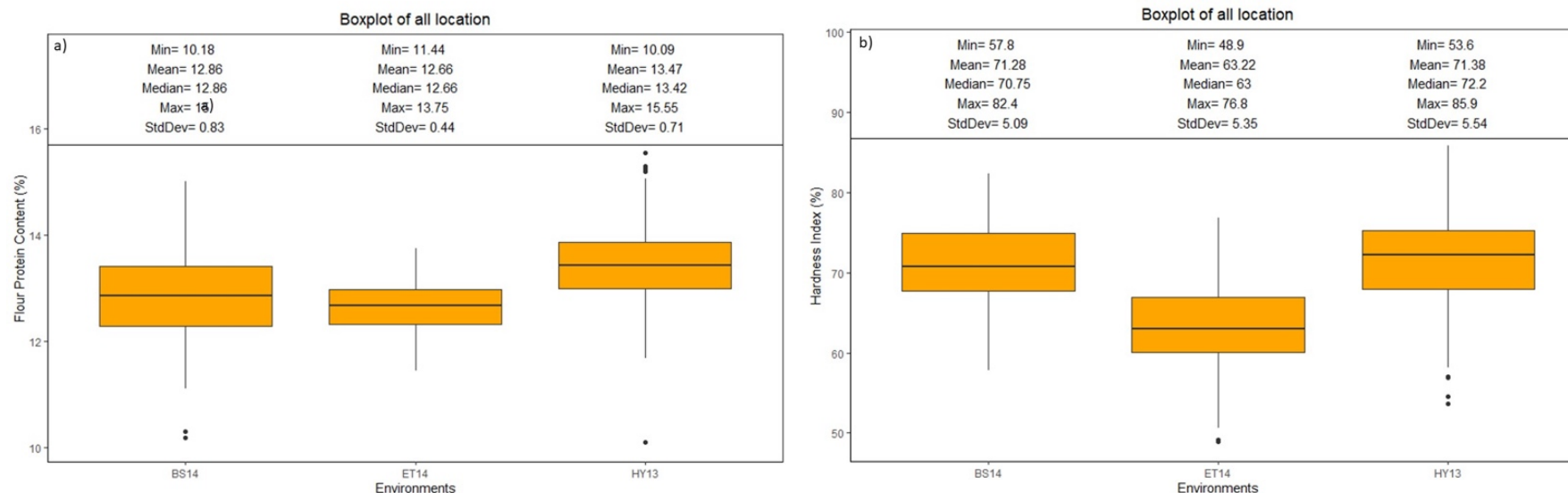
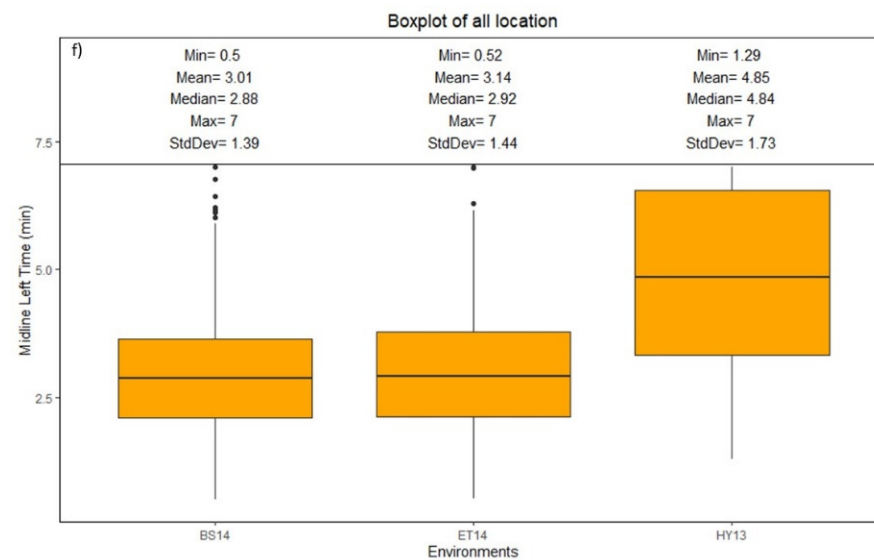
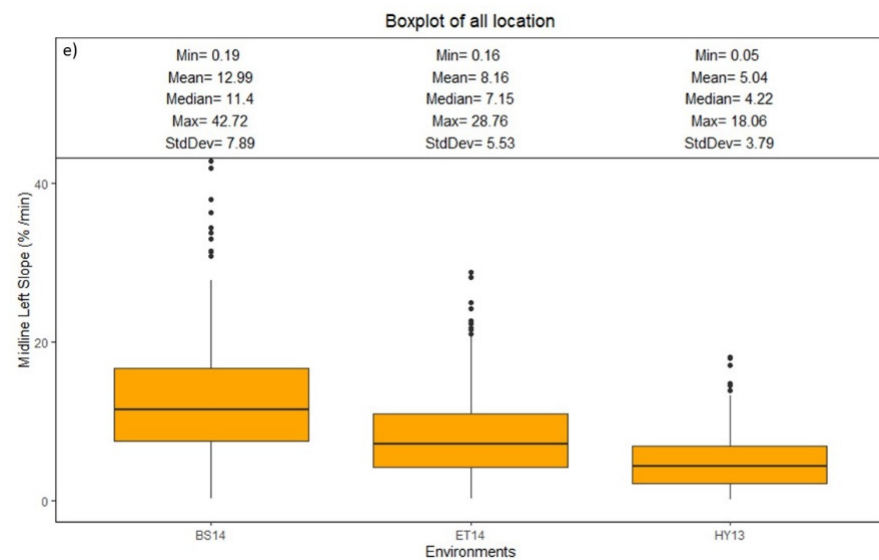
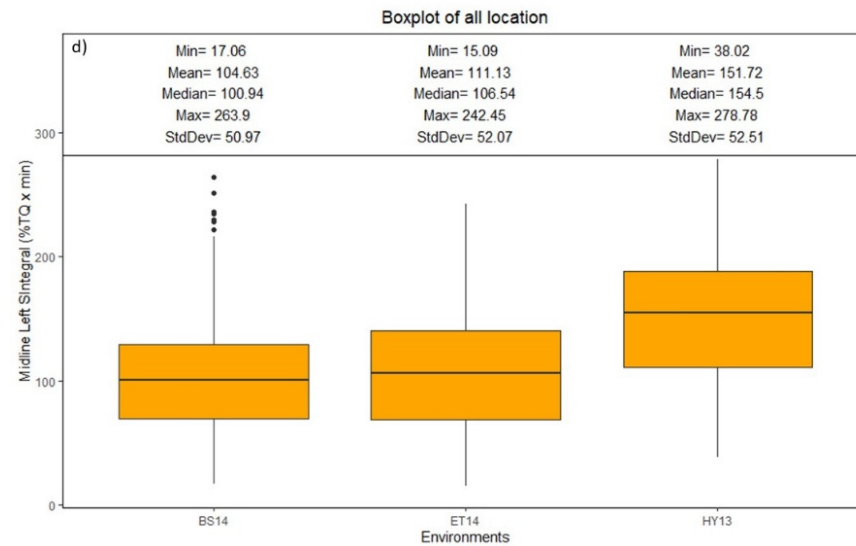
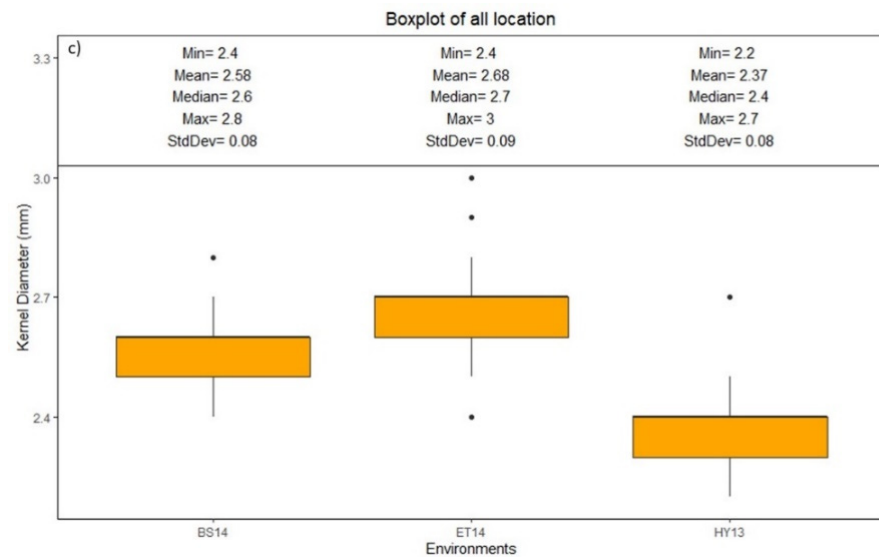
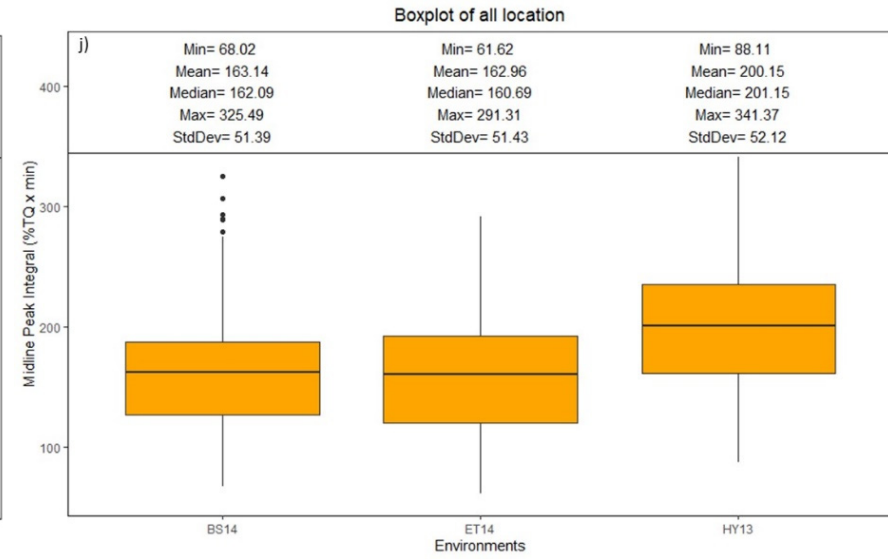
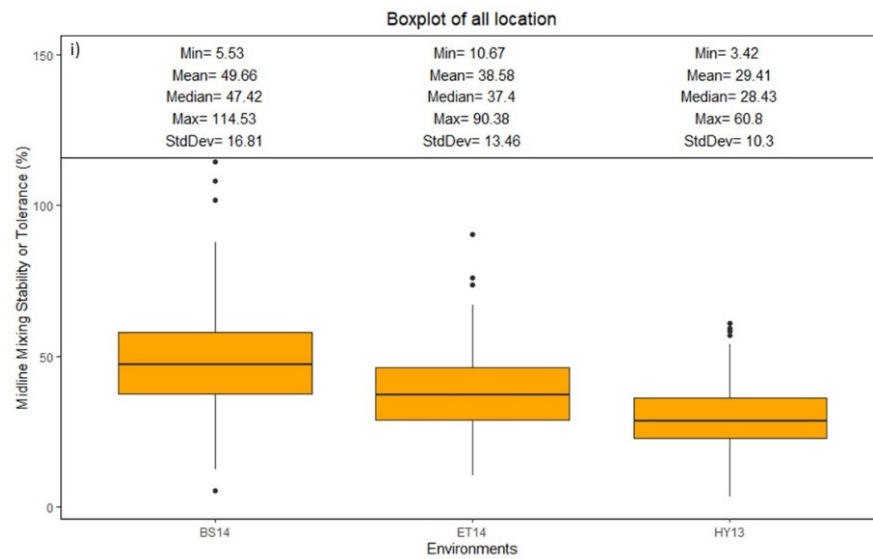
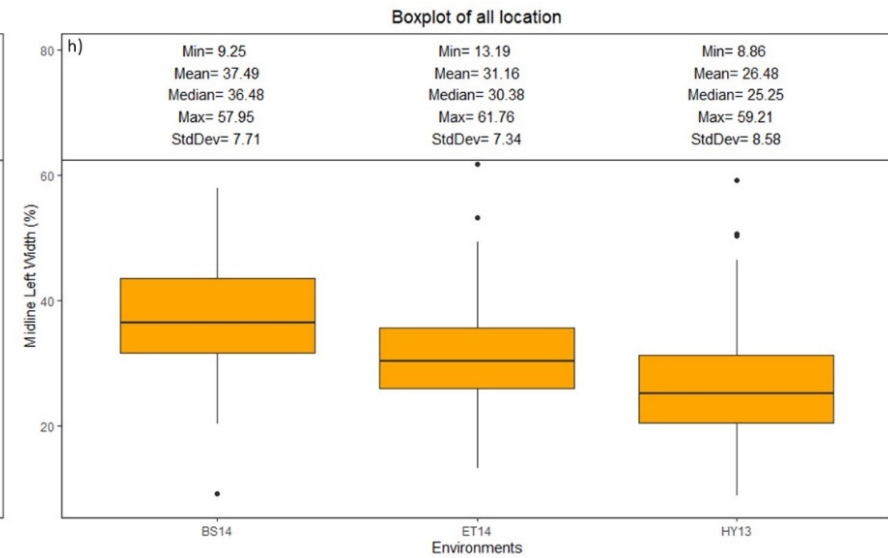
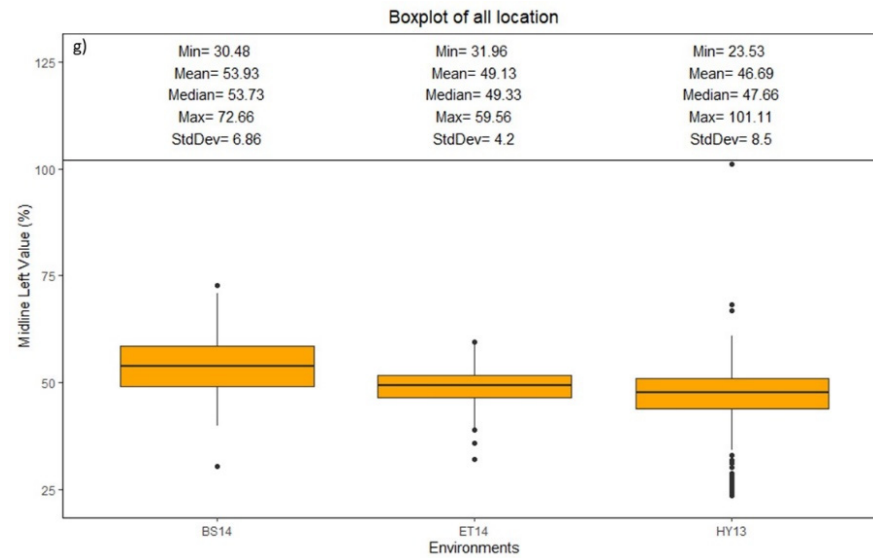
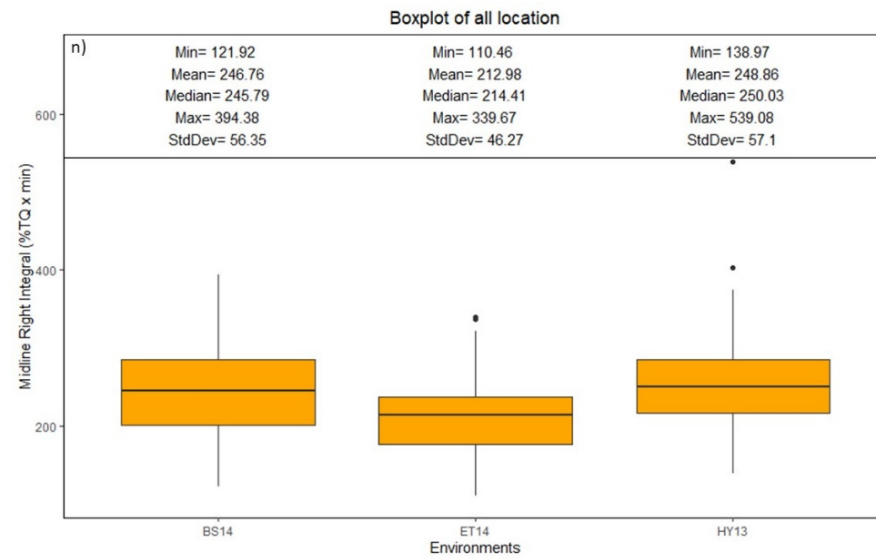
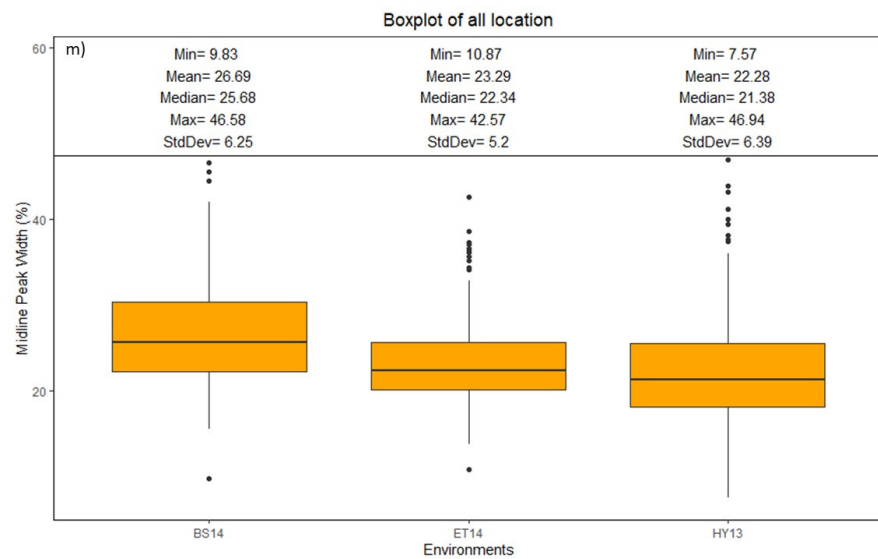
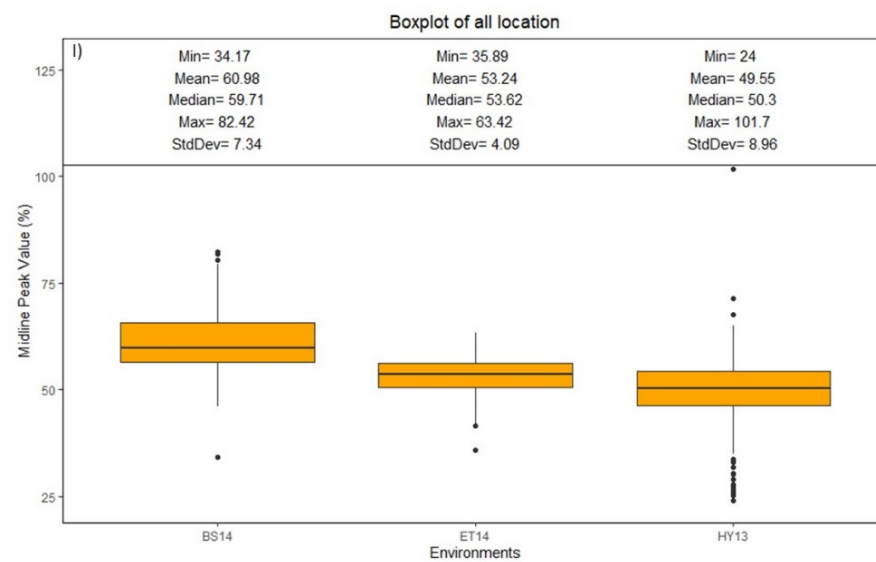
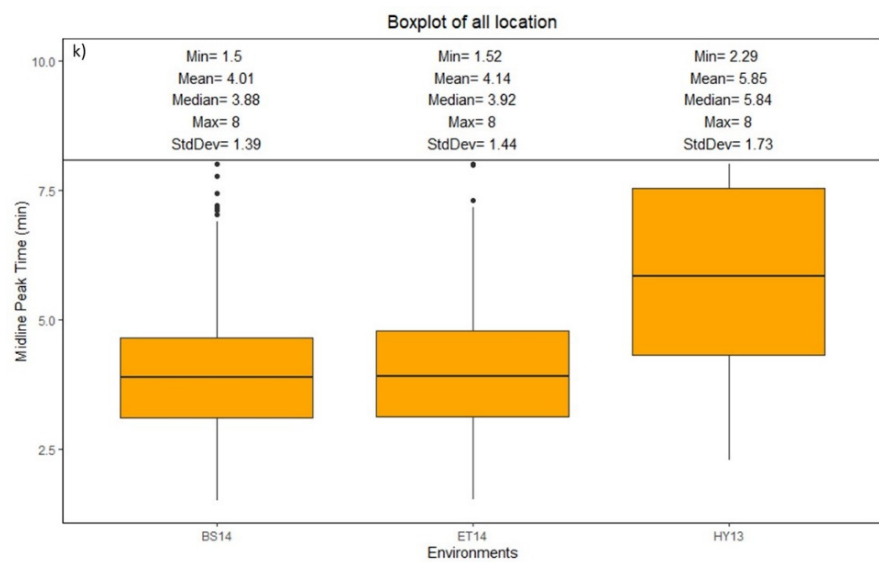


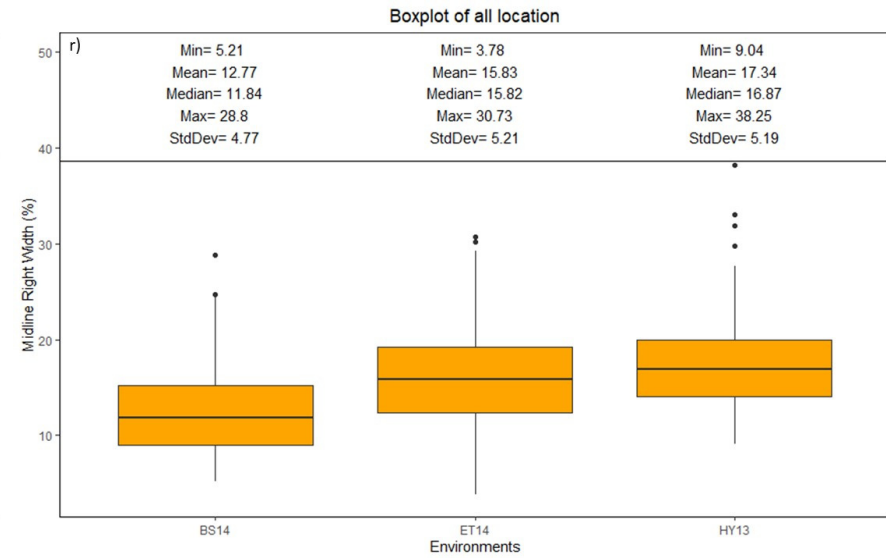
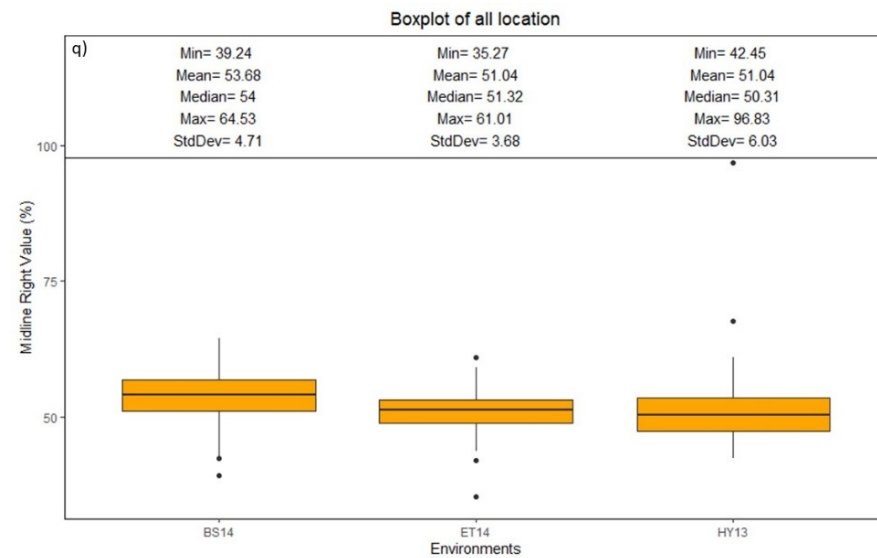
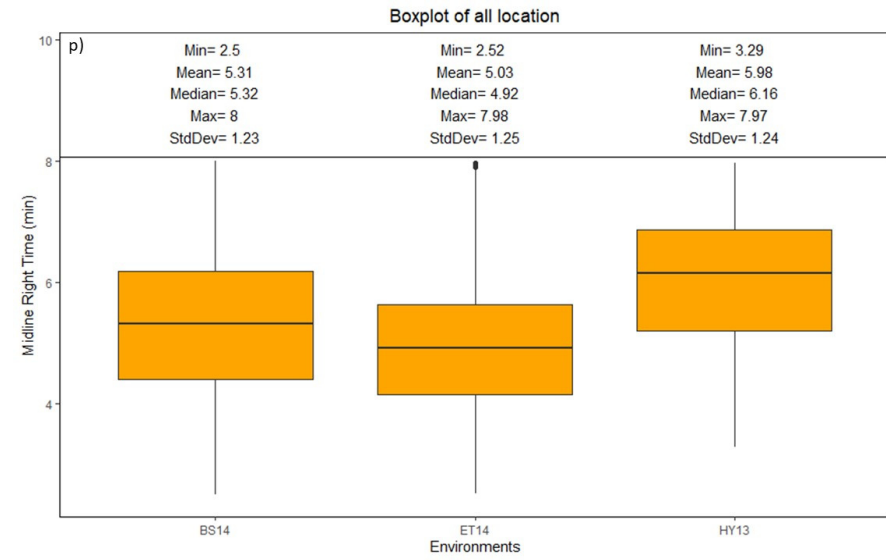
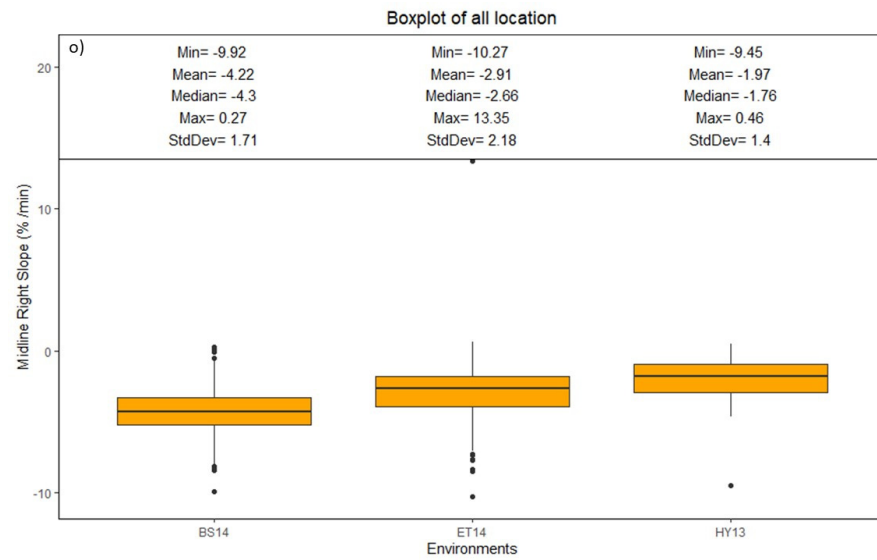
Supplemental Figure S1: Boxplot analysis of end-use quality traits. Traits included are: a) Flour protein content, b) Hardness index, c) Kernel diameter, d) Midline left integral, e) Midline left slope, f) Midline left time, g) Midline left value, h) Midline left width, i) Midline mixing stability or tolerance, j) Midline peak integral, k) Midline peak time, l) Midline peak value, m) Midline peak width, n) Midline right integral, o) Midline right slope, p) Midline right time, q) Midline right value, r) Midline right width, s) Midline tail integral, t) Midline tail slope, u) Midline tail value, v) Midline tail width, w) Midline time\_X integral, x) Midline time\_X slope, y) Midline time\_X value, z) Midline time\_X width, aa) Single kernel weight, ab) Water absorption, ac) As concentration, ad) Ca concentration, ae) Cd concentration, af) Co concentration, ag) Cu concentration, ah) Fe concentration, ai) K concentration, aj) Li concentration, ak) Mg concentration, al) Mn concentration, am) Mo concentration, an) Na concentration, ao) Ni concentration, ap) P concentration, aq) Rb concentration, ar) S concentration, as) Sr concentration, at) Ti concentration, au) Zn concentration. X-axis is environment: BS14, ET14, and HY13. Y-axis represents the corresponding trait value under the respective environments. Descriptive statistics are on top of each boxplot.

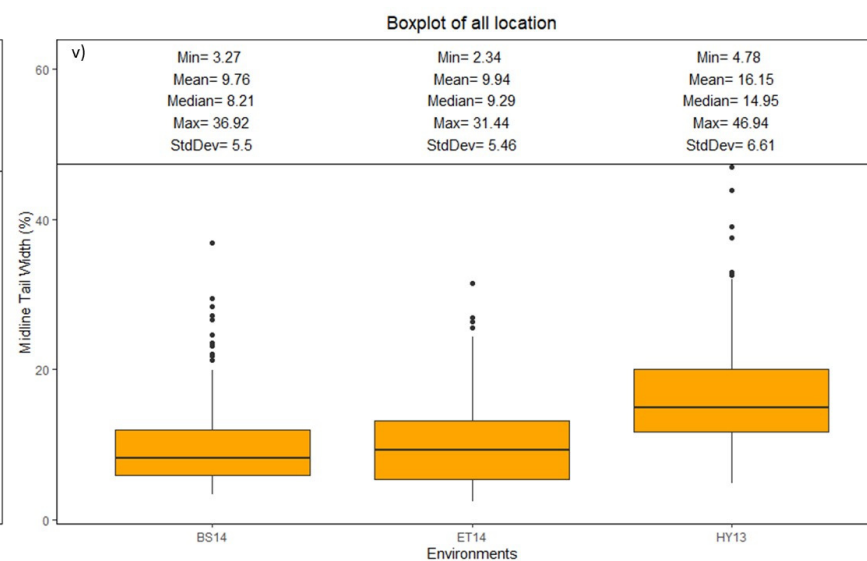
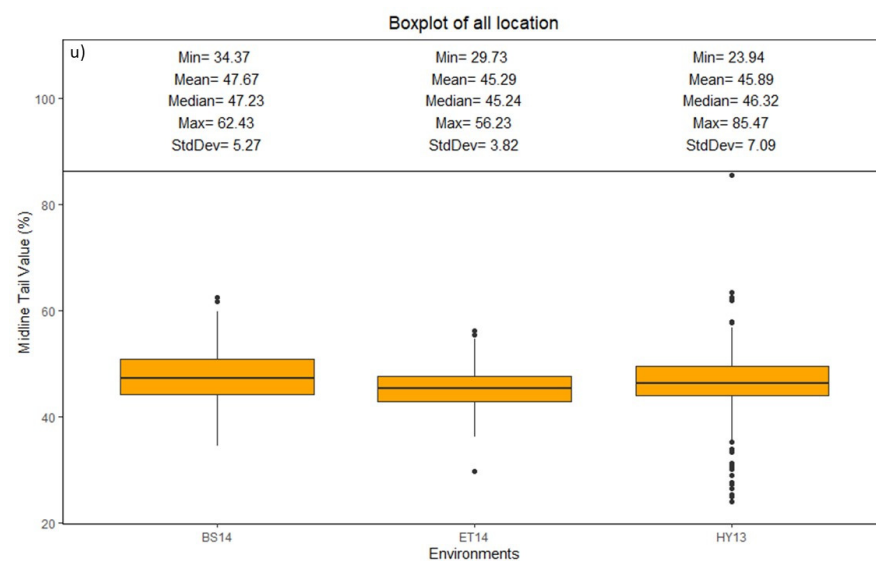
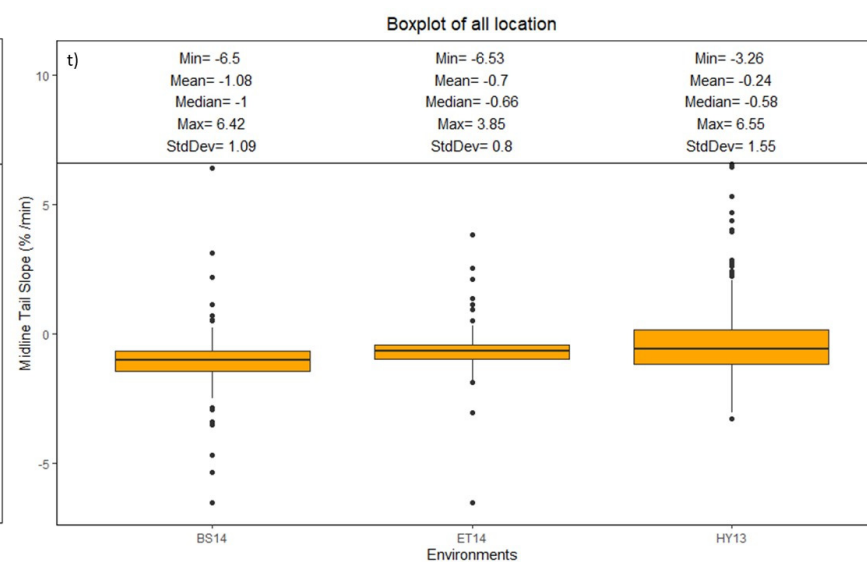
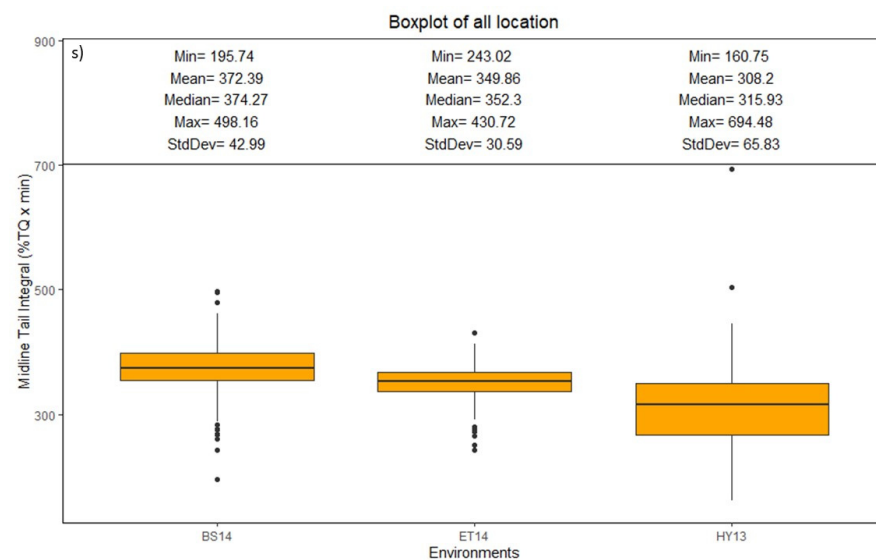


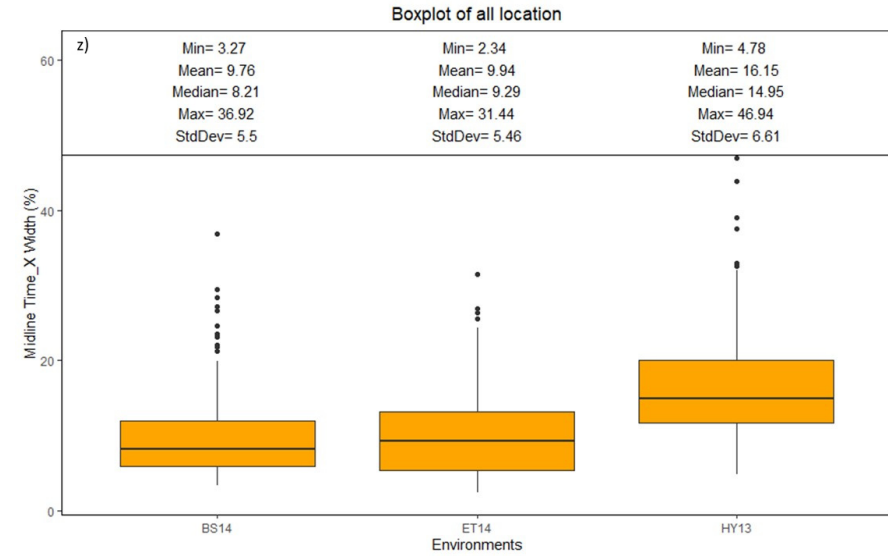
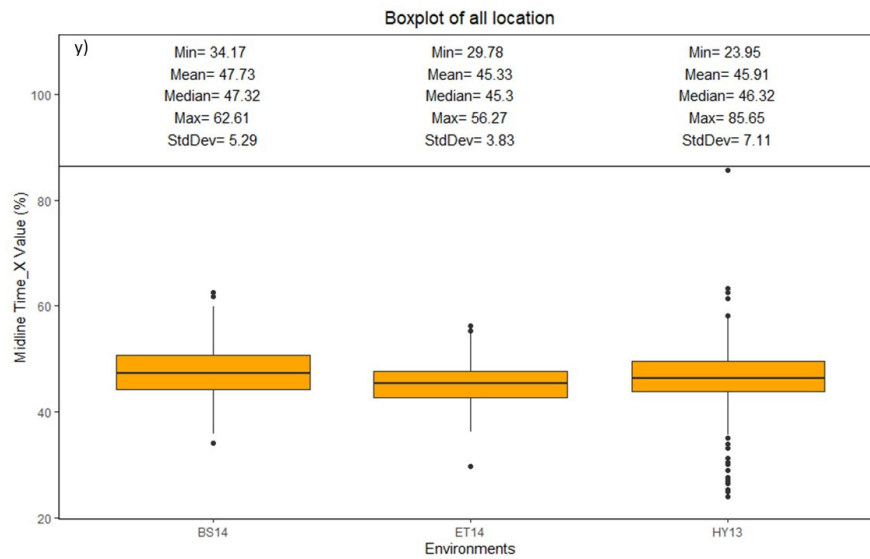
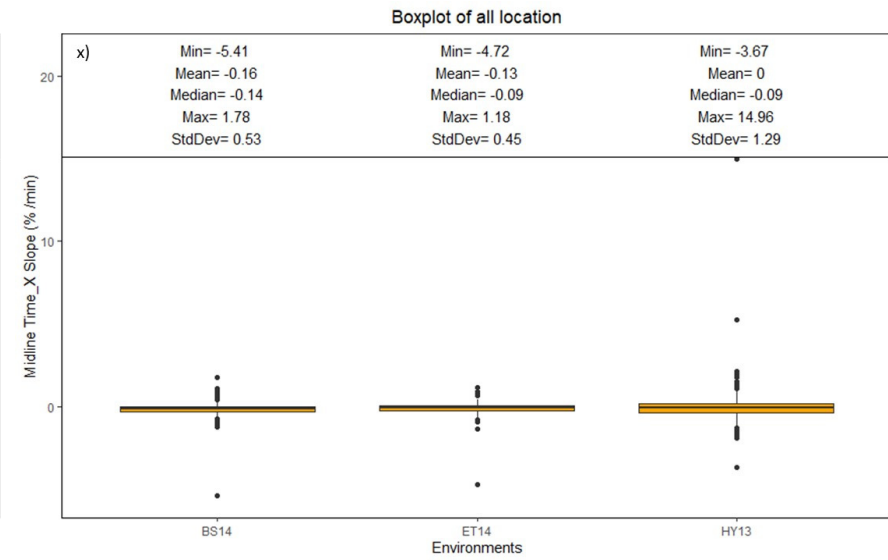
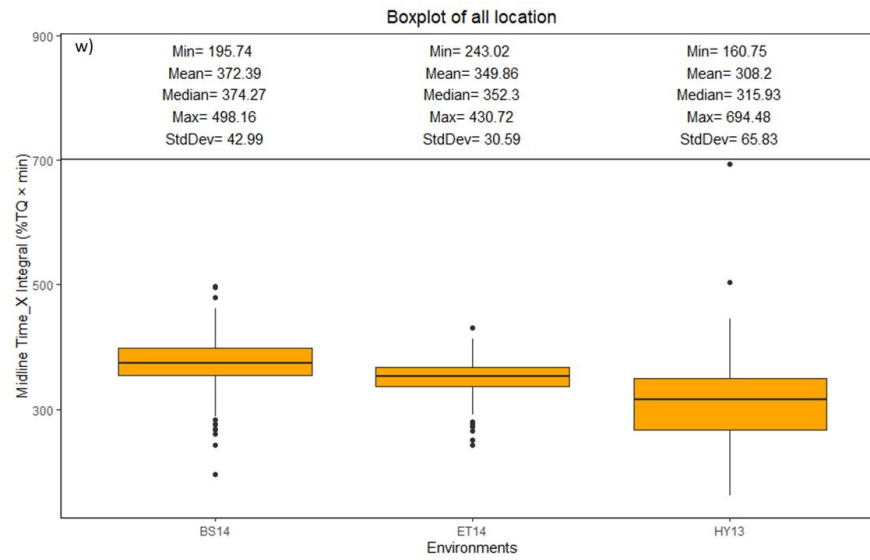


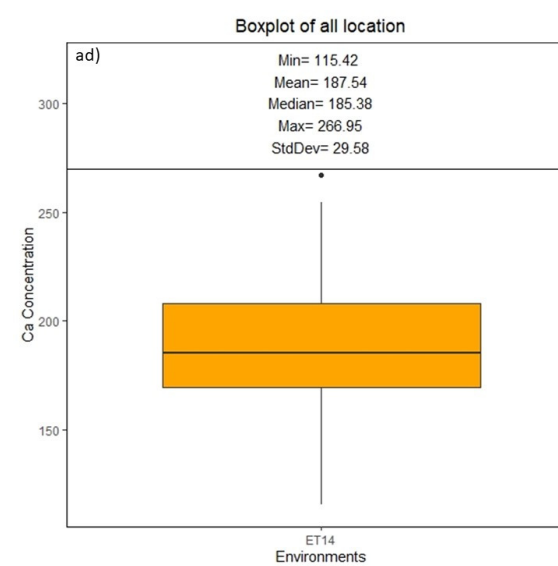
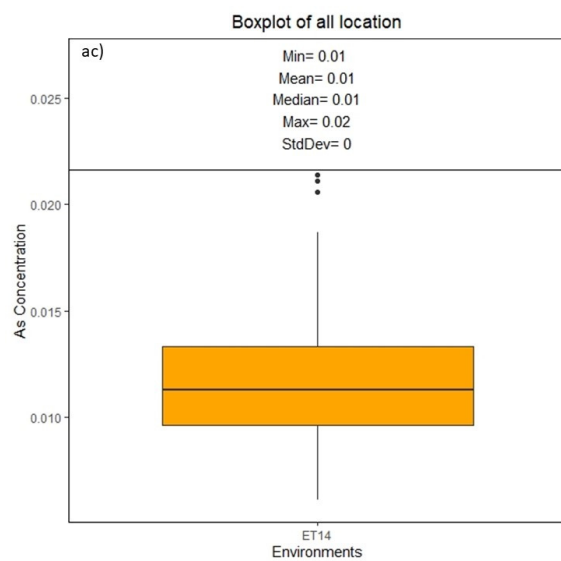
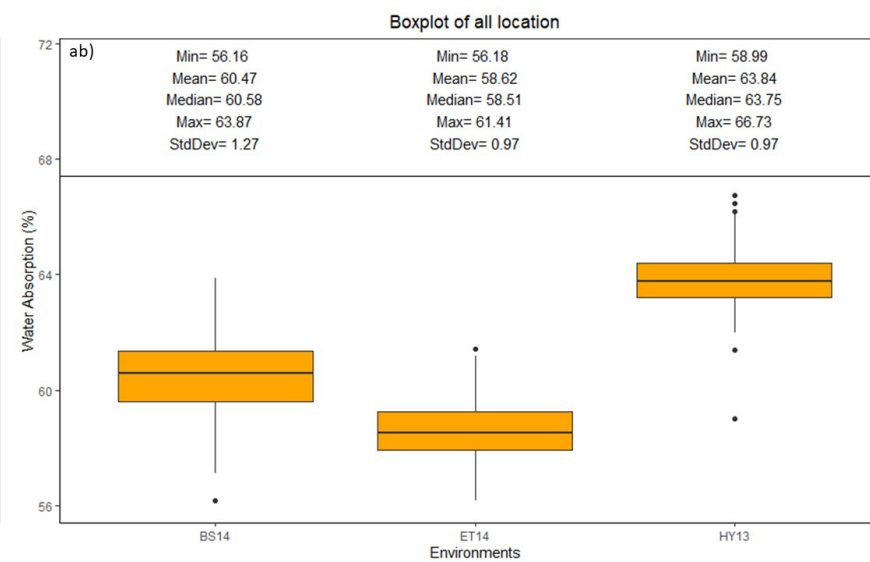
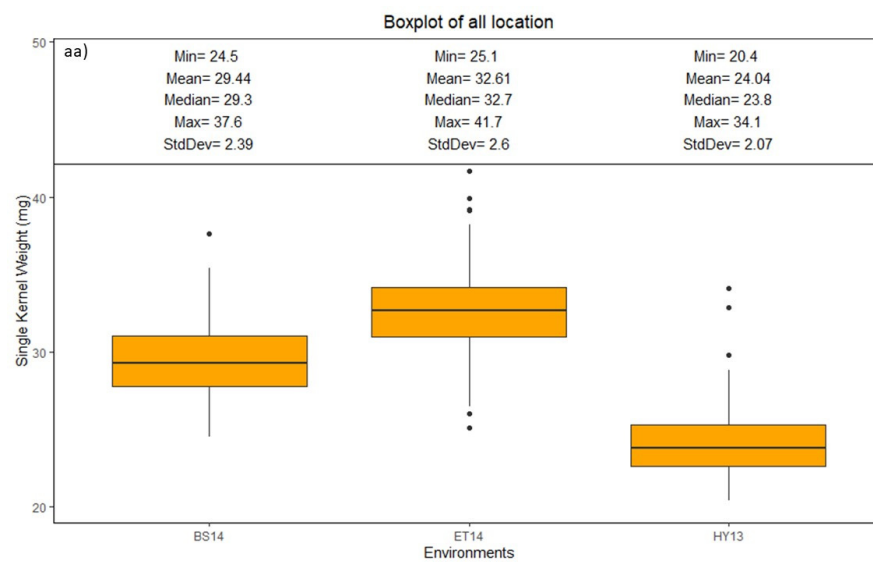


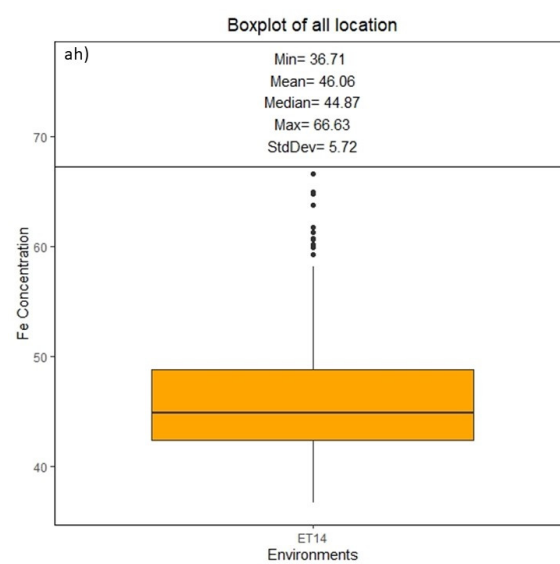
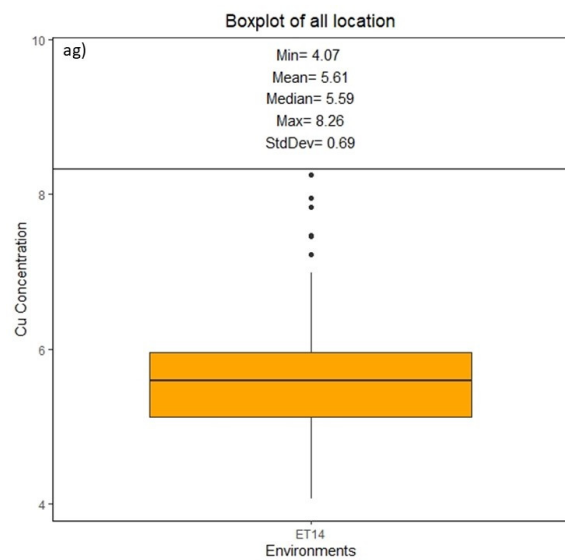
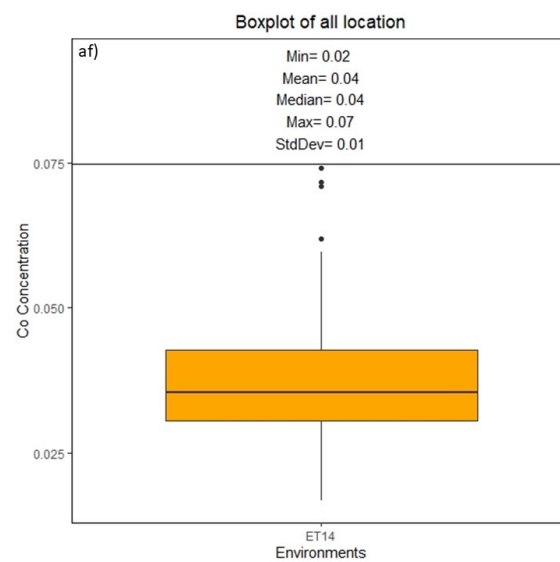
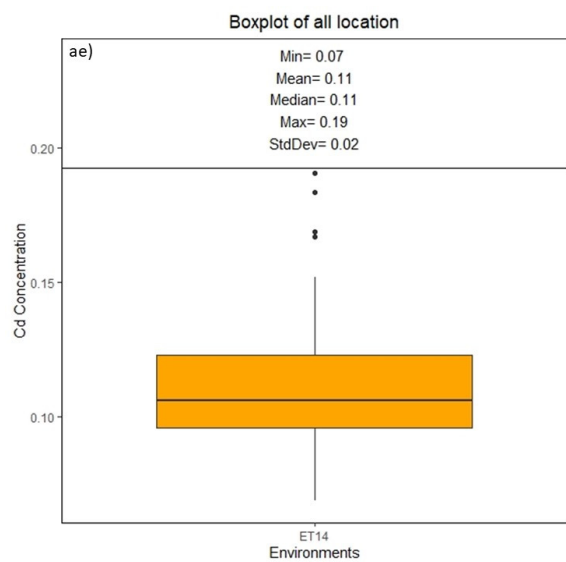


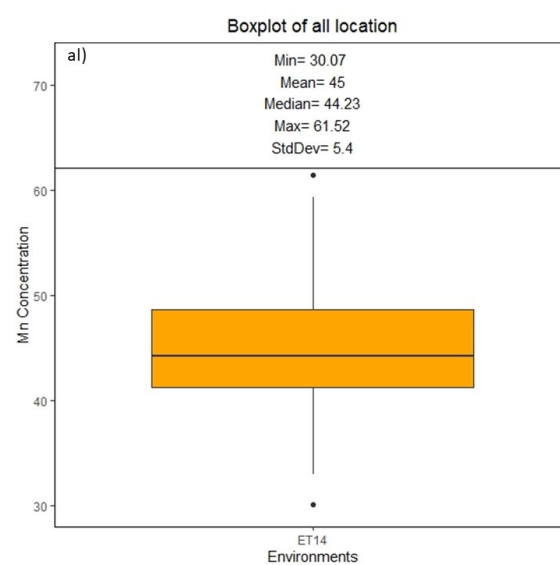
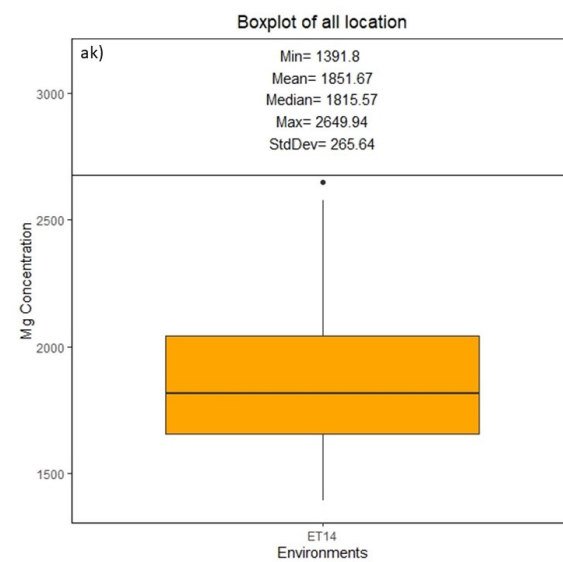
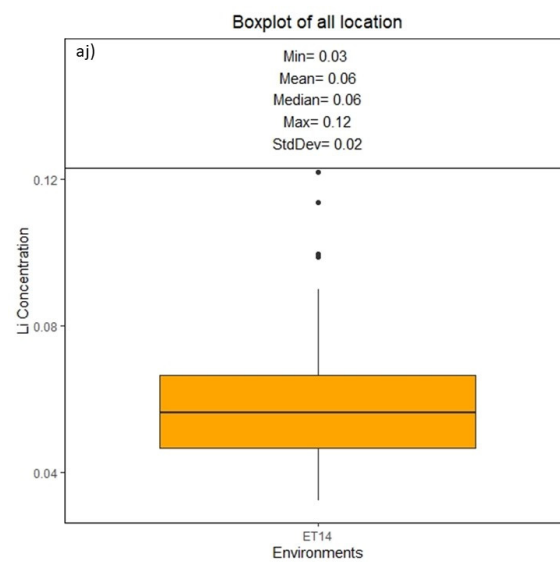
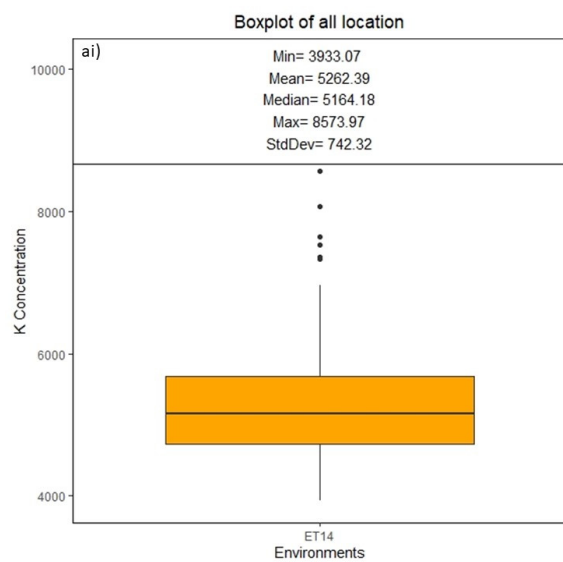


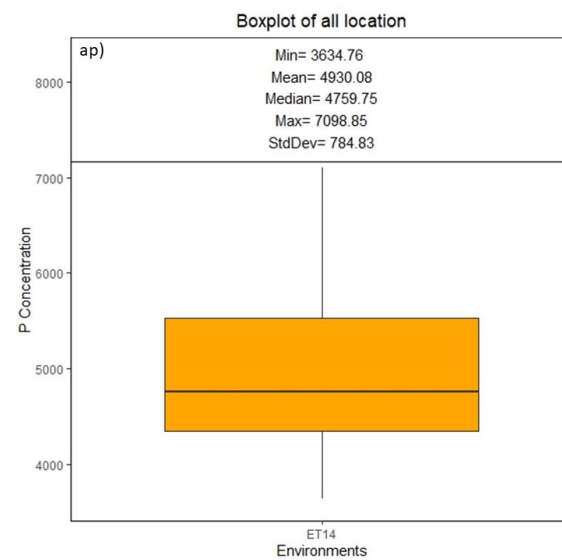
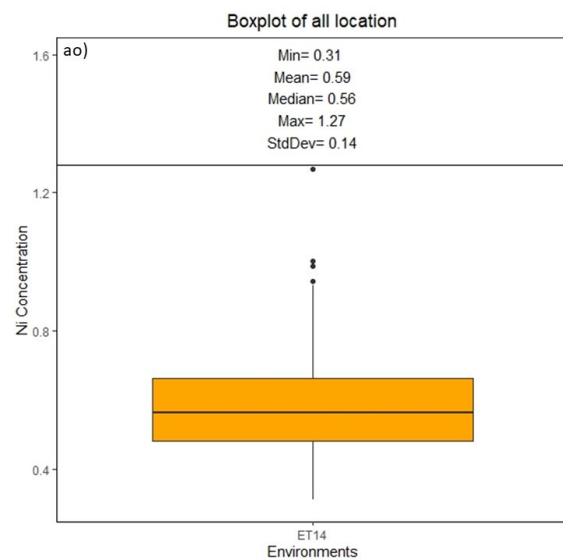
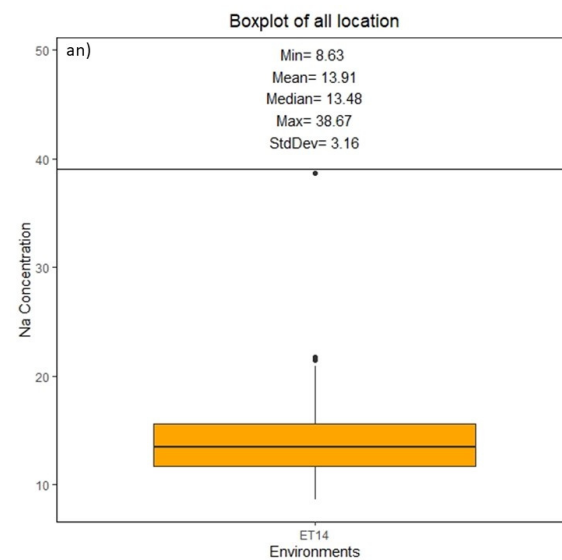
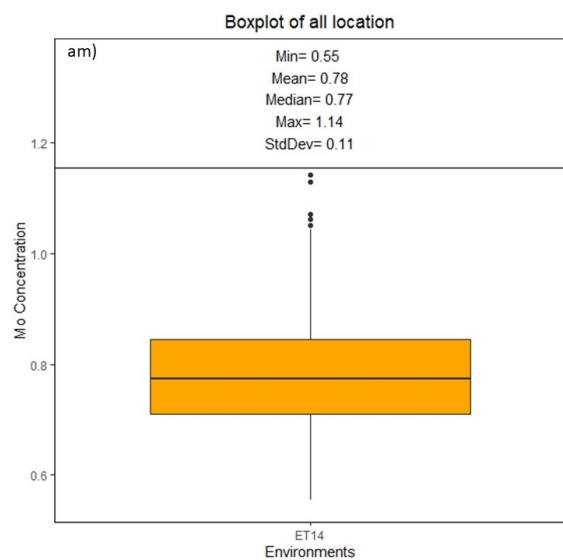


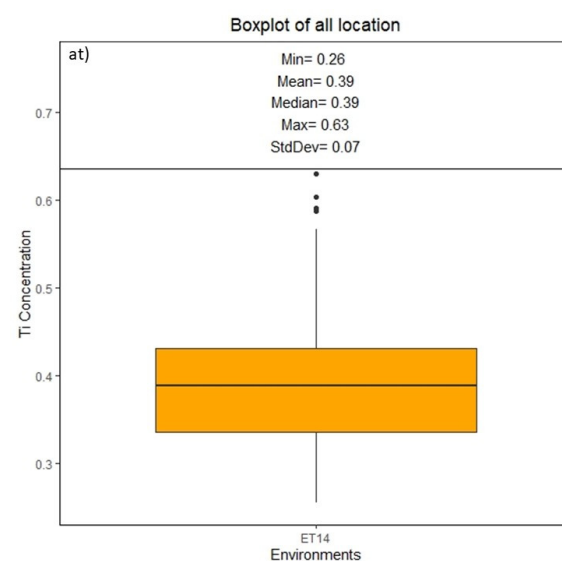
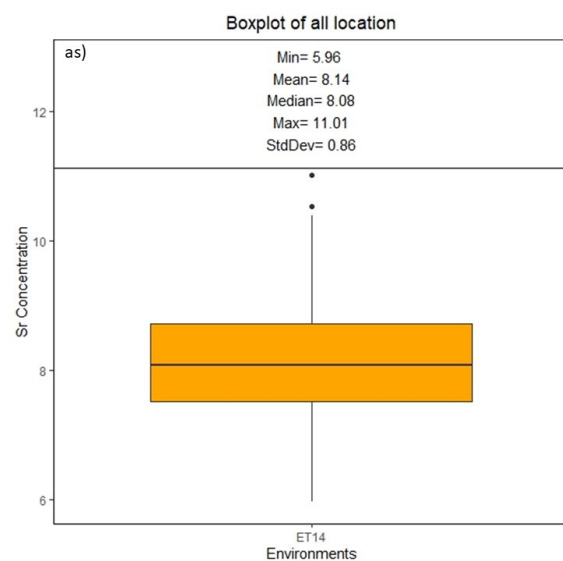
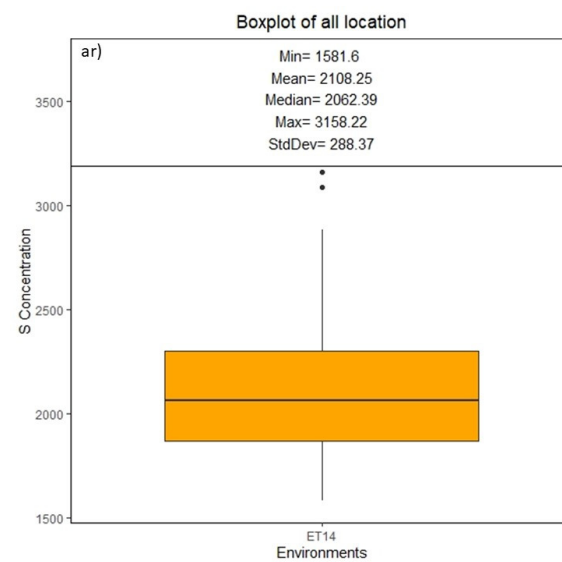
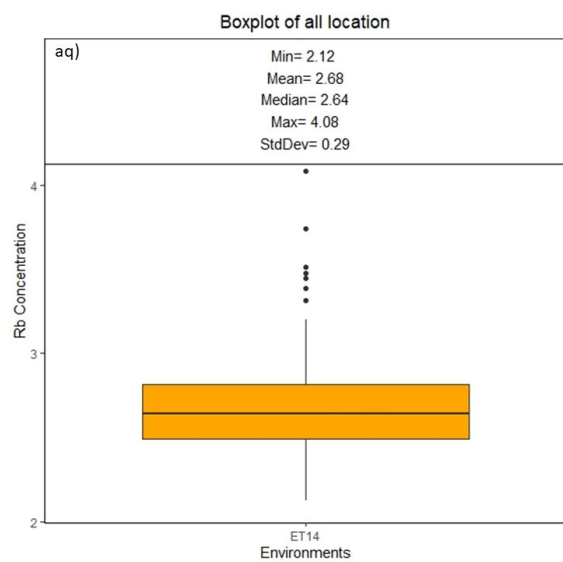


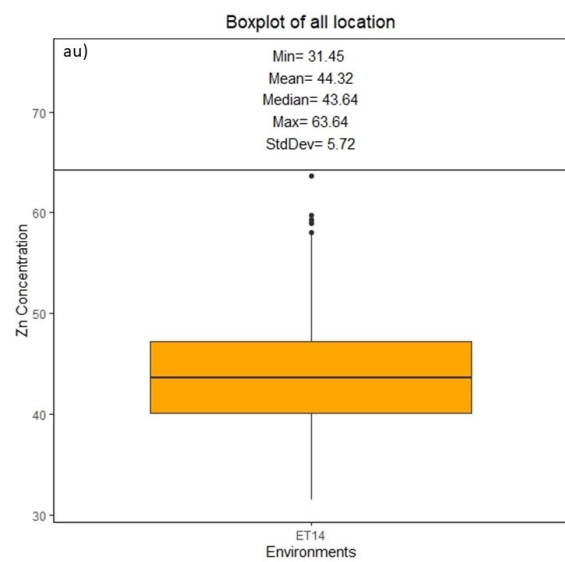




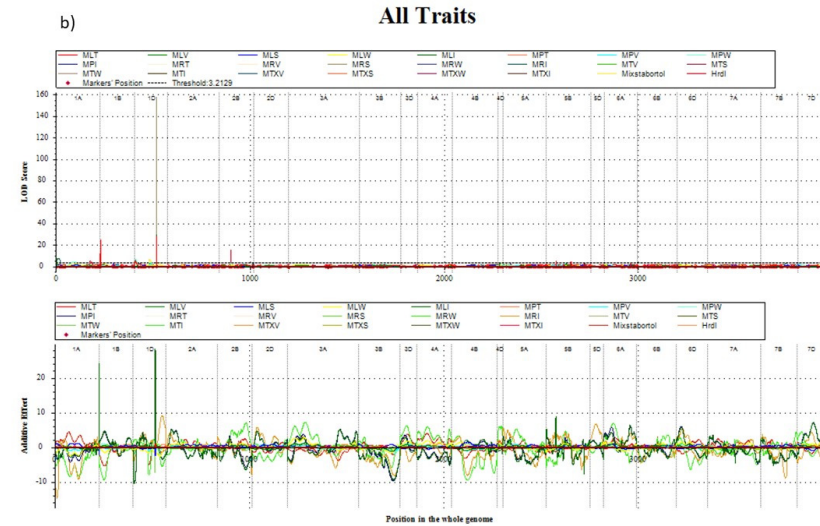


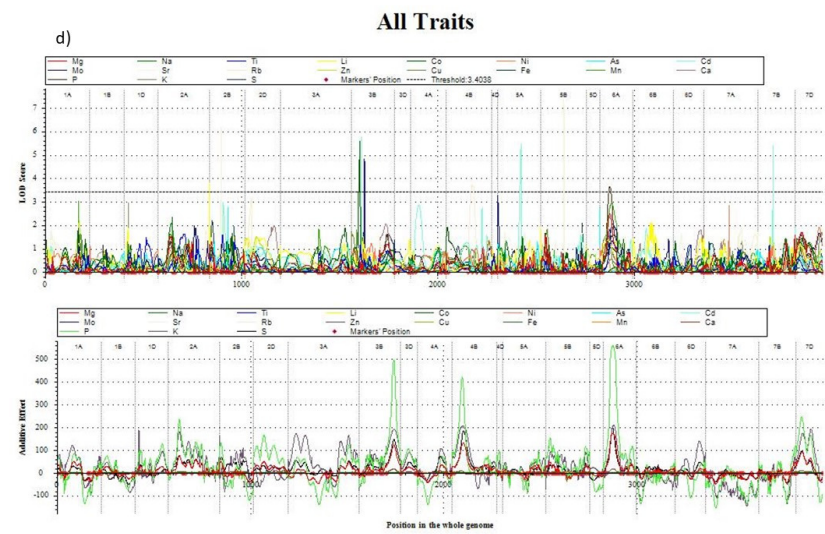




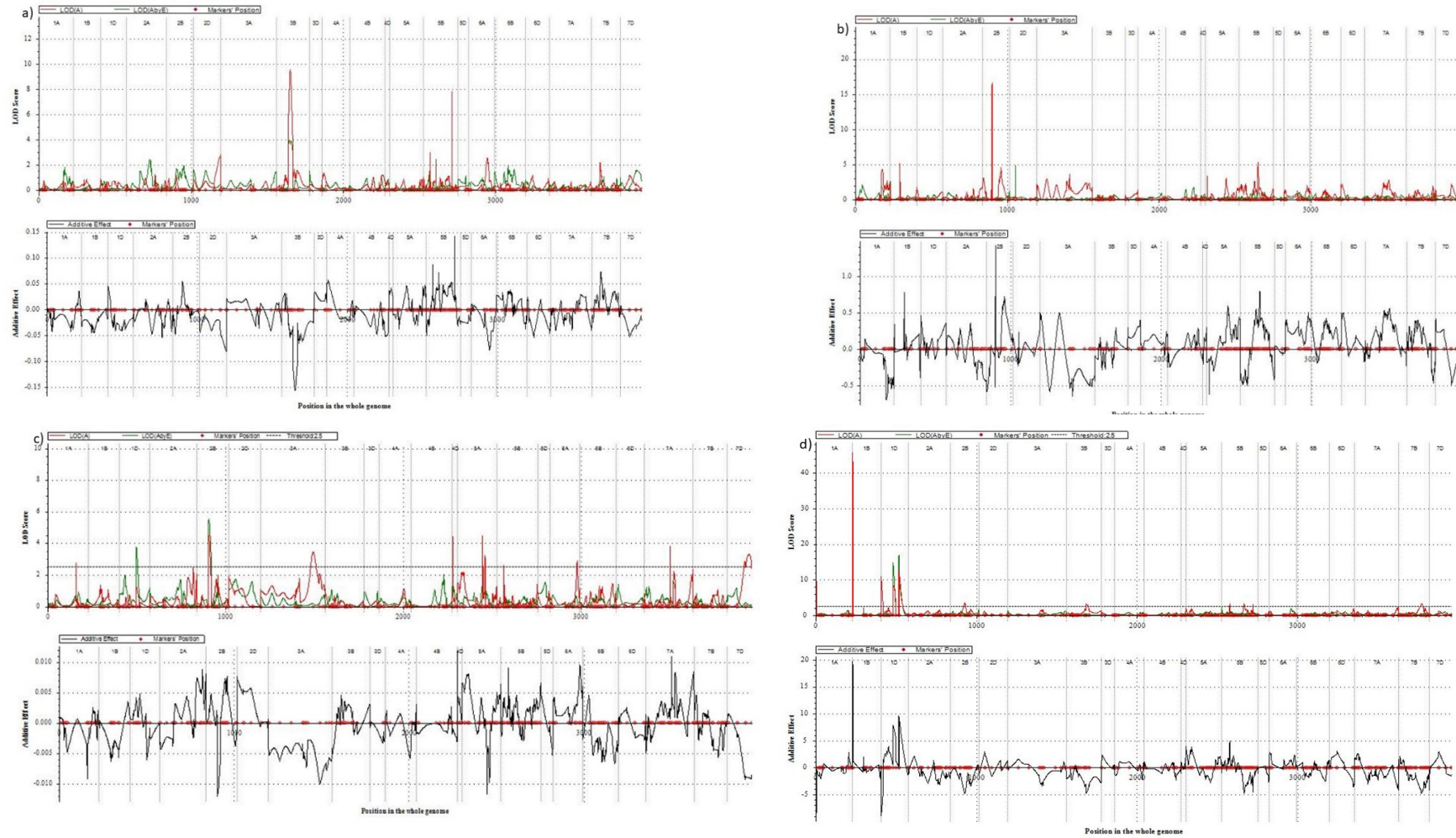


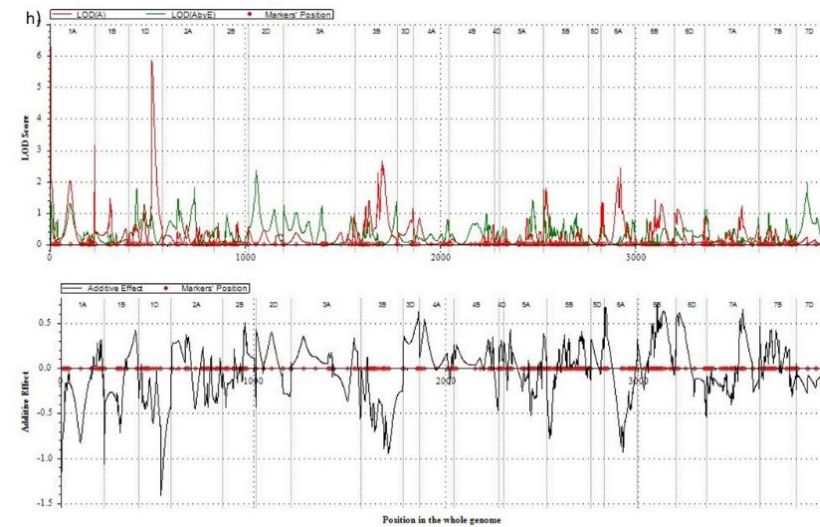
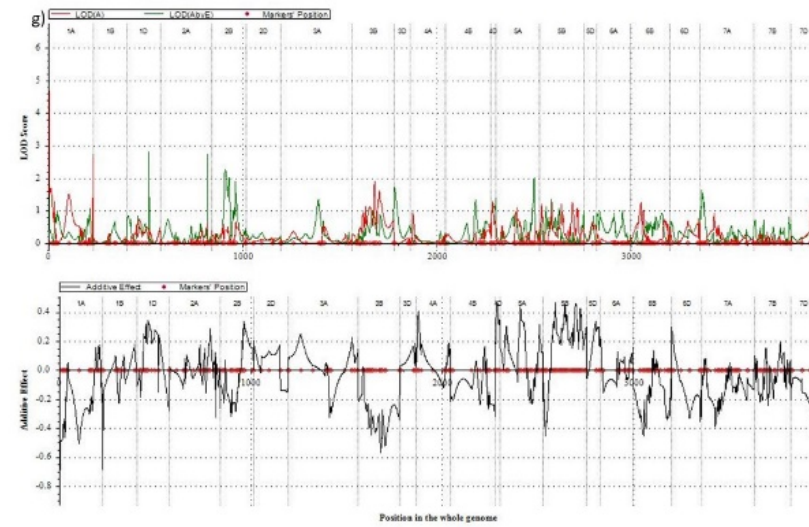
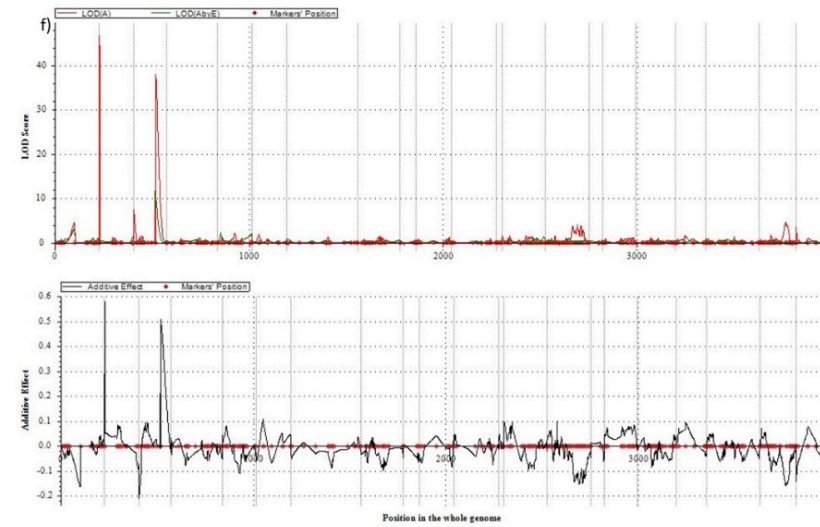
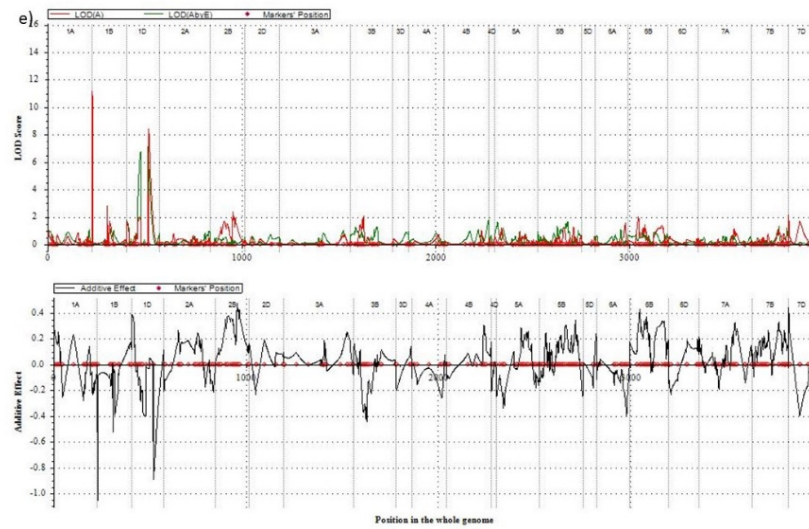
Supplemental Figure S2: LOD profile and additive effects of end-use quality QTL detected in the environments a)BS14, b) ET14, c) HY13, and grain mineral concentration in environment d) ET14. Traits are Flour protein content, Hardness index, Kernel diameter, Midline left integral, Midline left slope, Midline left time, Midline left value, Midline left width, Midline mixing stability or tolerance, Midline peak integral, Midline peak time, Midline peak value, Midline peak width, Midline right integral, Midline right slope, Midline right time, Midline right value, Midline right width, Midline tail integral, Midline tail slope, Midline tail value, Midline tail width, Midline time\_X integral, Midline time\_X slope, Midline time\_X value, Midline time\_X width, Single kernel weight, Water absorption, As concentration, As concentration, Ca concentration, Cd concentration, Co concentration, Cu concentration, Fe concentration, K concentration, Li concentration, Mg concentration, Mn concentration, Mo concentration, Na concentration, Ni concentration, P concentration, Rb concentration, S concentration, Sr concentration, Ti concentration, Zn concentration. The top panel of each figure shows LOD profile with chromosomal position along the x-axis (cM of 21 chromosomes) and LOD score on the y-axis. The bottom panel of each figure show an additive effect profile with chromosomal position along the x-axis (cM of 21 chromosomes) and additive effect values on the y-axis (values of each trait have different units). Positive additive effects means that the favorable alleles increasing traits were from CO960293-2 while negative values indicate that the favorable alleles increasing the traits were from TAM 111.

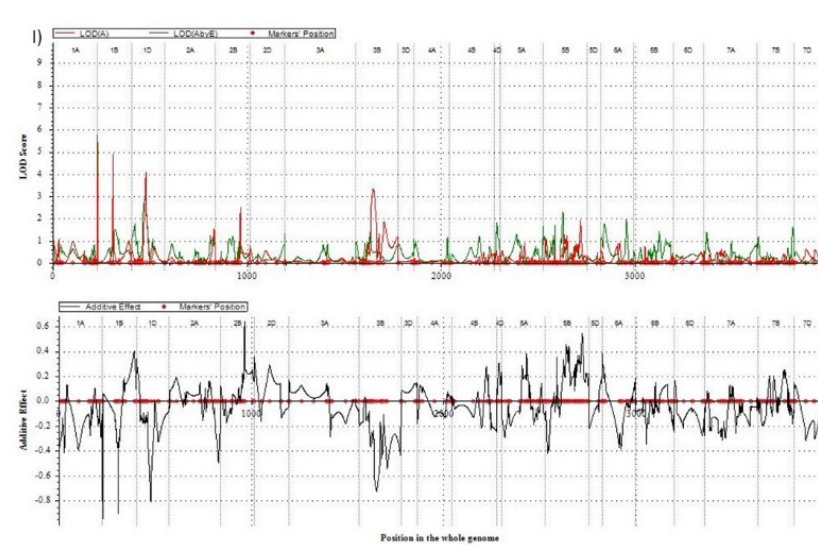
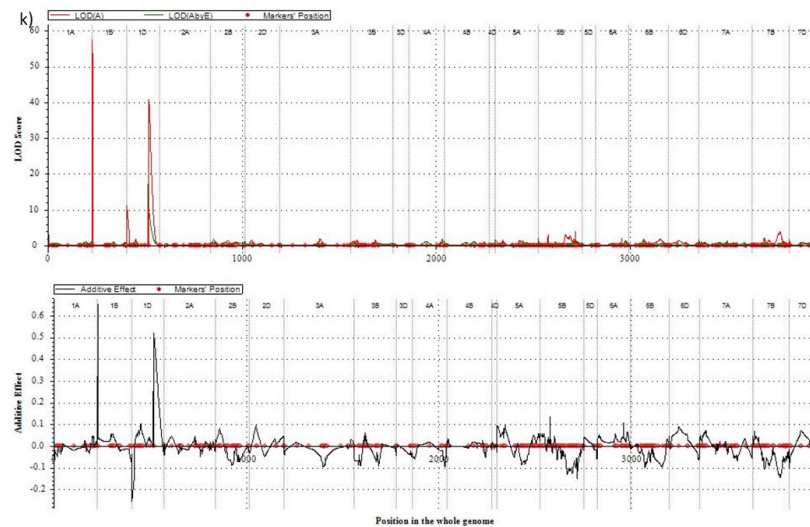
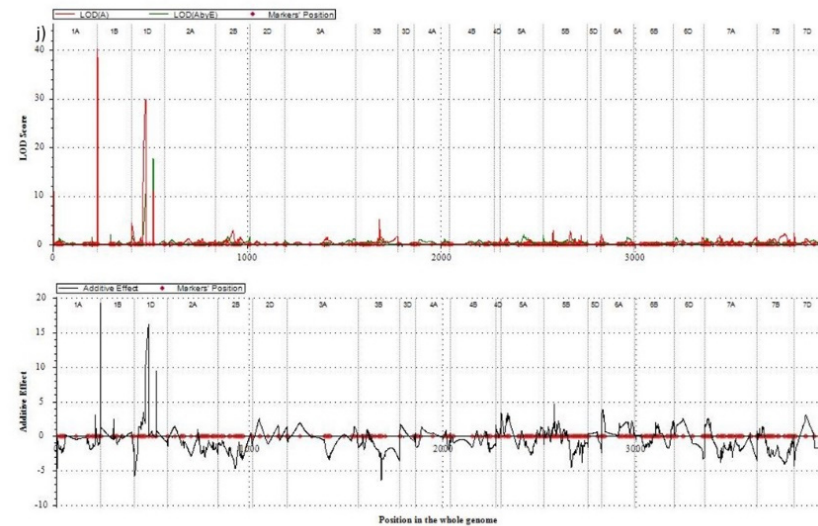
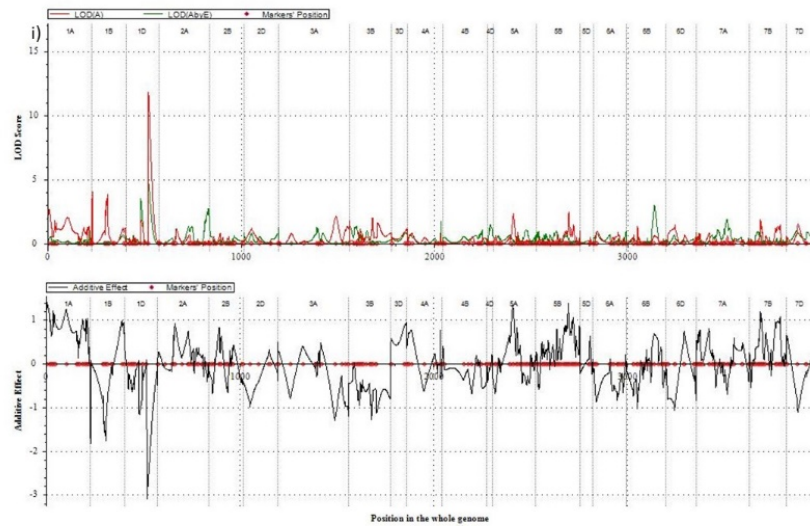


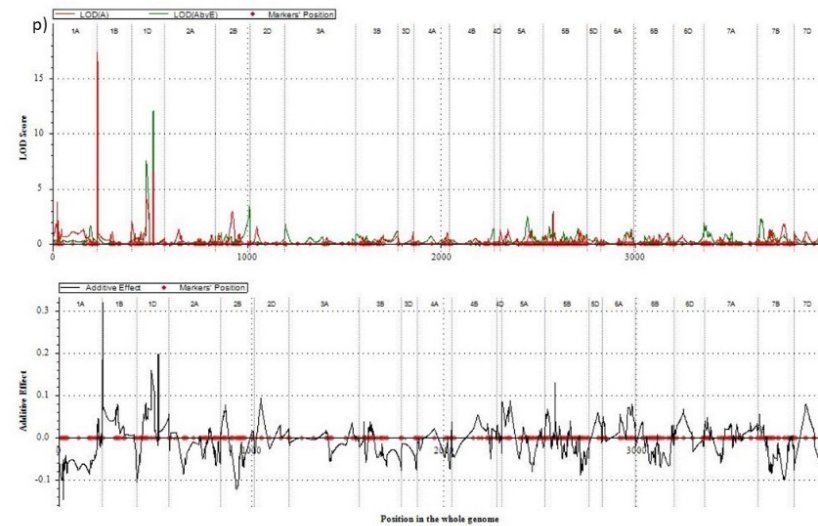
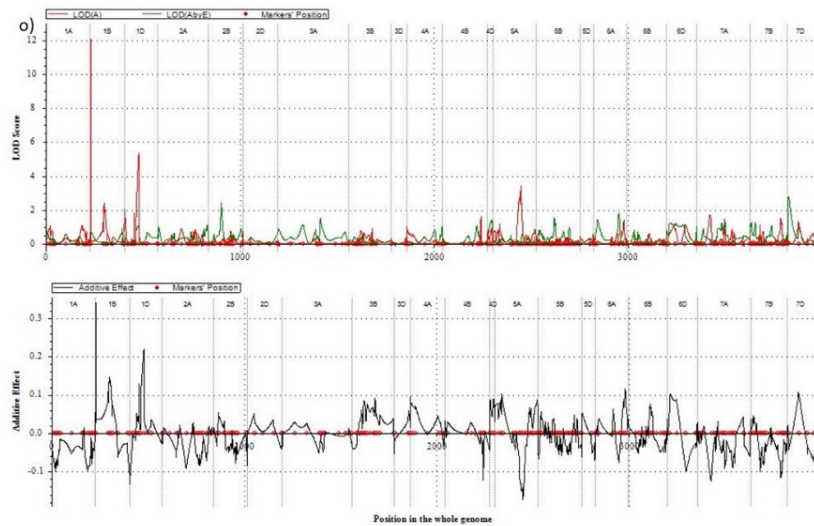
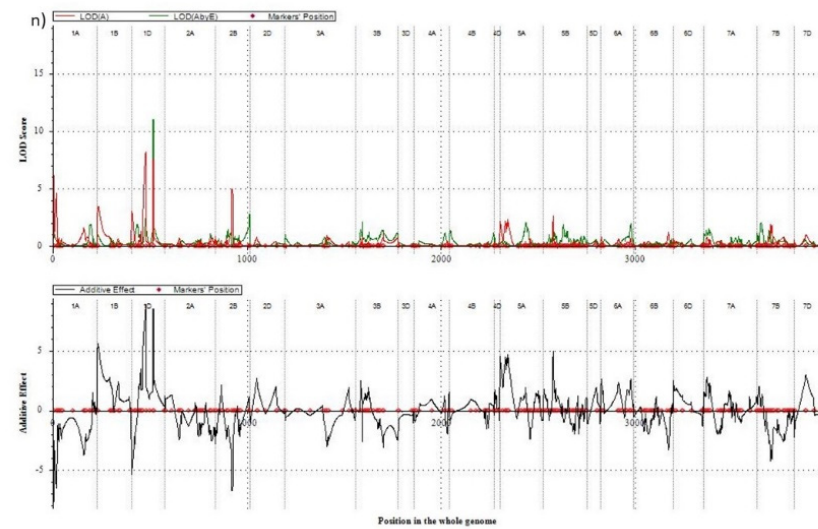
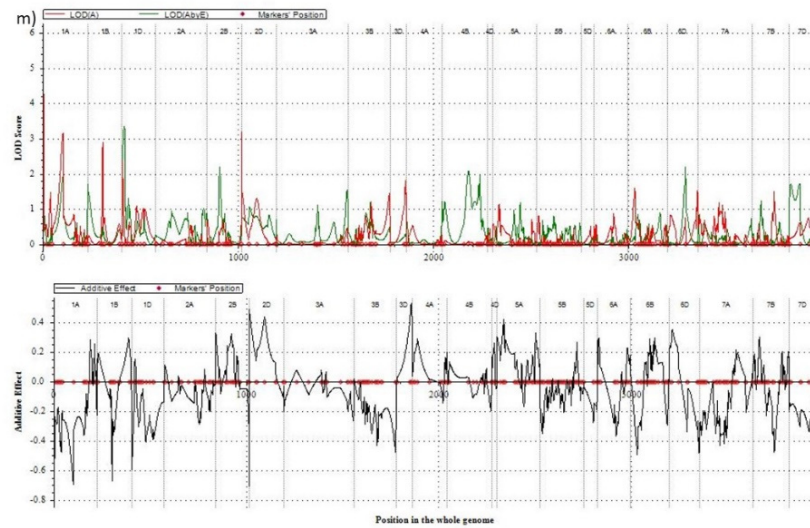


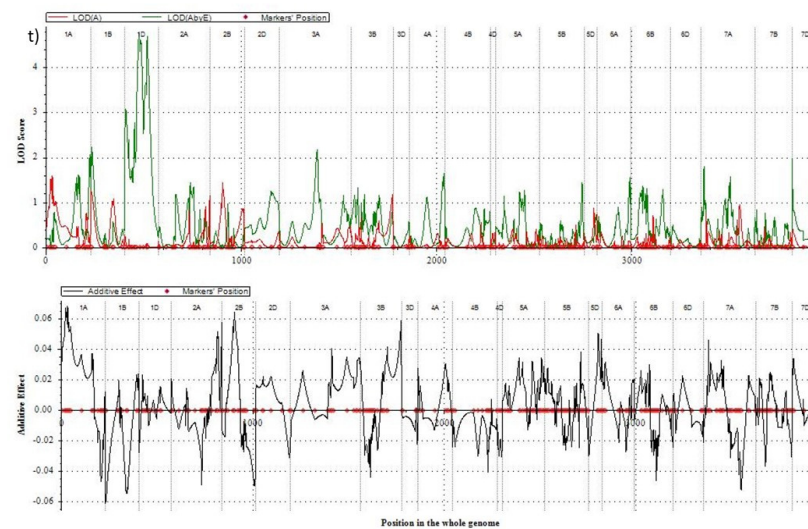
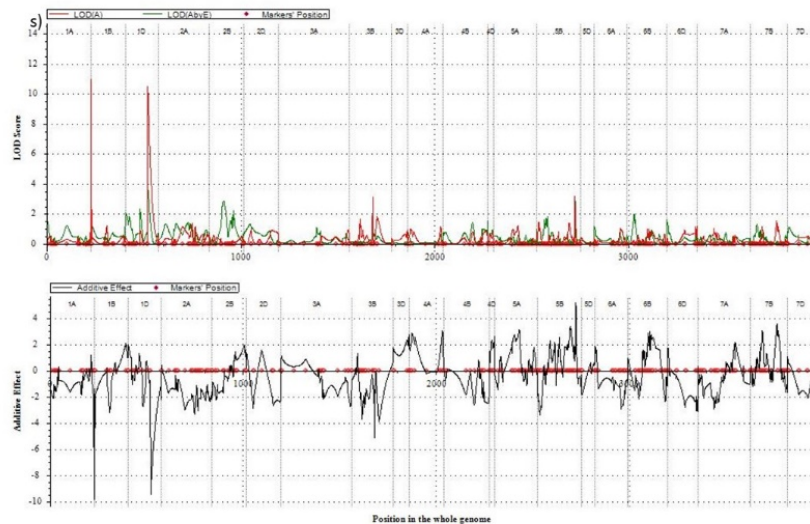
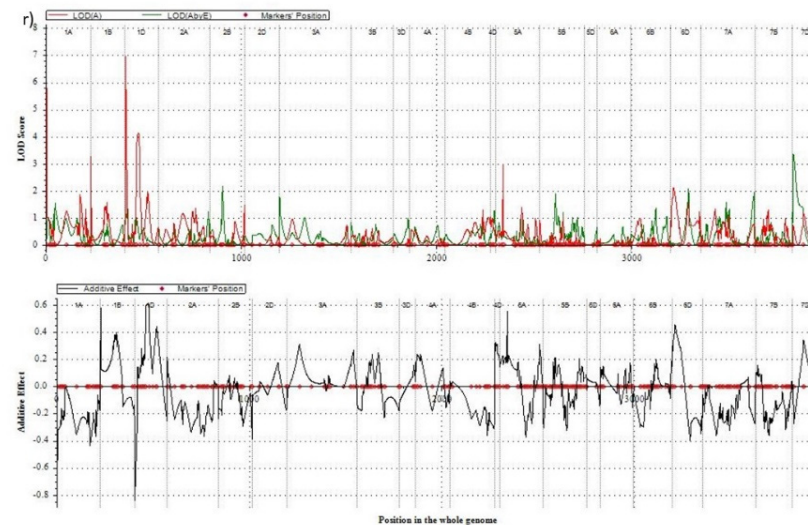
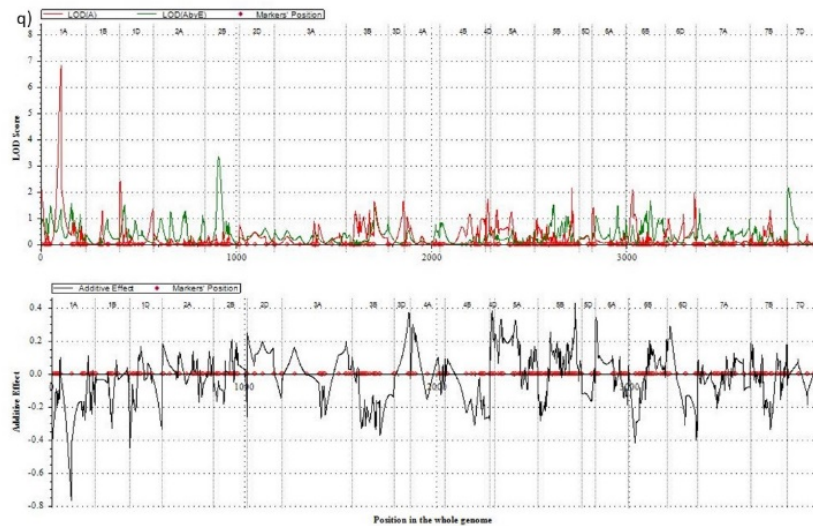
Supplemental Figure S3: LOD profile of additive, additive-by-environment detected in the multi-environment QTL analysis for a) Flour protein content, b) Hardness index, c) Kernel diameter, d) Midline left integral, e) Midline left slope, f) Midline left time, g) Midline left value, h) Midline left width, i) Midline mixing stability or tolerance, j) Midline peak integral, k) Midline peak time, l) Midline peak value, m) Midline peak width, n) Midline right integral, o) Midline right slope, p) Midline right time, q) Midline right value, r) Midline right width, s) Midline tail integral, t) Midline tail slope, u) Midline tail value, v) Midline tail width, w) Midline time\_X integral, x) Midline time\_X slope, y) Midline time\_X value, z) Midline time\_X width, aa) Single kernel weight, ab) Water absorption. LOD profile with chromosomal position is shown on the x-axis (cM of 25 LGs) and LOD score on the y-axis. Positive additive effects mean that the favorable alleles increasing traits were from CO960293-2 while negative values indicate that the favorable alleles increasing the traits were from TAM 111.

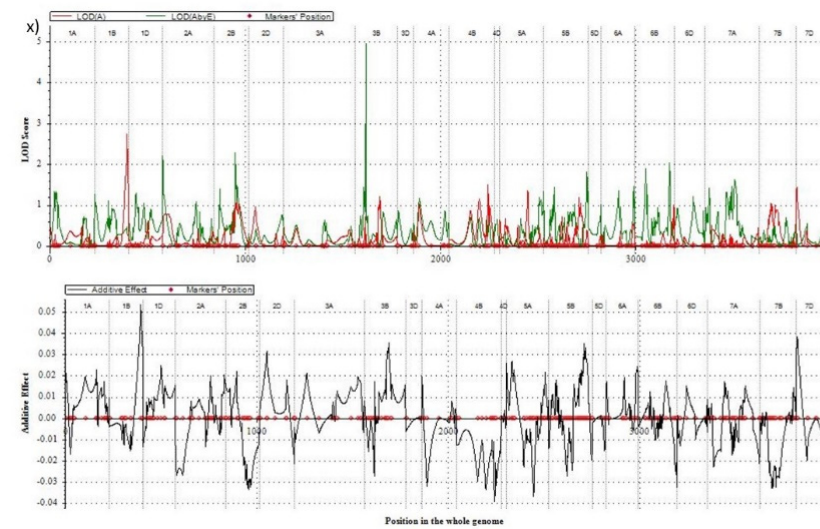
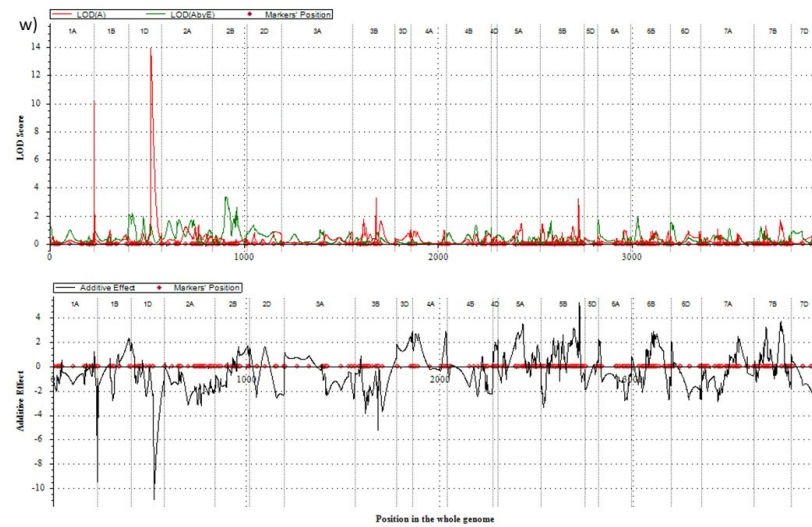
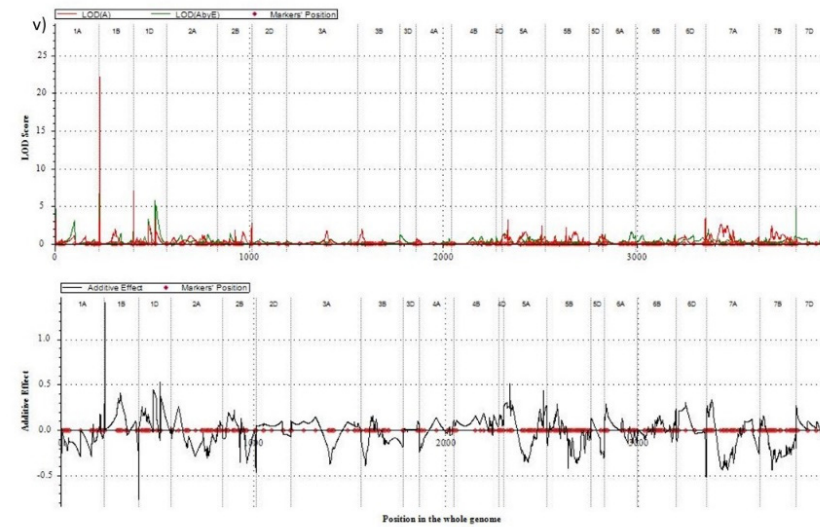
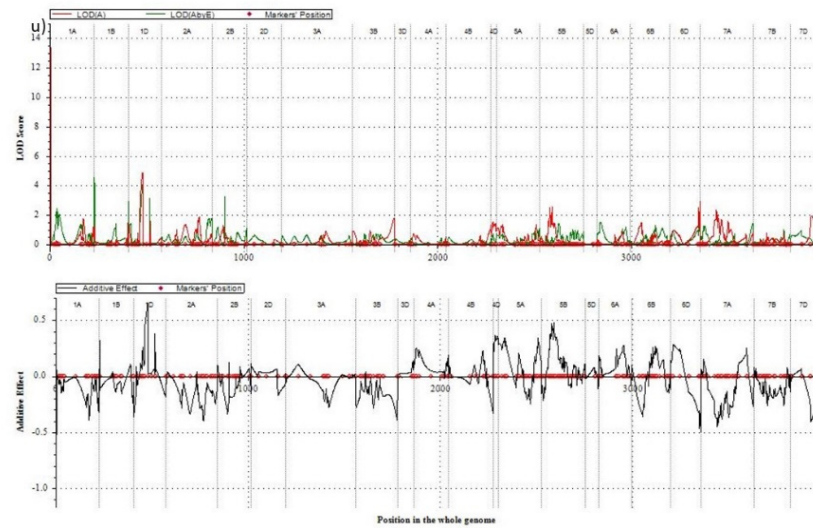


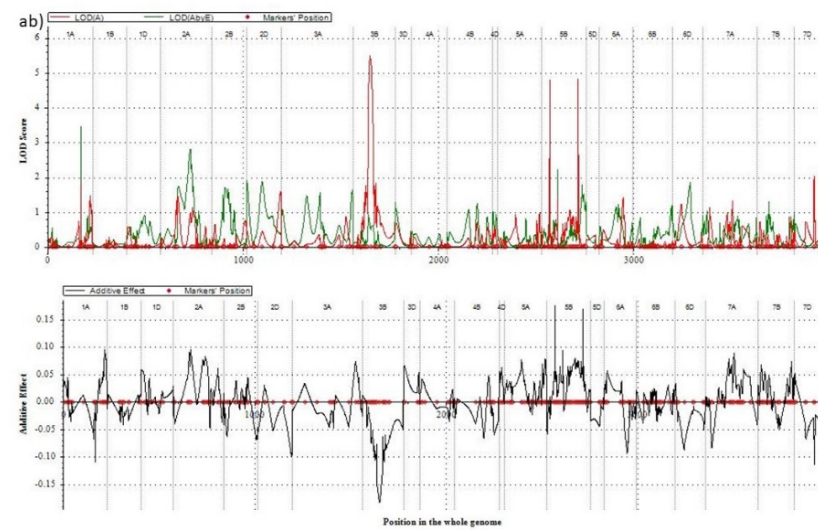
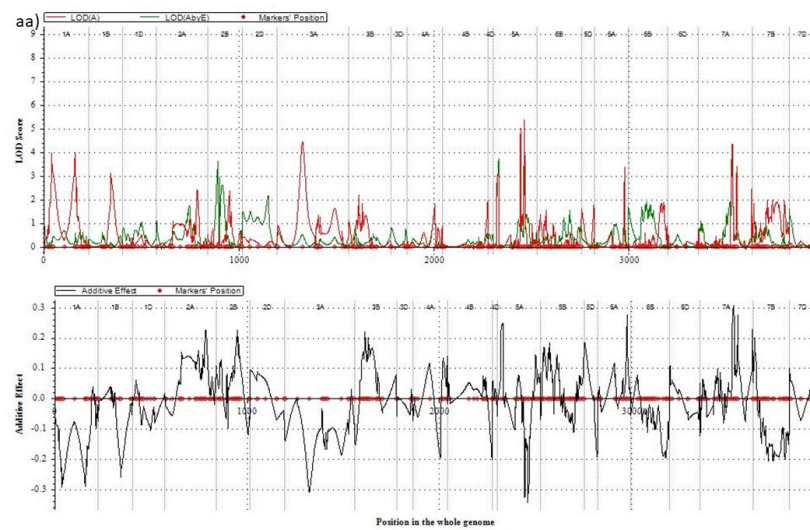
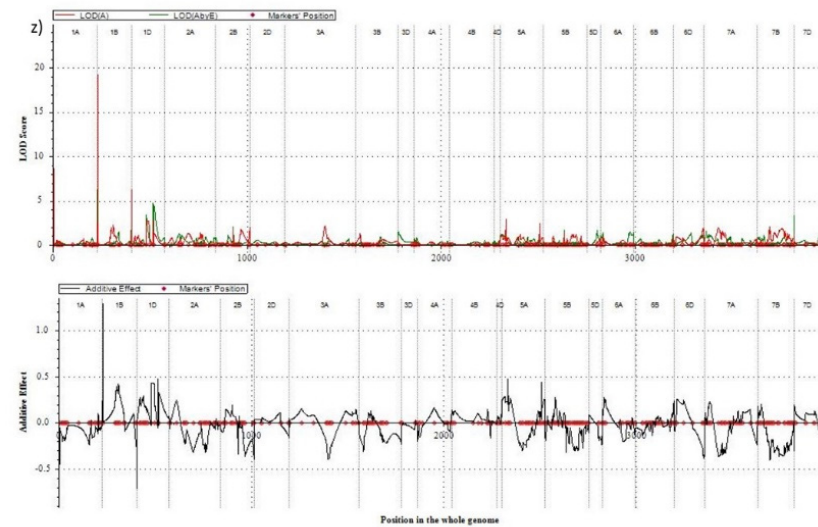
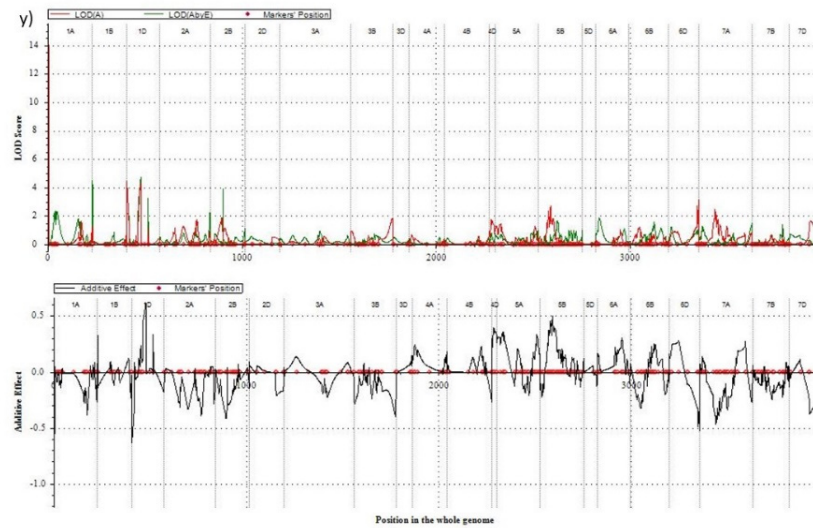




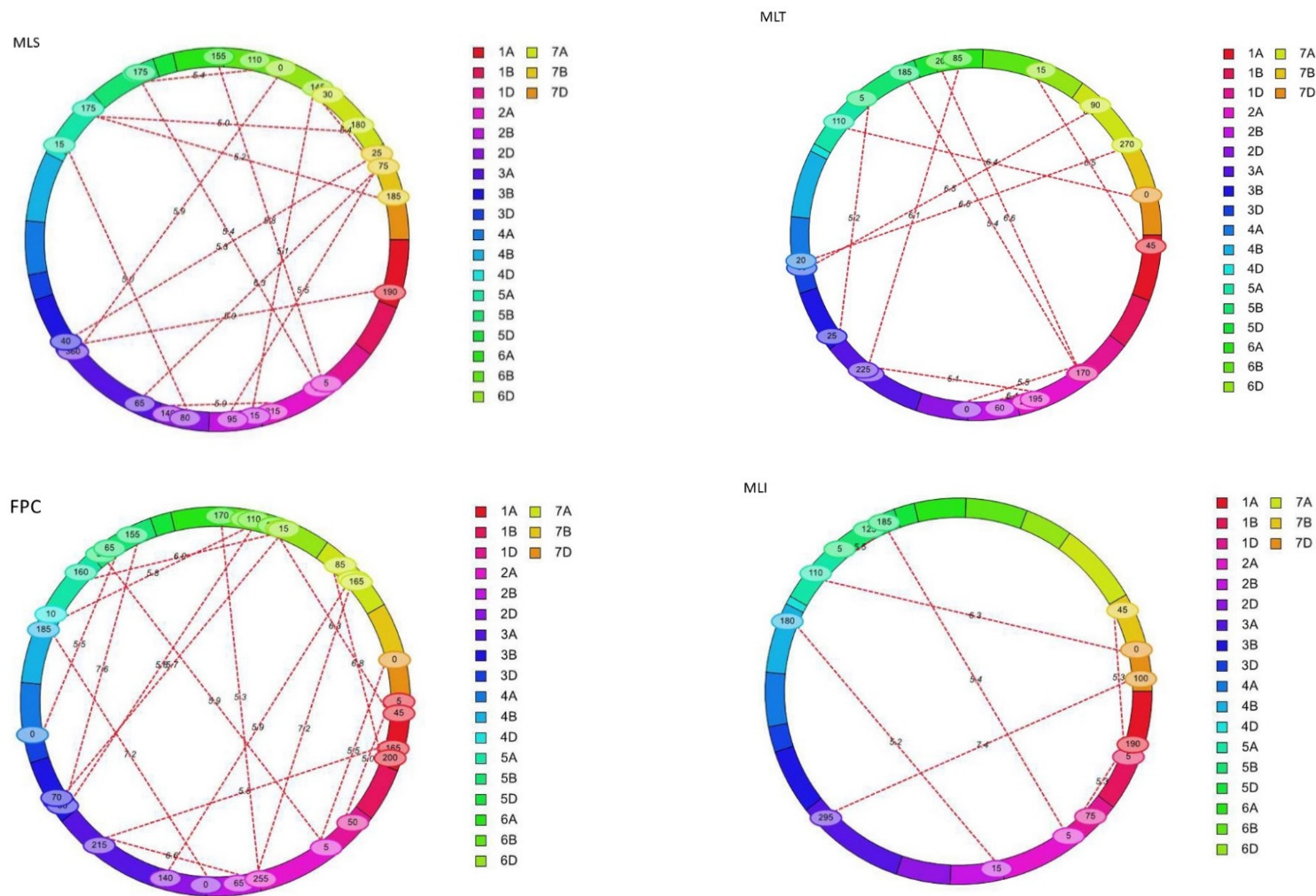




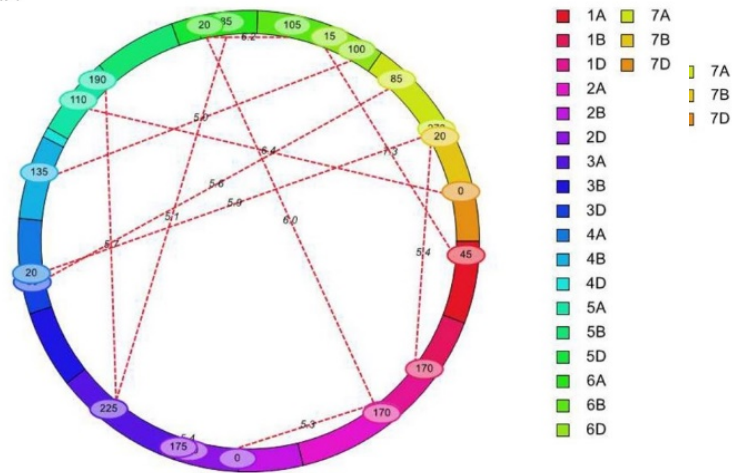




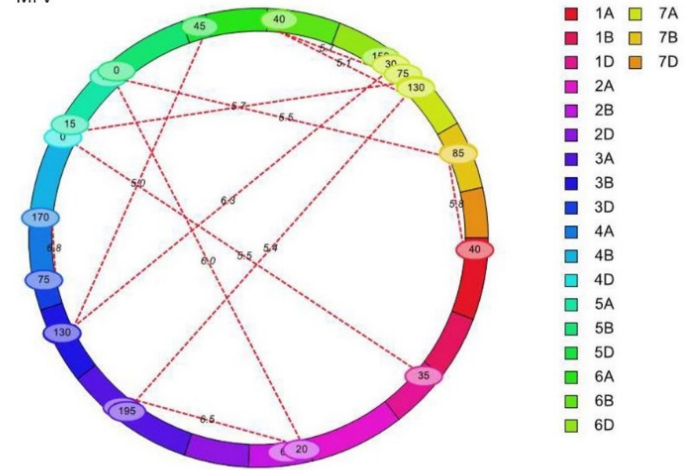
Supplemental Figure S4: Epistatic interaction for LOD > 5 between QTL for flour protein content, midline left integral, midline left slope, midline left time, midline left value, midline left width, midline mixing stability or tolerance, midline peak integral, midline peak time, midline peak value, midline peak width, midline right integral, midline right slope, midline right time, midline right value, midline right width, midline tail integral, midline tail slope, midline tail value, midline tail width, midline time\_X integral, midline time\_X value, midline time\_X width, single kernel weight, water absorption. The numbers on the rings represent the peak cM position of the on chromosomes and numbers on each line show the total LOD score of that epistasis effects. The detailed information were listed in Table S7.



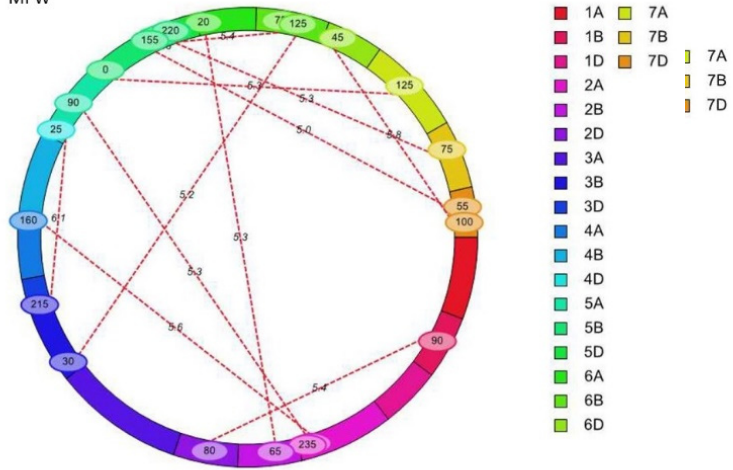
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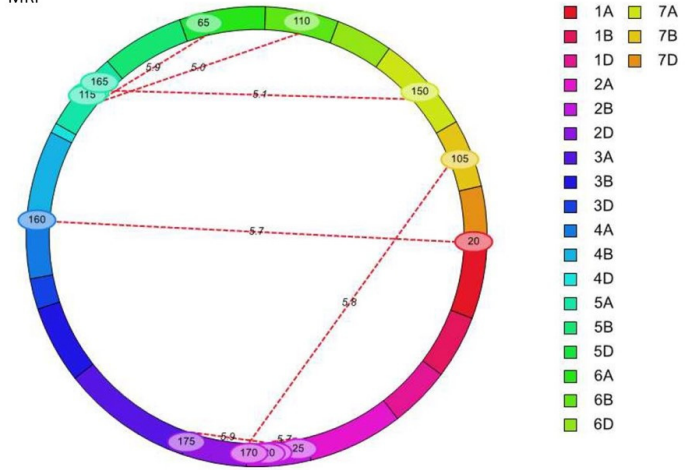
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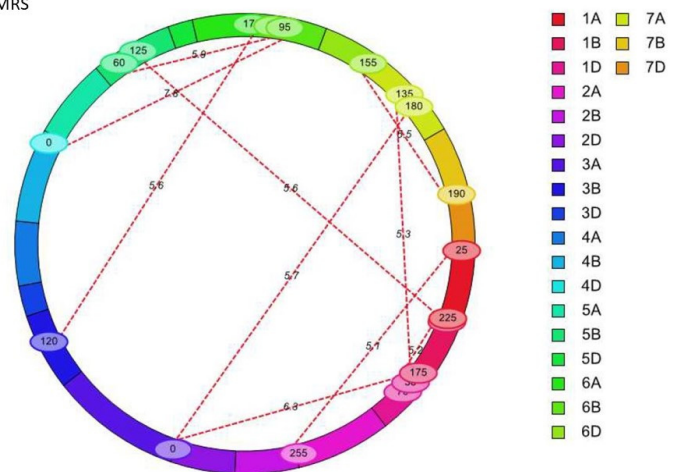
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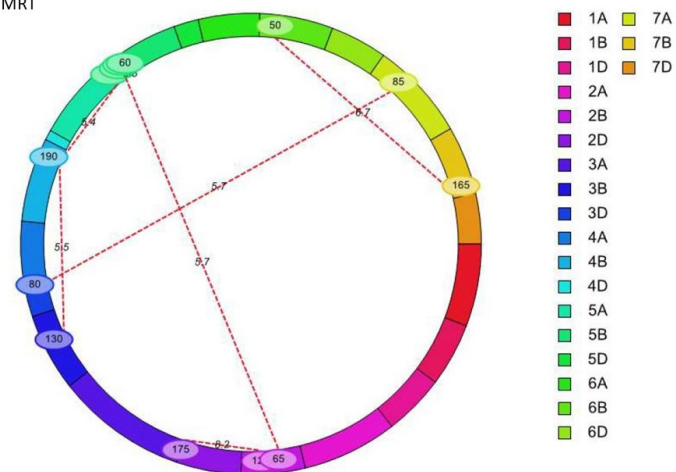
MRI



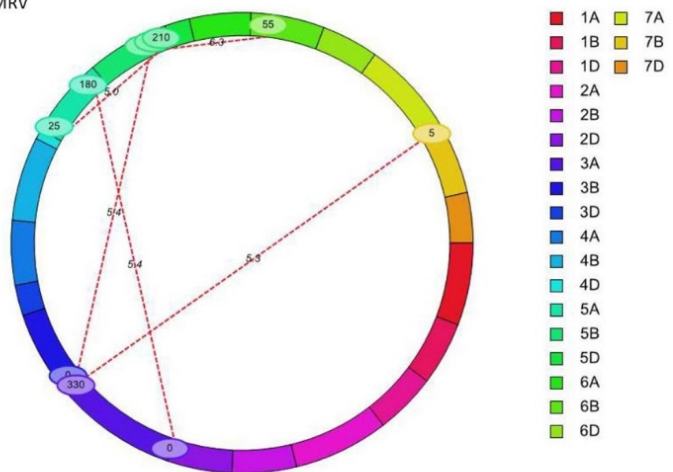
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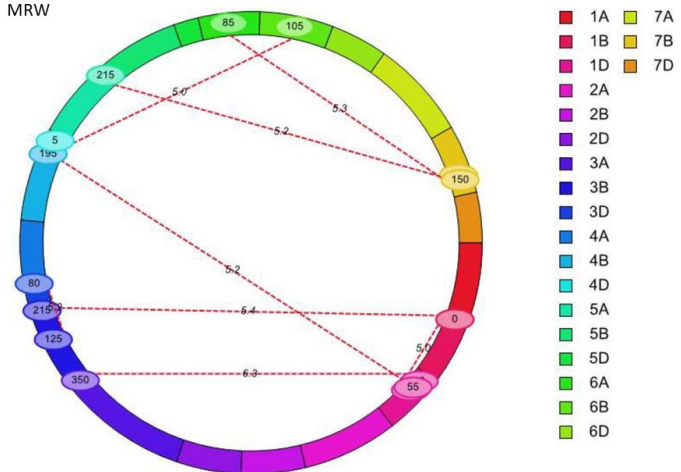
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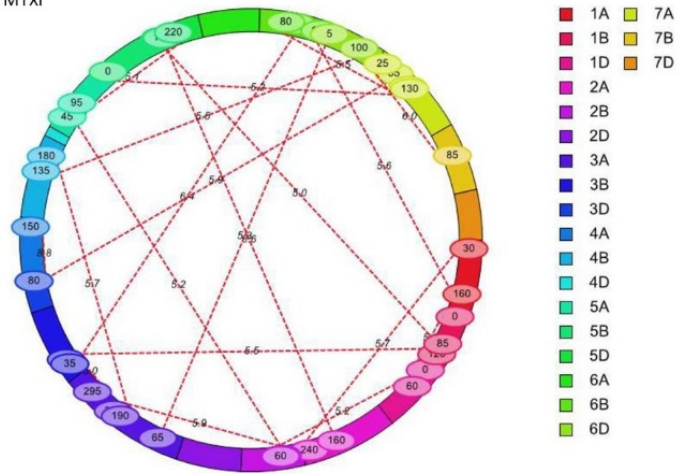


MRW

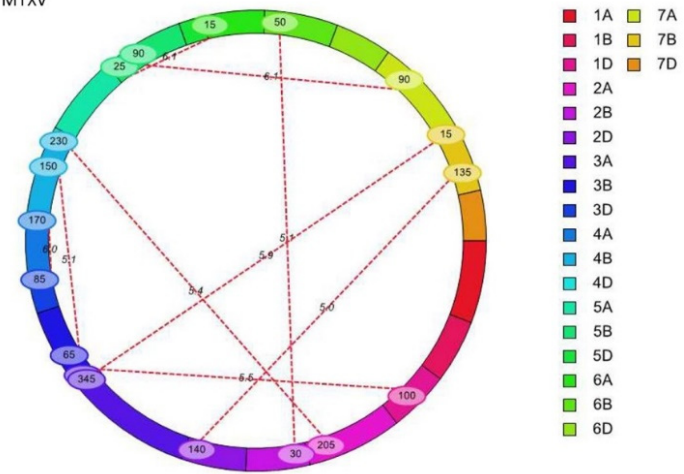




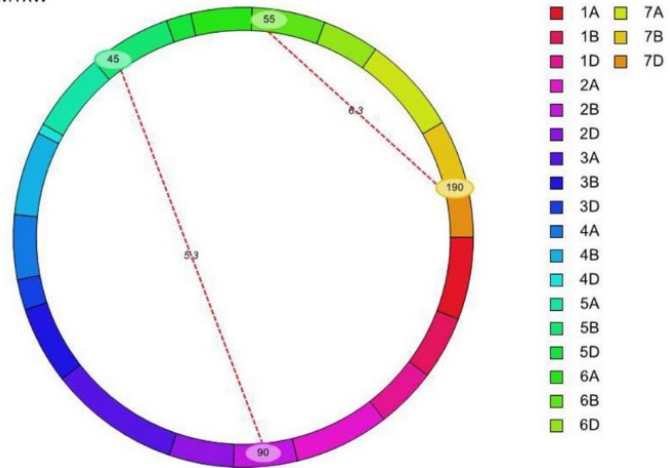
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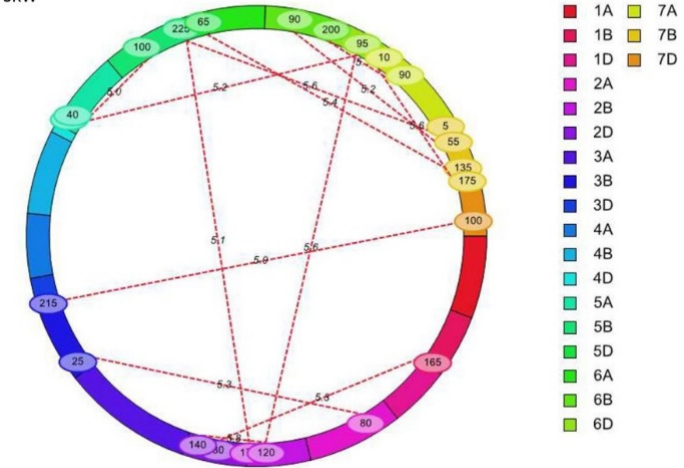
MTXV



MTXW



SKW



WAB

