Figure S2: EpiQTL mapping of Indolic glucosinolate means. Plots show composite interval mapping results and significance estimated from 1000 permutations. The x-axis shows the genome by chromosome and y-axis shows the LOD score. The significance thresholds are plotted for each trait and significant QTLs are re marked with red arrows. The light grey line shows the QTL map using the means from experiment 1, dark grey shows experiment 2, and black lines represent the pooled data from experiment 1 and 2. Marker names show the position of significant makers after using a linear model to assess loci. An asterisk after a marker shows that the marker was not significant in both experiments. Beneath plots are shown the additive effect of markers, i.e. the percentage phenotypic change when the marker is *ddm1* within the epiRIL lines compared to WT. EpiQTLs not assigned a marker were rejected in the subsequent ANOVA. Analyzed indolic glucosinolates are A) I3M, B) NMOI3M, C) 4MOI3M, D) Pooled indolic glucosinolates.