



Figure S5 *Lactuca sativa* pseudo-chromosome distribution of $-\log_{10} P$ -values for 646 LKAM associations with *N. ribisnigri* count data obtained from the VeGIN lettuce diversity set. Panels' a., b., and c. represent SNP associations with mean count data for alate, apterous, total-aphid count respectively. Horizontal dashed line represents a threshold of $-\log_{10} P$ -value >2 . Pseudo-chromosomes 1-9 and group-10 (un-mapped SNPs) alternately coloured blue and red. Each panel is accompanied with a Q-Q plot following genomic control for the three phenotype groups.