**Supplementary Figures**

**Supplementary Figure 1:** Population structure visualizations from PCA performed on a population of F2:3 table beet individuals selected for extreme geosmin concentration (n = 87) using 8,651 biallelic SNP markers. (A) Percent genotypic variation explained by principal components 1-10, and frst and second principal component locations of individuals by (B) F2:3 family indicated by unique color and (C) high (red) or low (blue) geosmin tail.

**Supplementary Figure 2:** Locations on principal components 1-4 of F3 table beet individuals selected for extreme geosmin concentration (n = 87) genotyped on 8,651 biallelic SNP markers. F2:3 families are indicated by number and color.

**Supplementary Figure 3:** Percent genotypic variation explained by principal components 1-10 from PCA performed on 8,651 SNP markers for **(A)** a population of F3 table beet individuals selected for extreme geosmin concentration (n = 87); **(B)** a balanced subpopulation including one individual from each of the 24 F2:3 families in the selected population; and the **(C)** low (n = 43) and (**B**) high (n = 44) geosmin tails of the selected population.

**Supplementary Figure 4**: QQ plots by chromosome for association analysis performed on untransformed geosmin for a population of F3 table beet individuals selected for extreme geosmin concentration (n = 87) using 8,651 SNP markers.

**Supplementary Figure 5:** Manhattan plots for association analyses performed on the **(A)** low and (**B)** high geosmin tails of an F3 individual table beet population selected for extreme geosmin concentration (n=W and n=44 F3 individuals, respectively) using 8,651 SNP markers and thresholds derived from 1000 permutations (α = 0.05).

**Supplementary Figure 6**: QQ plots for association analysis of geosmin concentration with 8,651 SNP markers in (**A**) low (n = 43) and (**B**) high (n = 44) geosmin tails of an F3 individual table beet population selected for extreme geosmin concentration.

## Supplementary Files

**Supplementary File 1:** R code used to analyze phenotypic data found in Files S2 and S3.

**Supplementary File 2:** Phenotypic data for entire mapping population plus check individuals.

**Supplementary File 3:** Phenotypic data for selected individuals.

**Supplementary File 4:** R code used for association analysis and PCA. Association analysis uses phenotypic data found in File S5, and PCA uses categorical data in File S6. Both analyses use the filtered marker data set in File S7.

**Supplementary File 5:** Phenotypic data for 87 individuals selected for genotyping.

**Supplementary File 6:** Classification data for 87 individuals selected for genotyping.

**Supplementary File 7:** Marker genotypes for filtered set of 8,651 SNP’s used for association analysis and PCA. Marker names include original EL10.2 scaffold names that were later renamed according to Butterfass nomenclature as: Scaffold 1 = Chr 6; Scaffold 2 = Chr 5; Scaffold 3 = Chr 4; Scaffold 4 = Chr 1; Scaffold 5 = Chr 8; Scaffold 6 = Chr 7; Scaffold 7 = Chr 3; Scaffold 8 = Chr 2; Scaffold 9 = Chr 9.

**Supplementary File 8:** Unfiltered genomic data in Variant Call Format. Marker names include original EL10.2 scaffold names that were later renamed according to Butterfass nomenclature as: Scaffold 1 = Chr 6; Scaffold 2 = Chr 5; Scaffold 3 = Chr 4; Scaffold 4 = Chr 1; Scaffold 5 = Chr 8; Scaffold 6 = Chr 7; Scaffold 7 = Chr 3; Scaffold 8 = Chr 2; Scaffold 9 = Chr 9.