

Supplementary Information

Genomic predictions and genome-wide association studies based on RAD-seq of quality-related metabolites for the genomics-assisted breeding of tea plants

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Supplementary Figure S1. Correlations of tea quality-related metabolites in 150 accessions between 2018 and 2019. NS; Not significant ($P > 0.01$)

Supplementary Figure S2. Distribution of genome-wide SNPs in the tea chromosome-scale genome. UA; Un-anchored SNPs.

Supplementary Figure S3. Genetic structure analyses using 9,523 SNPs among 150 tea accessions. Estimated genetic structure for $K = 2$ and $K = 3$ by fastSTRUCTURE (A). Plot of first and second principal components computed by PCA (B). Dendrogram of Ward's hierarchical clustering based on Euclidean distance (C).

Supplementary Figure S4. QQ-plots from a GWAS based on the MLM (A) and GLM (B) of five phenotypes of tea quality-related metabolites.

Supplementary Figure S5. Correlation matrix between tea quality-related metabolites.

Supplementary Data file includes:

Supplementary Table S1. List of candidate genes linked to the top 80 SNPs in a GWAS of EC content.

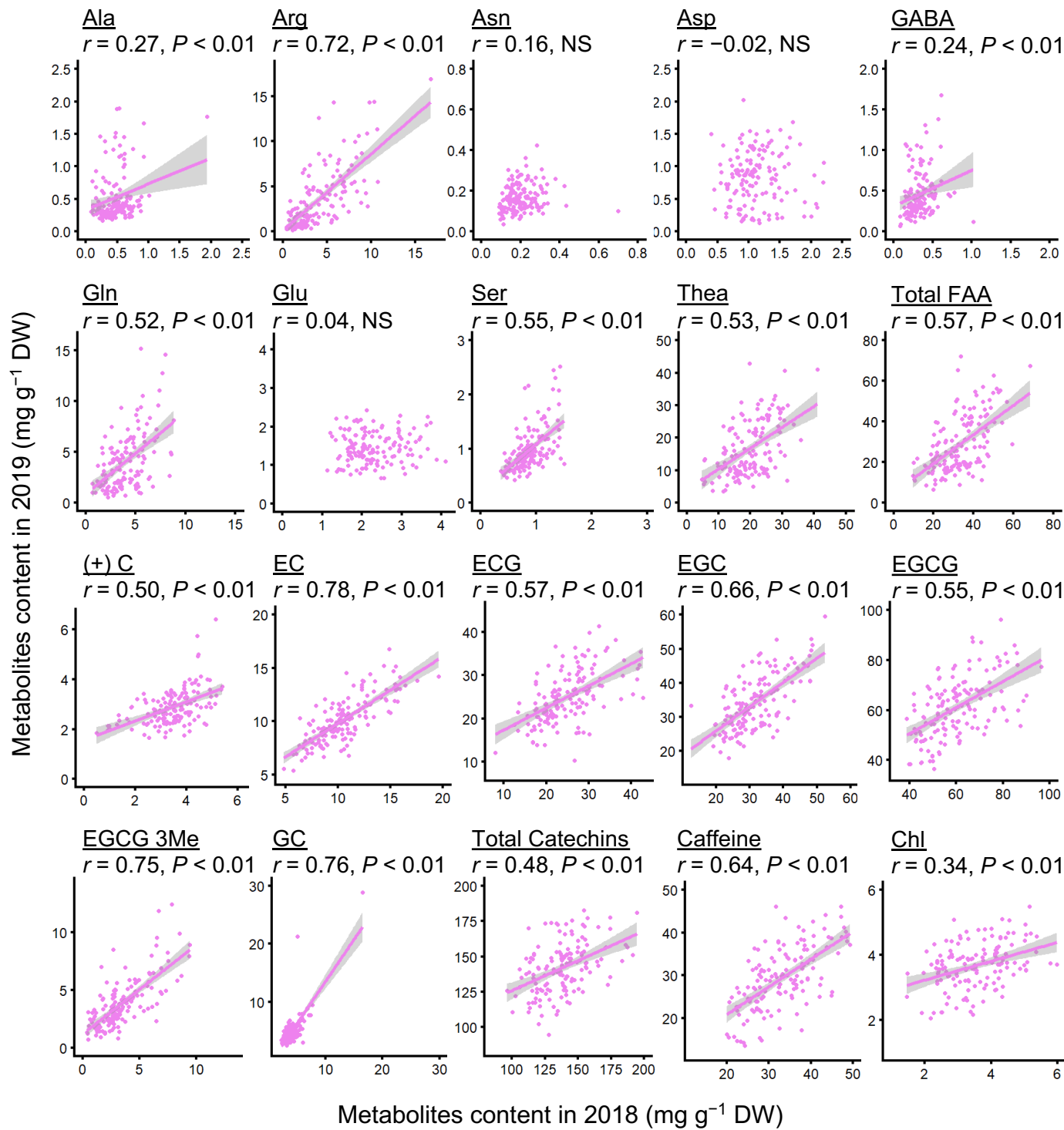
Supplementary Table S2. List of candidate genes linked to the top 140 SNPs in a GWAS of ECG content.

Supplementary Table S3. List of candidate genes linked to the top 140 SNPs in a GWAS of EGCG content.

Supplementary Table S4. List of candidate genes linked to the top 140 SNPs in a GWAS of total catechin content.

Supplementary Table S5. List of candidate genes linked to the top 160 SNPs in a GWAS of caffeine content.

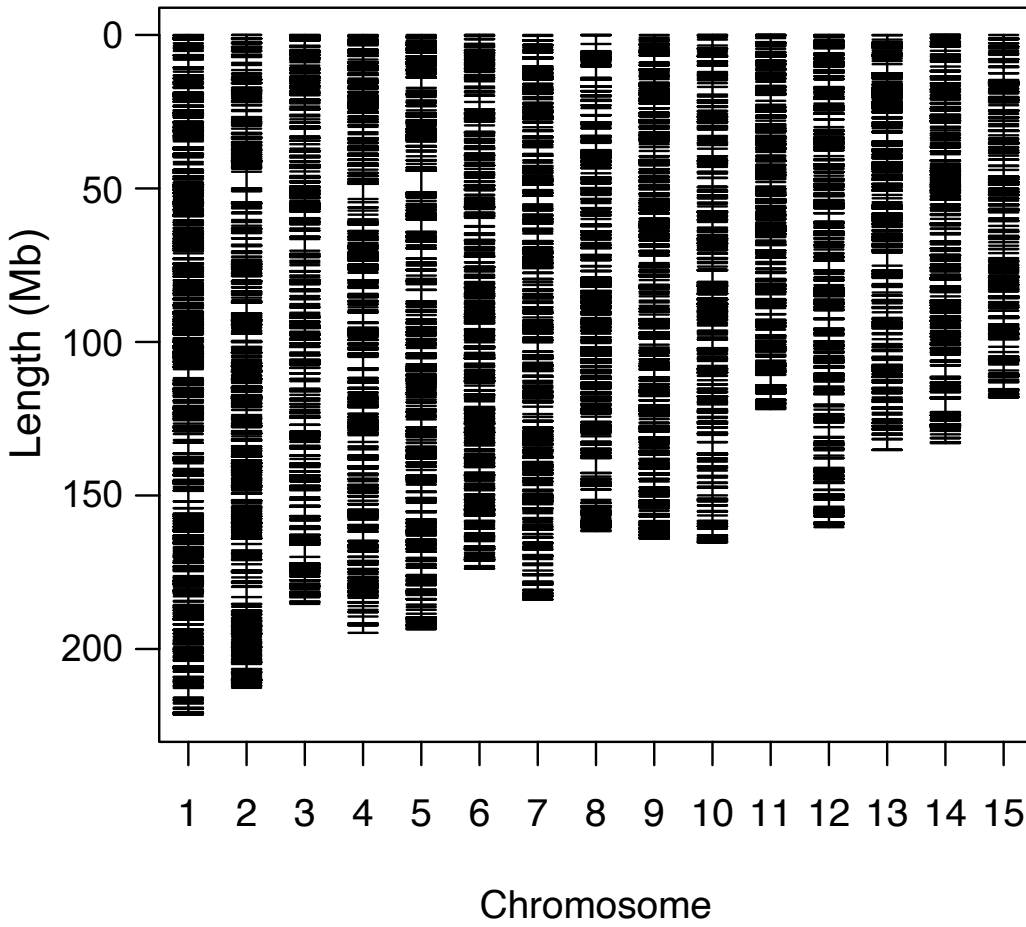
Supplementary Table S6. Tea accessions used in this study.



Supplementary Figure S1. Correlations of tea quality-related metabolites in 150 accessions between 2018 and 2019.

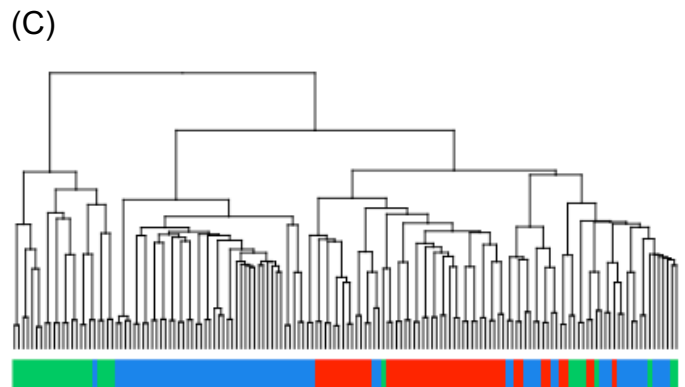
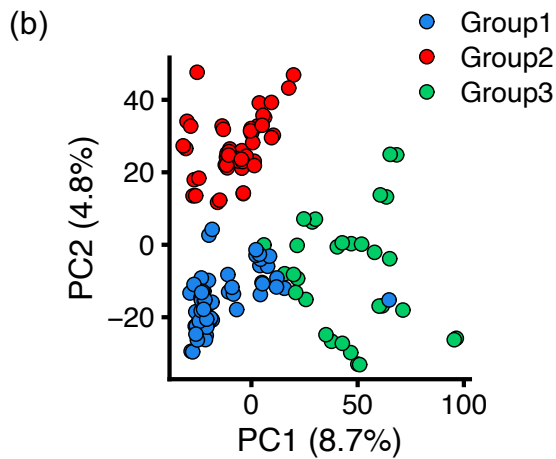
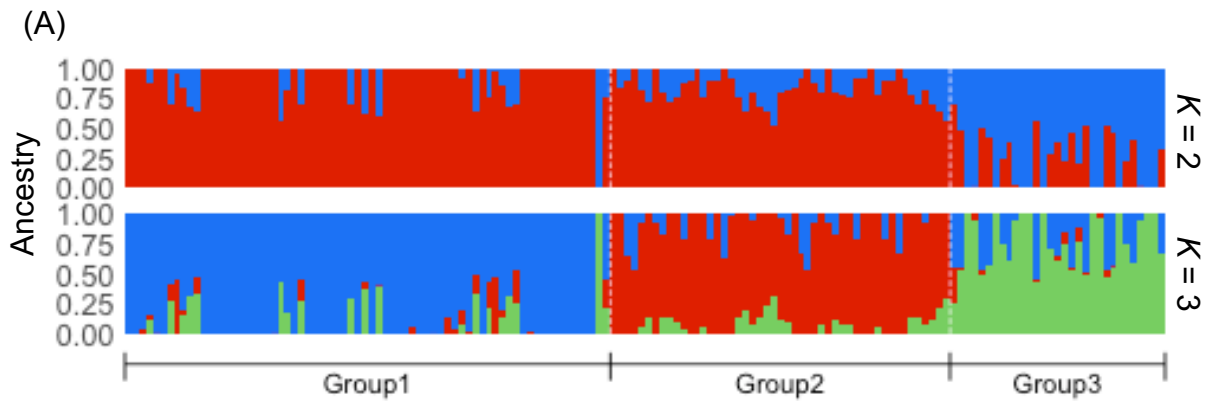
NS; Not significant ($P > 0.01$)

Genetic map

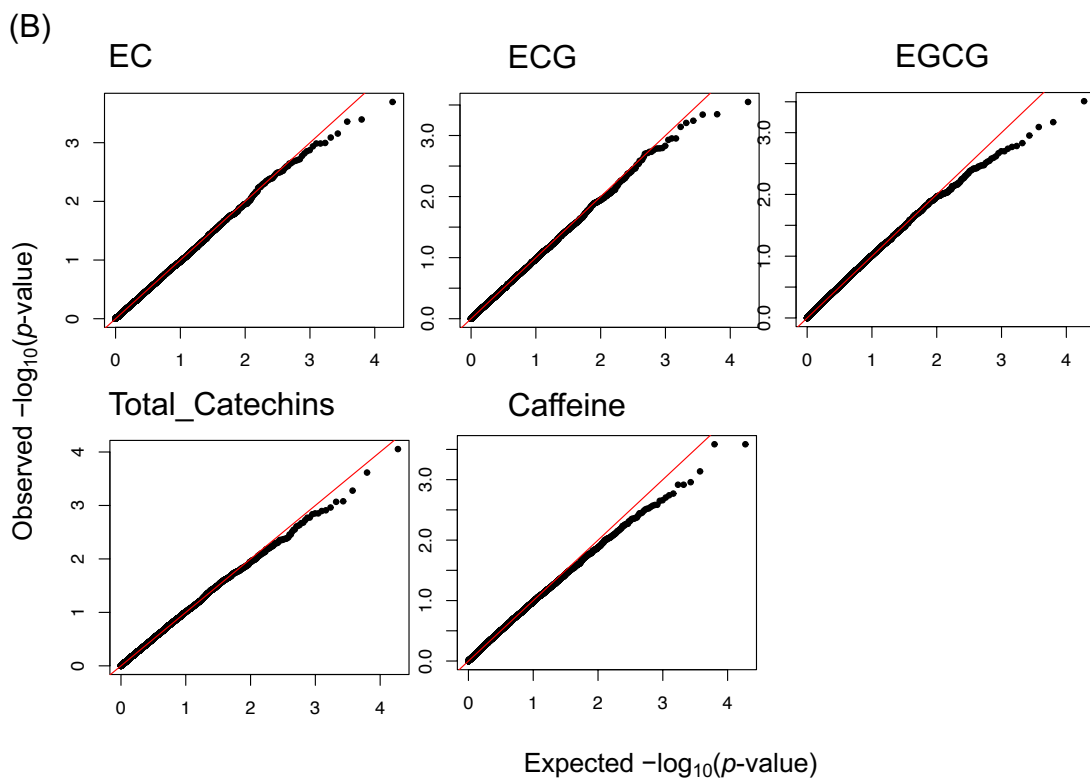
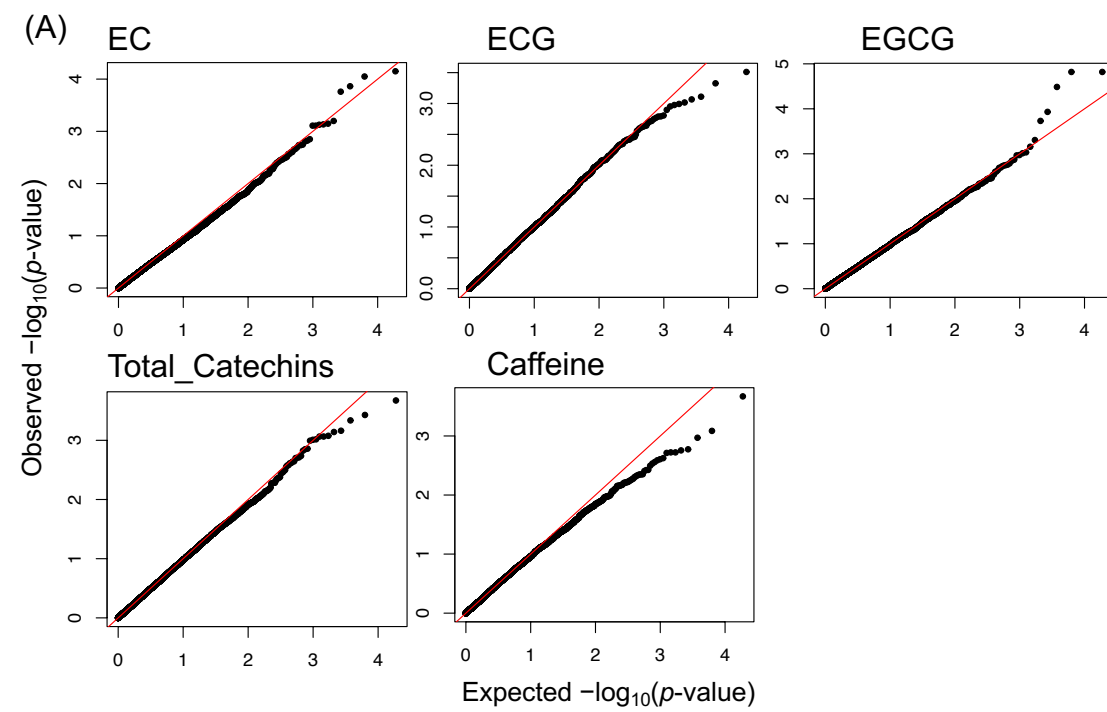


Chr	Number of SNPs
1	911
2	781
3	571
4	606
5	626
6	612
7	609
8	541
9	639
10	480
11	485
12	521
13	493
14	446
15	380
UA	822
Total	9,523

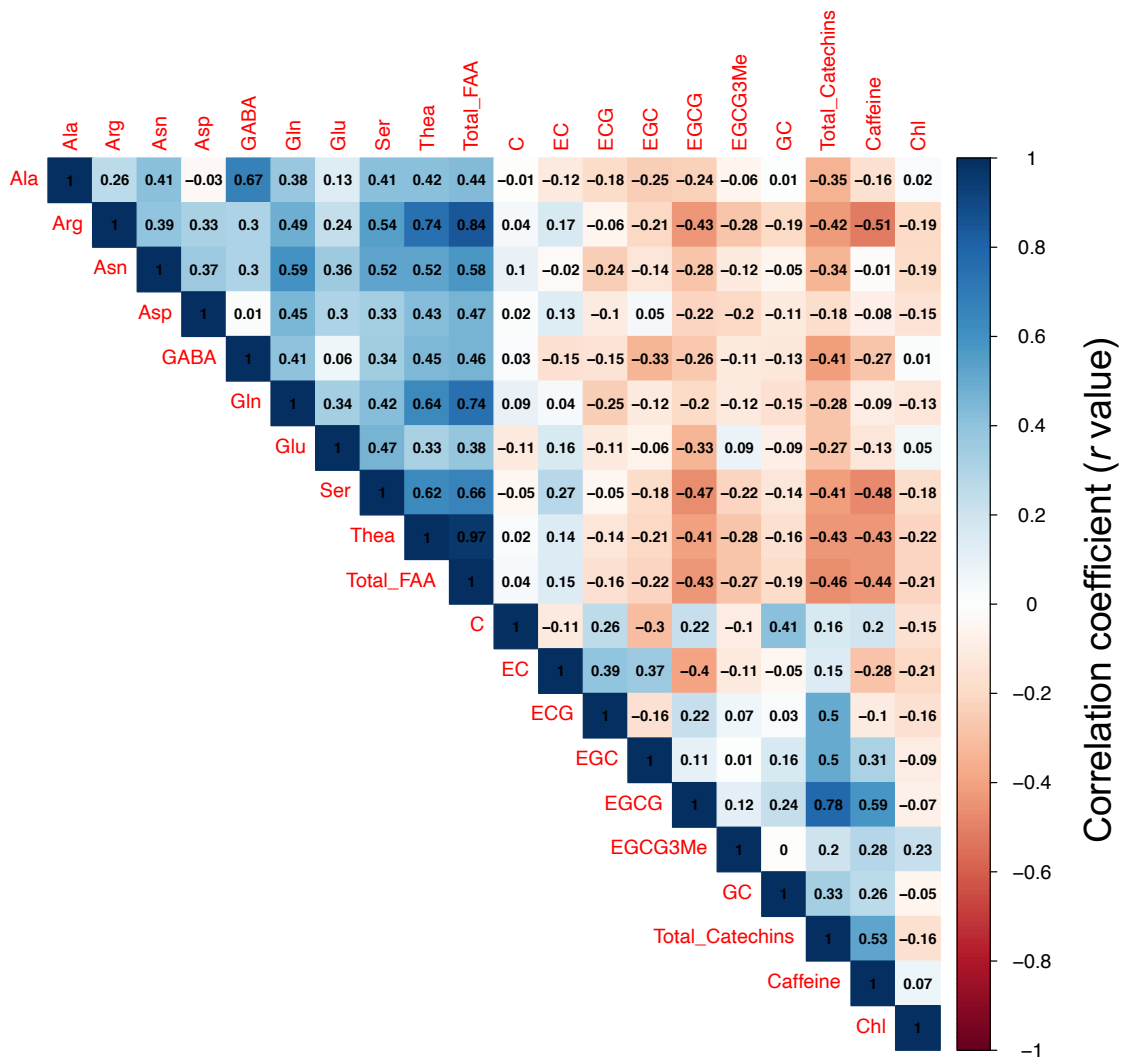
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