

A method for identifying a quantitative trait locus associated with desirable nutritional traits in canola includes: analyzing a population of canola plants or germplasm for desirable nutritional traits; determining the genotype of the canola plants or germplasm using at least one marker selected from the group consisting of SEQ SN NO:1 through SEQ ID NO:111; mapping the canola plants or germplasm for the presence of a quantitative trait locus (QTL) associated with the markers; and associating the QTL with the desirable nutritional trait. An isolated and/or recombinant nucleic acid includes a sequence associated with a quantitative trait locus (QTL), wherein the QTL is associated with a desirable nutritional trait in a canola plant or germplasm and wherein the QTL is further associated with at least one marker selected from the group consisting of SEQ ID NO:1 through SEQ ID NO:111.