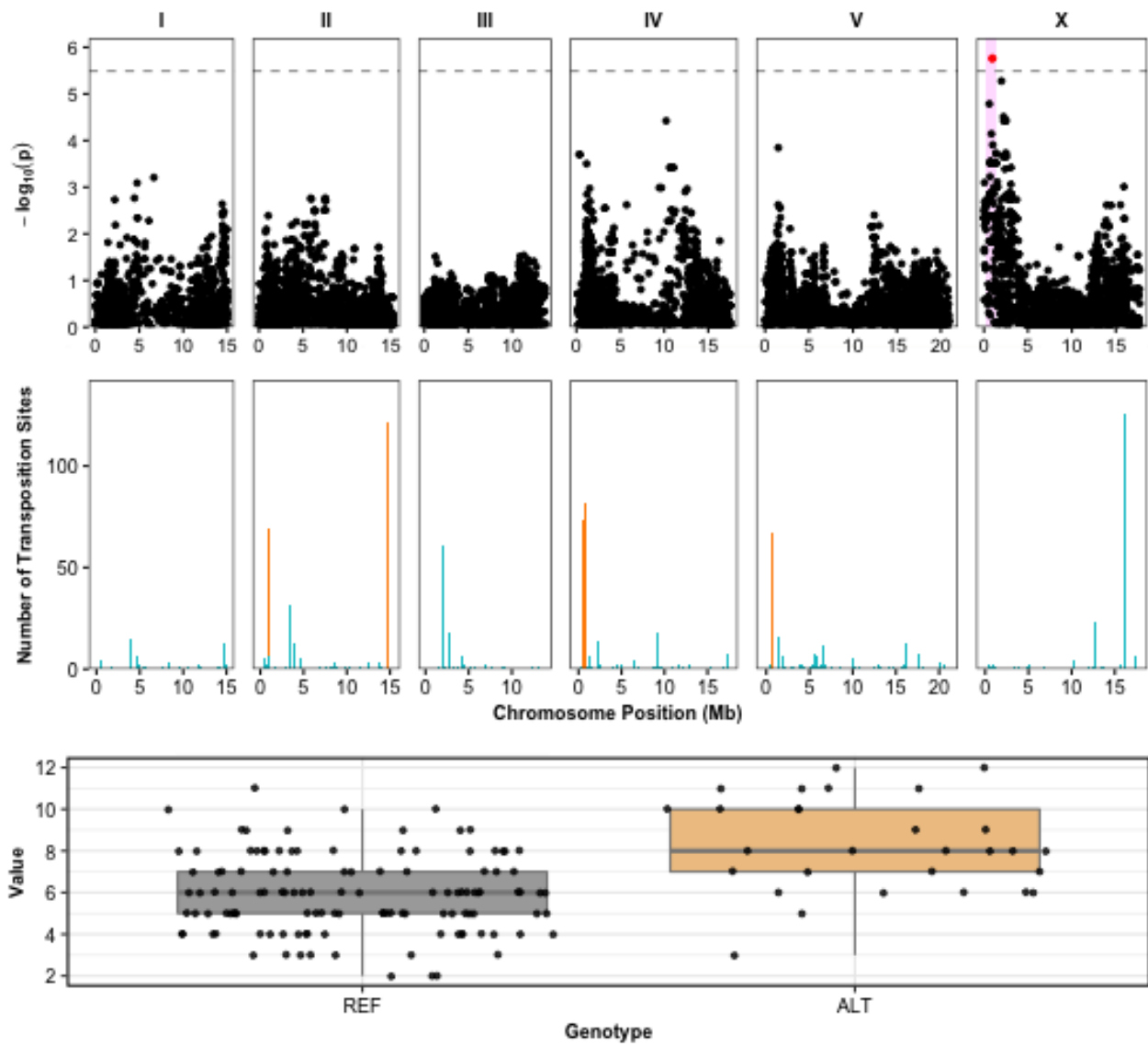
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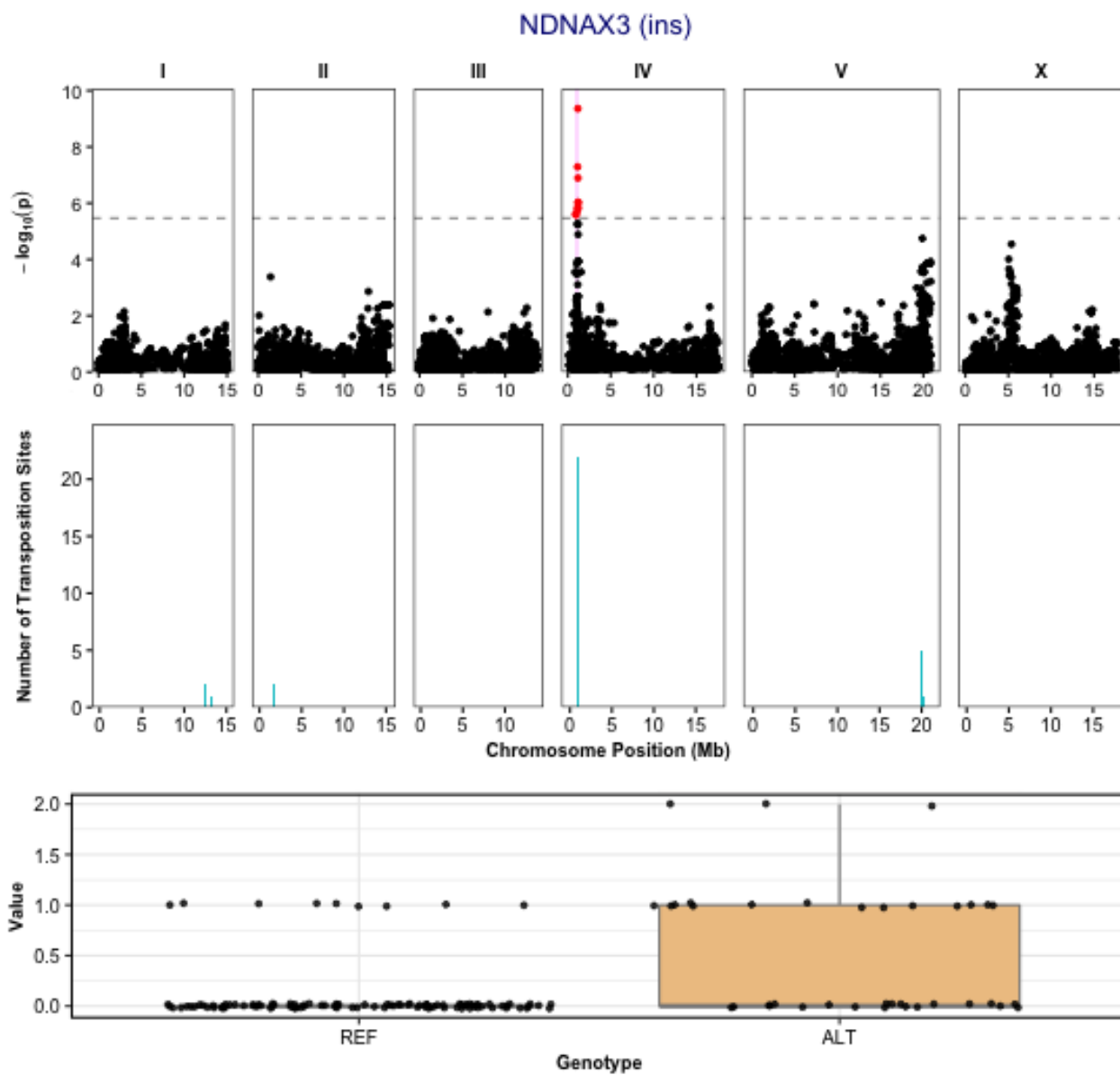


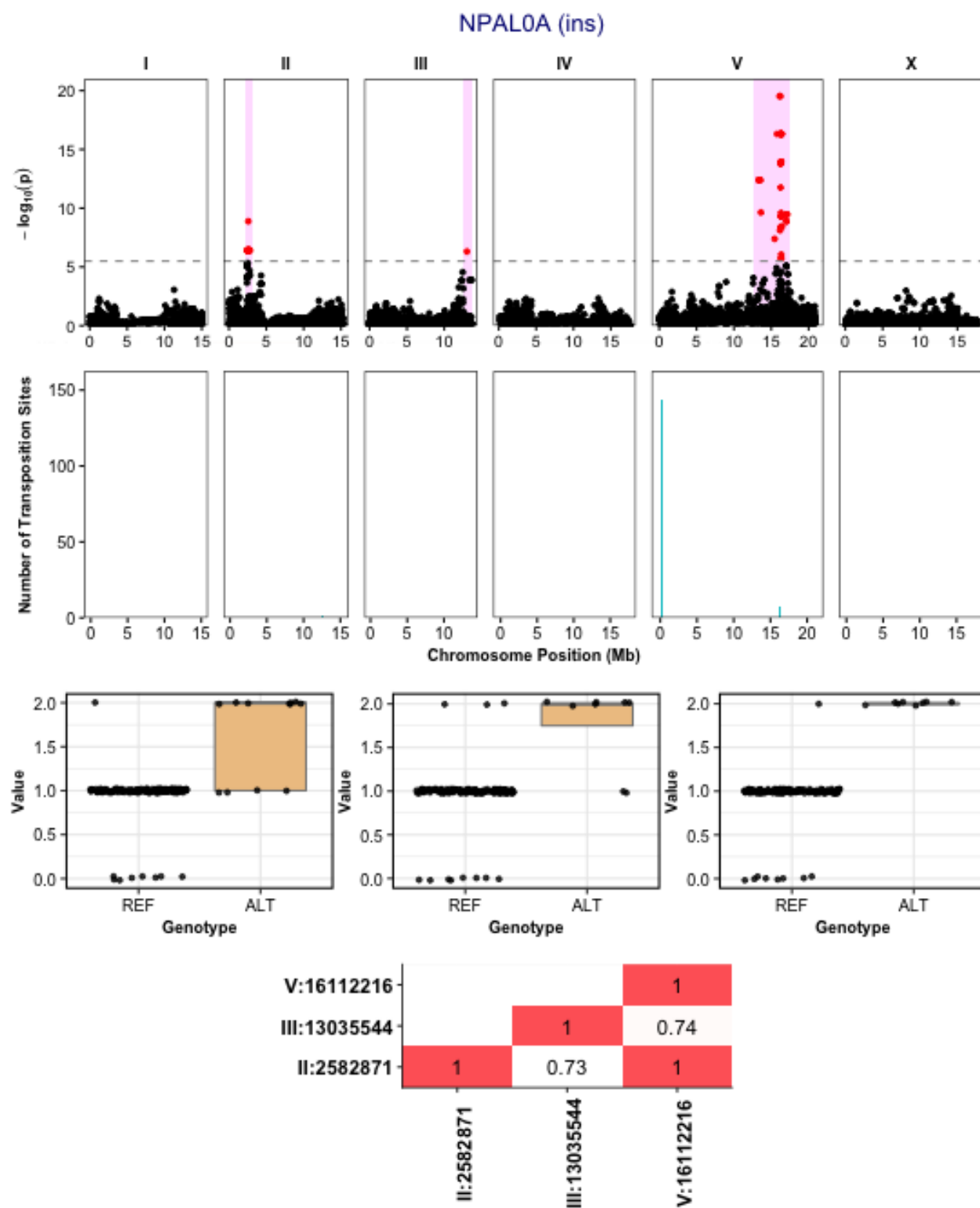


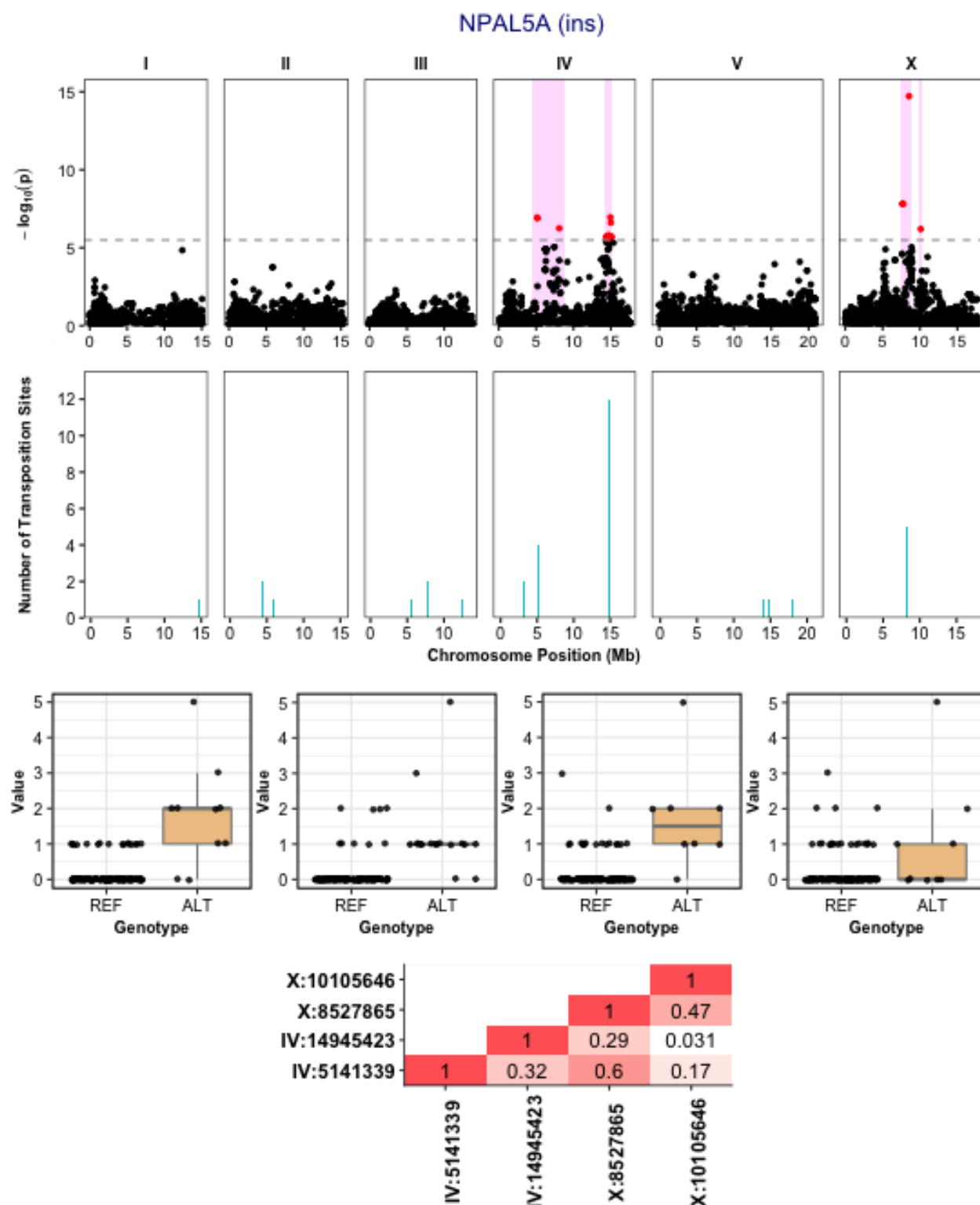


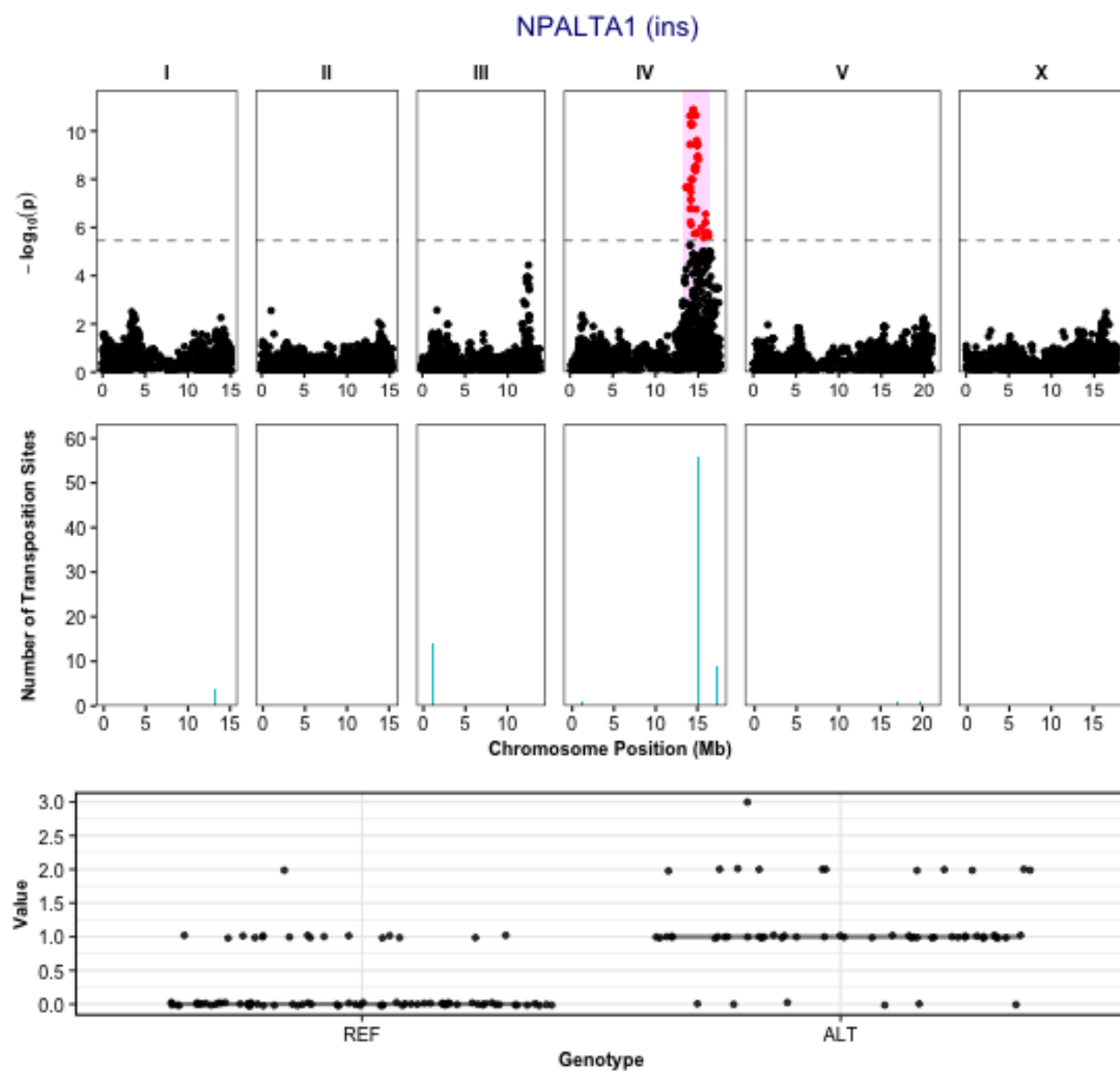
MIRAGE1 (all)

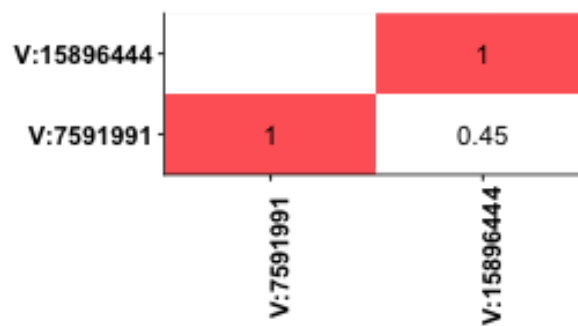
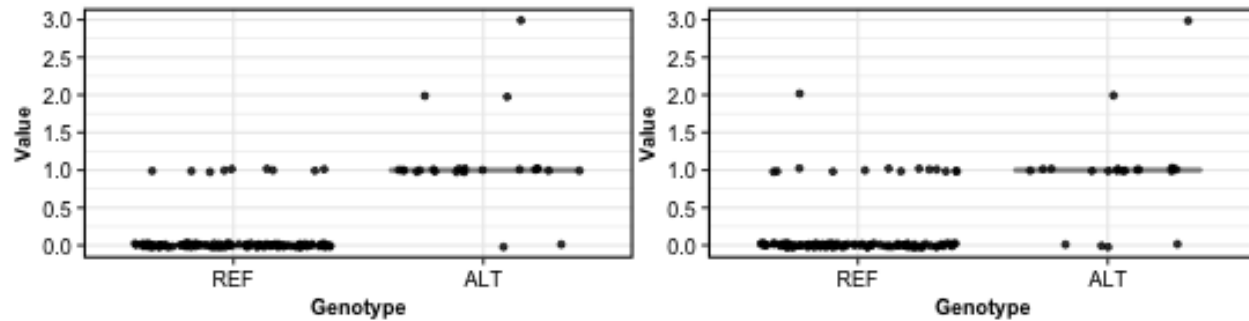
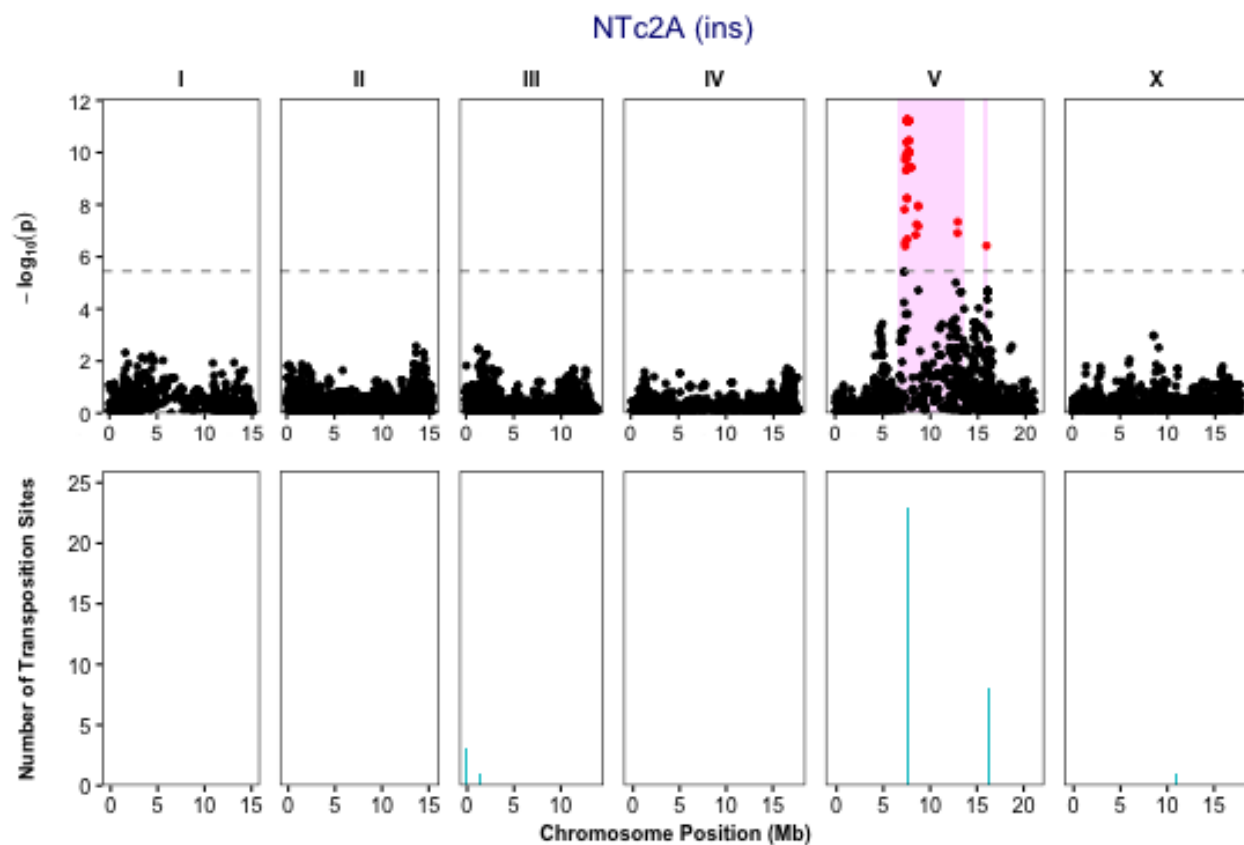


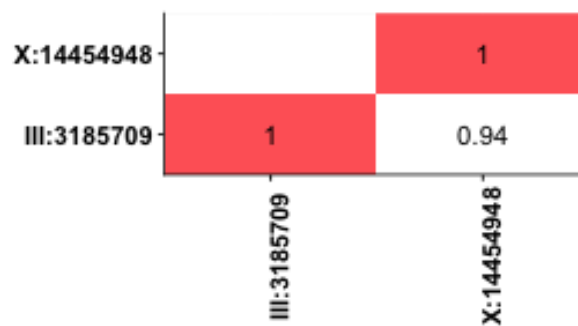
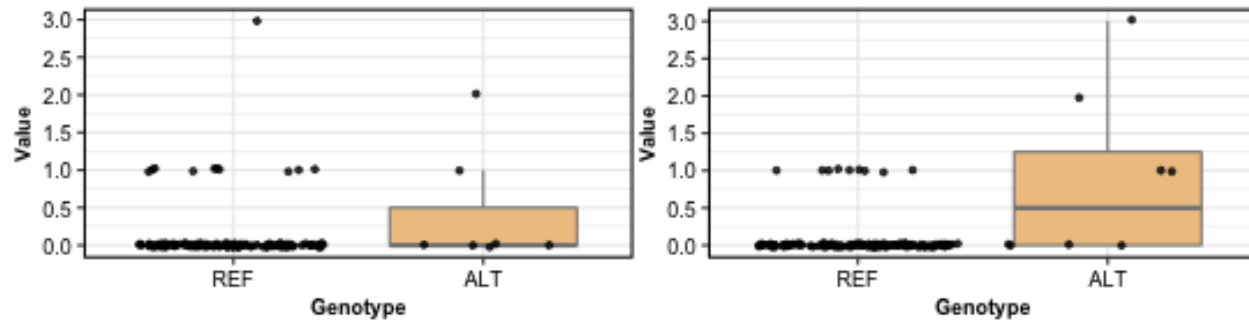
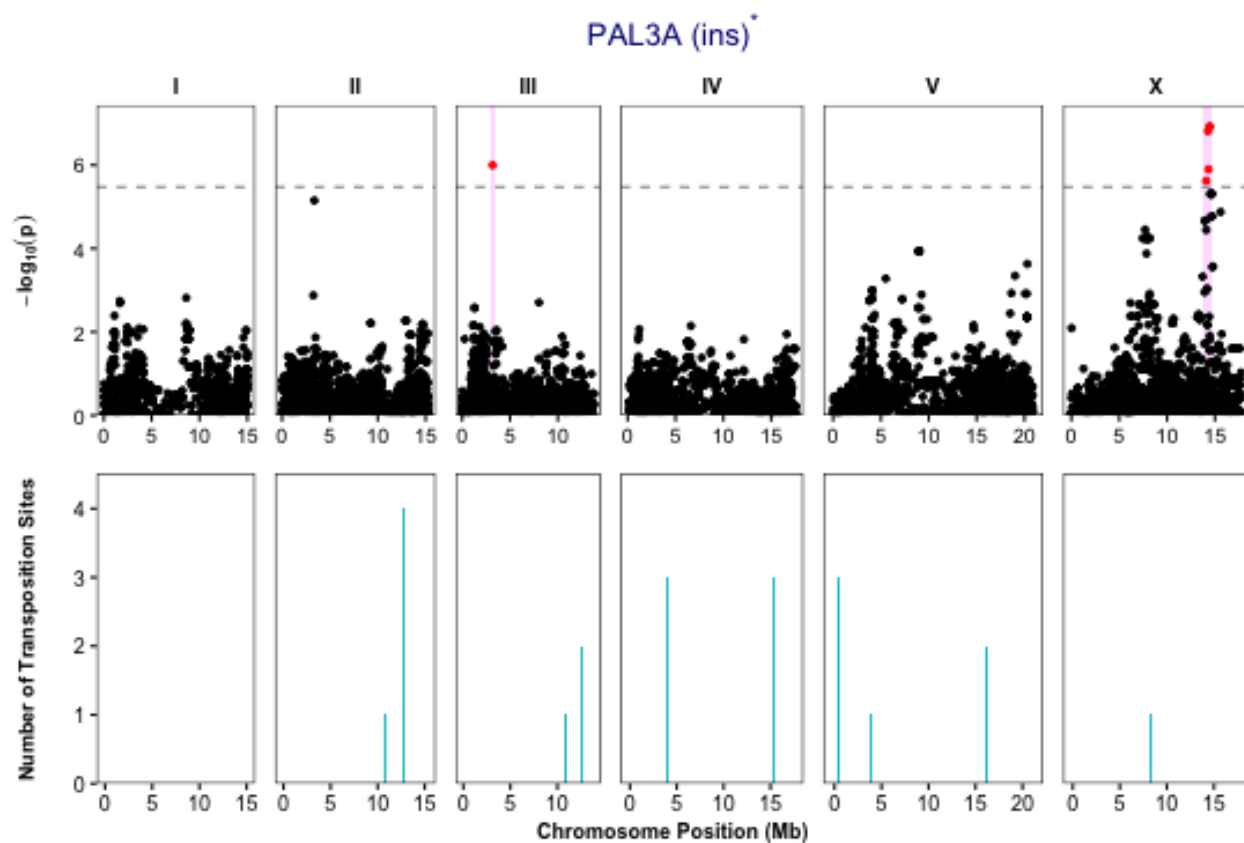


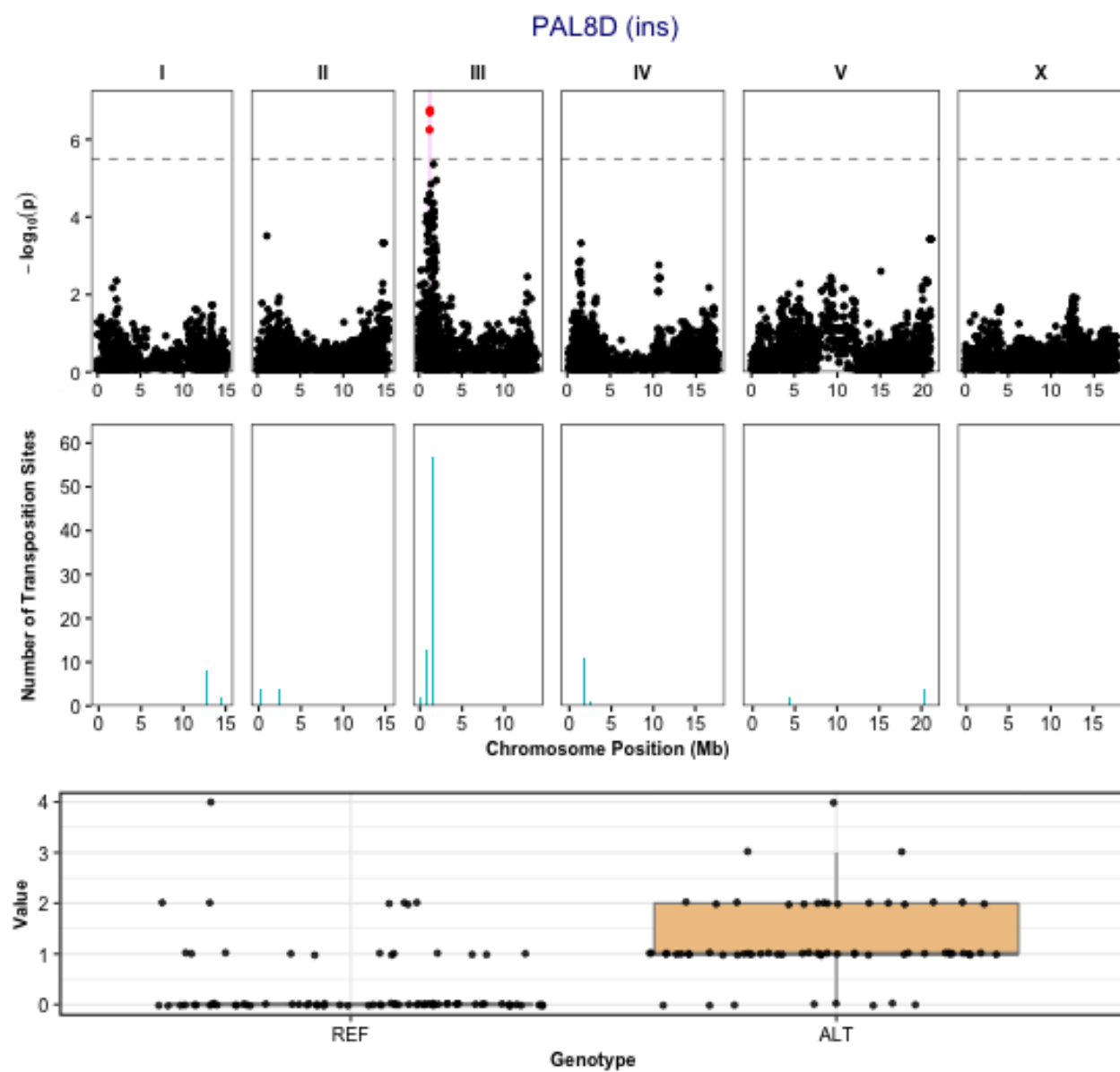


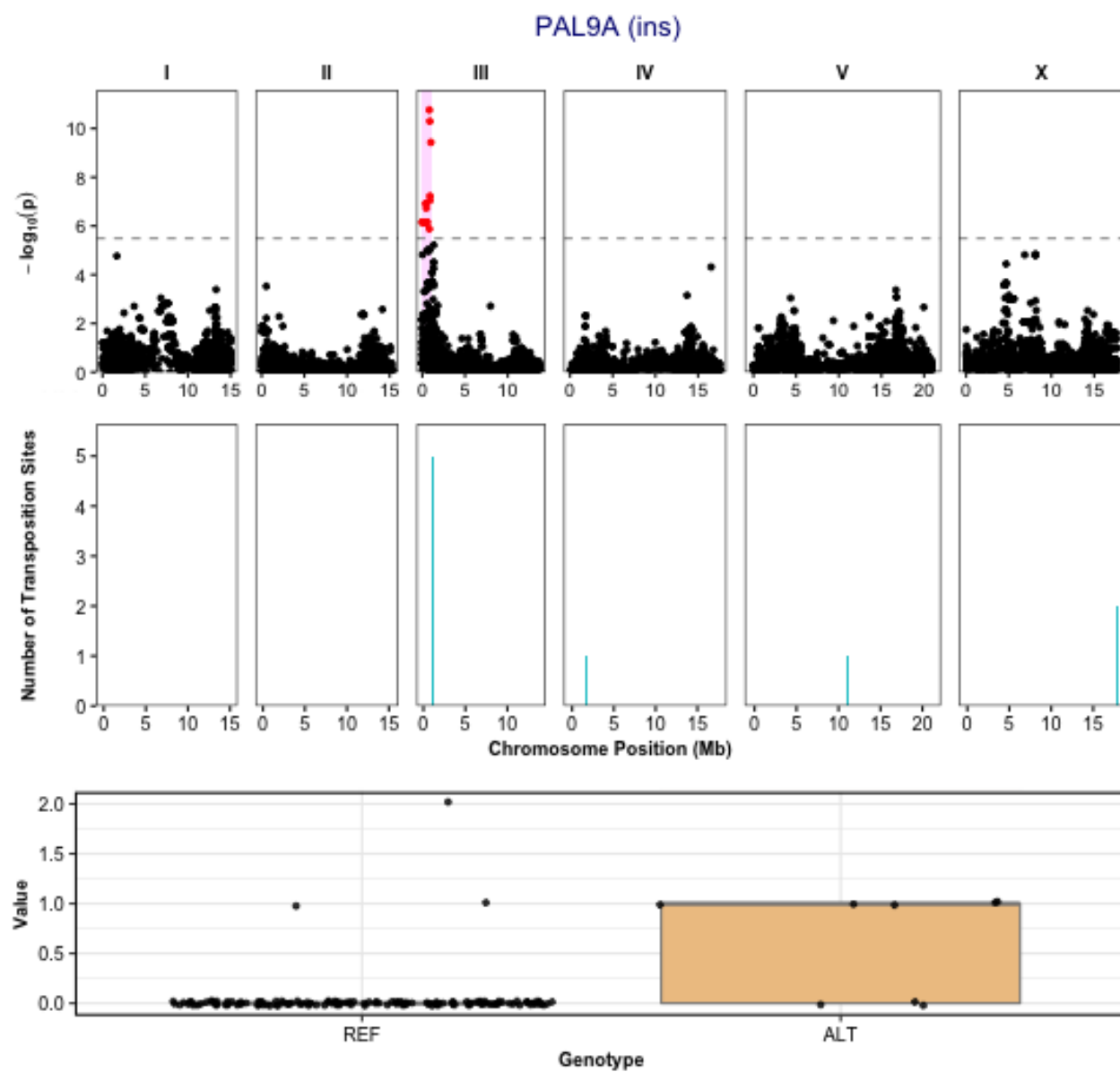


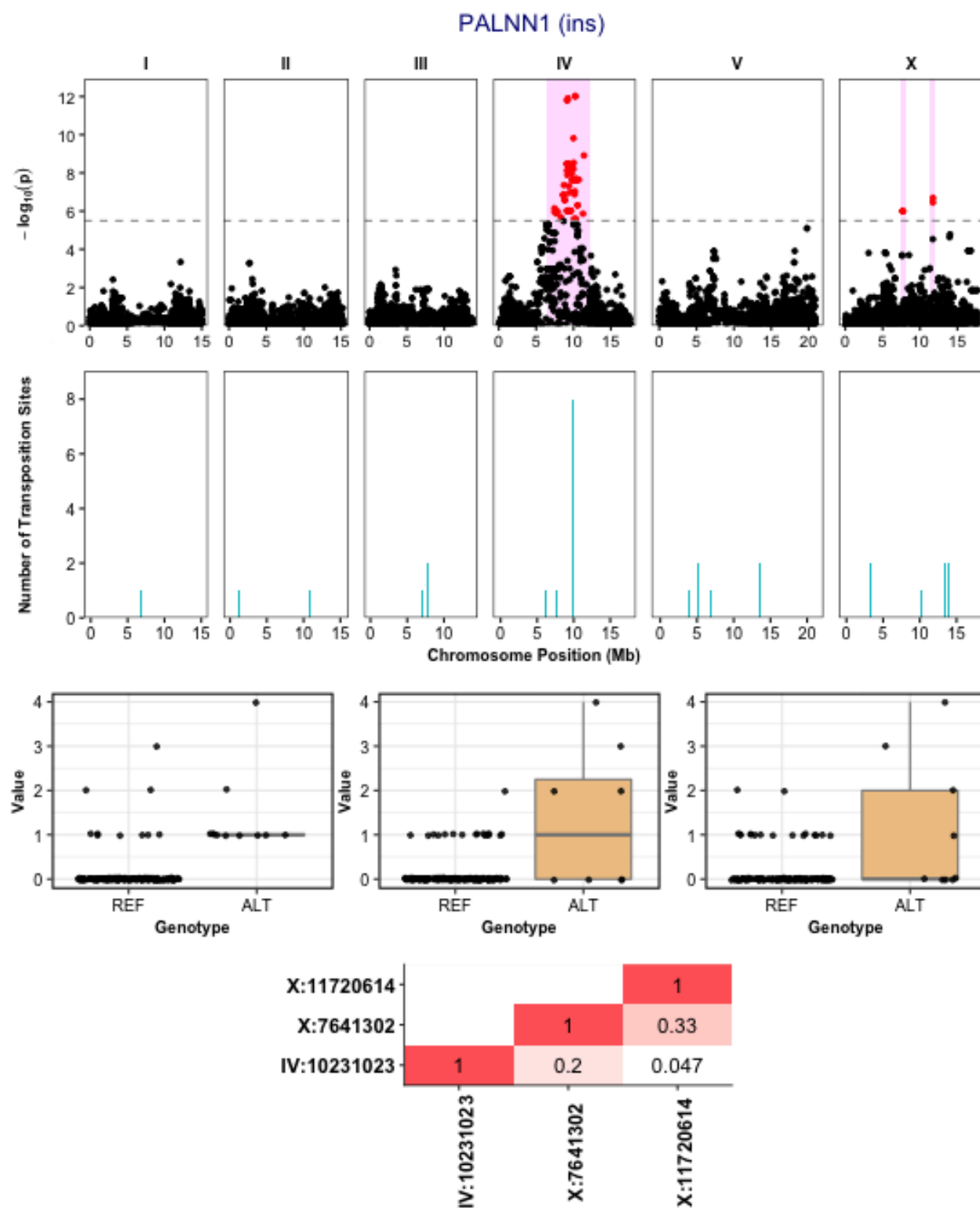


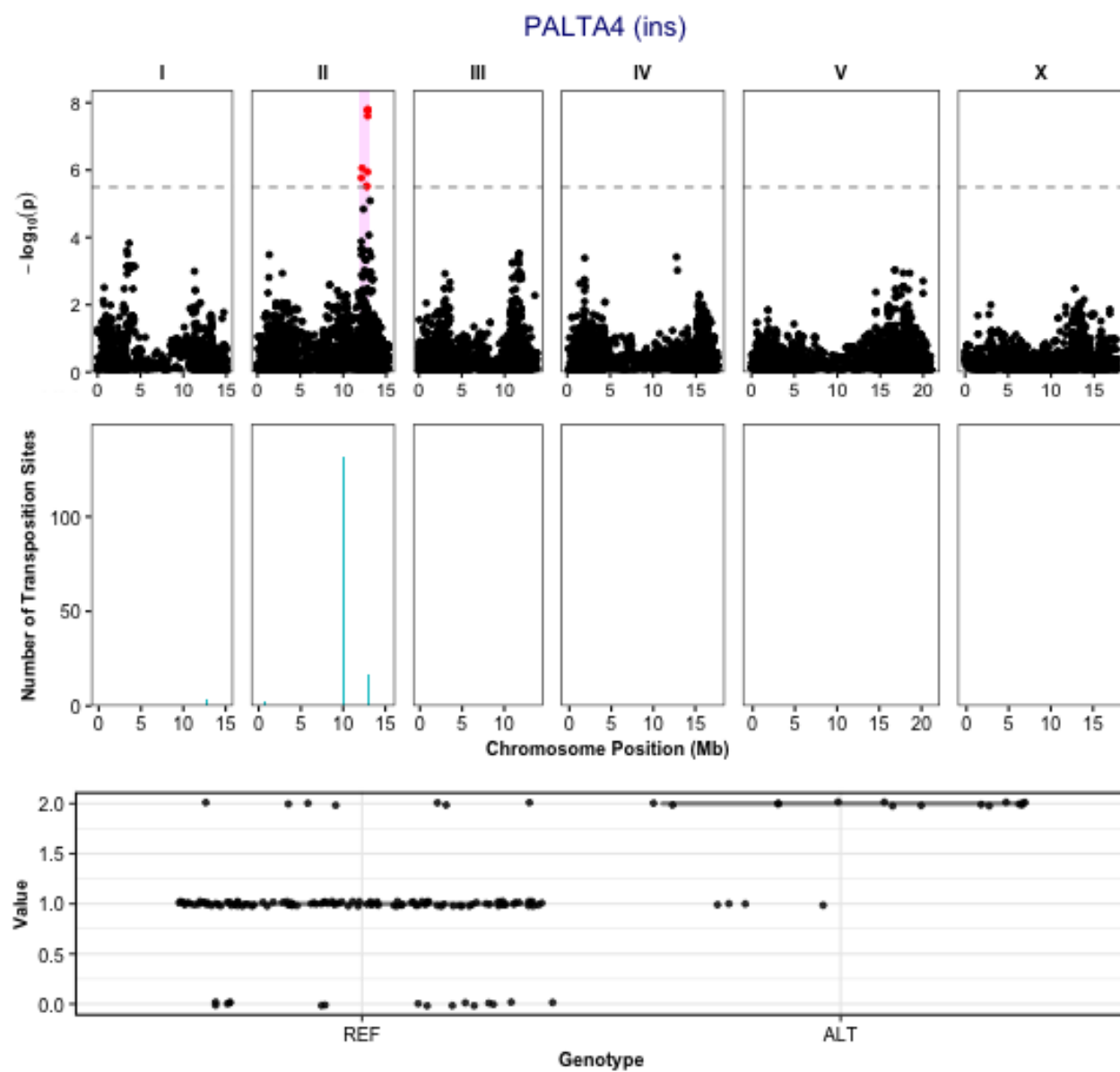


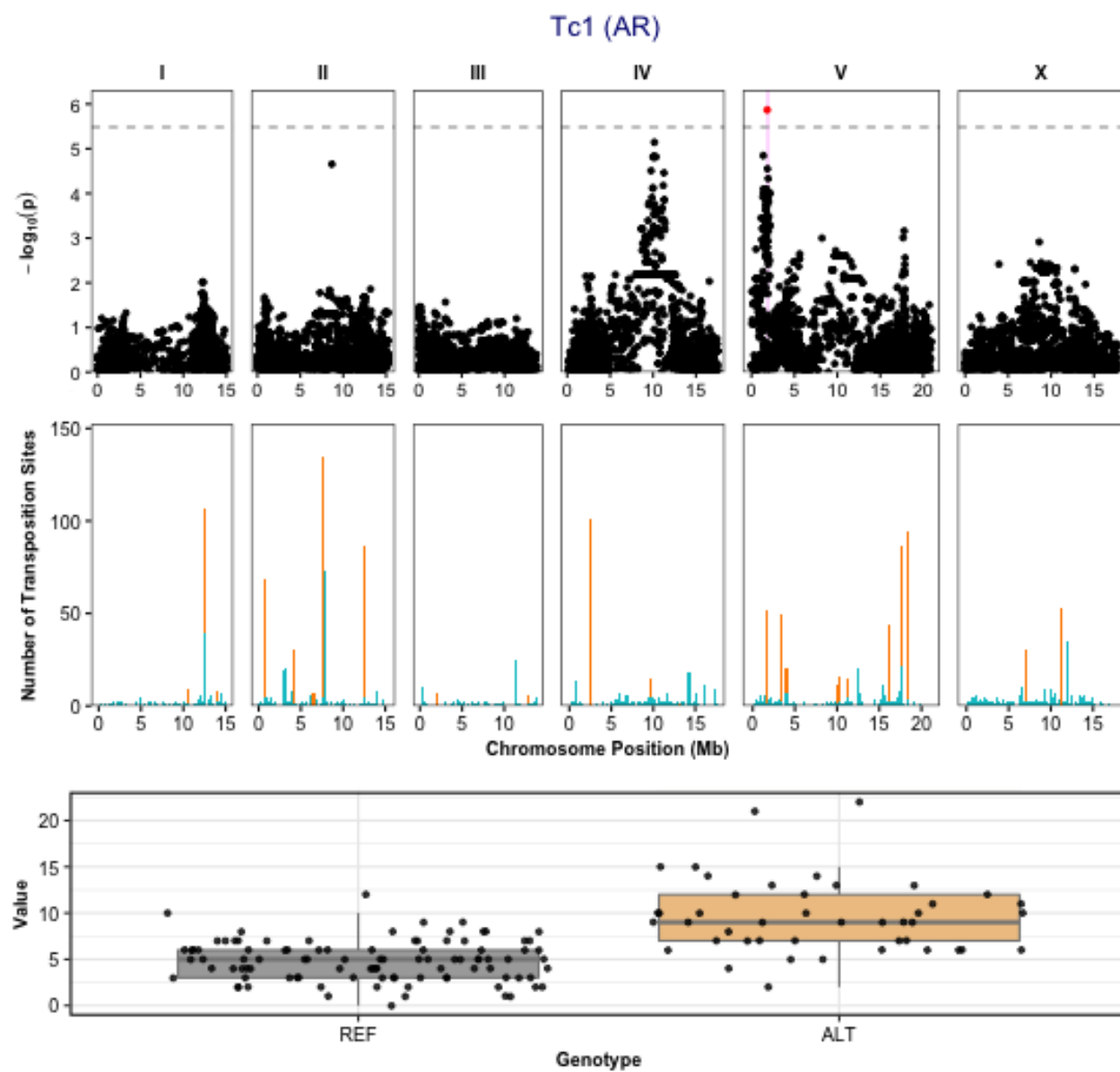


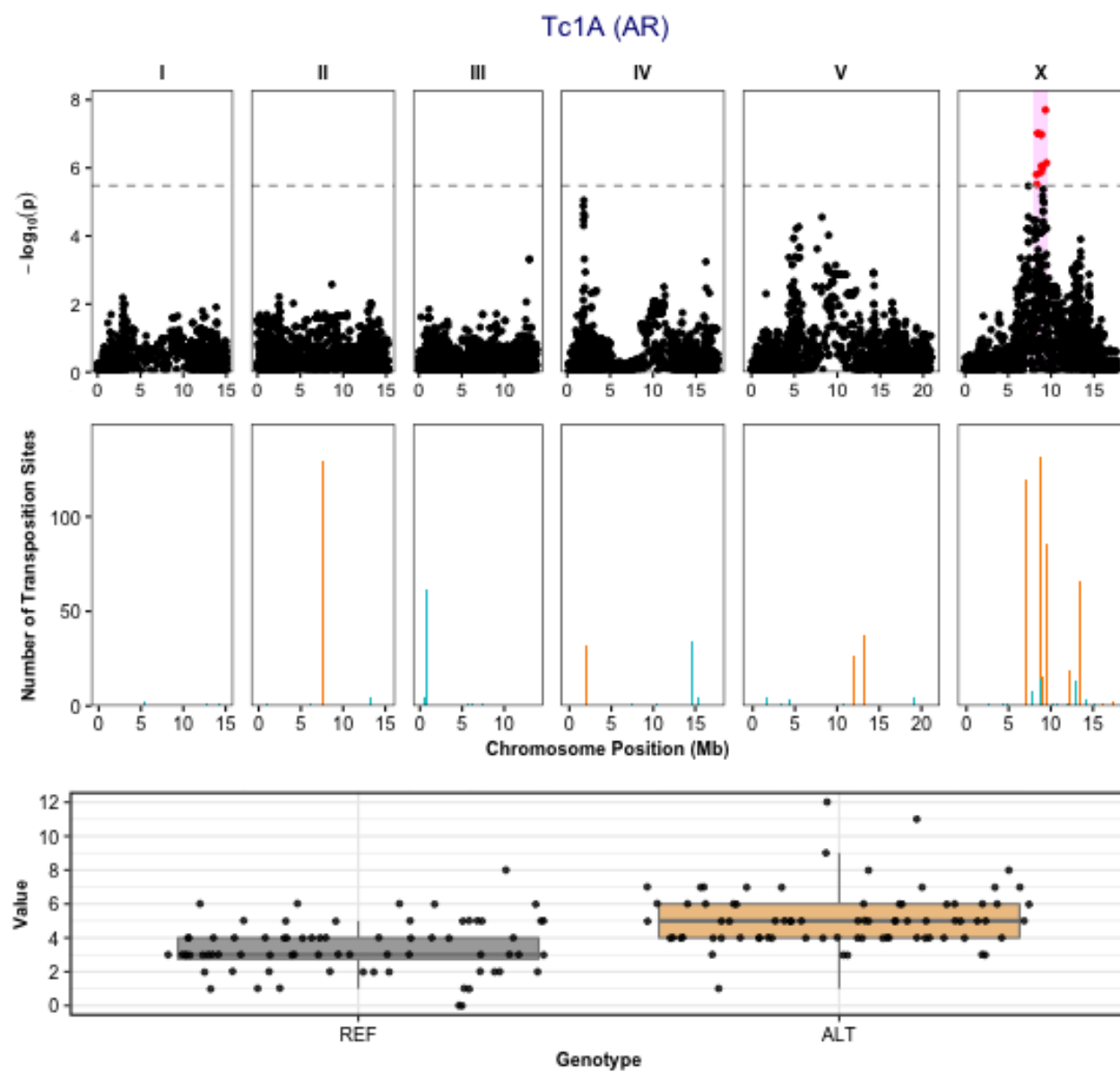




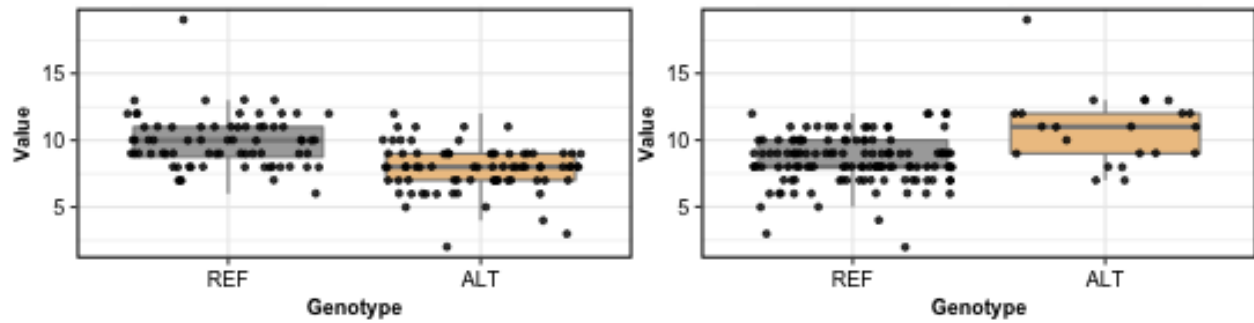
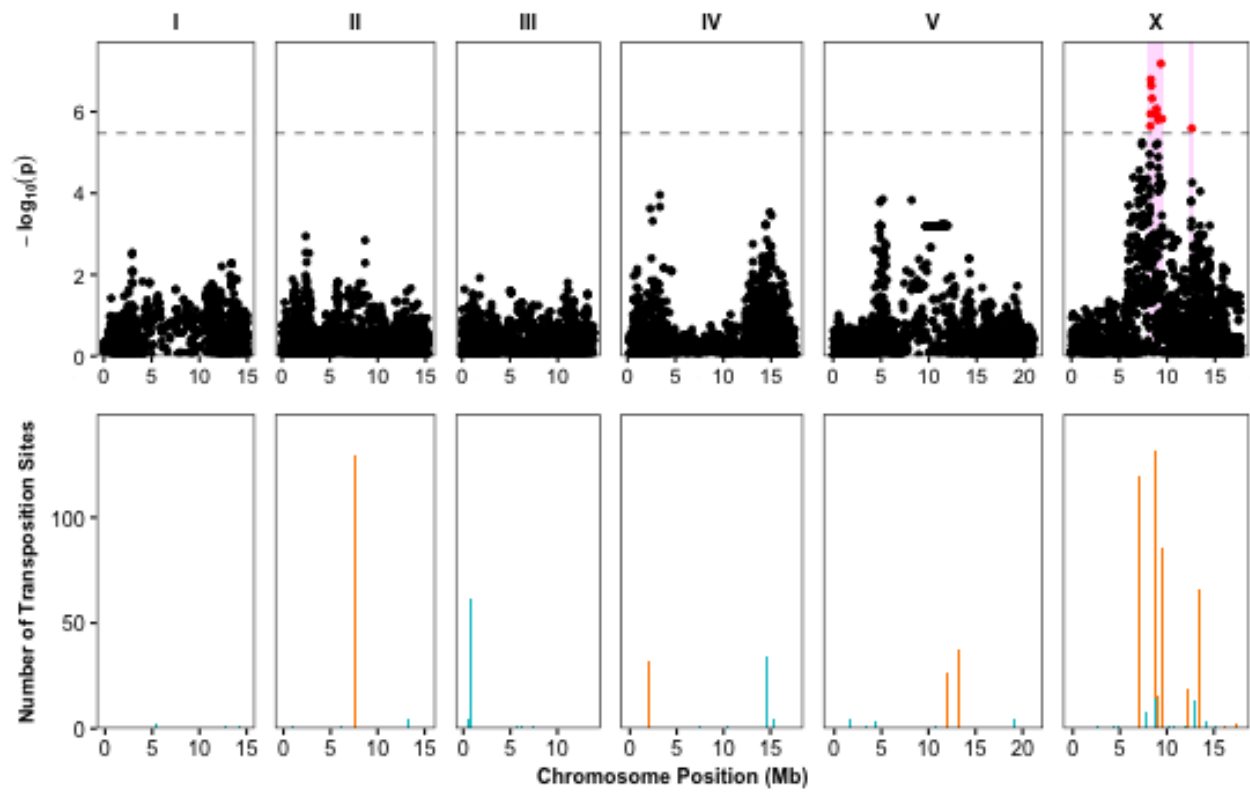




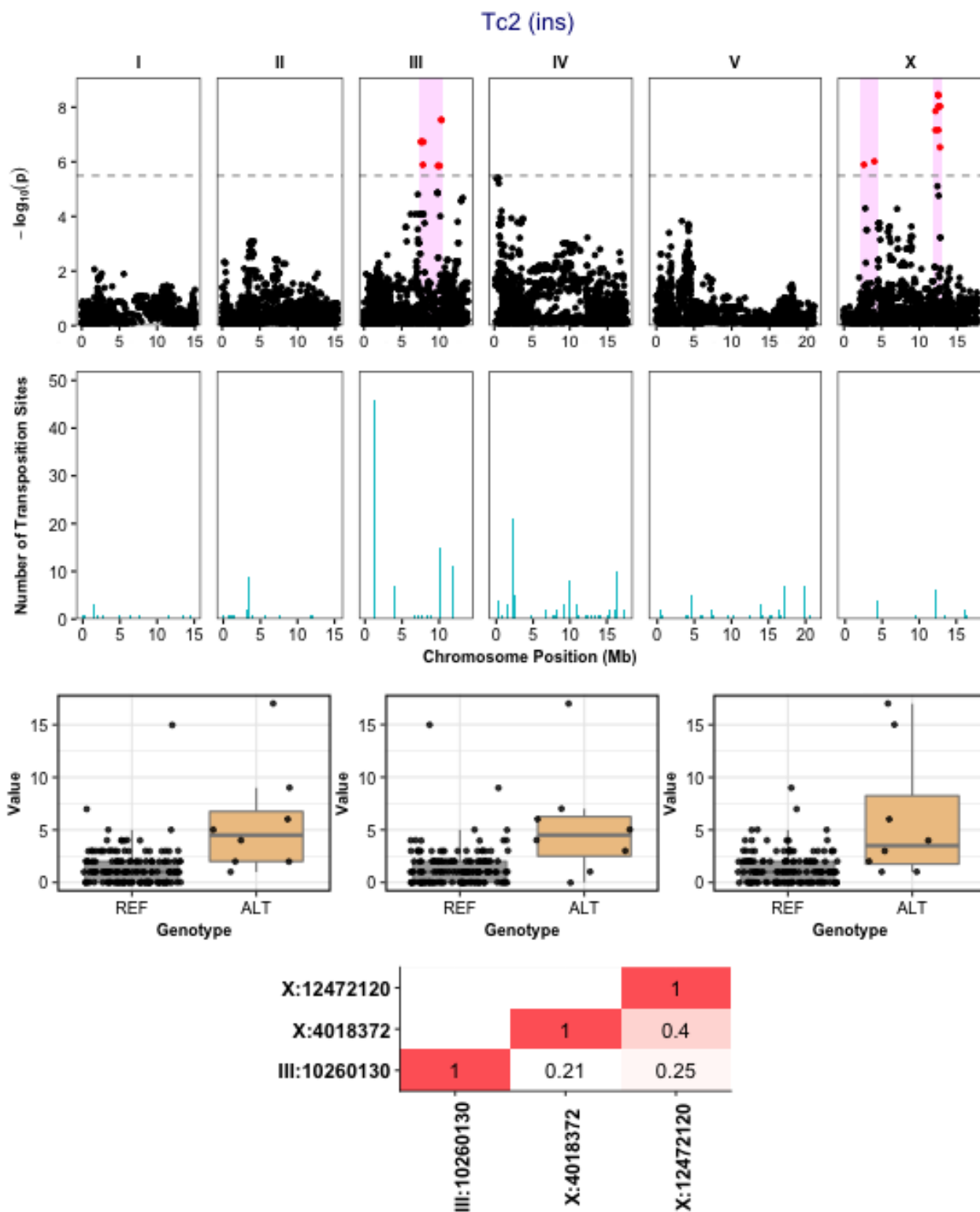


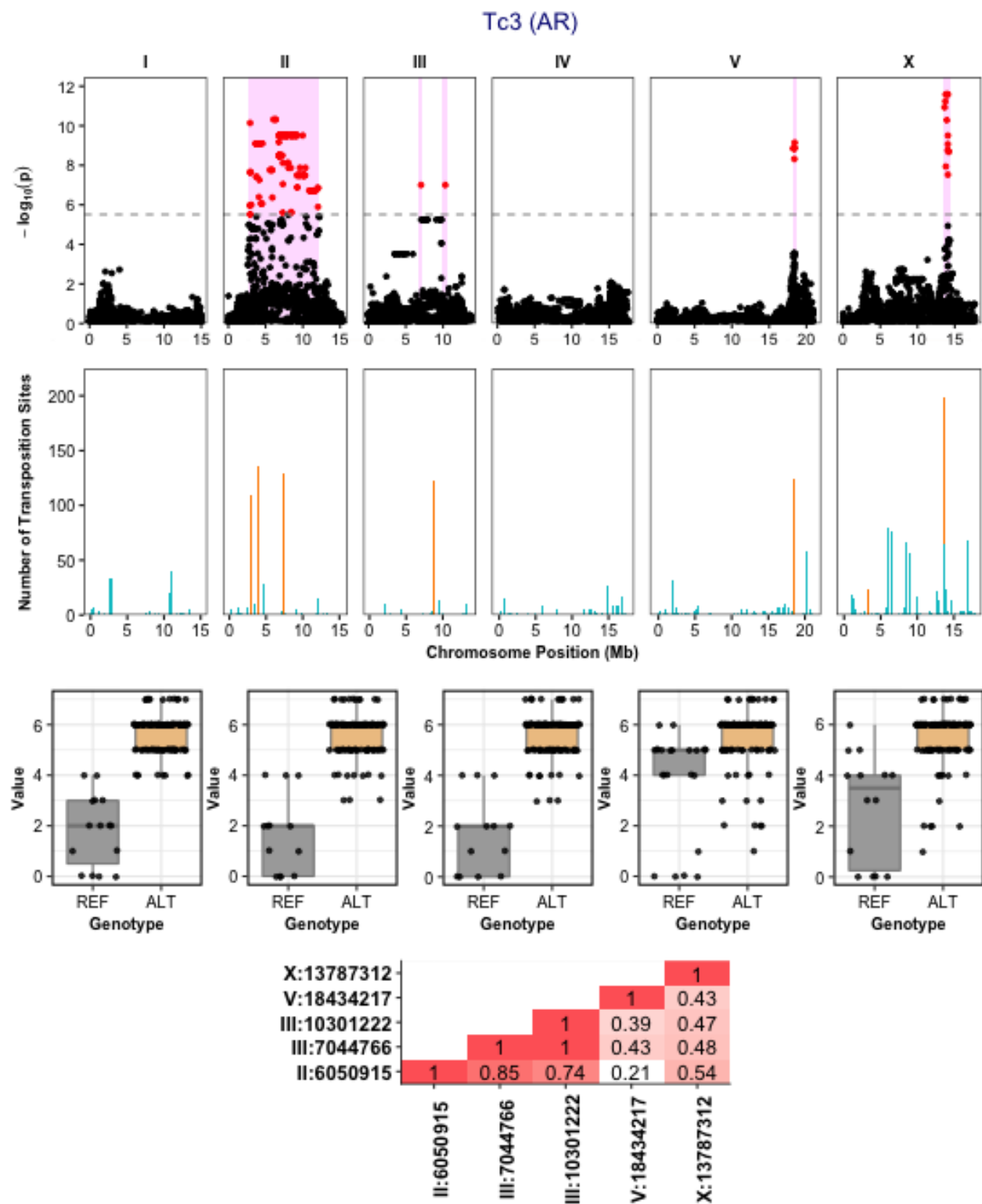


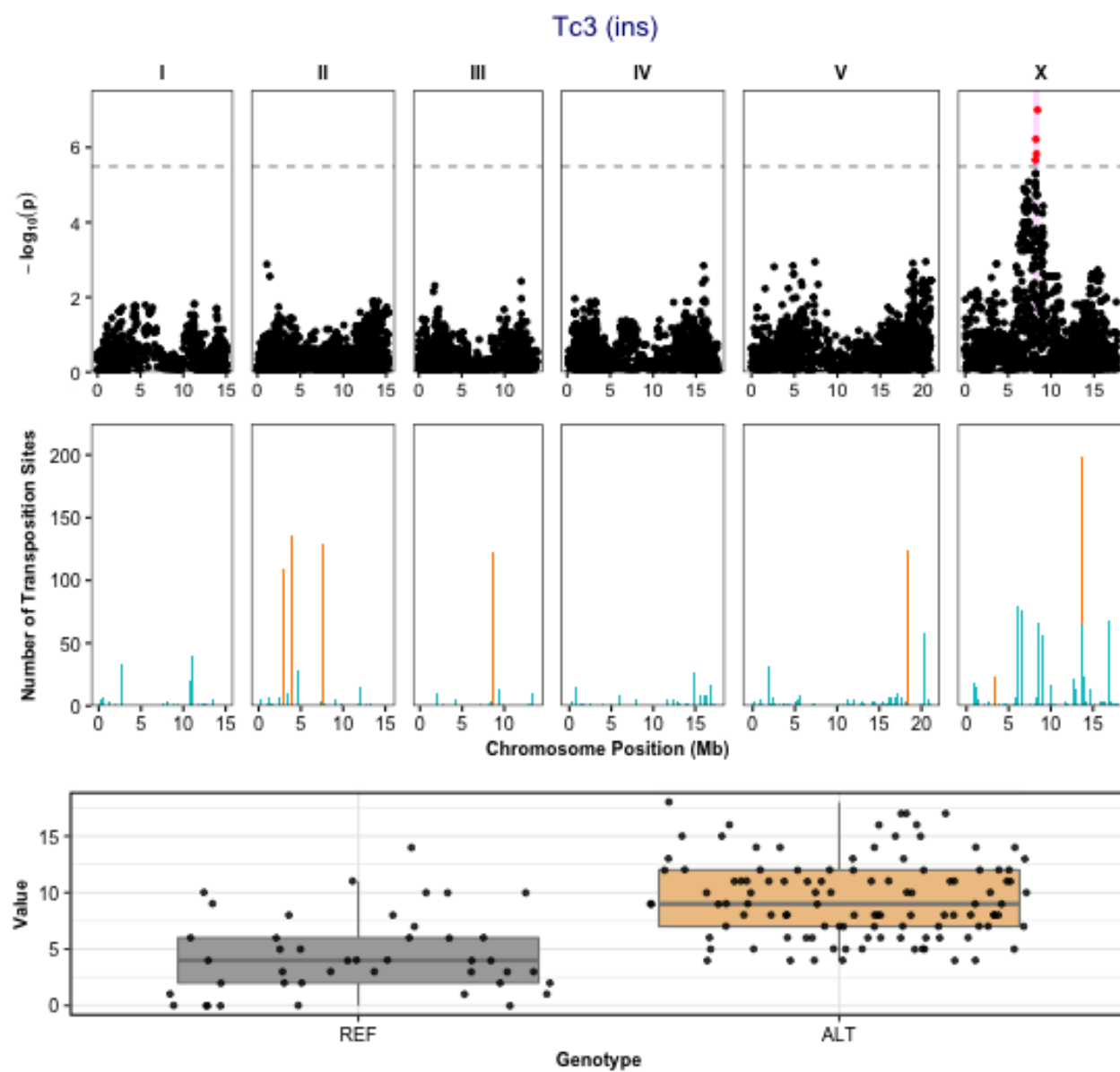
Tc1A (all)

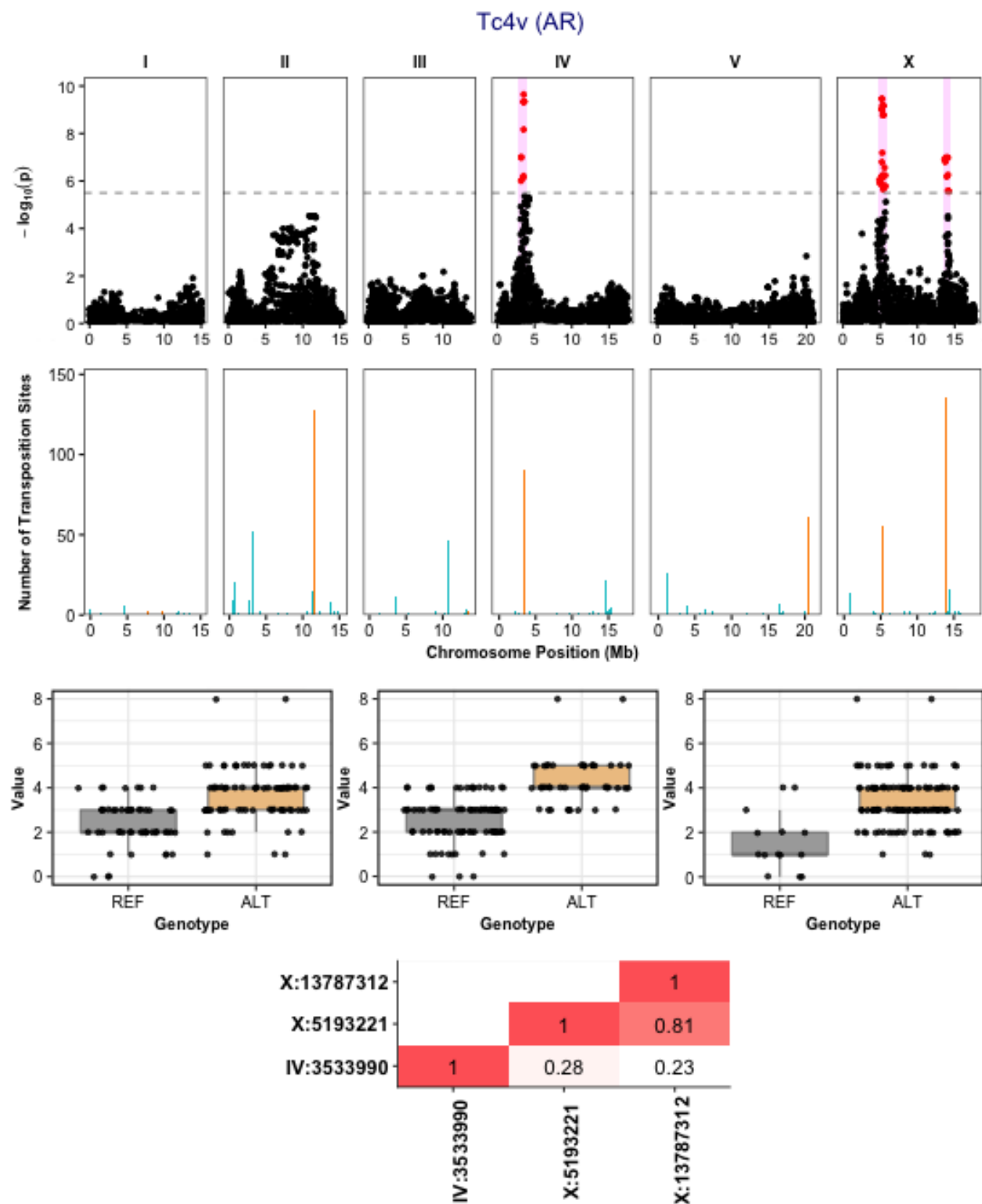


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X:9350385	1	0.83
	X:9350385	X:12576756

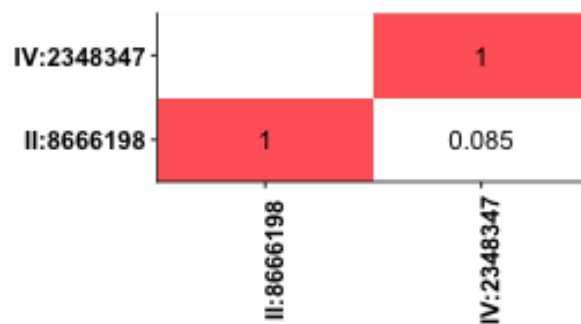
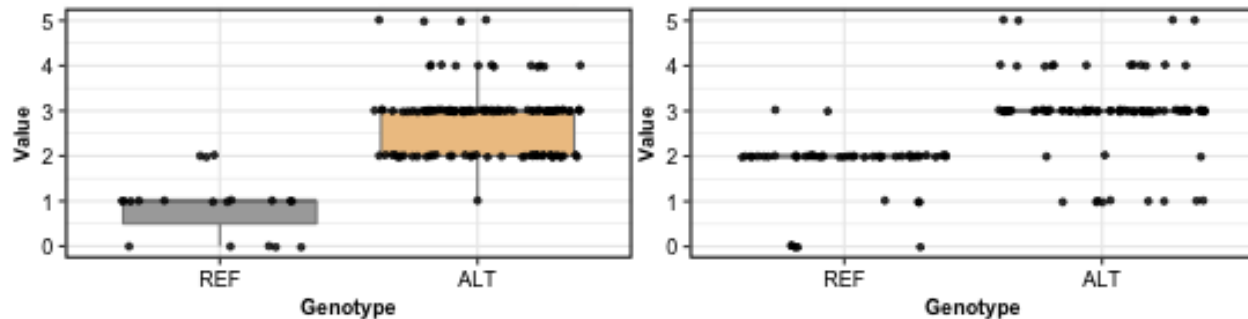
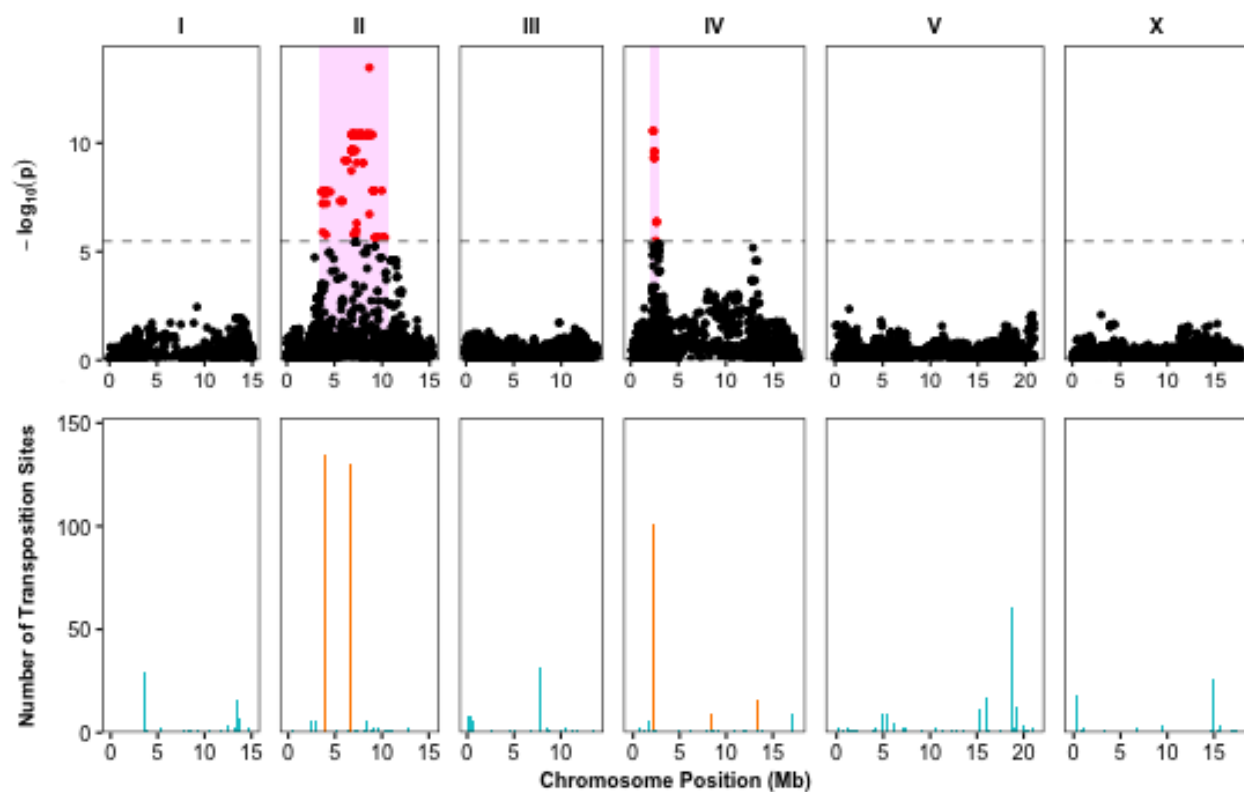


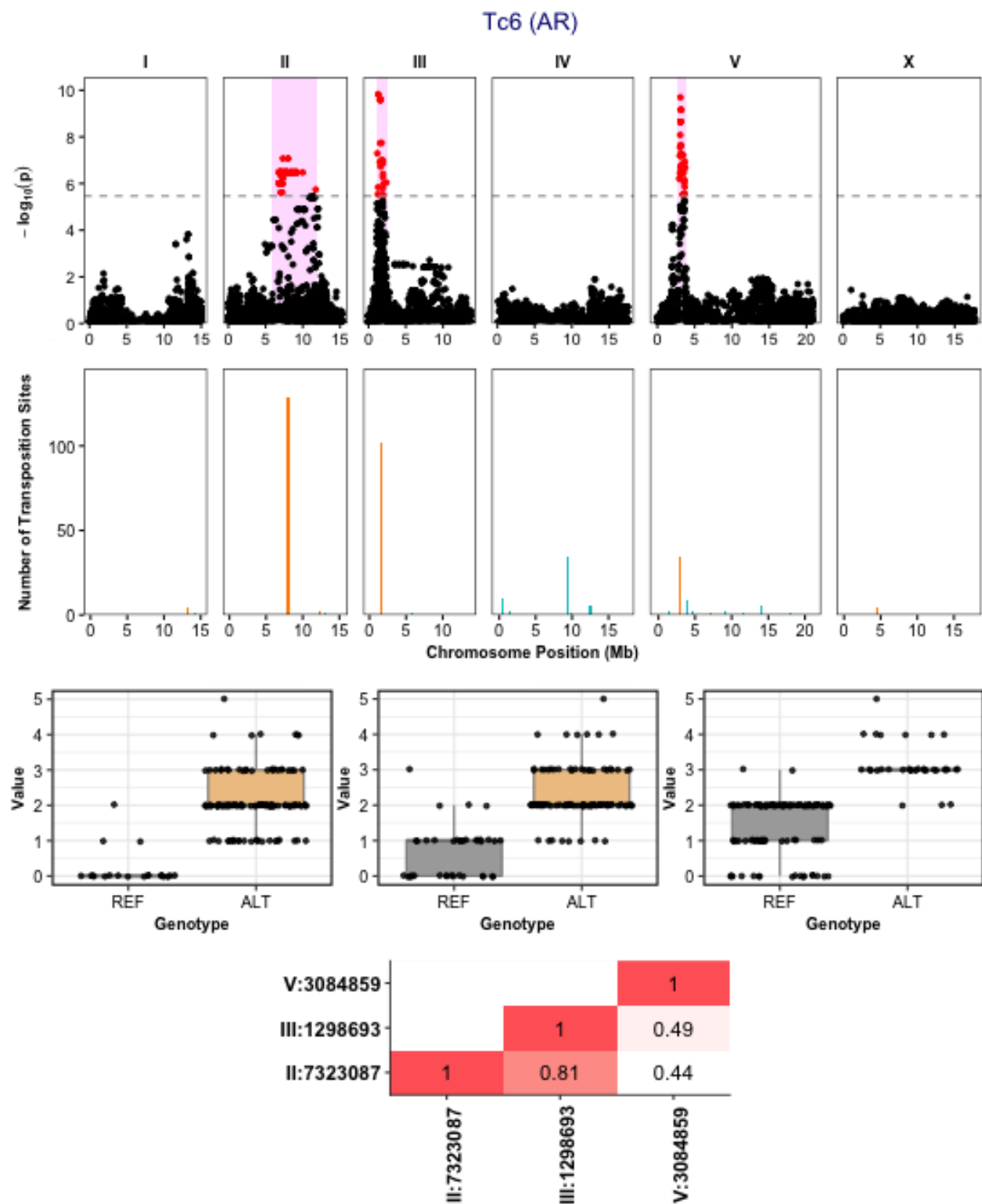


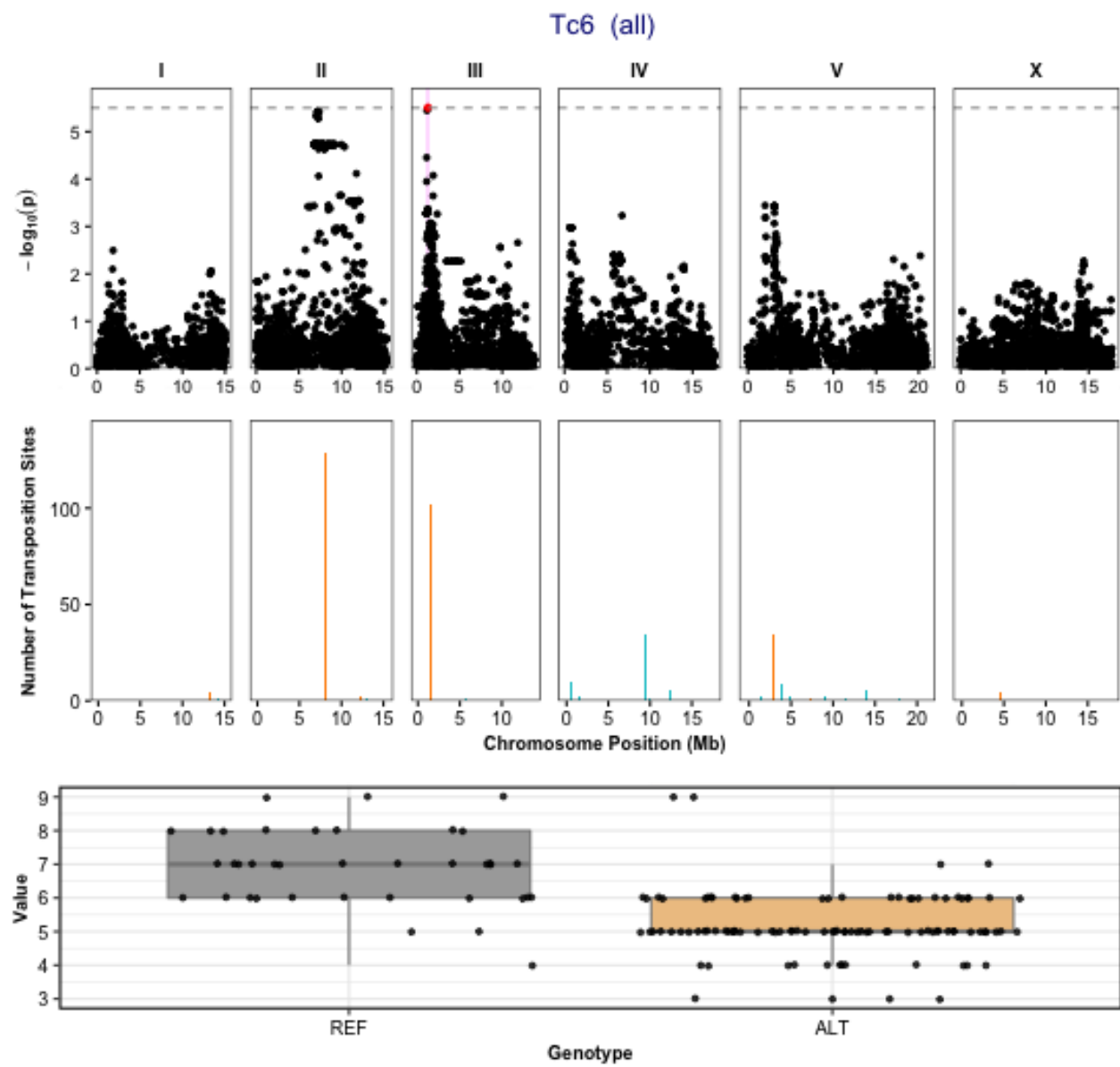


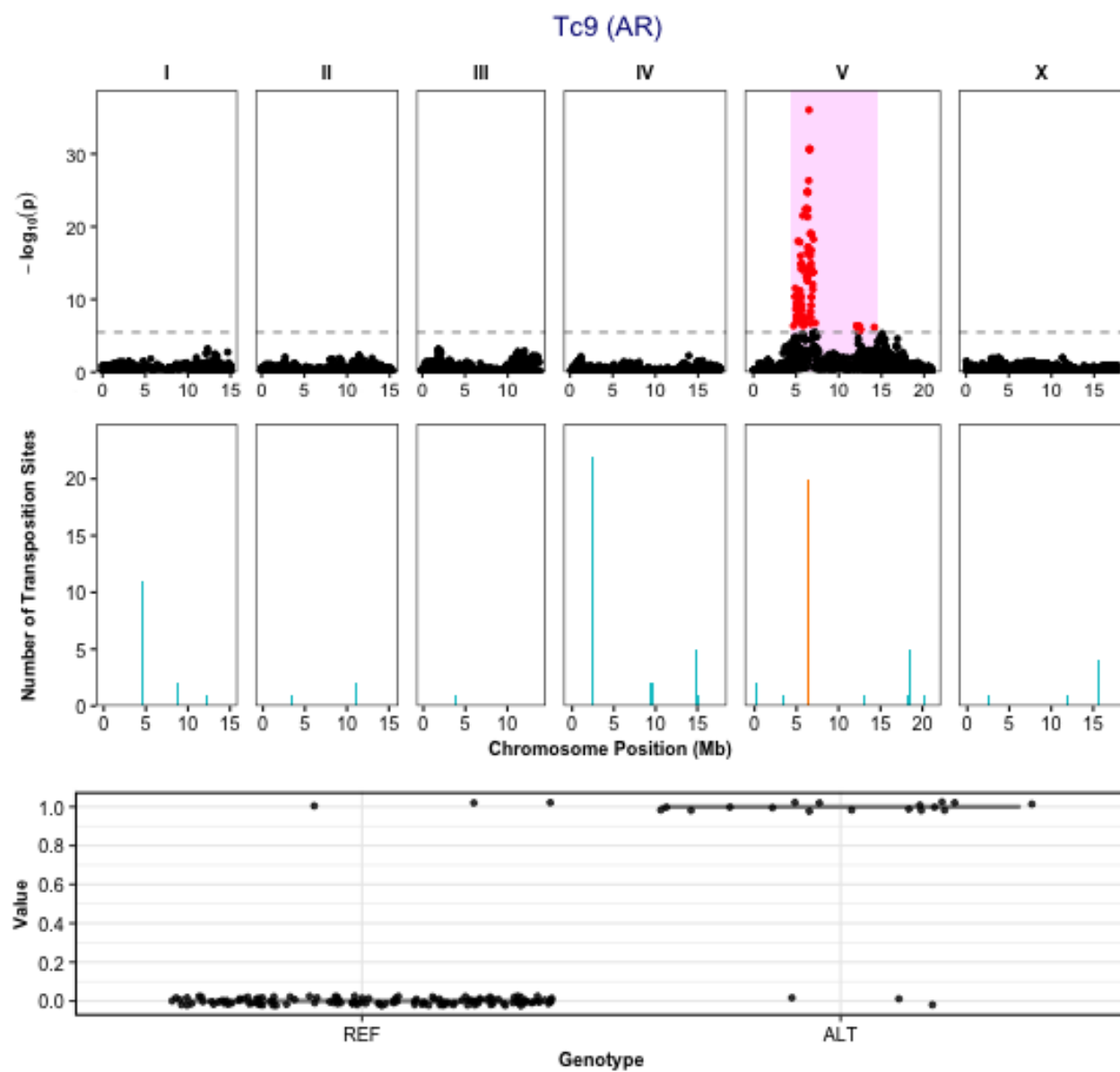


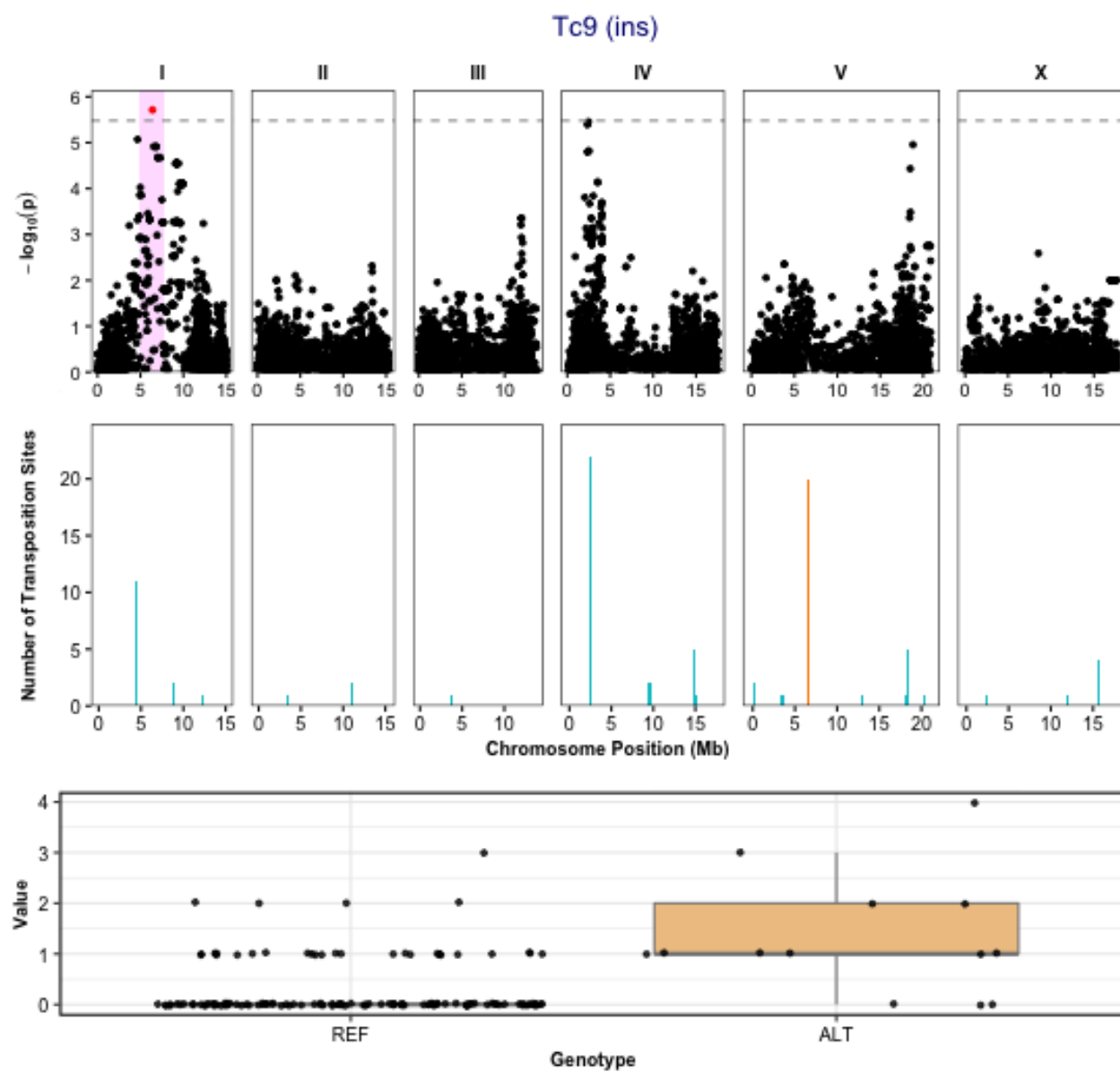
Tc5 (AR)

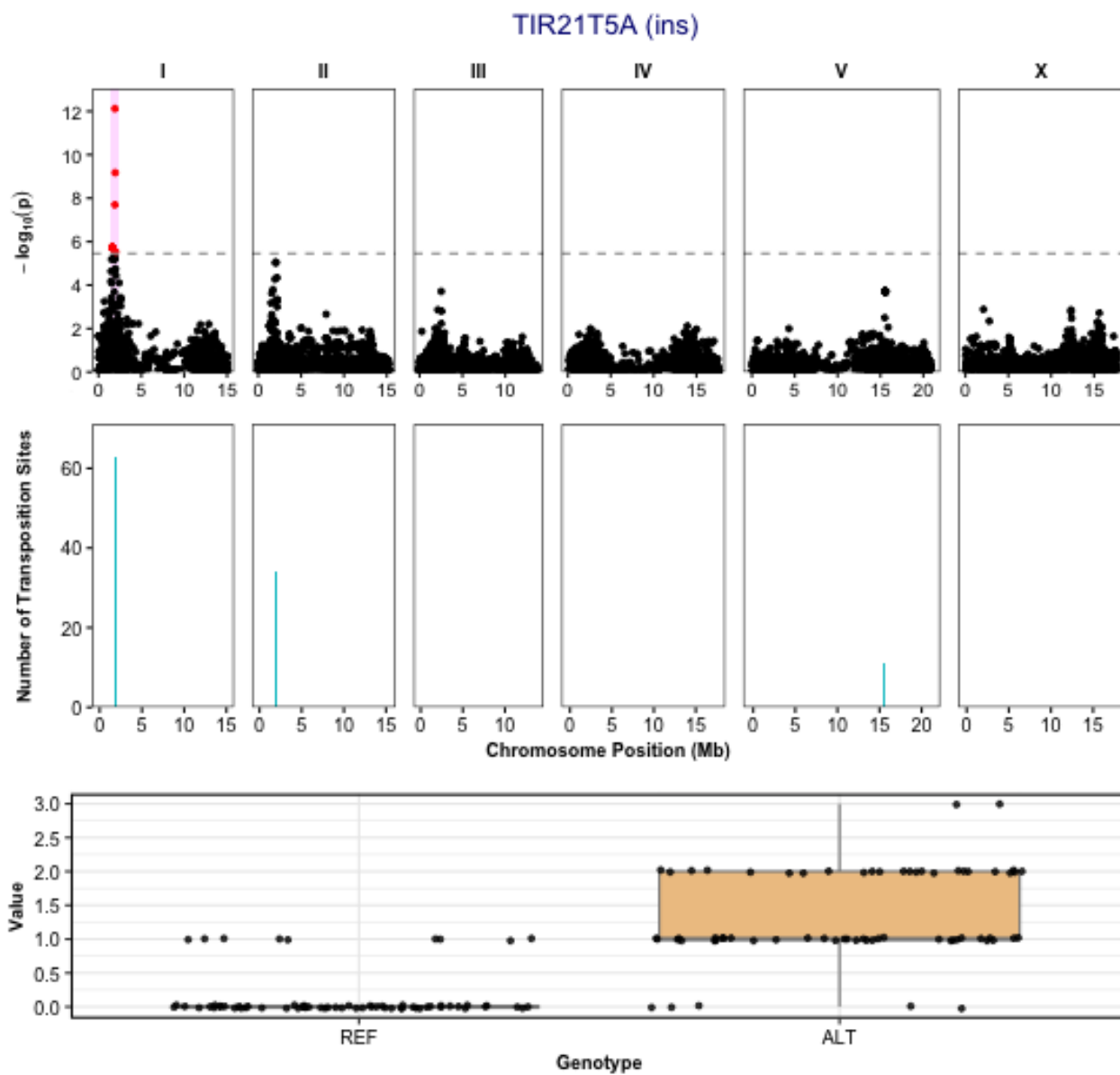


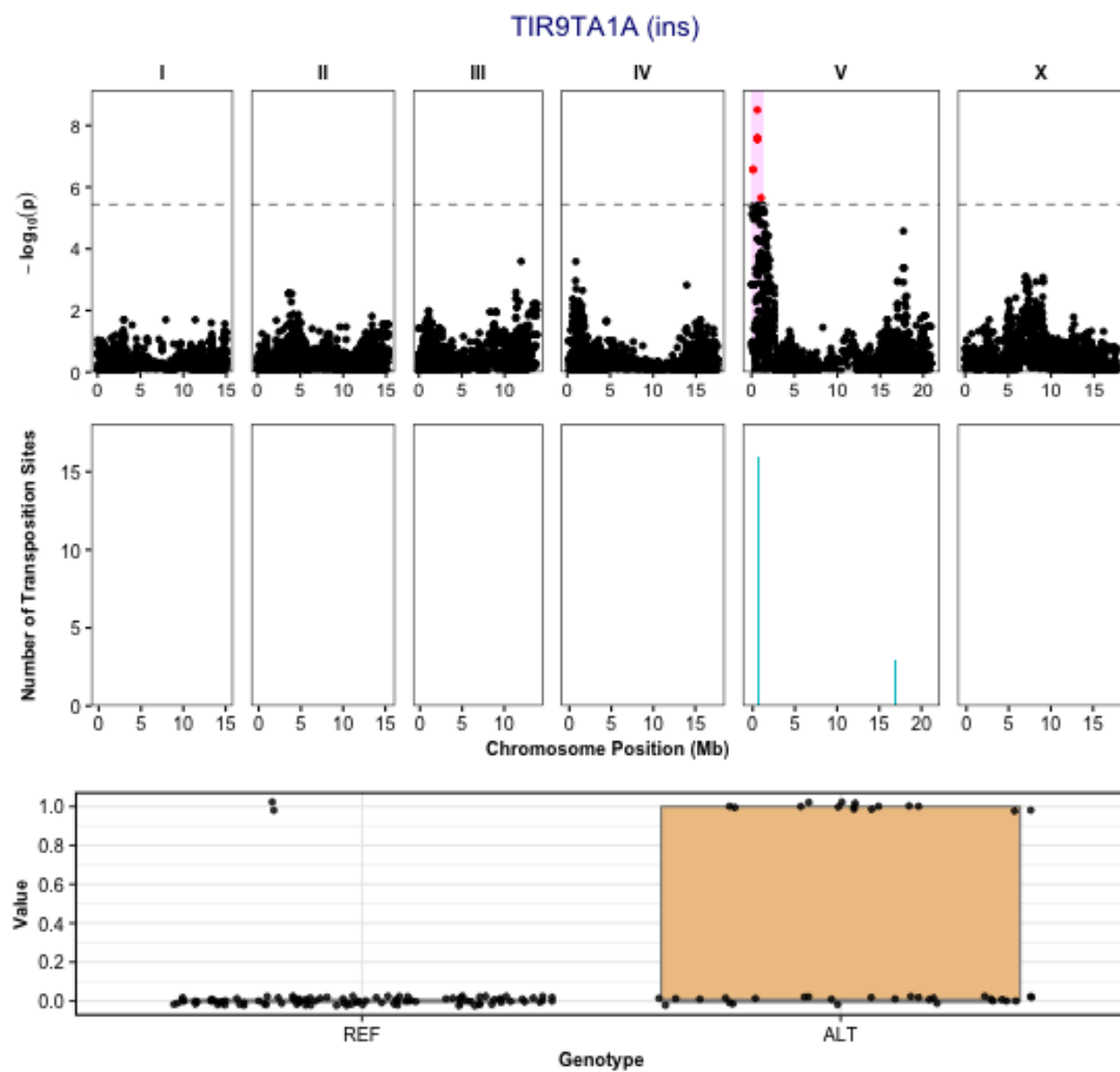




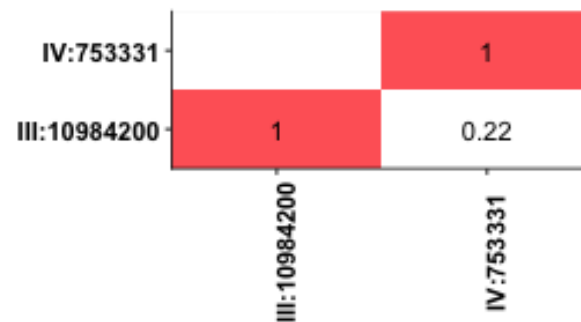
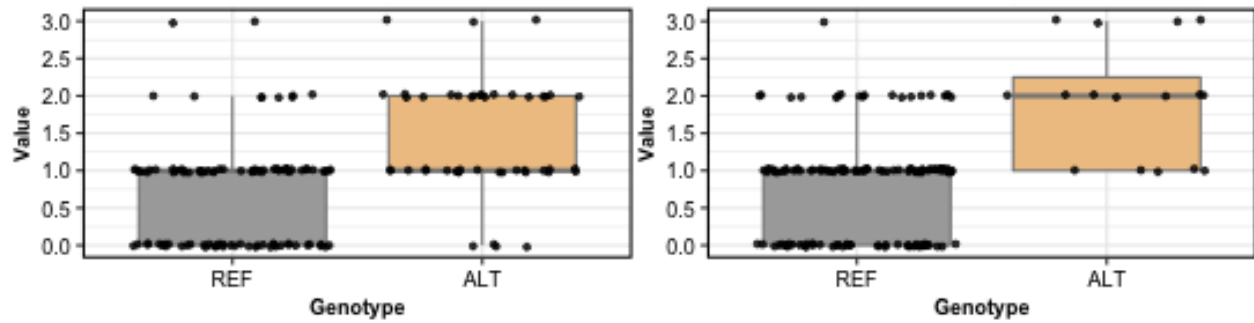
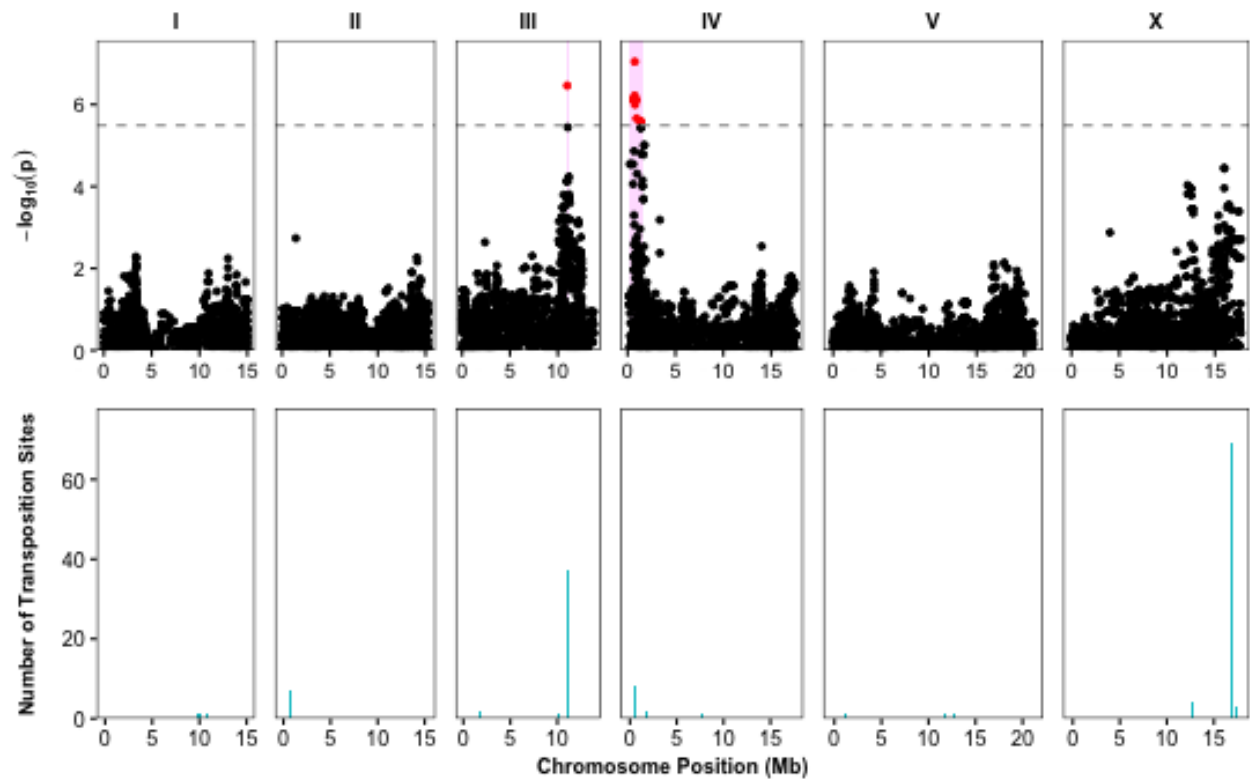




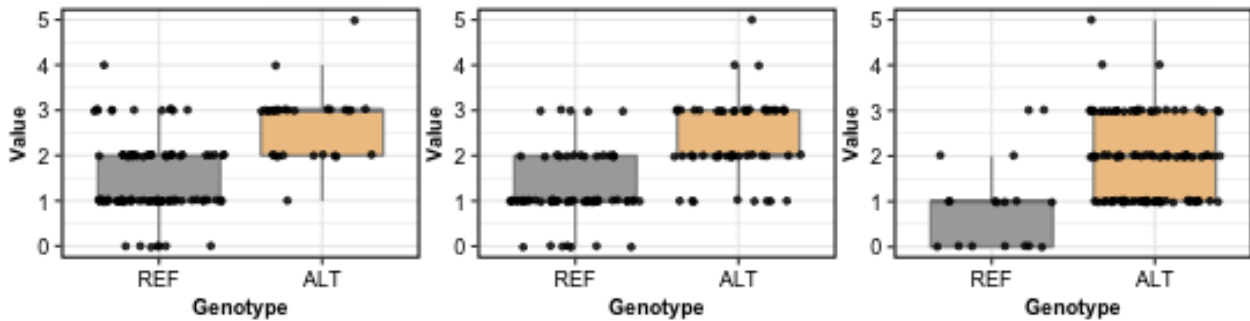
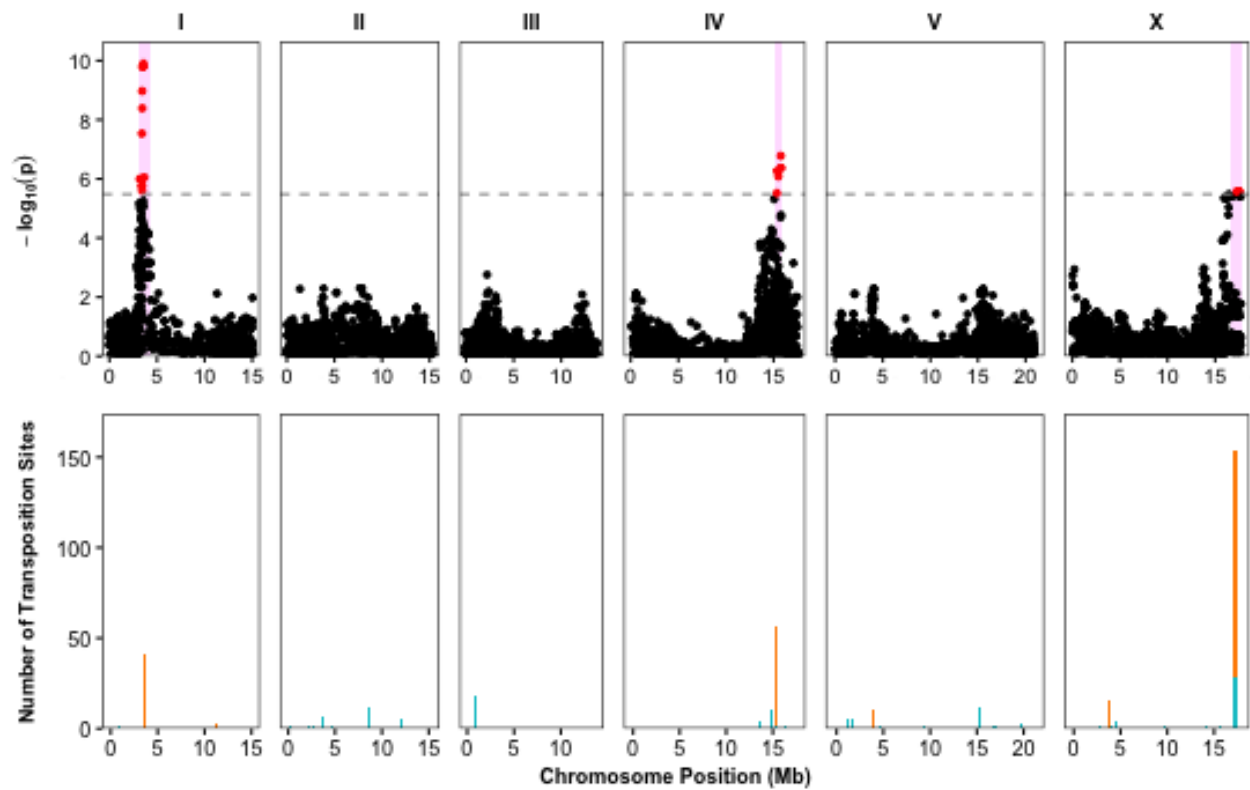




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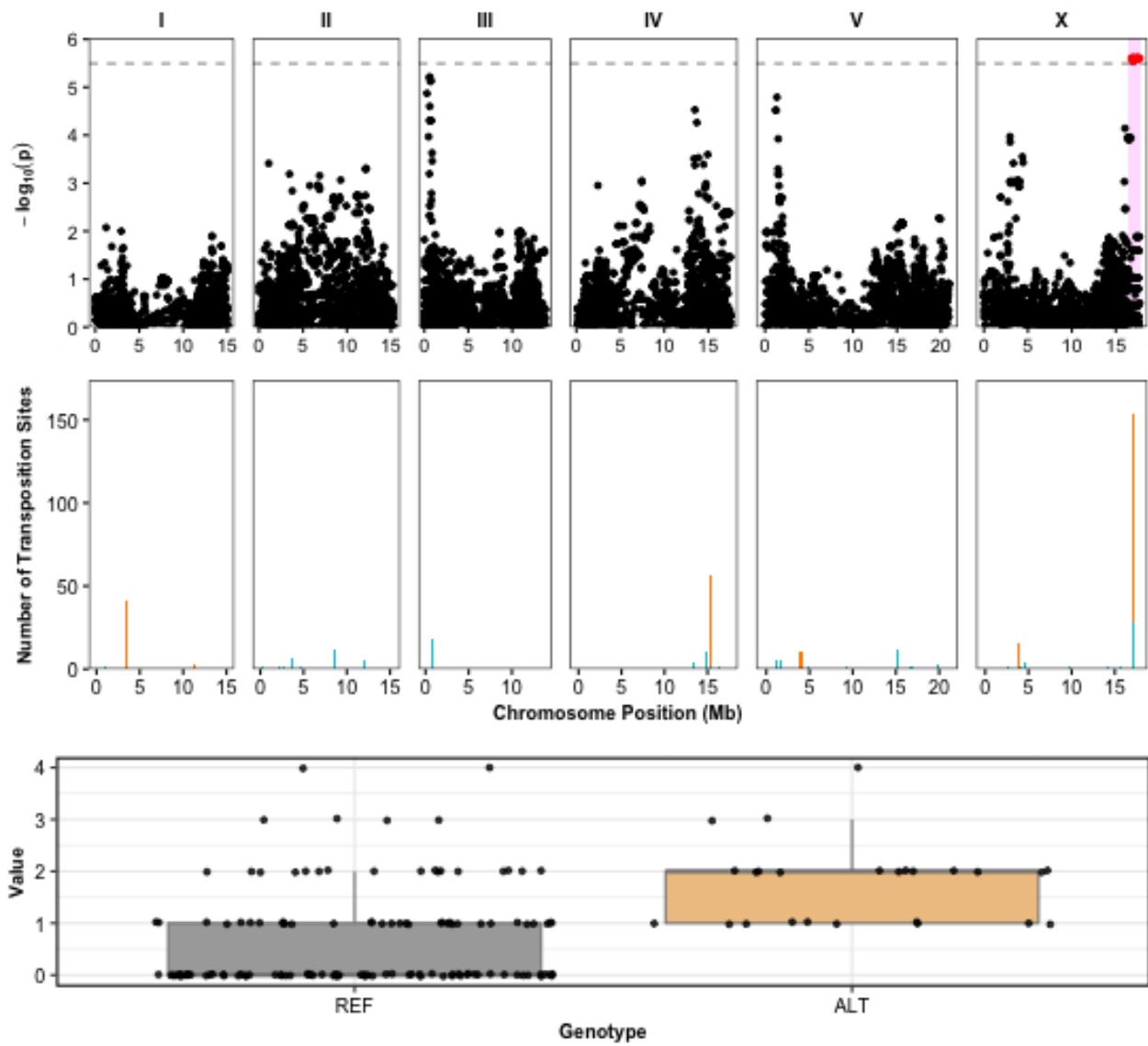


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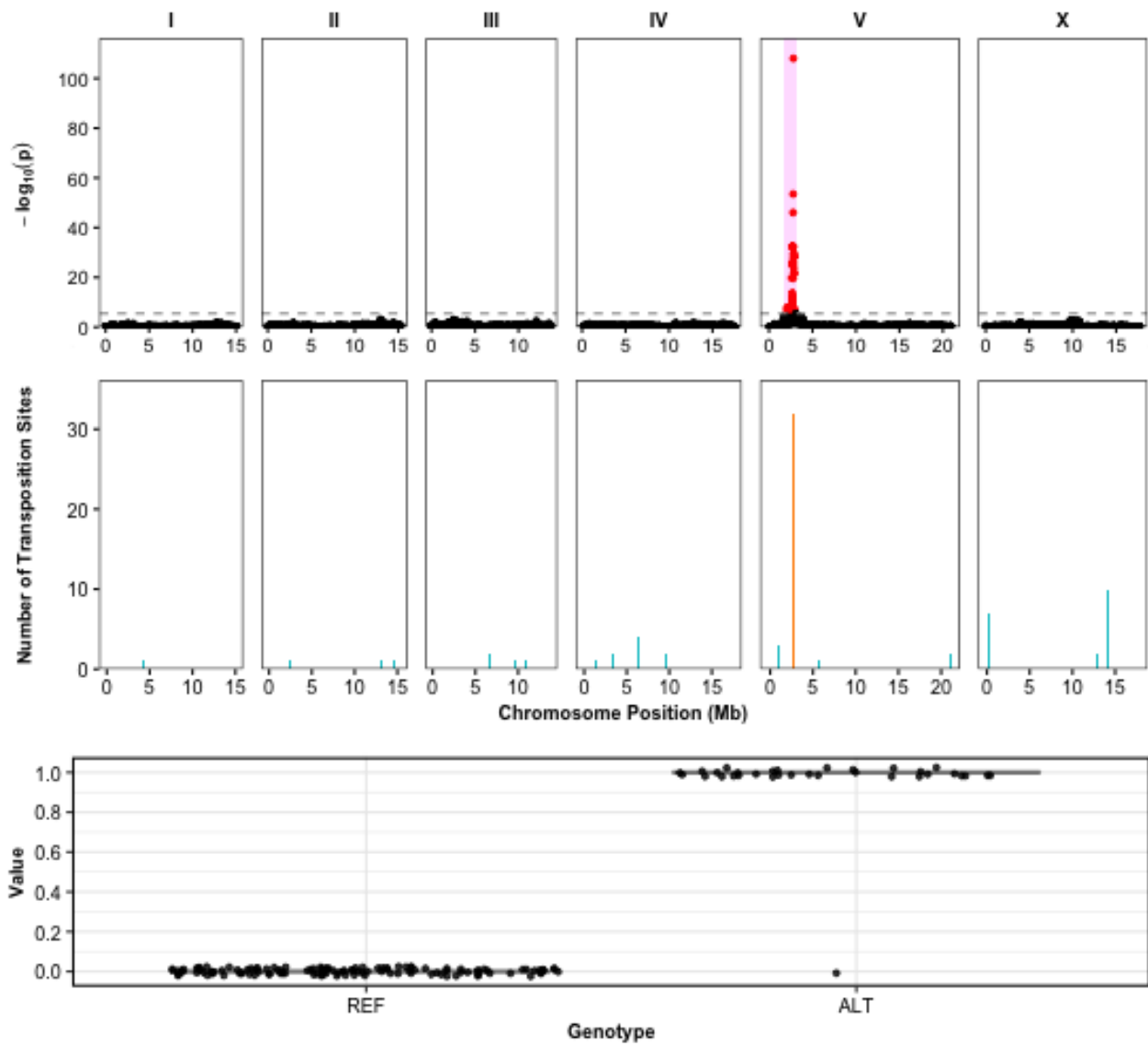


X:17274823			1
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I:3573372	1	0.14	0.23
I:3573372		IV:15763697	X:17274823

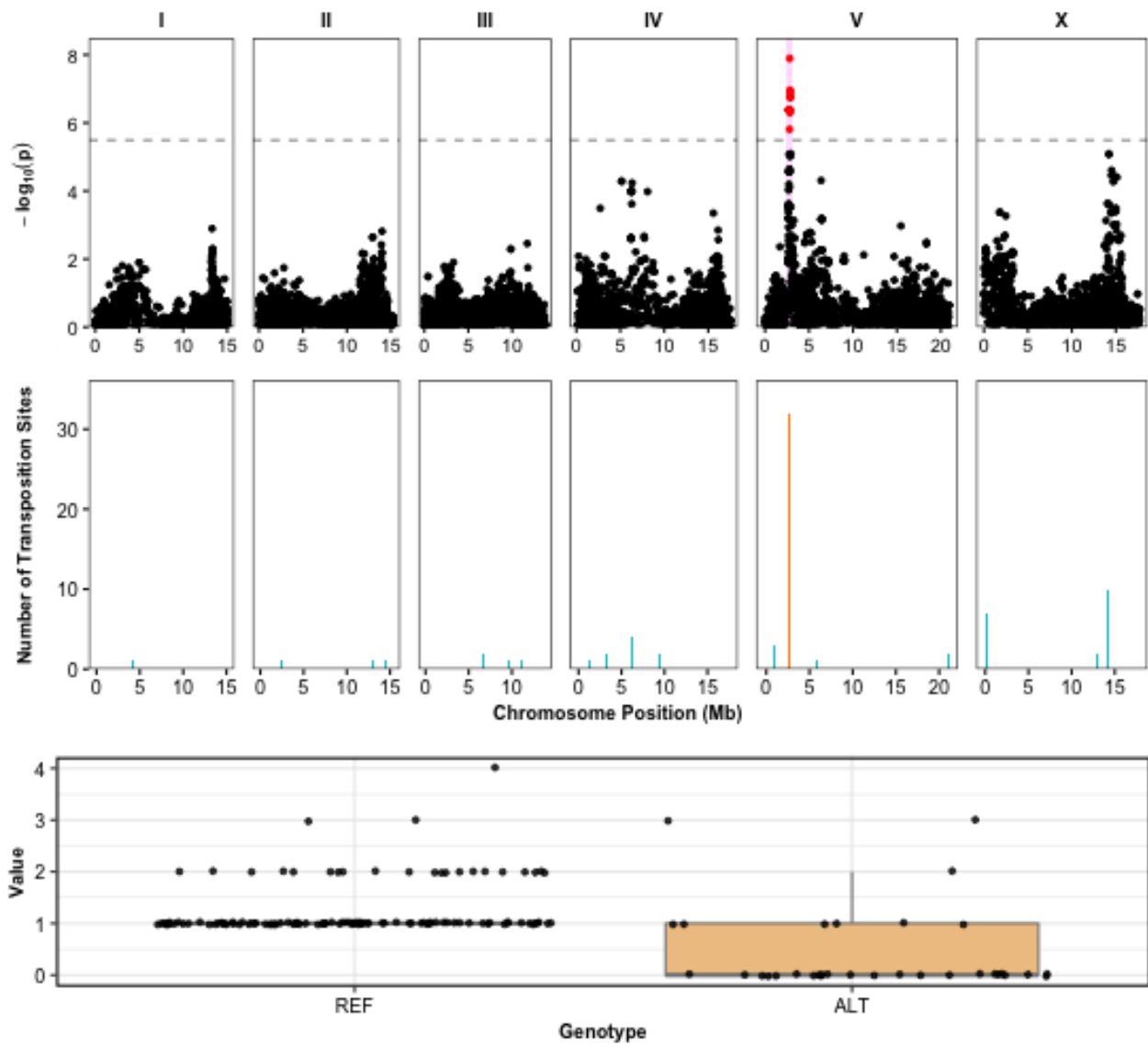
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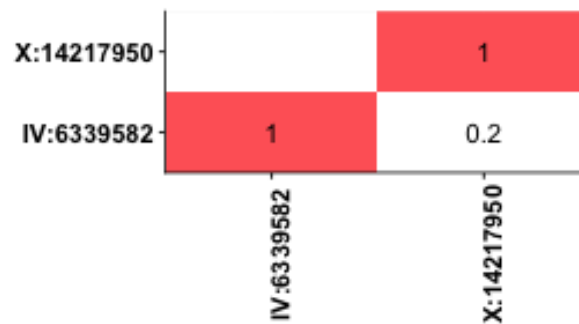
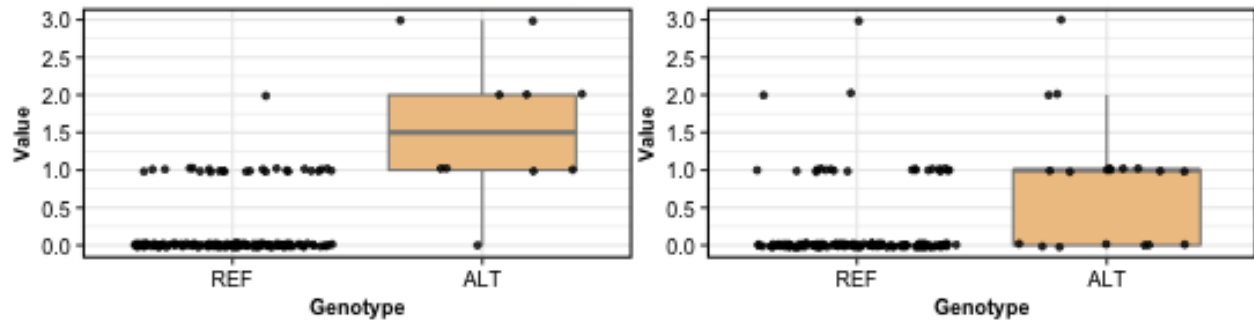
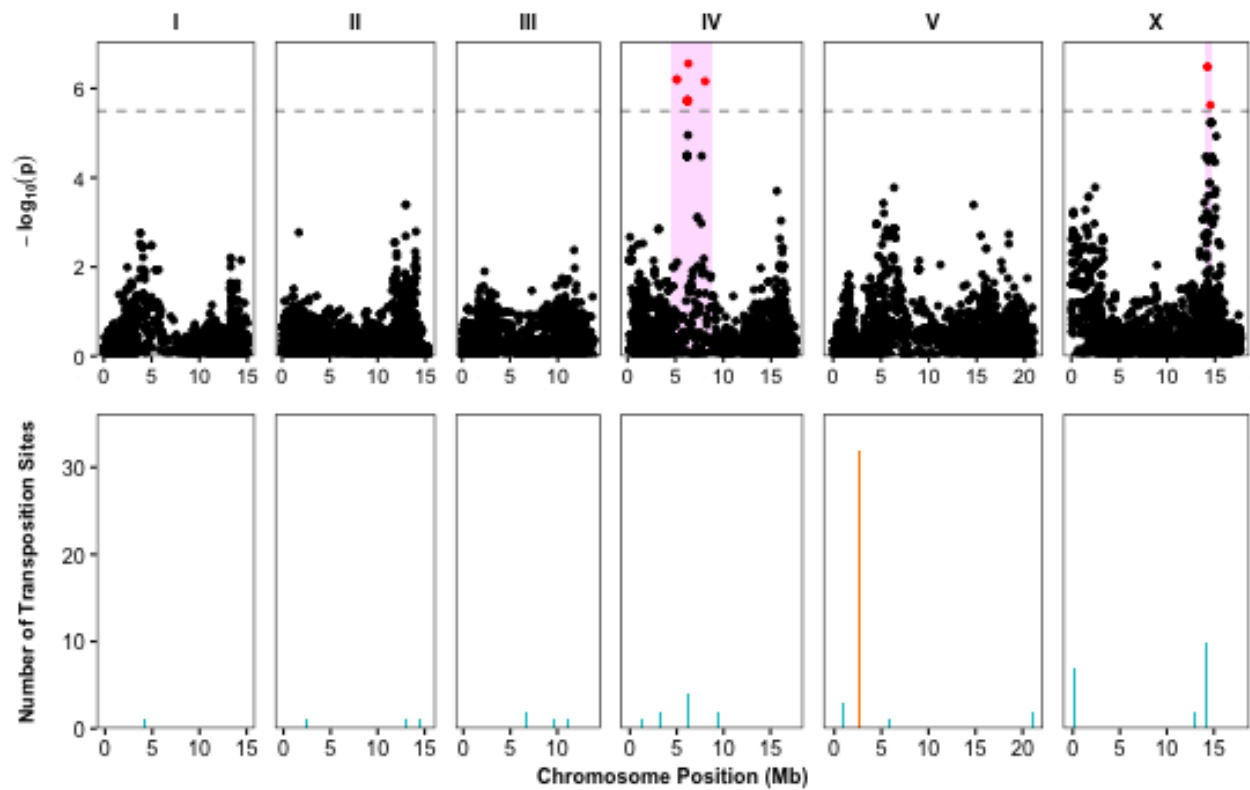
WBT00000416 (AR)

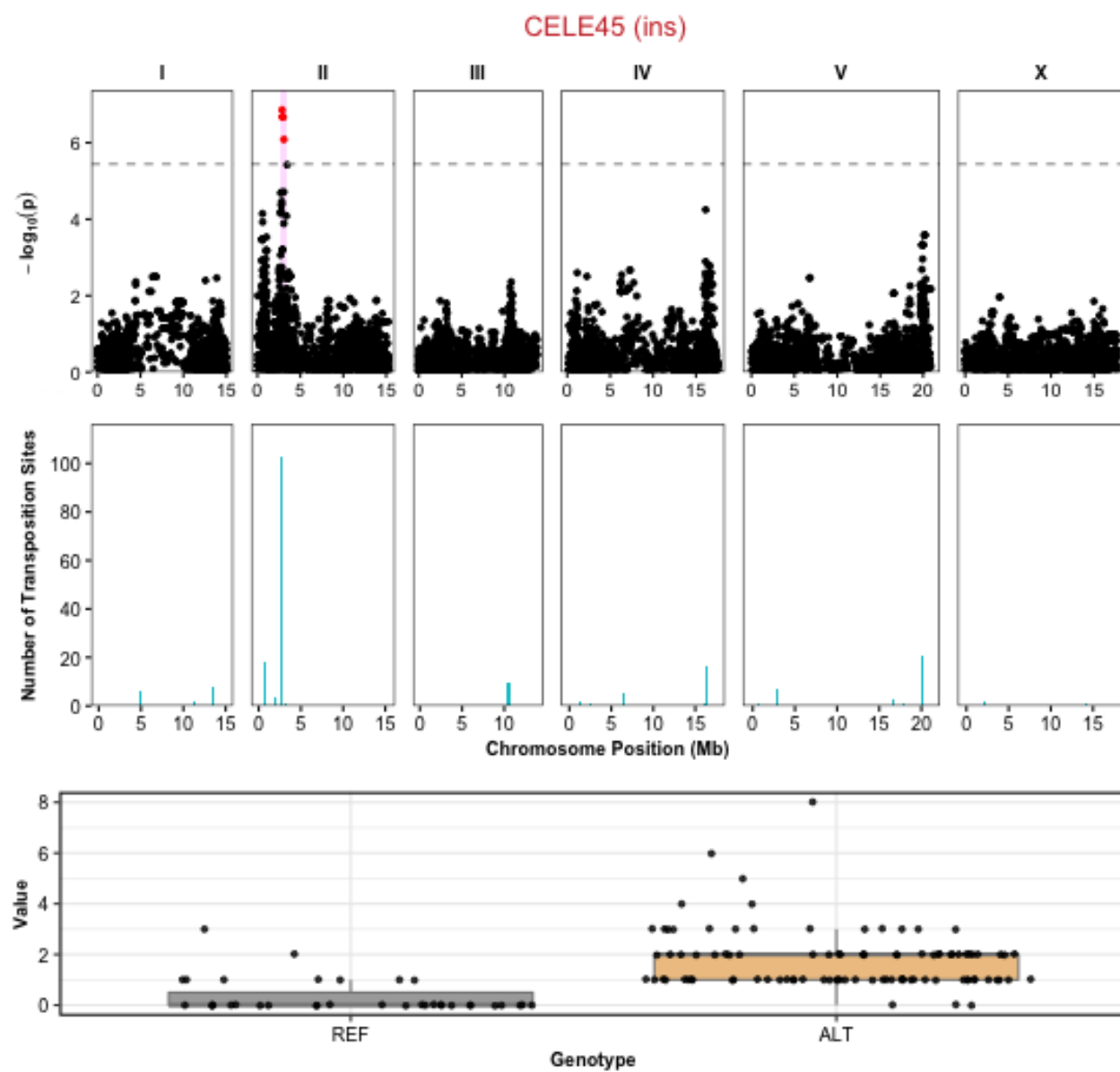


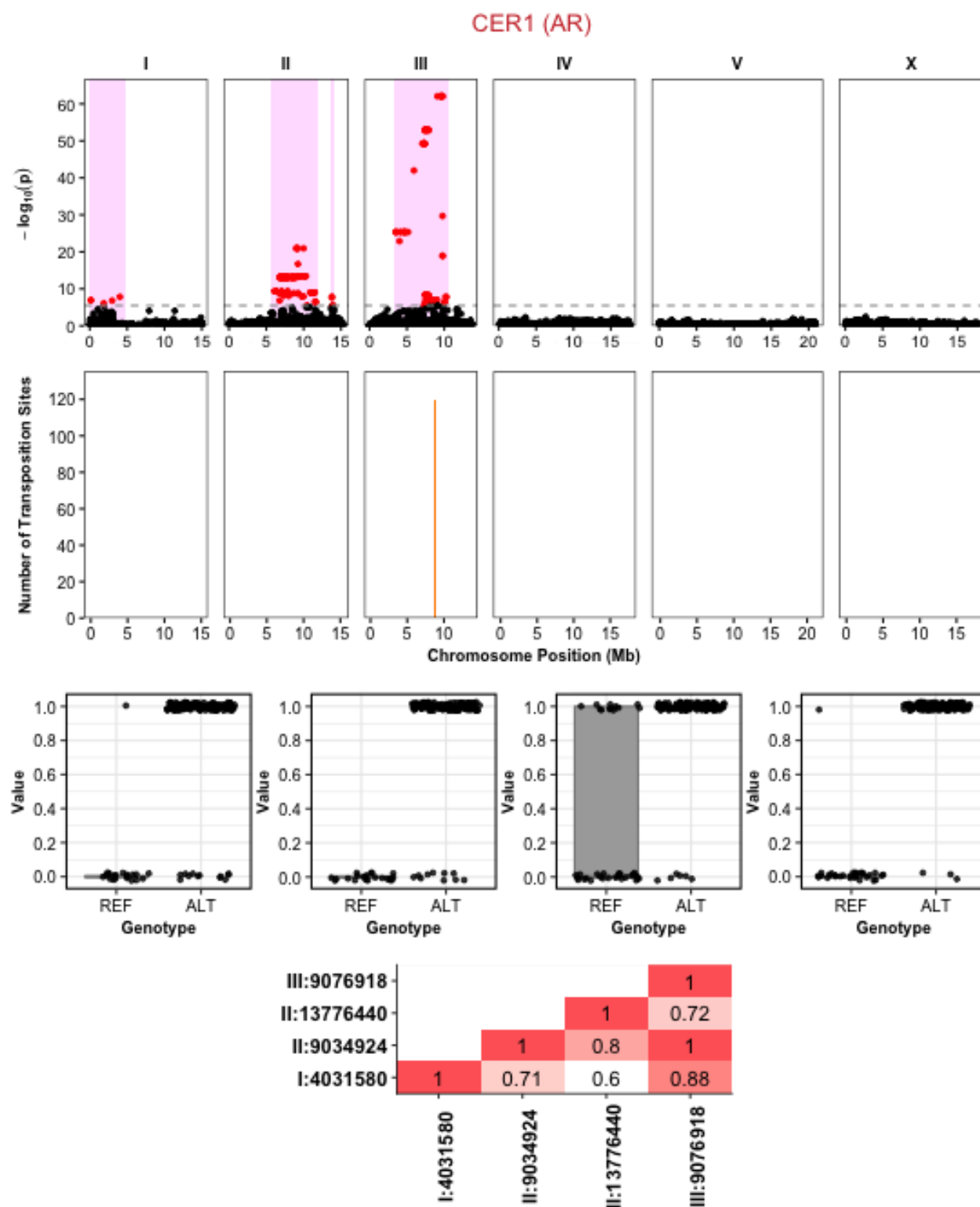
WBT00000416 (all)



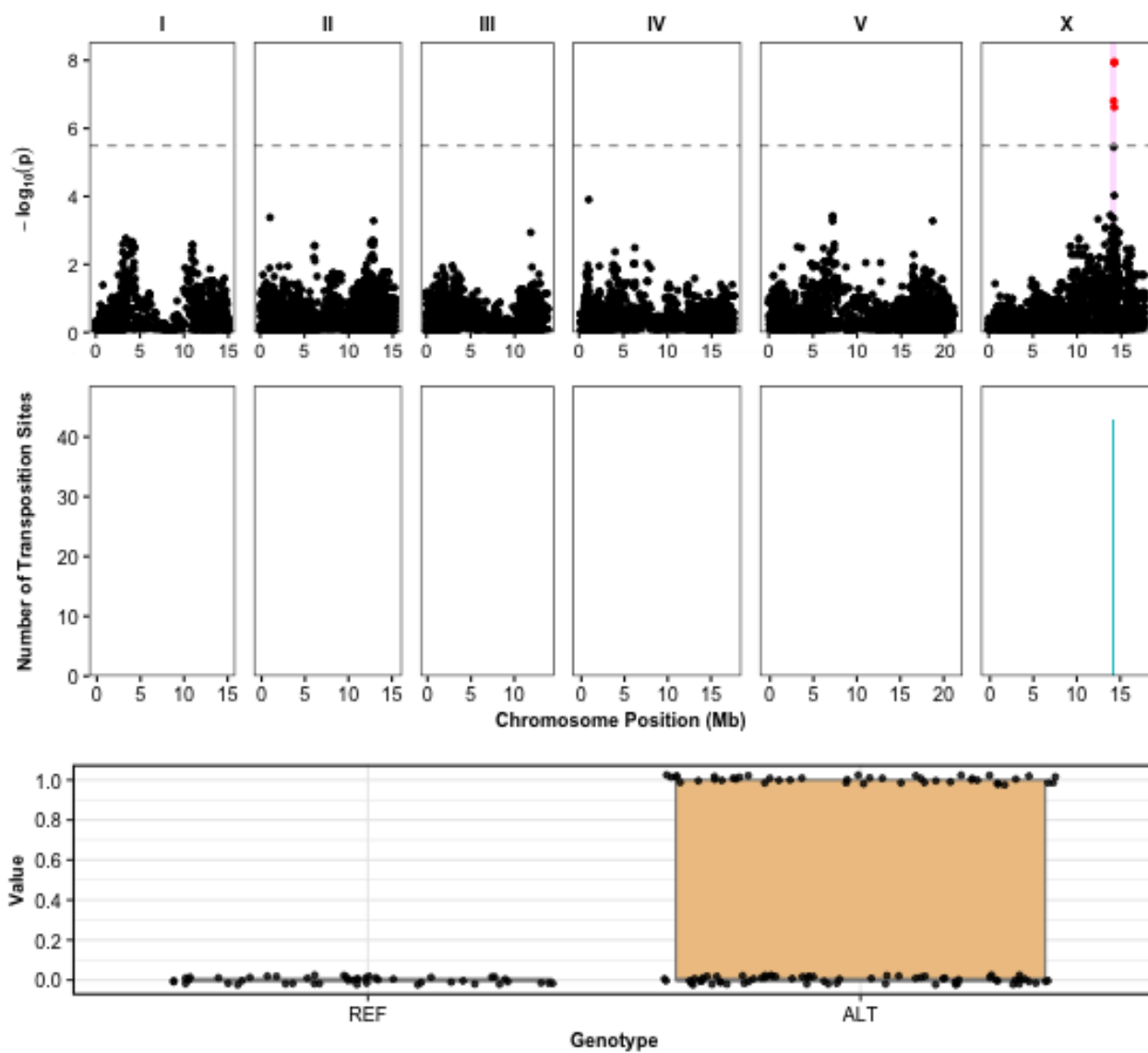
WBT00000416 (ins)

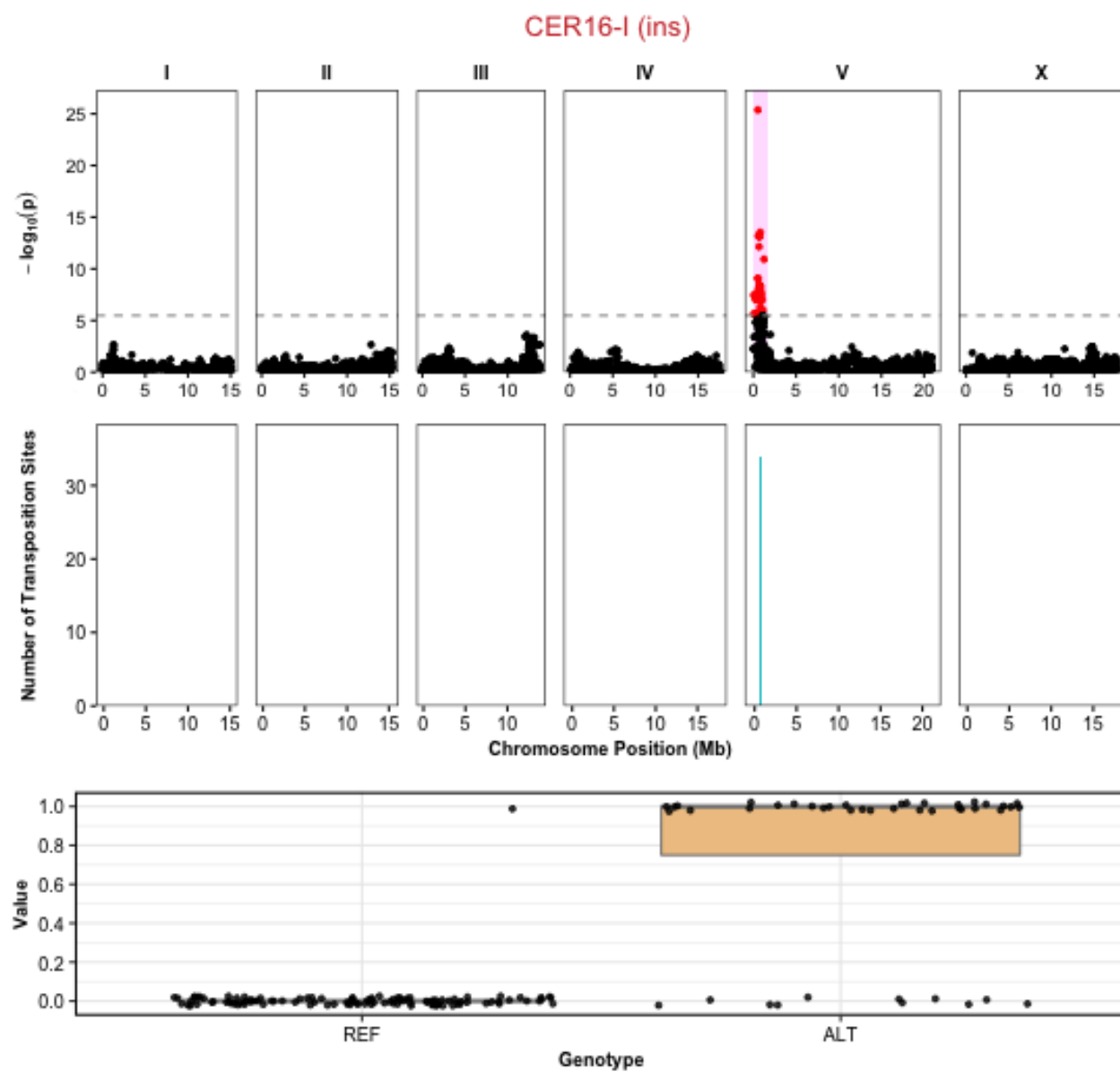


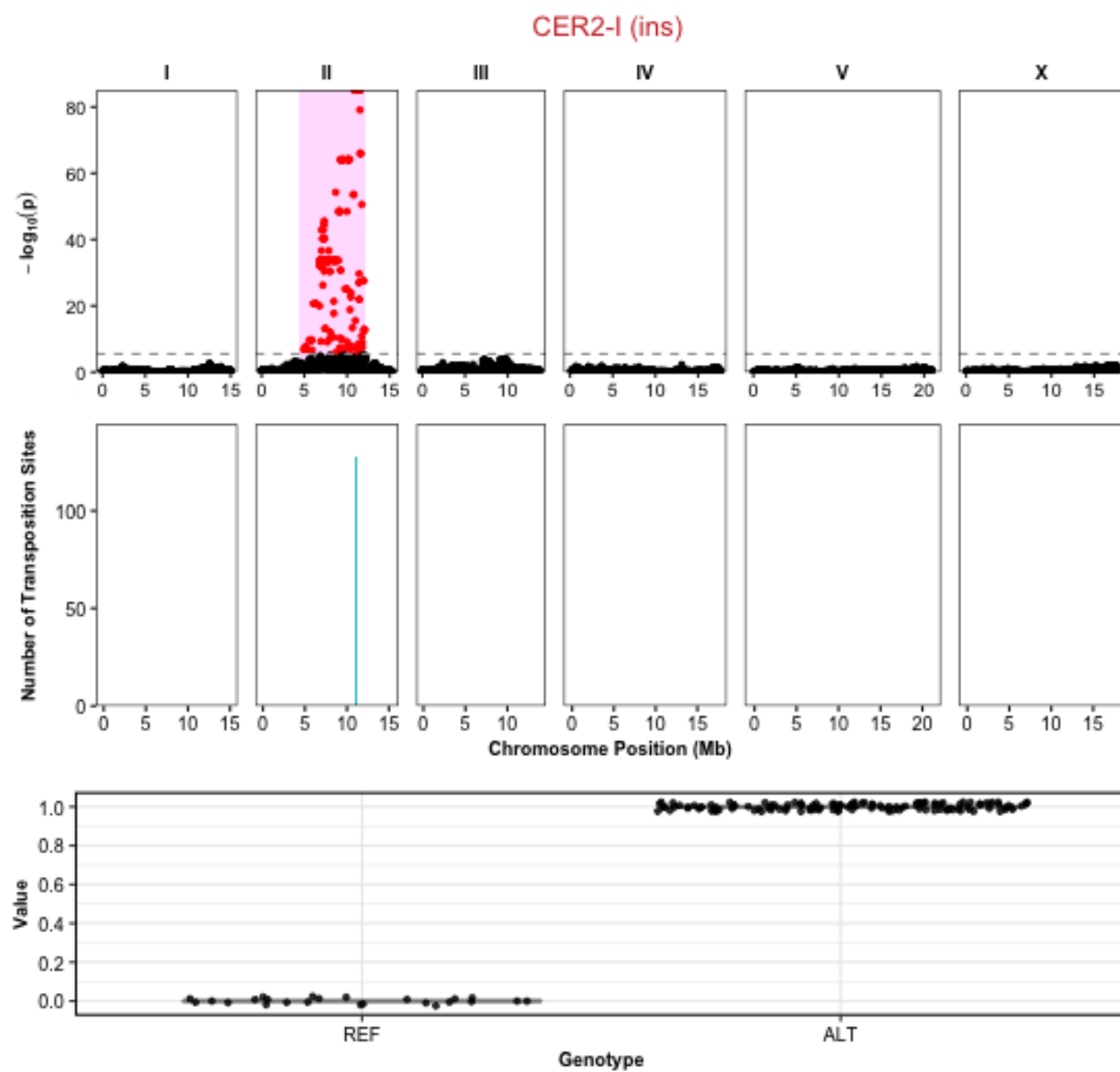


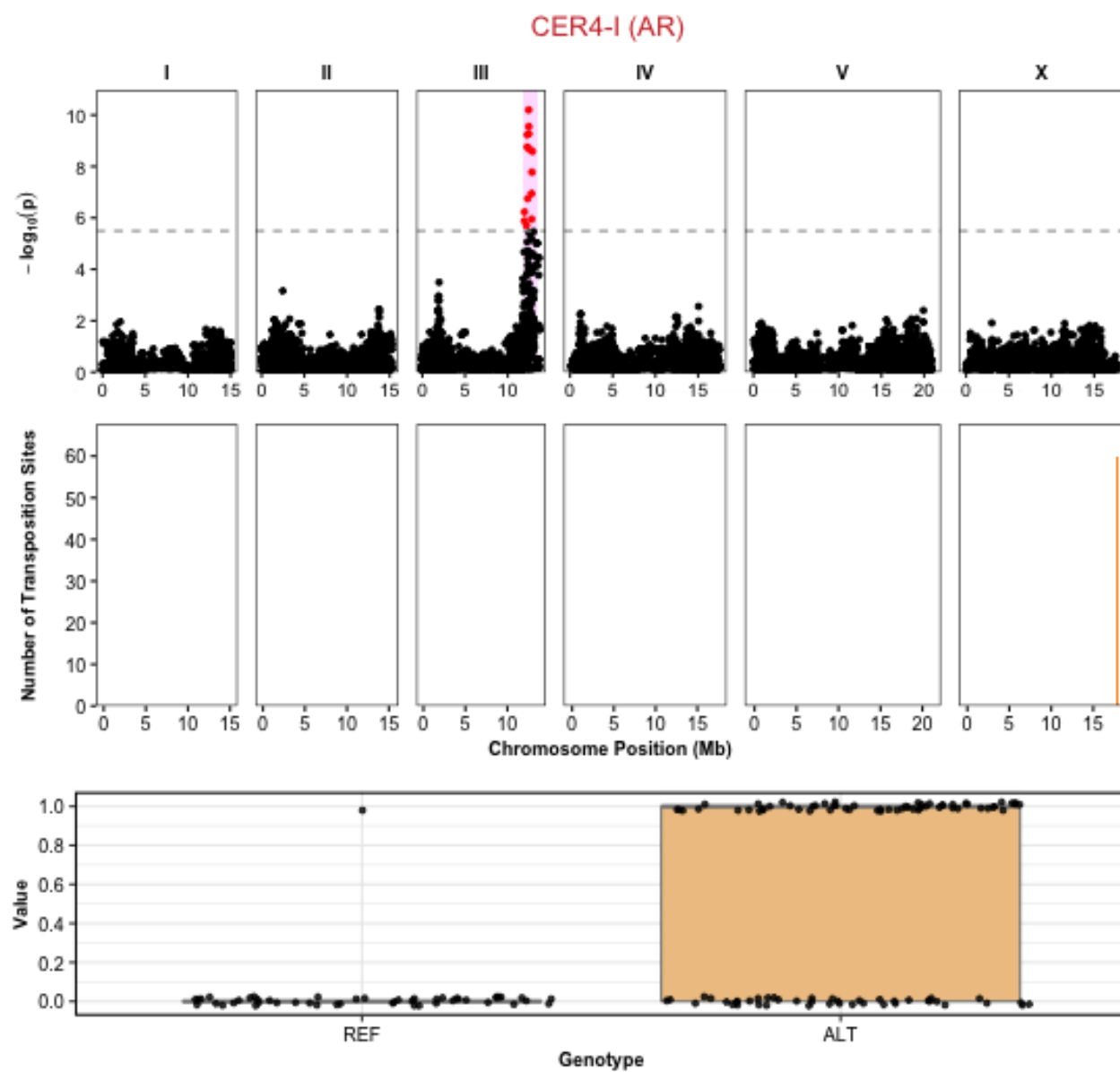


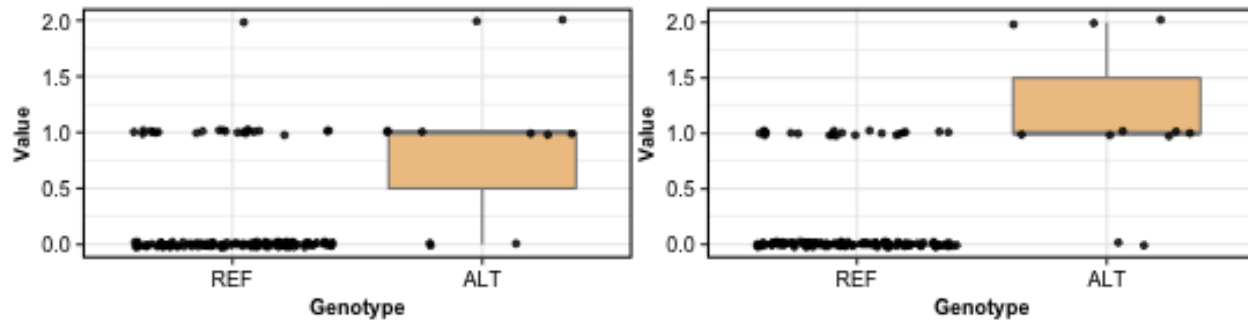
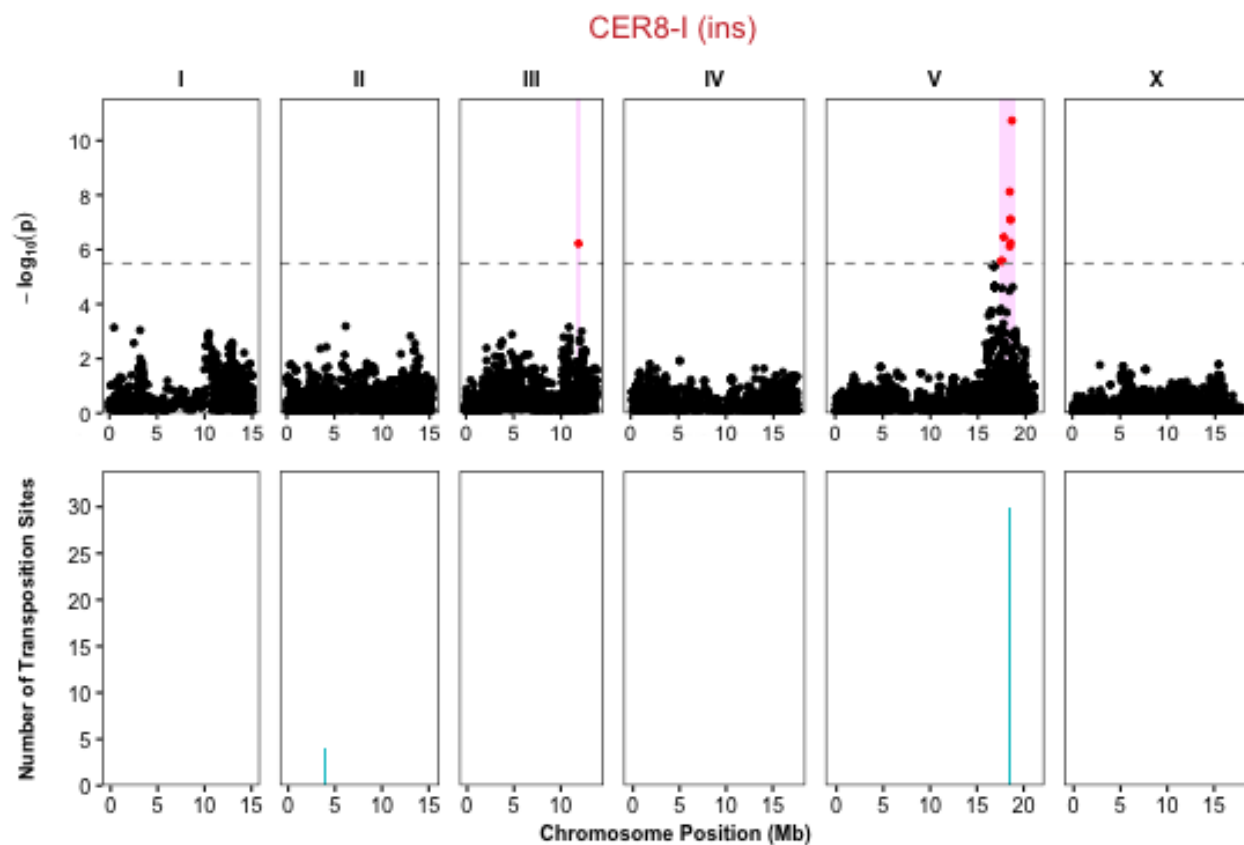
CER16-2-LTR (ins)



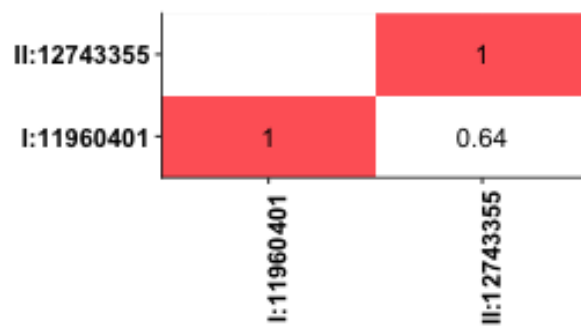
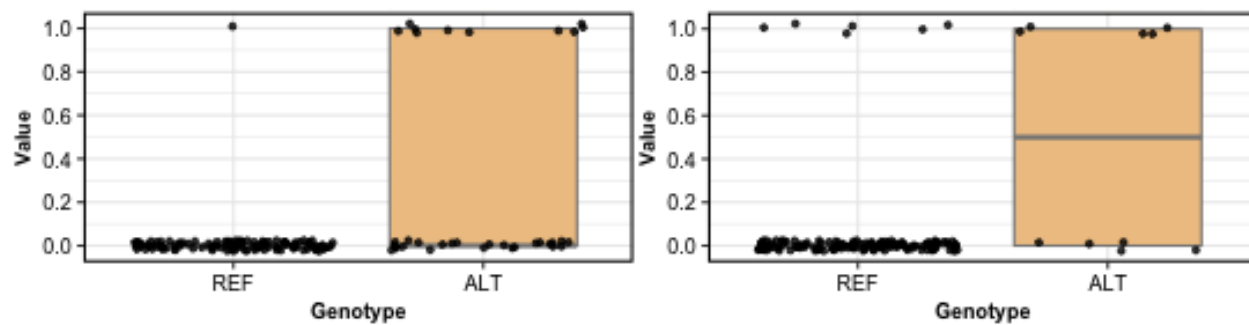
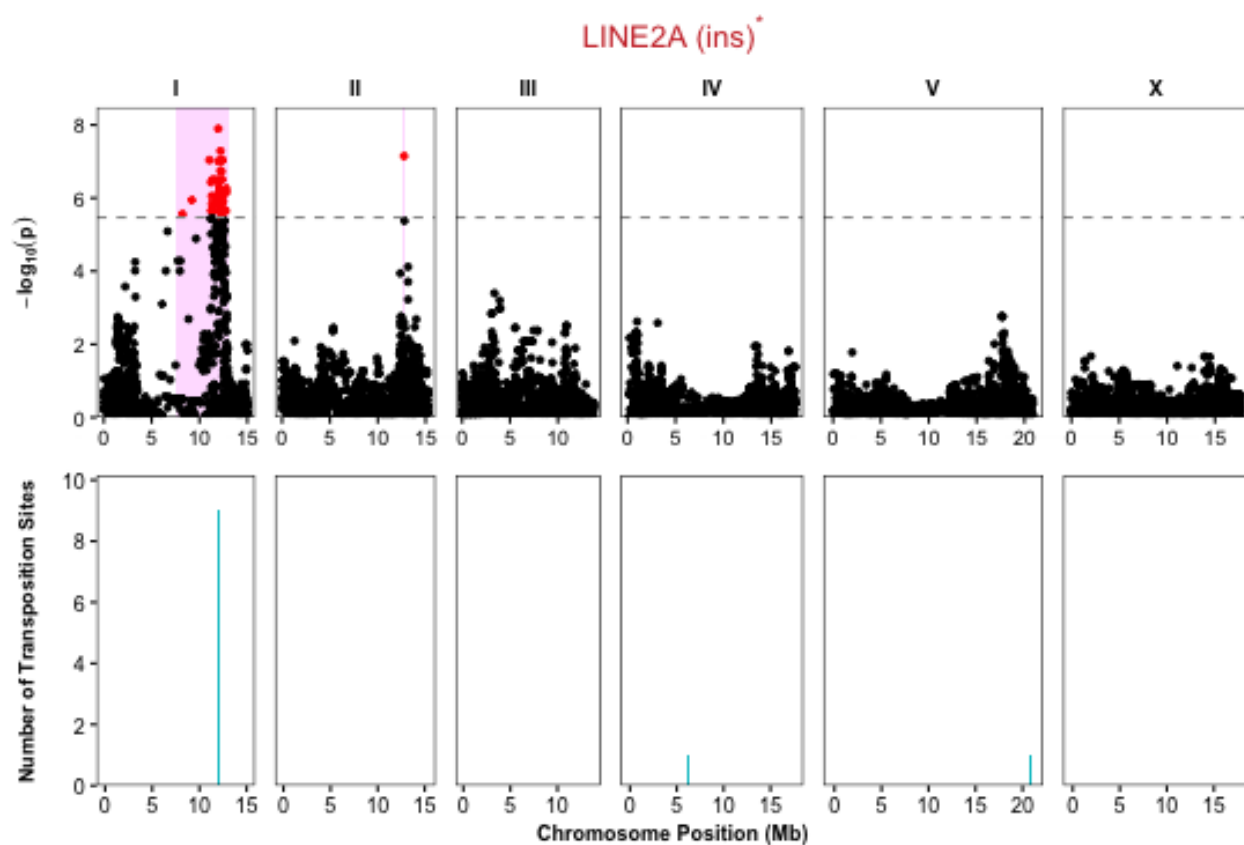


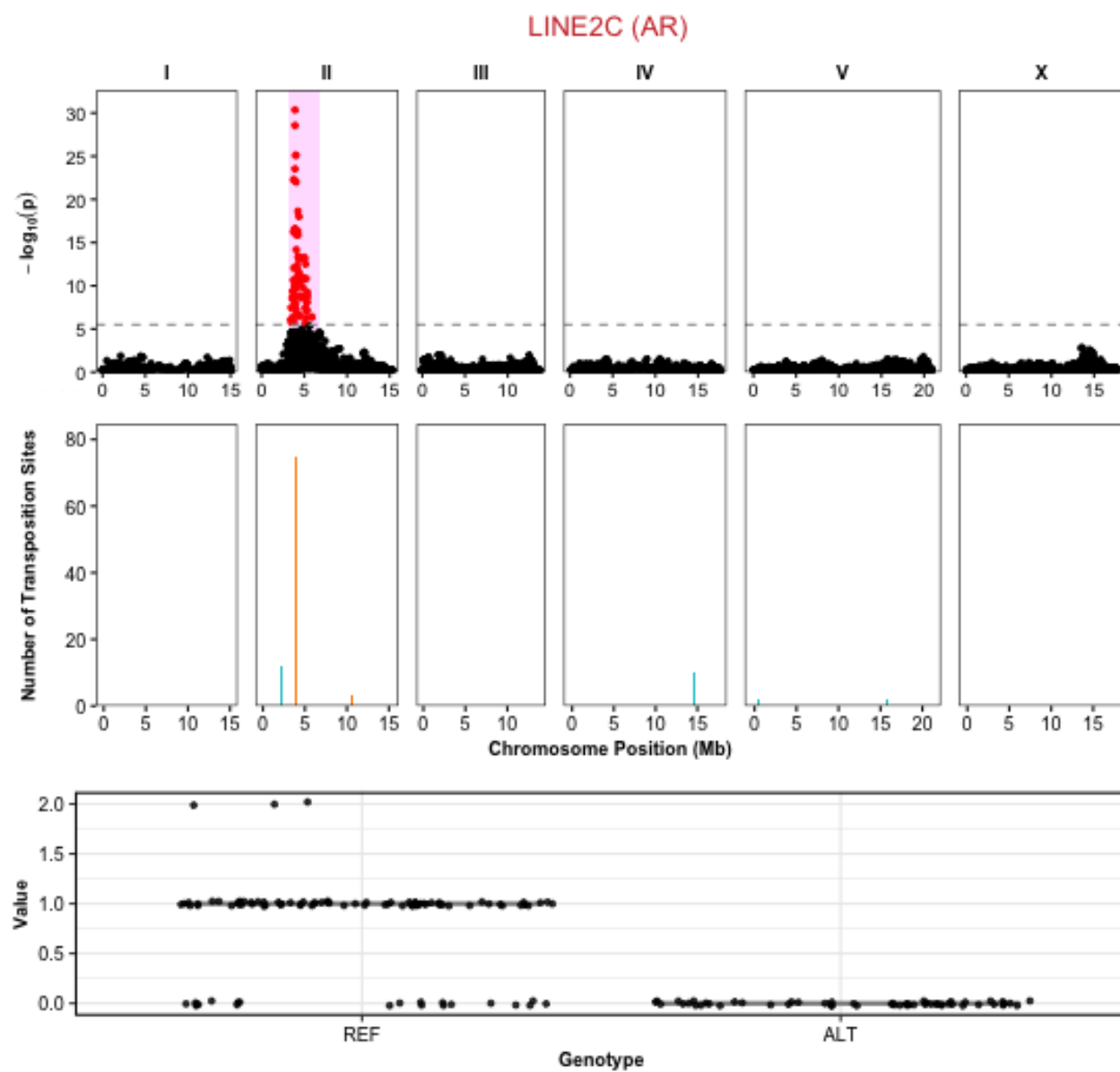


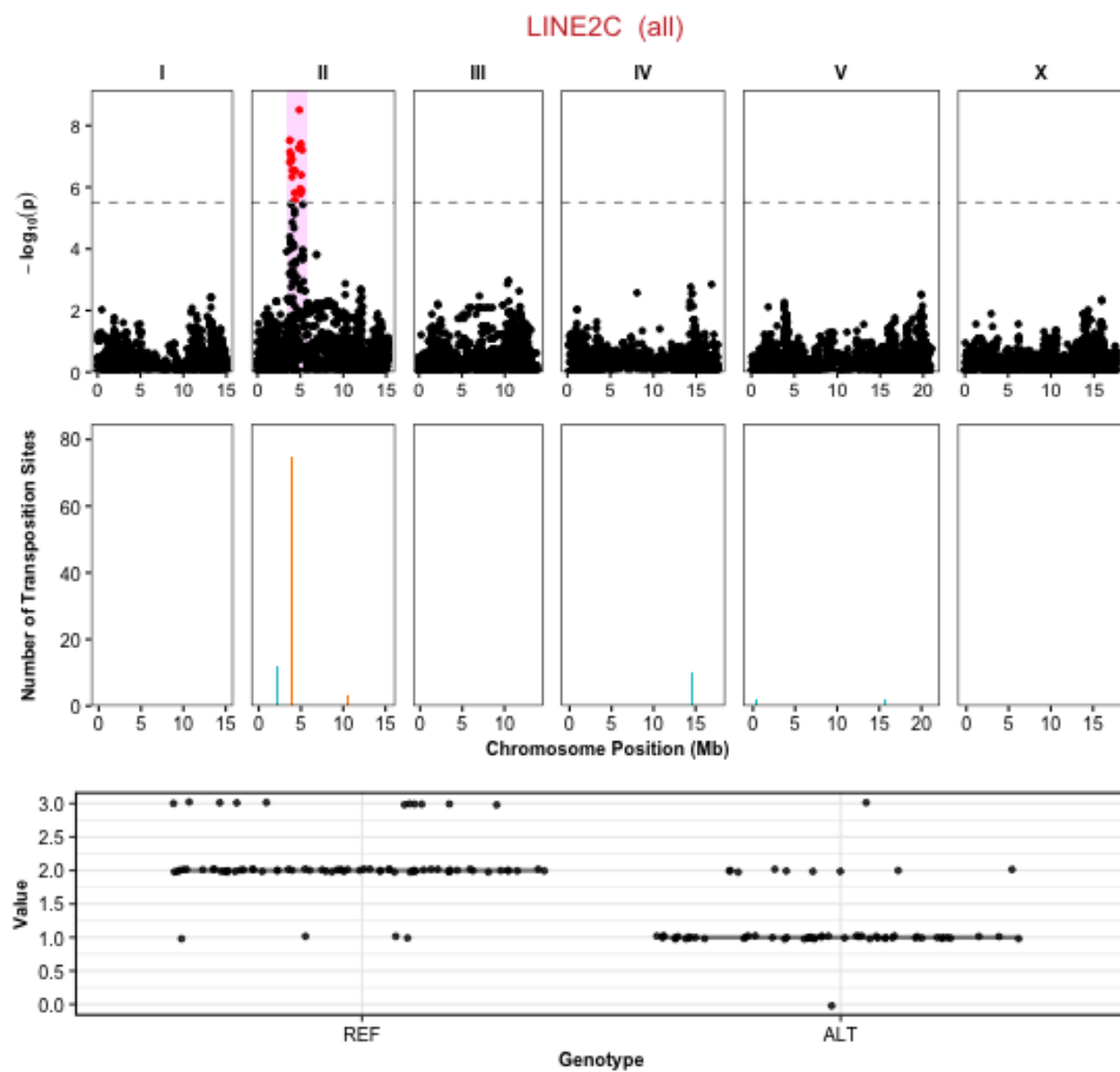


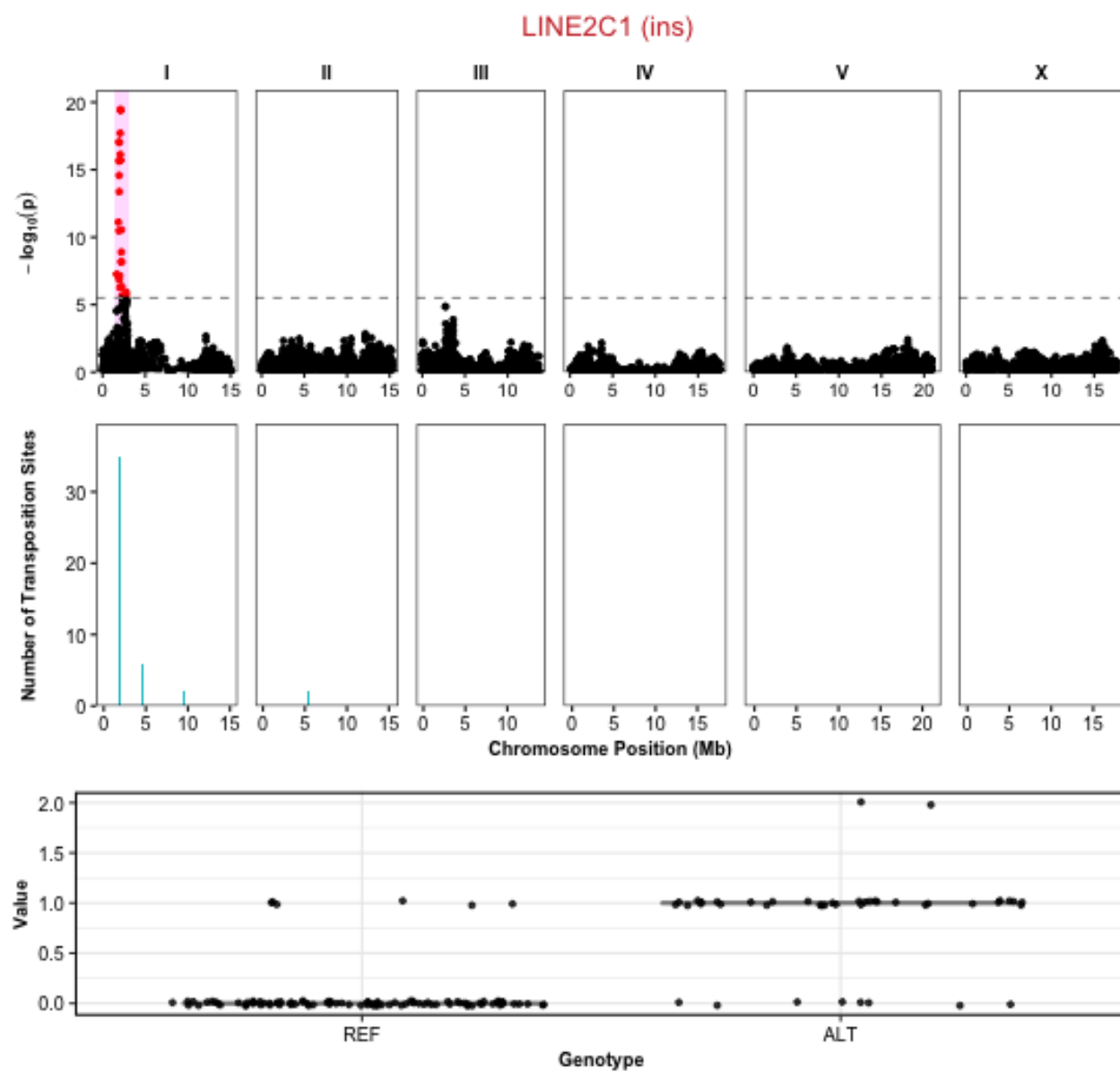


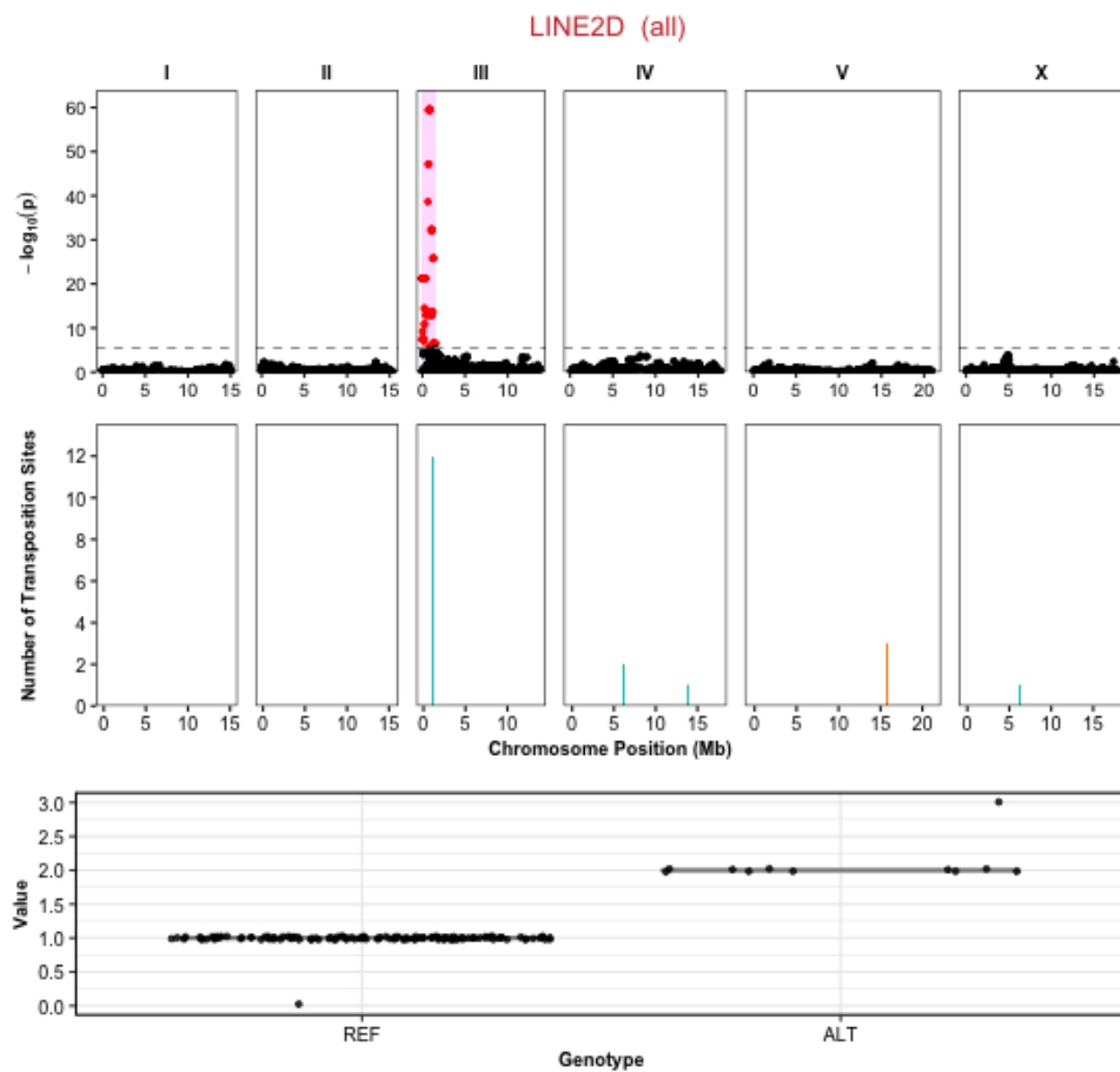
V:18565003		1
III:11820342	1	0.049
	III:11820342	V:18565003

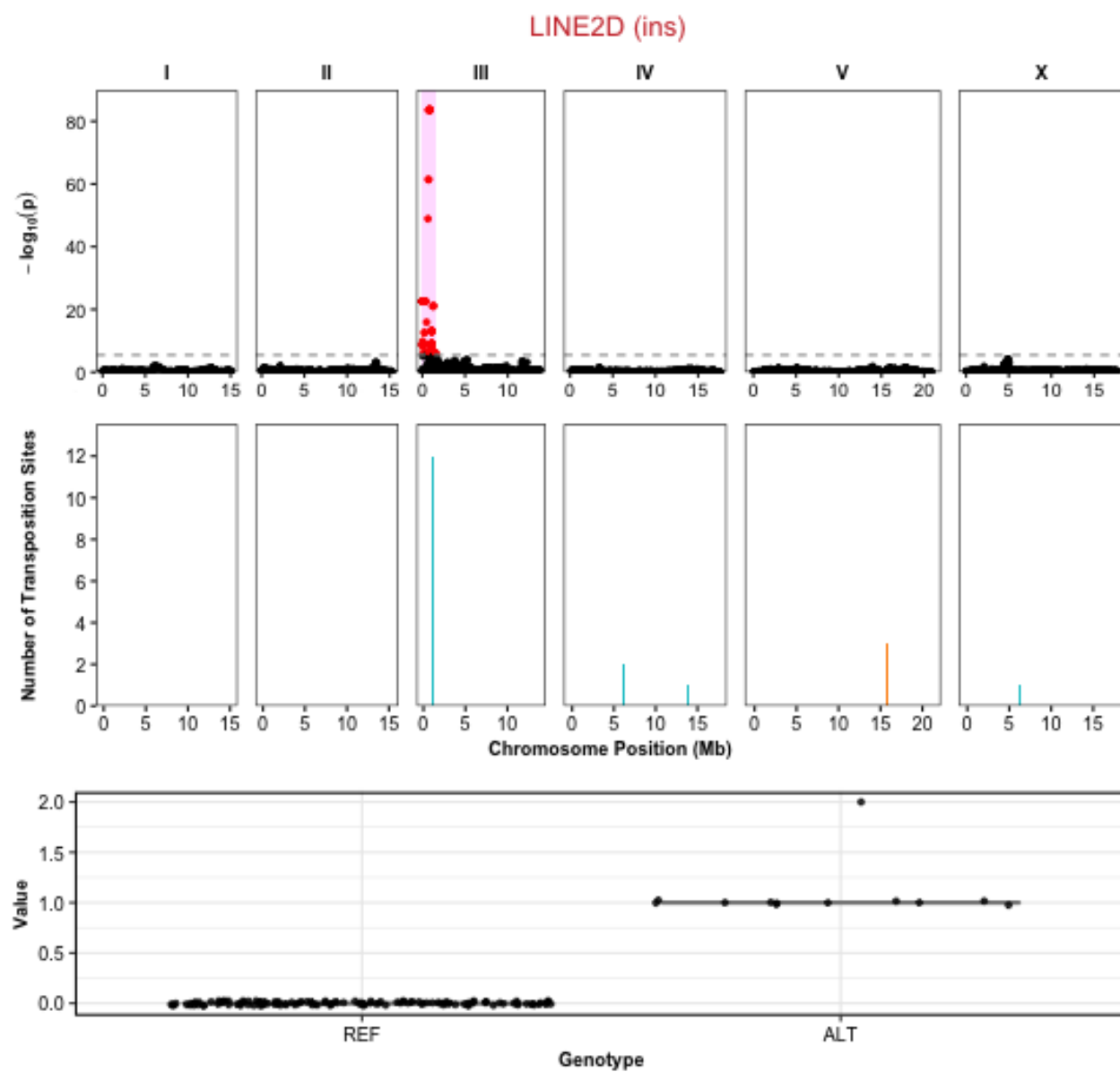


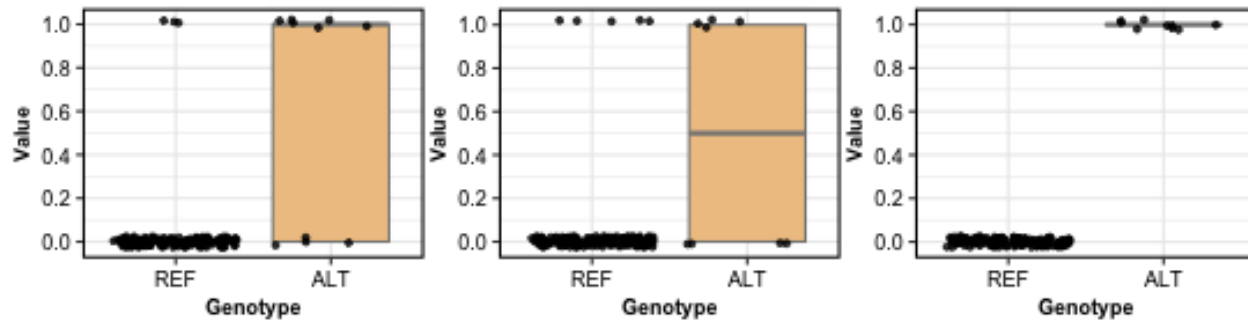
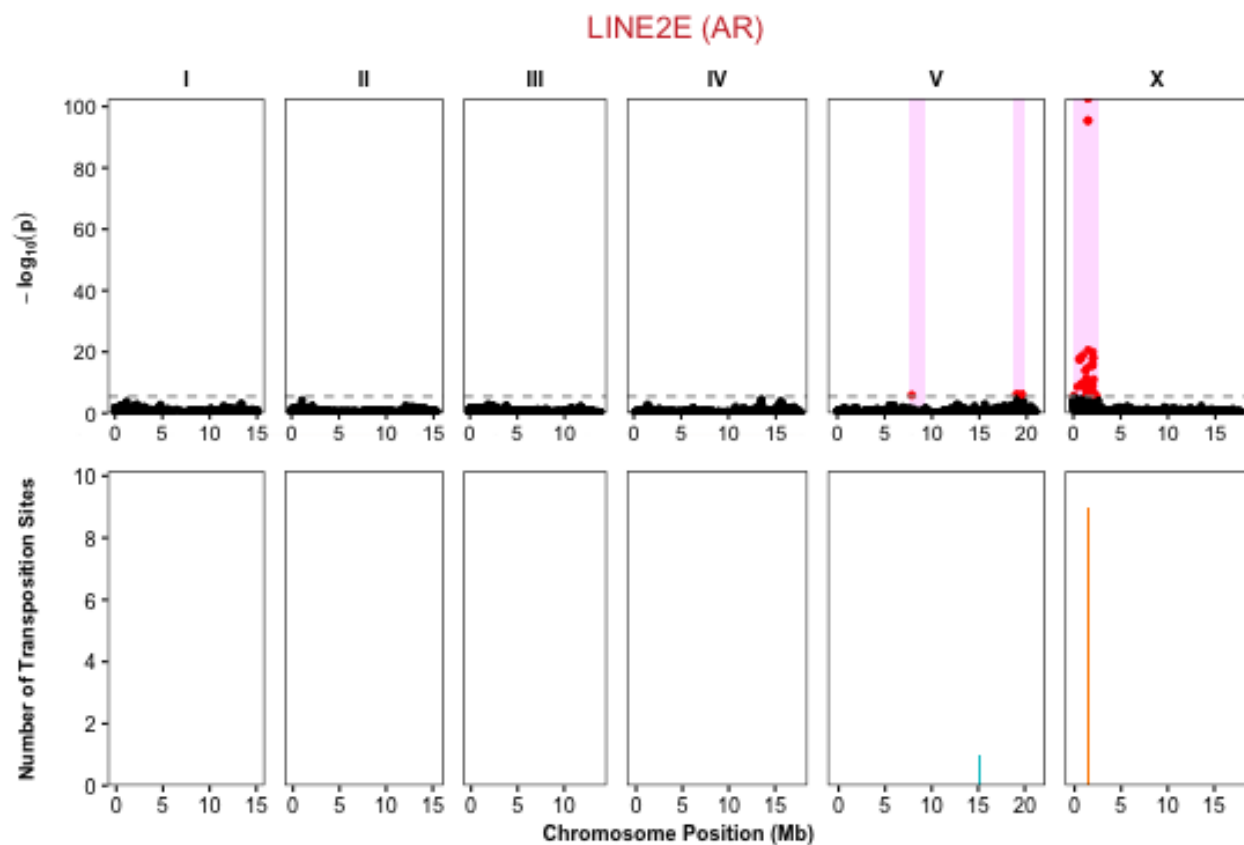




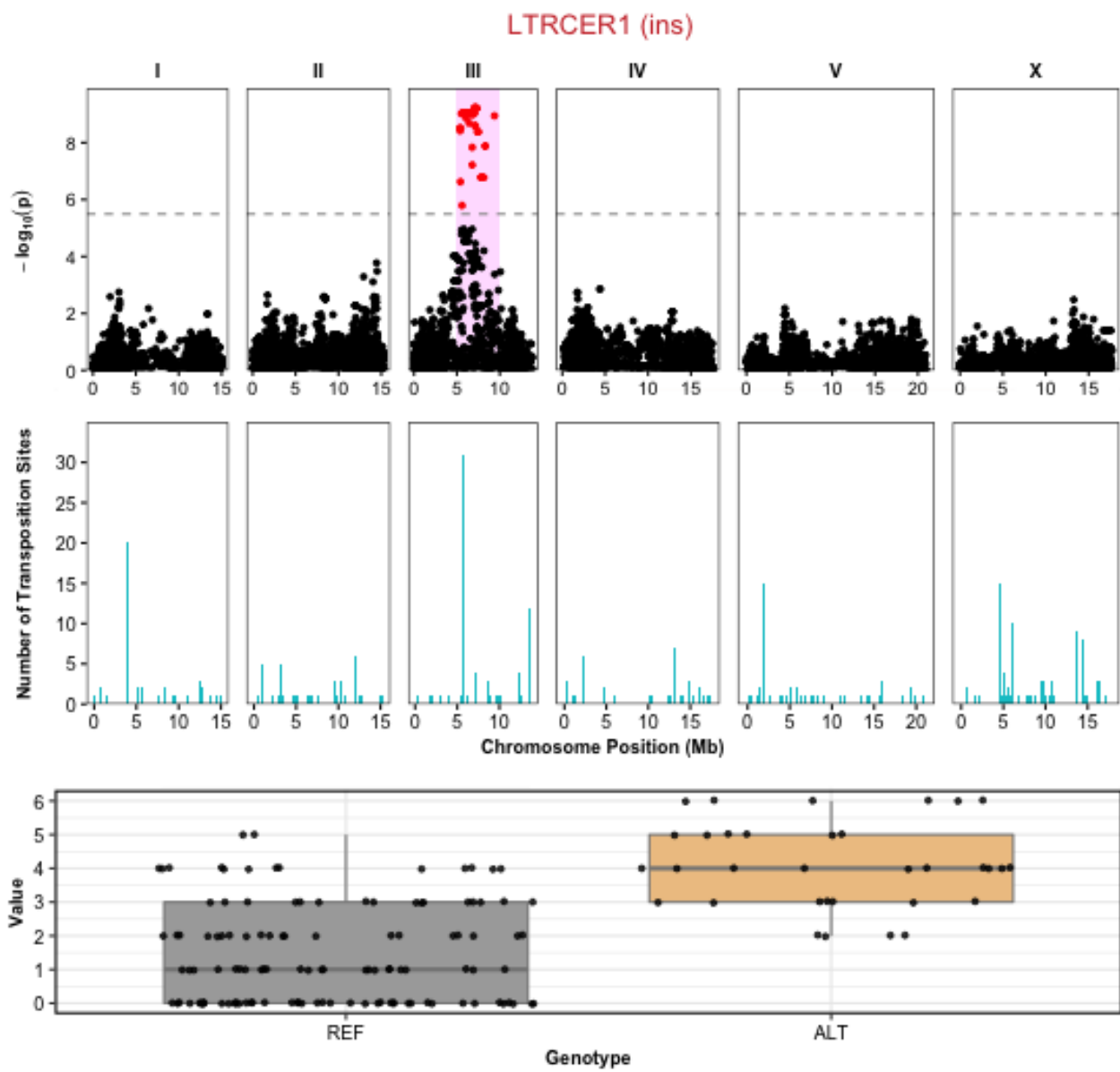


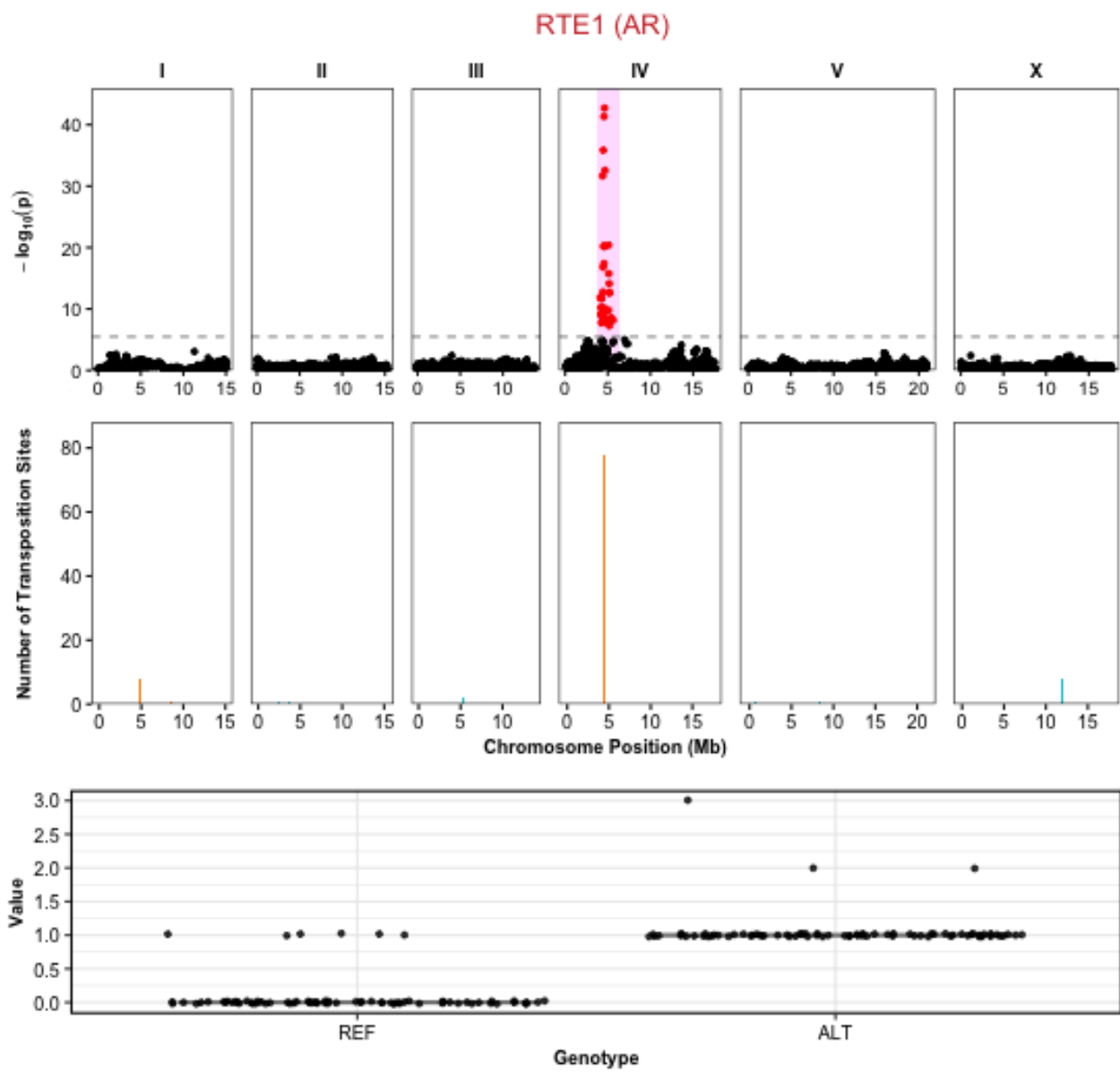


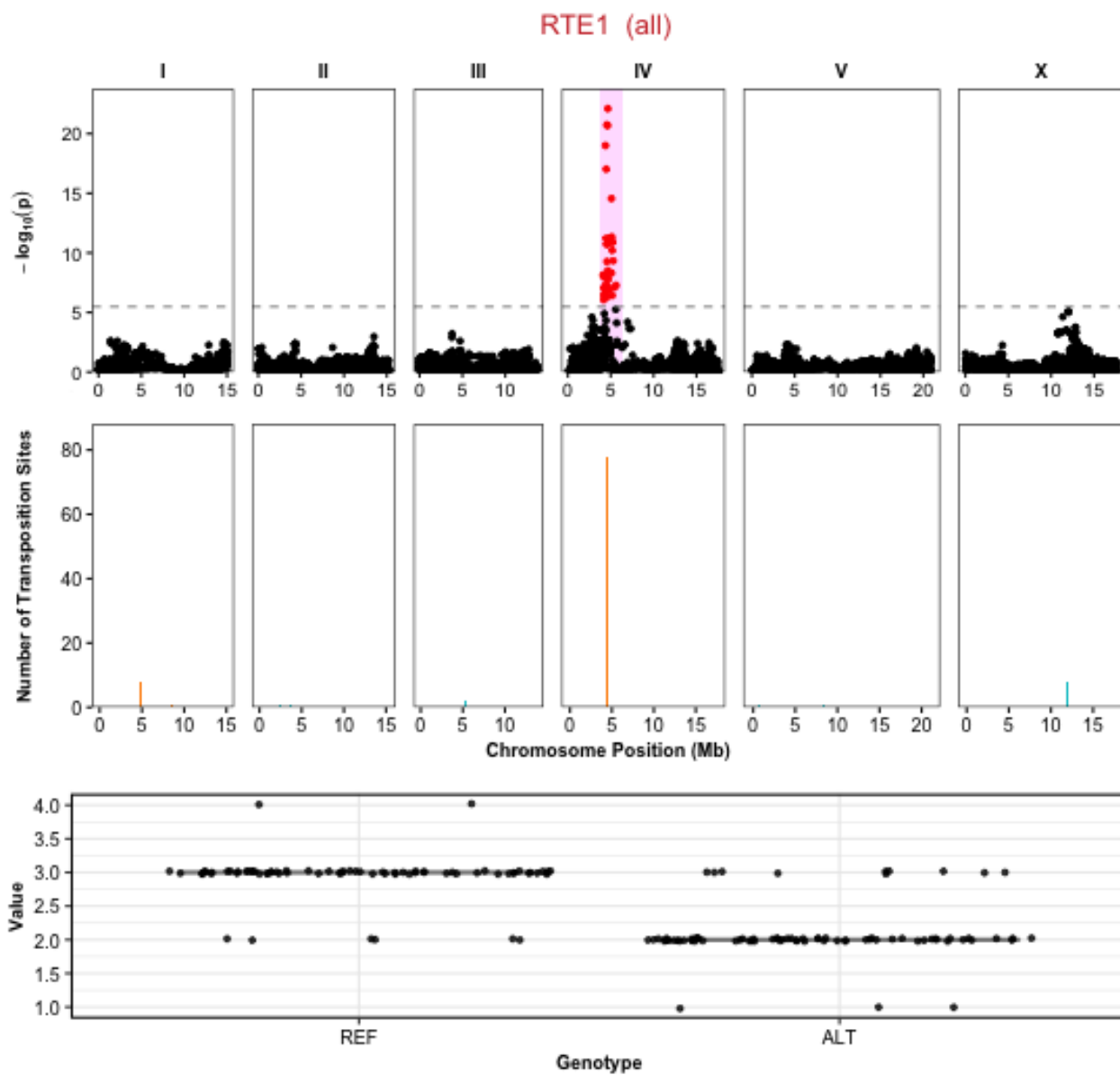


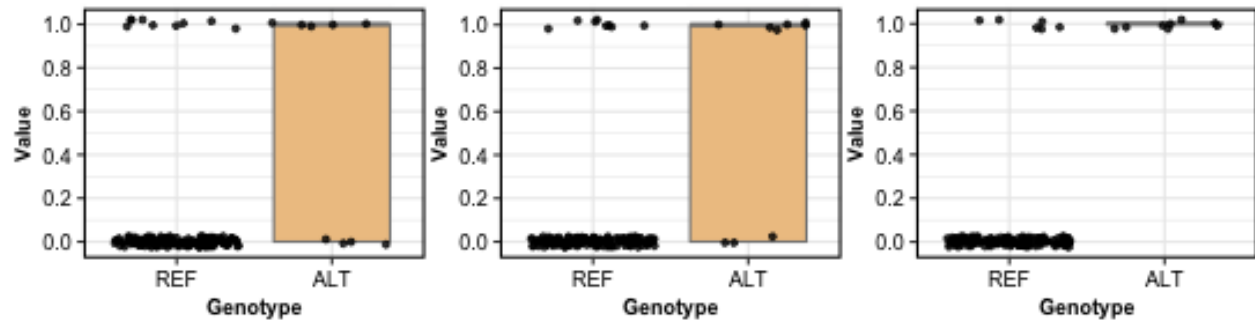
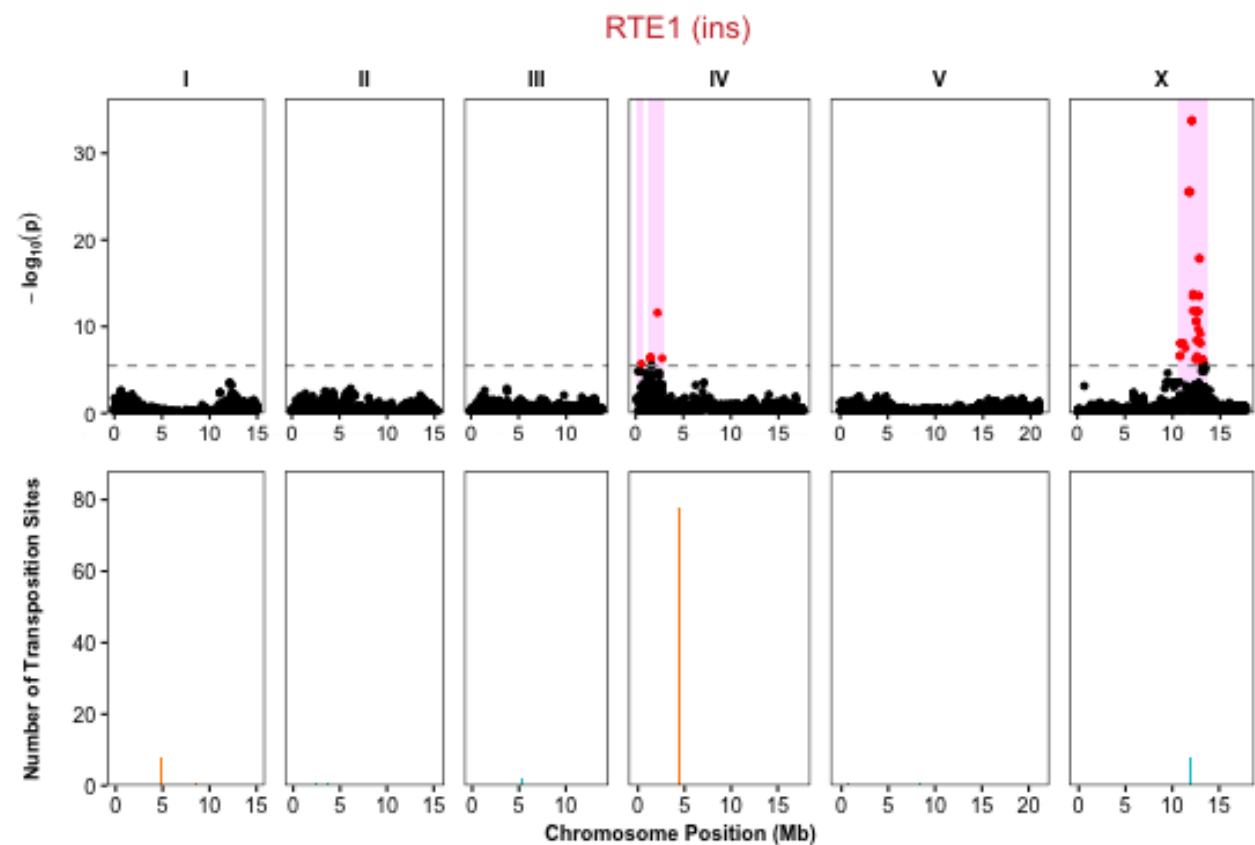


X:1559986			1
V:19511037		1	0.47
V:7857946	1	0.46	0.64
	V:7857946	V:19511037	X:1559986

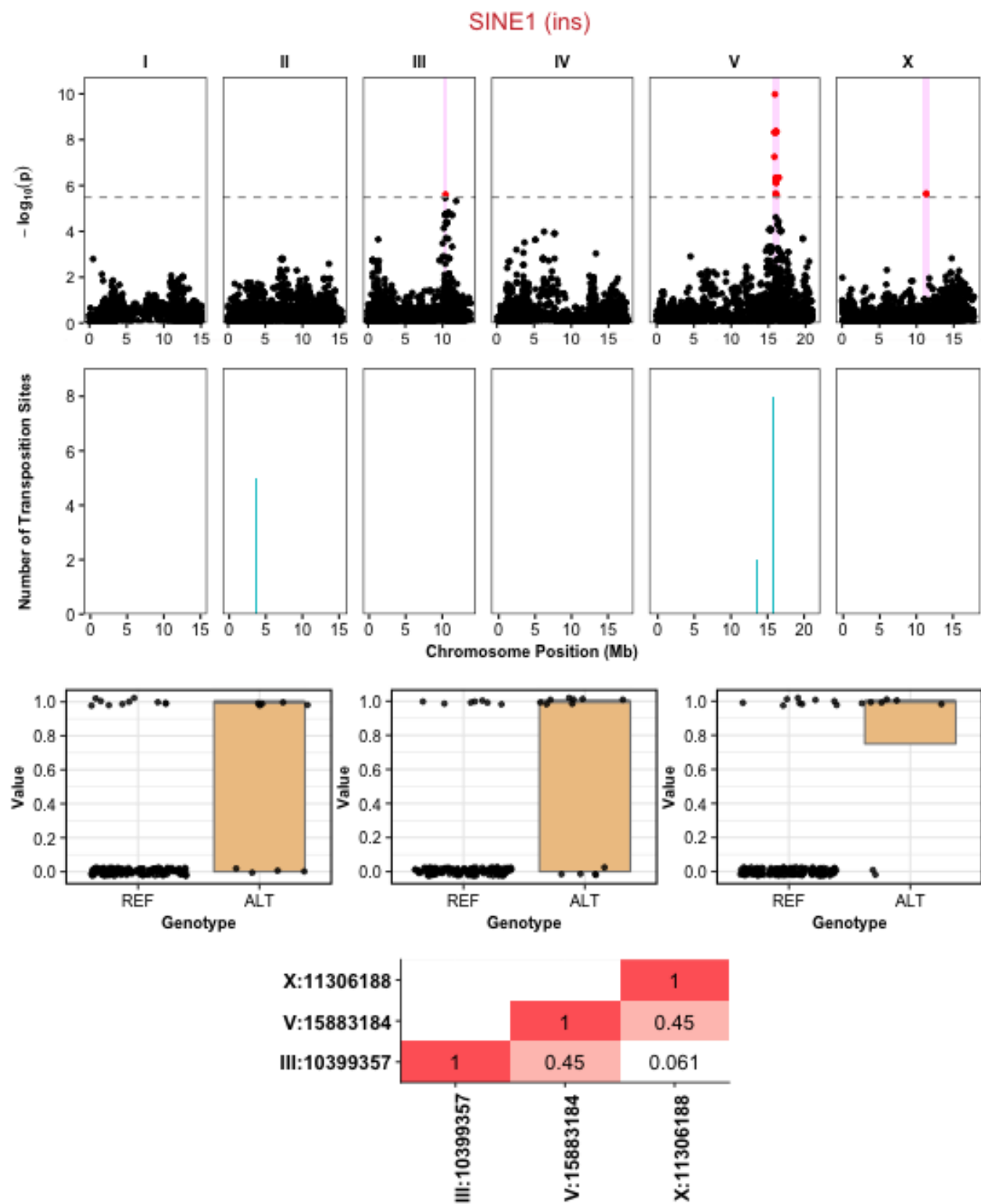


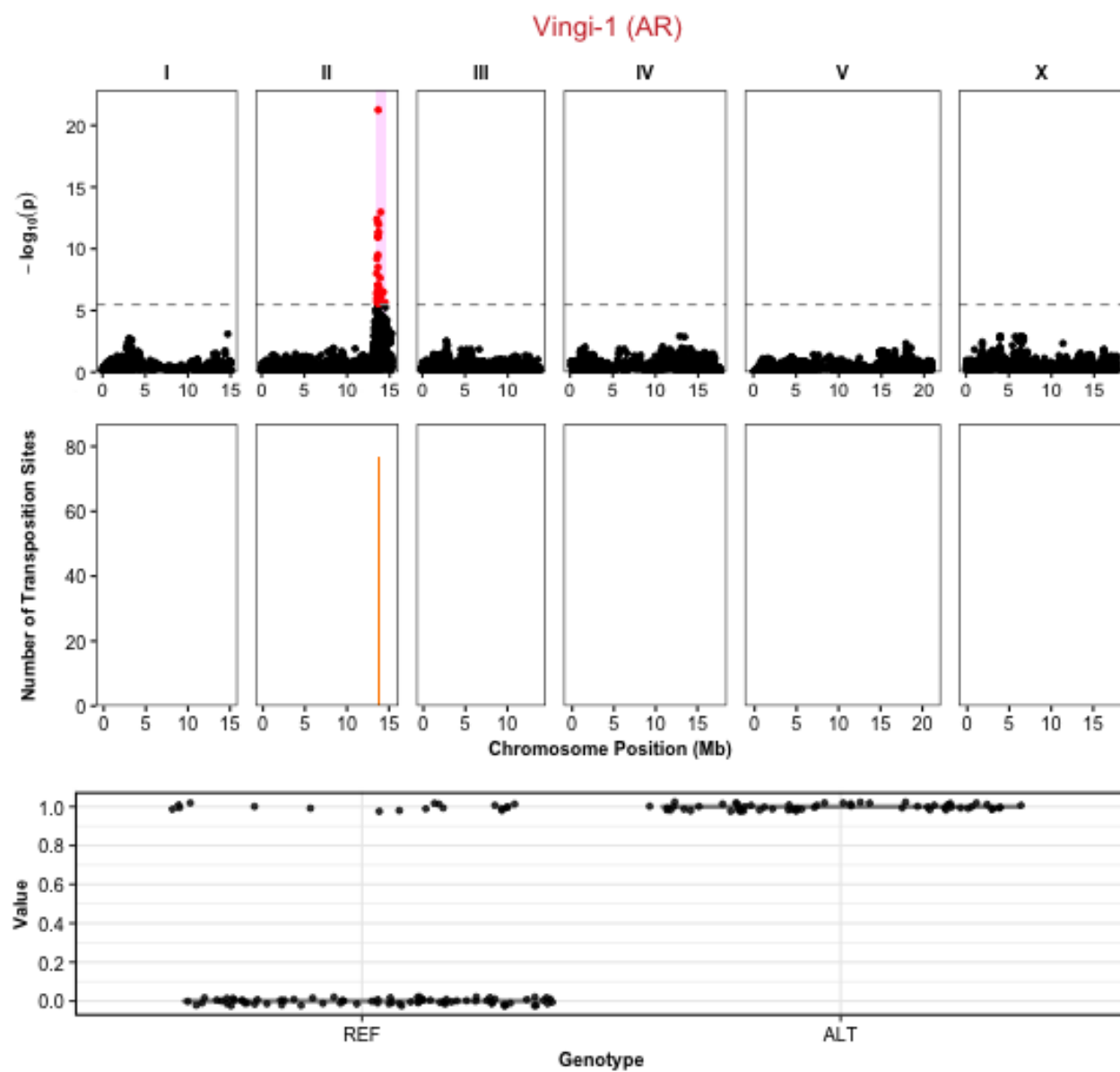




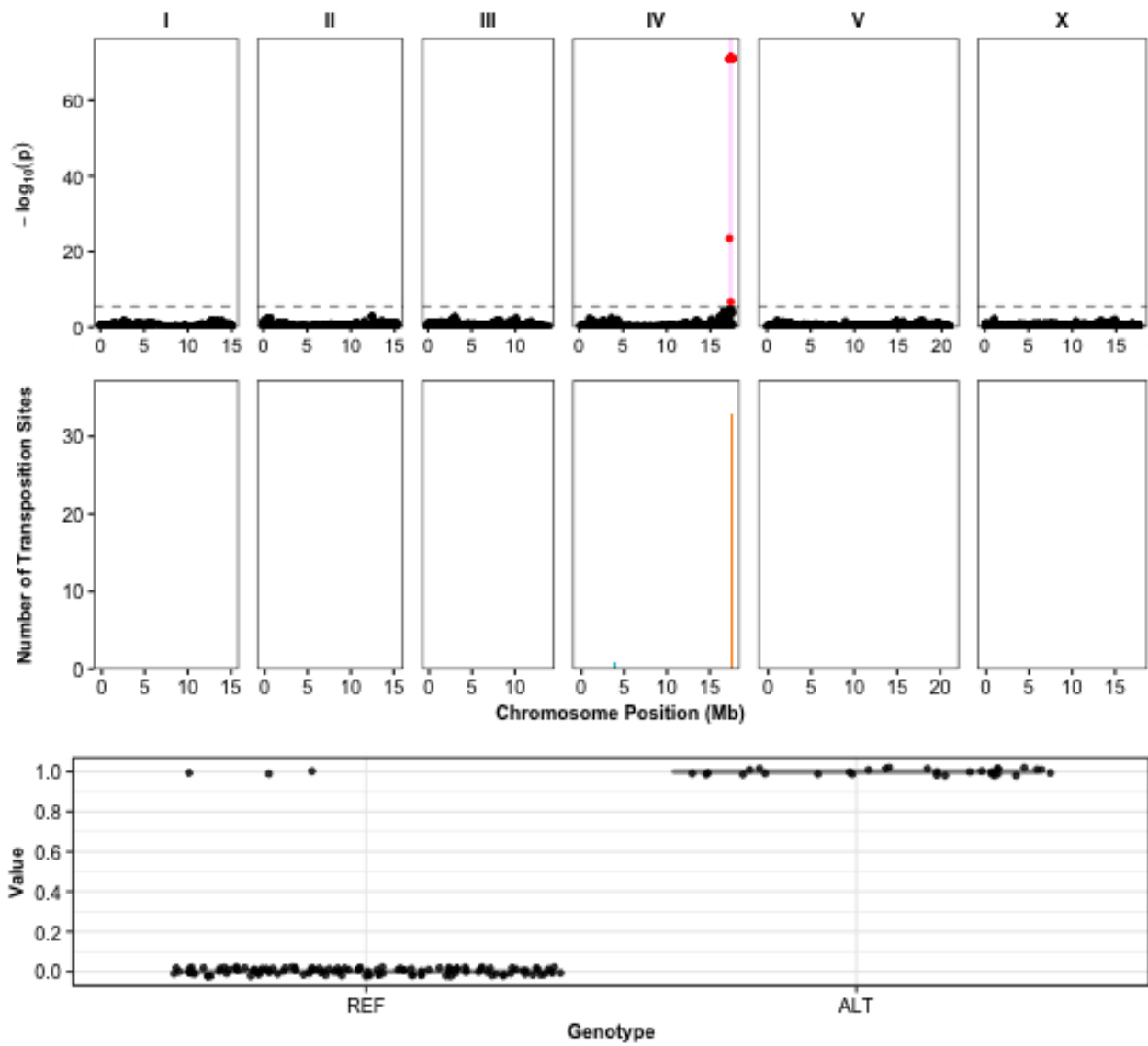


X:11991311			1
IV:2286383		1	0.39
IV:577864	1	0.068	0.55
	IV:577864	IV:2286383	X:11991311

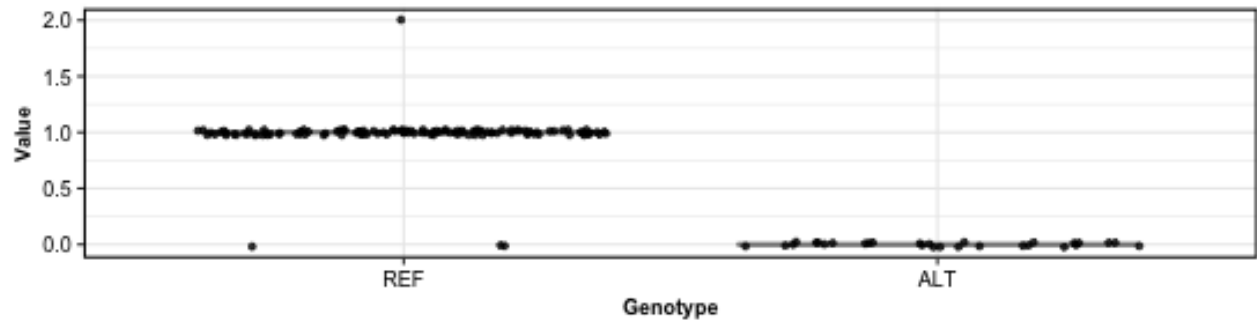
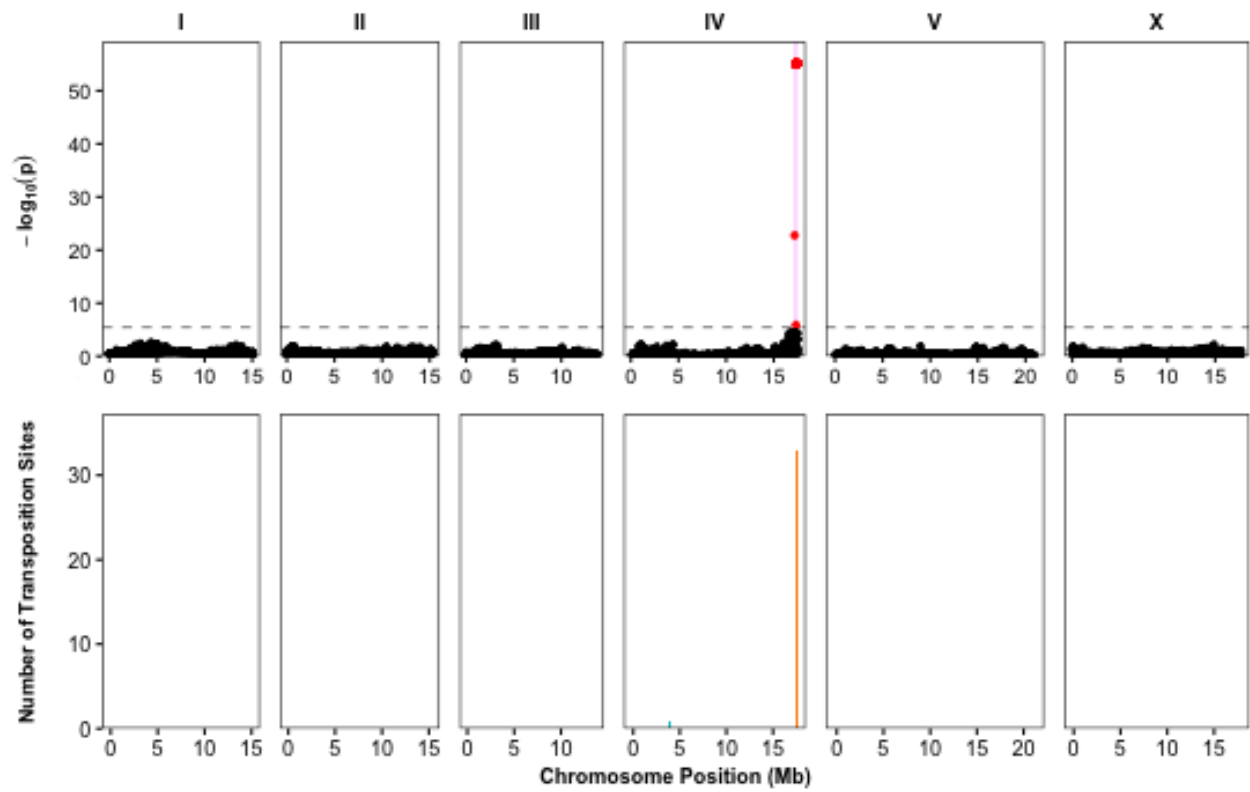




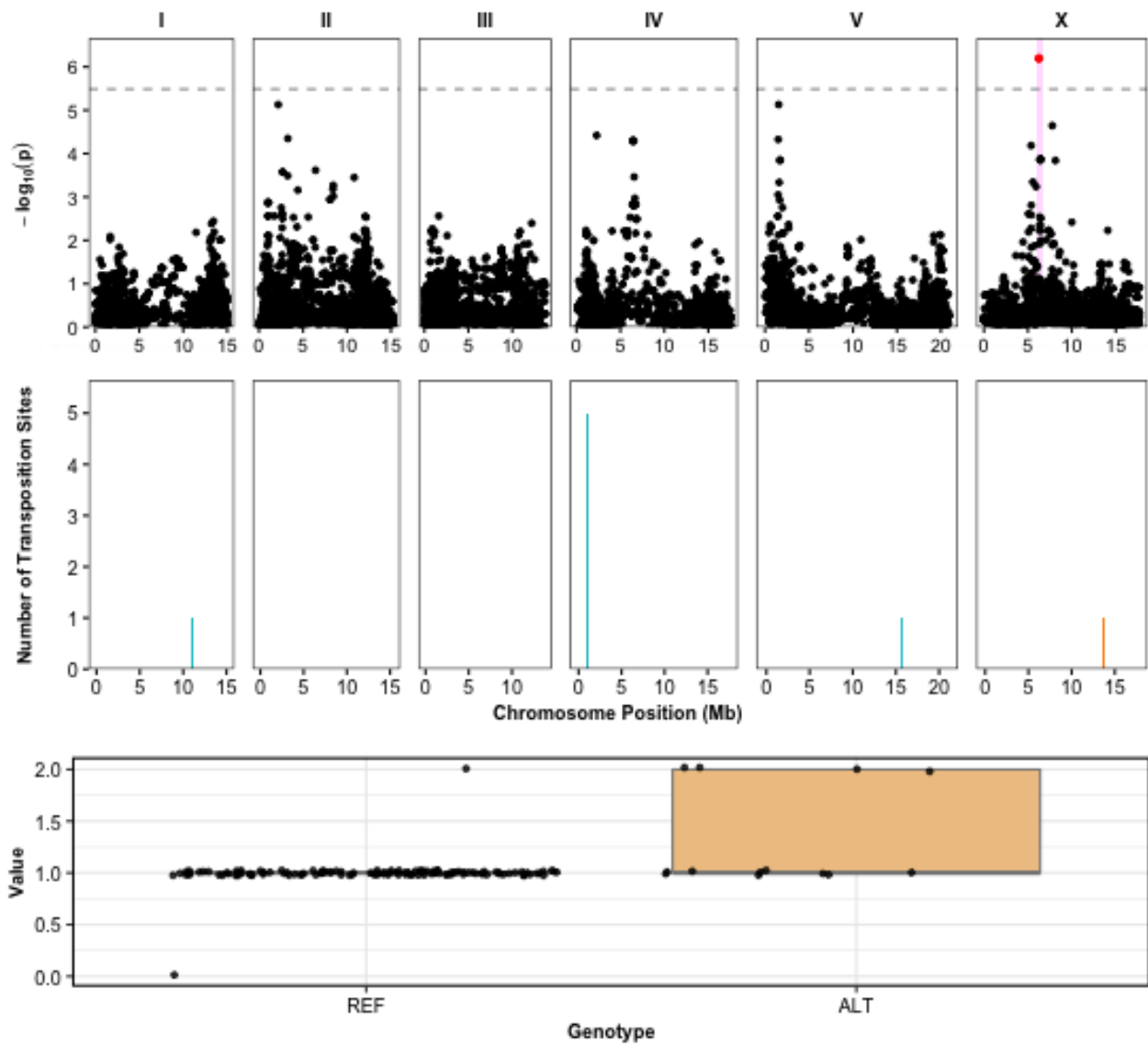
WBT00000134 (AR)



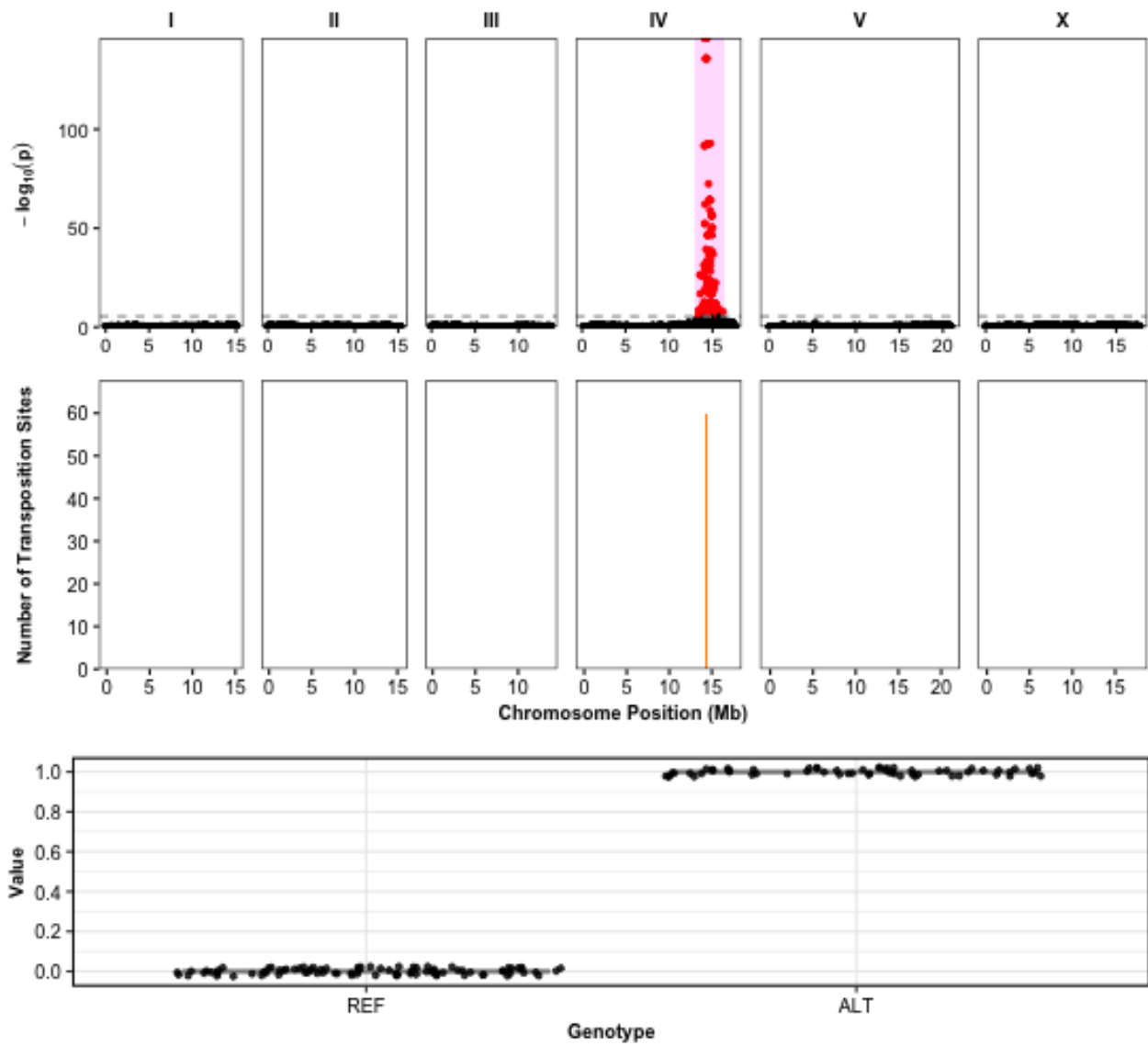
WBT00000134 (all)



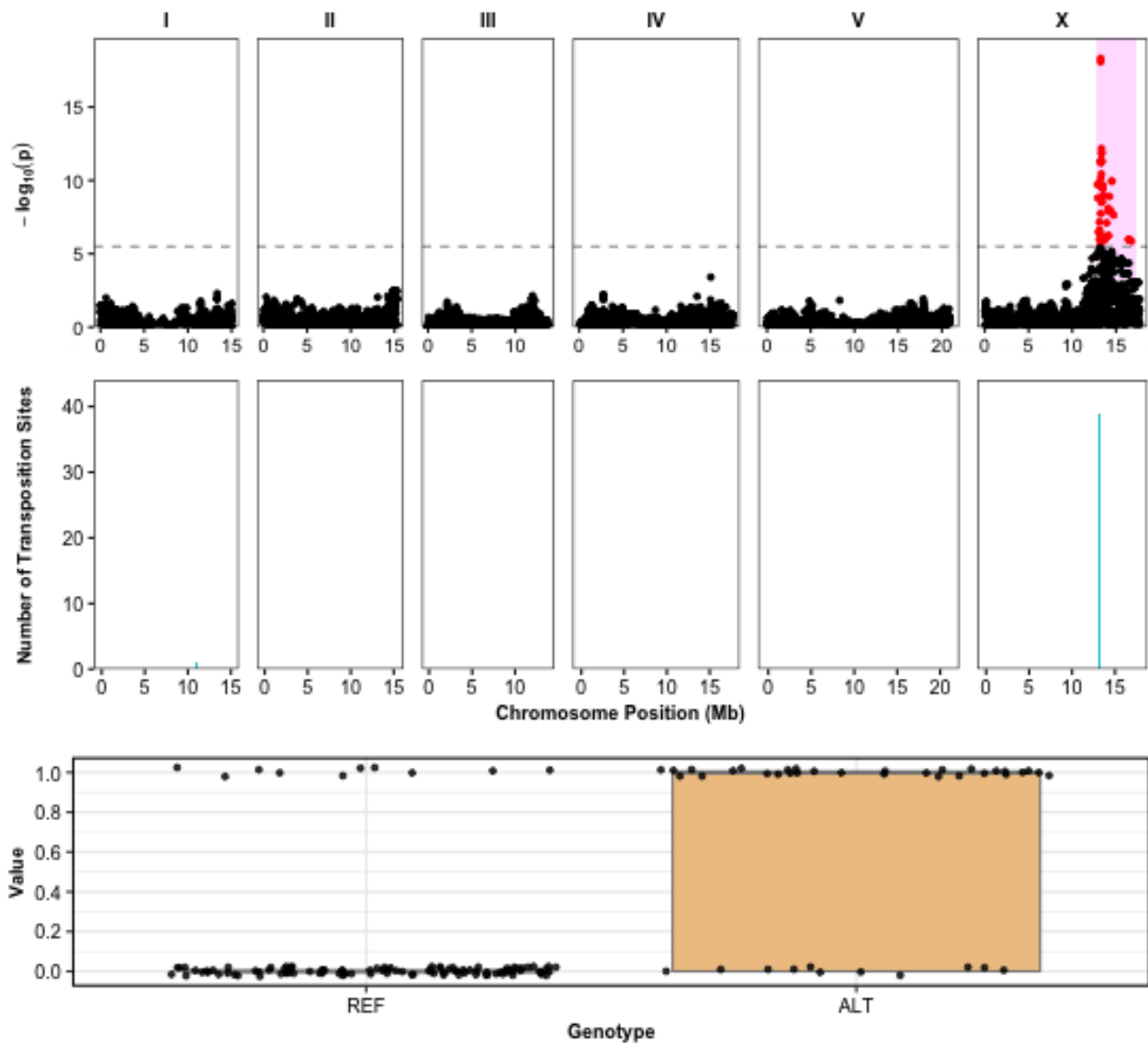
WBT00000581 (all)



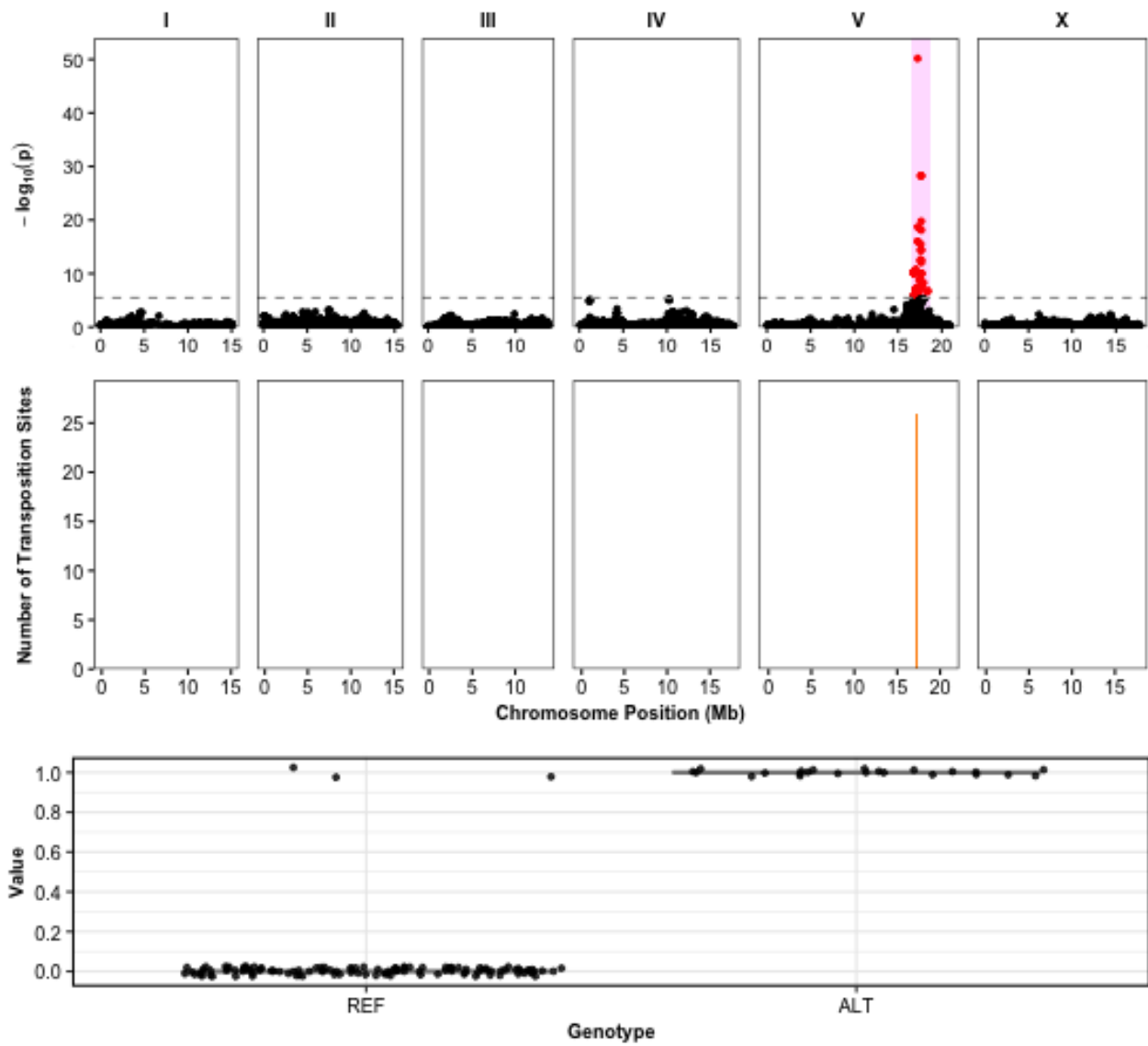
WBT00000617 (AR)



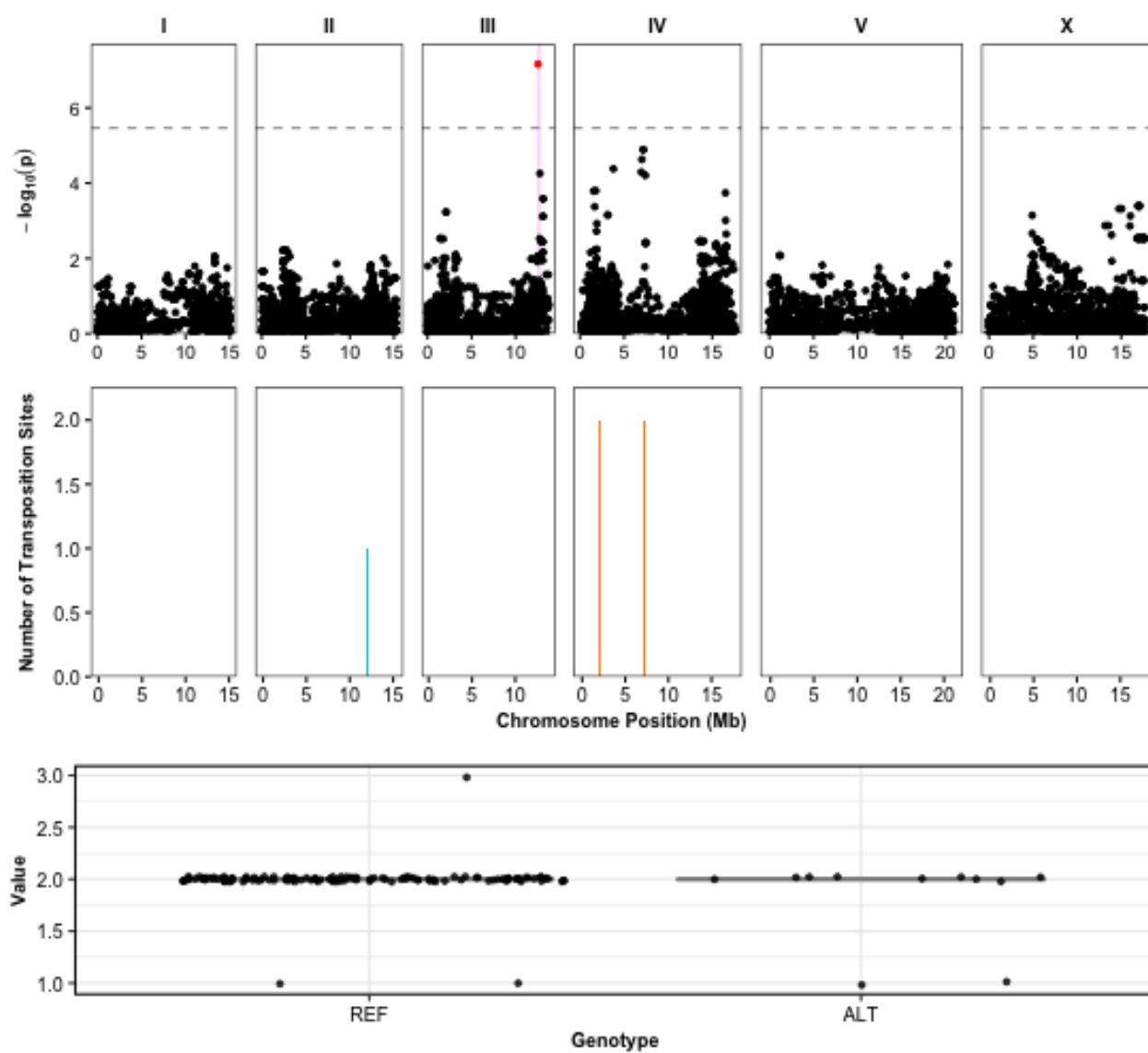
WBT00000628 (ins)



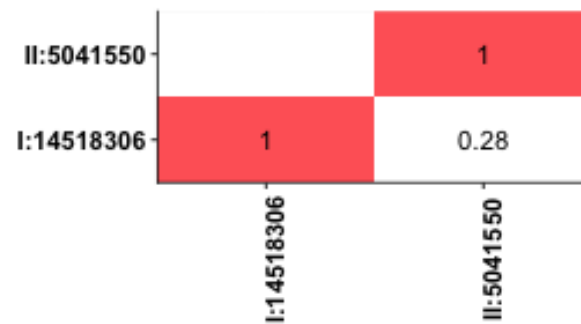
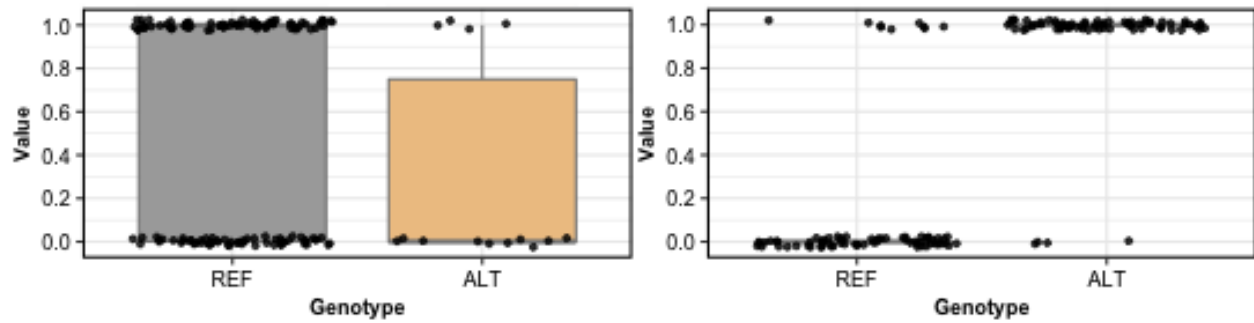
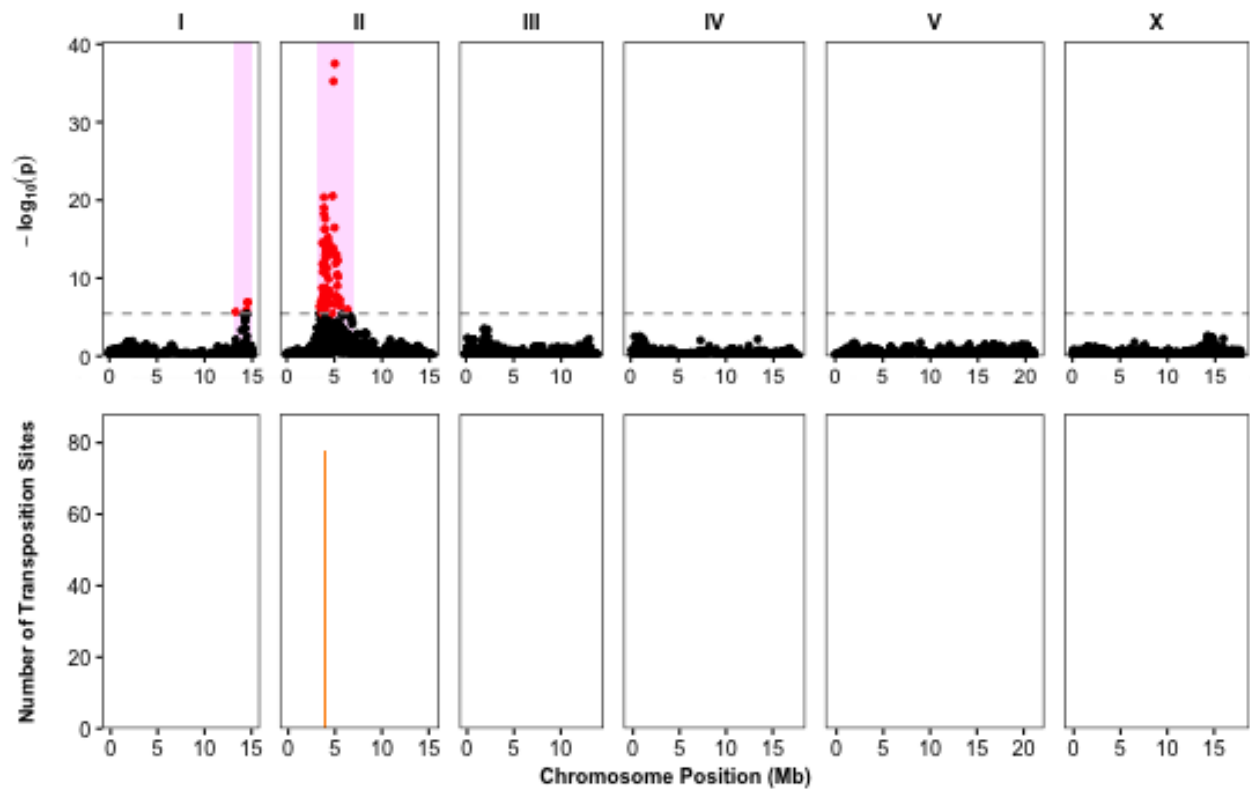
WBT00000634 (AR)



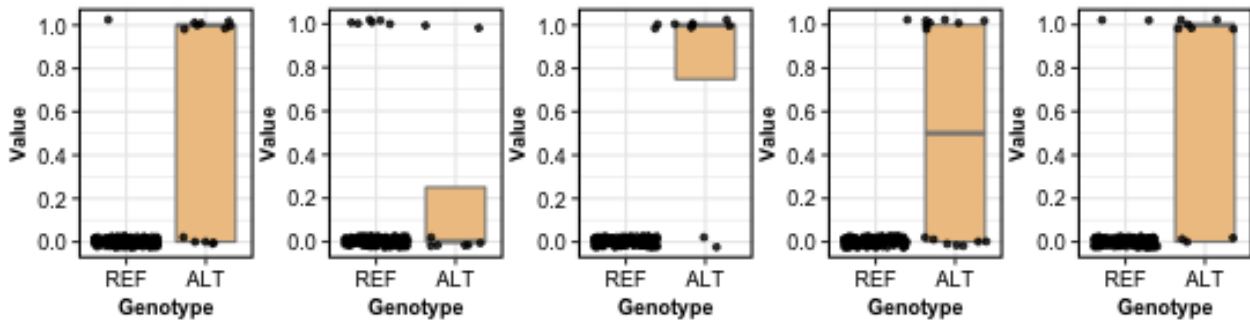
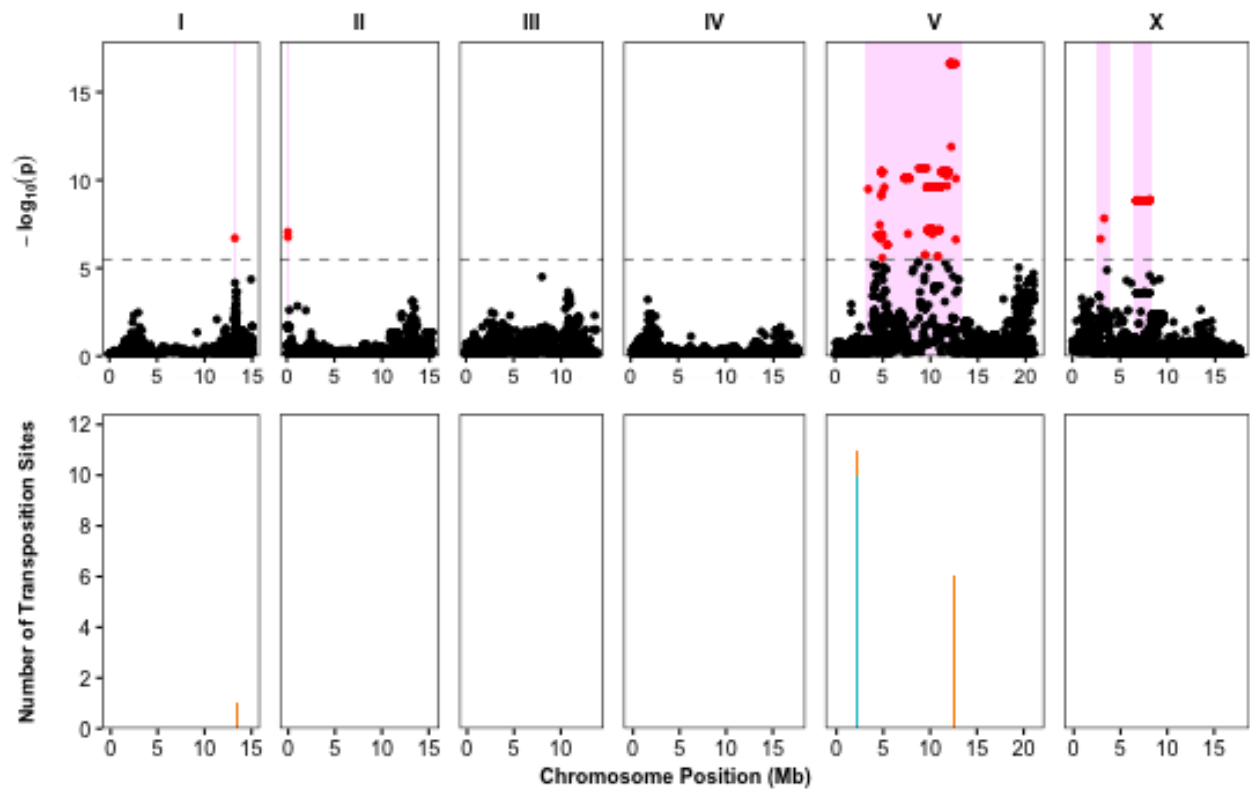
WBT00000661 (all)



WBT00000665 (AR)

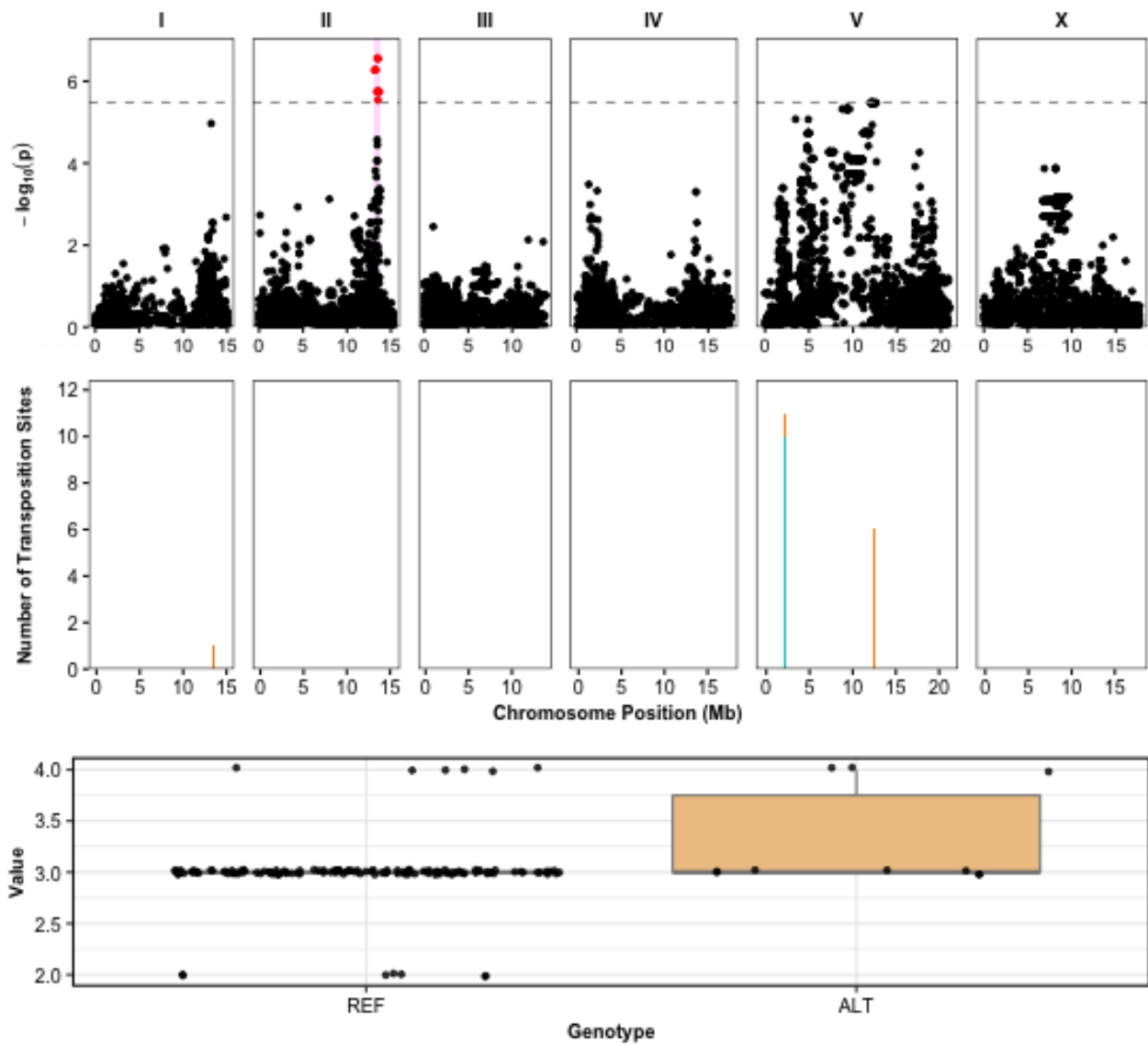


WBT00000746 (AR)

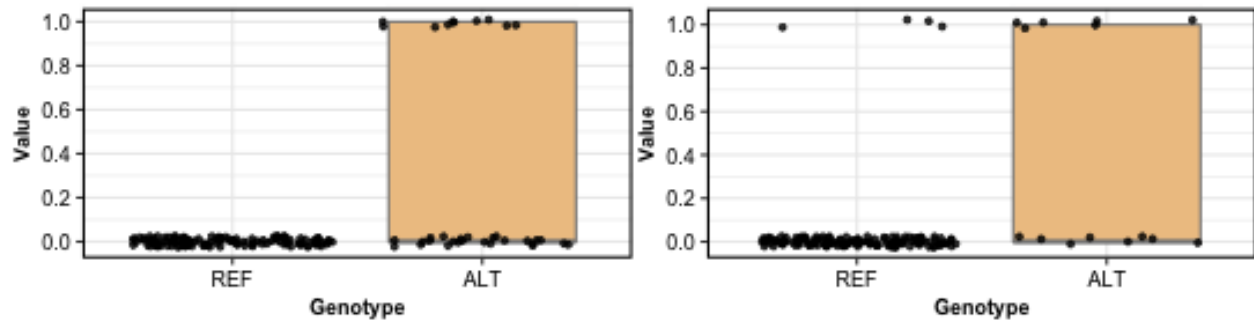
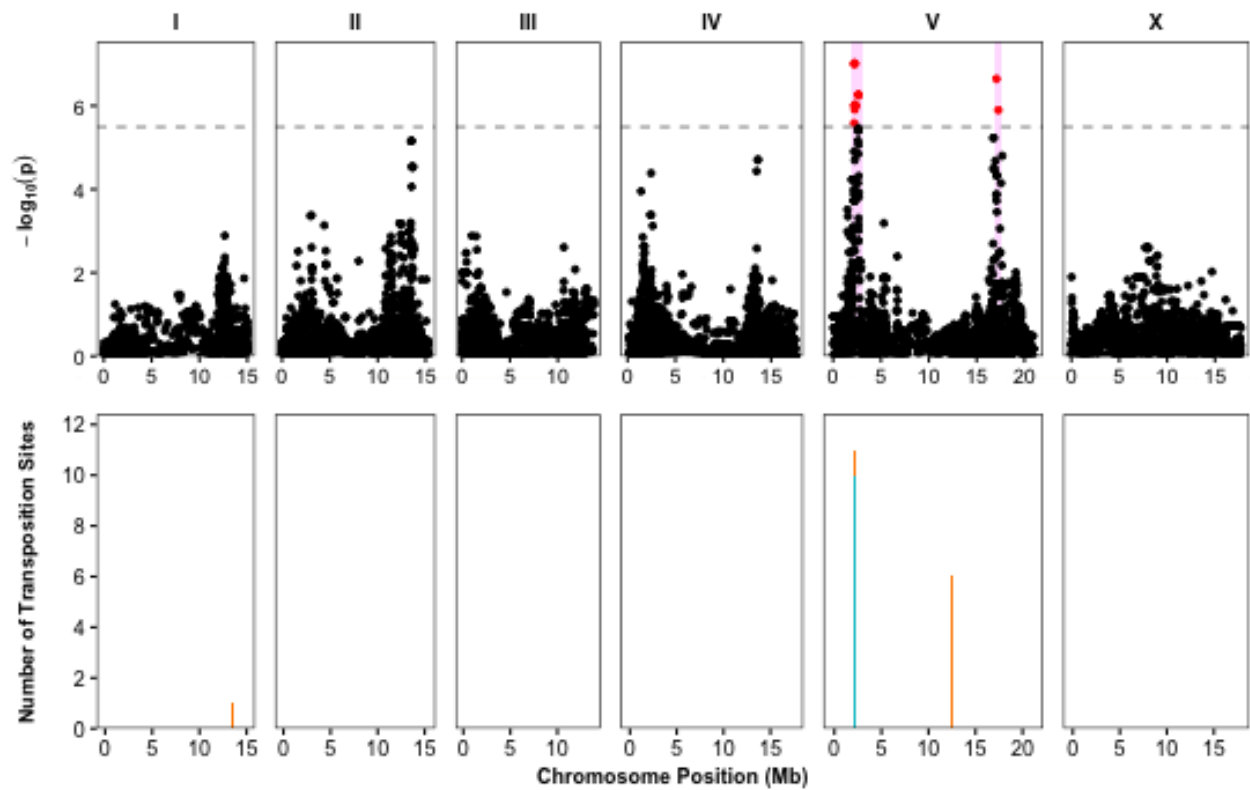


X:6871942				1
X:3342241			1	0.67
V:12045766		1	0.59	1
II:104876	1	0.33	0.75	0.52
I:13183418	1	0.88	0.73	0.91
I:13183418				
II:104876				
V:12045766				
X:3342241				
X:6871942				

WBT00000746 (all)



WBT00000746 (ins)



V:17072655		1
V:2199997	1	0.43
	V:2199997	V:17072655