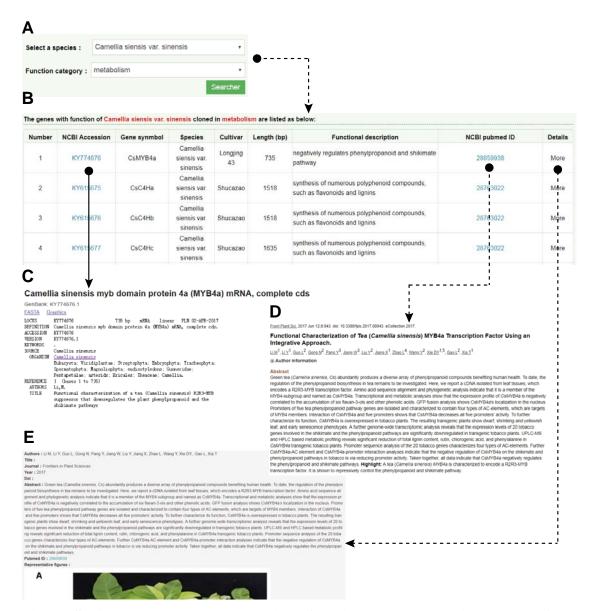
## **Additional Files**



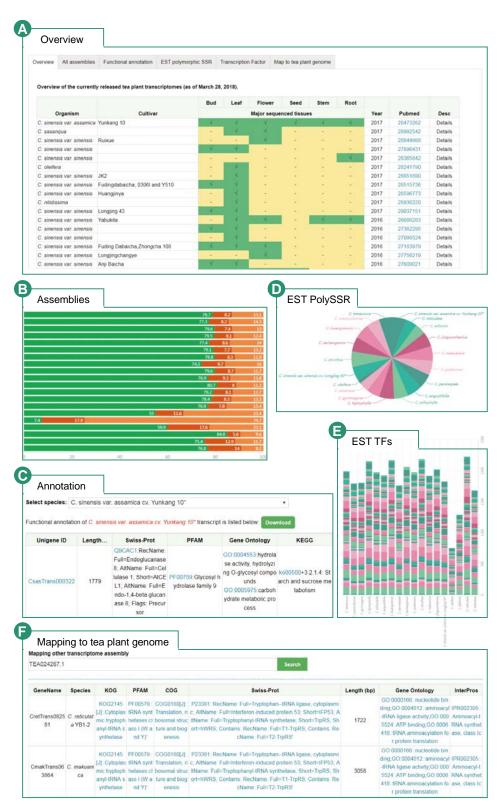
**Figure S1 Analysis of SSRs in tea plant genome**. (A) SSR selection; (B) SSR statistic; (C) Search result of specific SSRs; (D) SSR Polymorphism among 11 representative tea plant species; and (E) Three primer pairs designed for each polymorphic SSR.



**Figure S2 Analysis of repeat sequences in tea plant genome**. (A) Annotation method, repeat type and scaffolds selection; (B) Search result of specific repeat sequences with download; and (C) Visualization of repeat sequences using JBrowser.



**Figure S3 Abundant and well organized functionally characterized genes of tea plant**. (A) Species and functional category selection; (B) Search result of metabolism related genes in *Camellia sinensis* var. *sinensis*; (C) Sequence records in NCBI nucleotide database; (D) Related reference in PubMed; and (E) Detail information of the collected genes, particularly the representative figures of functional experiments.



**Figure S4 Collection and utilization of tea plant transcriptomes**. (A) Overview of the transcriptome collection; (B) Assemblies; (C) Functional annotations, (D) EST polymorphic SSRs, (E) EST transcription factors, and (F) Mapping the transcripts to tea plant genome.

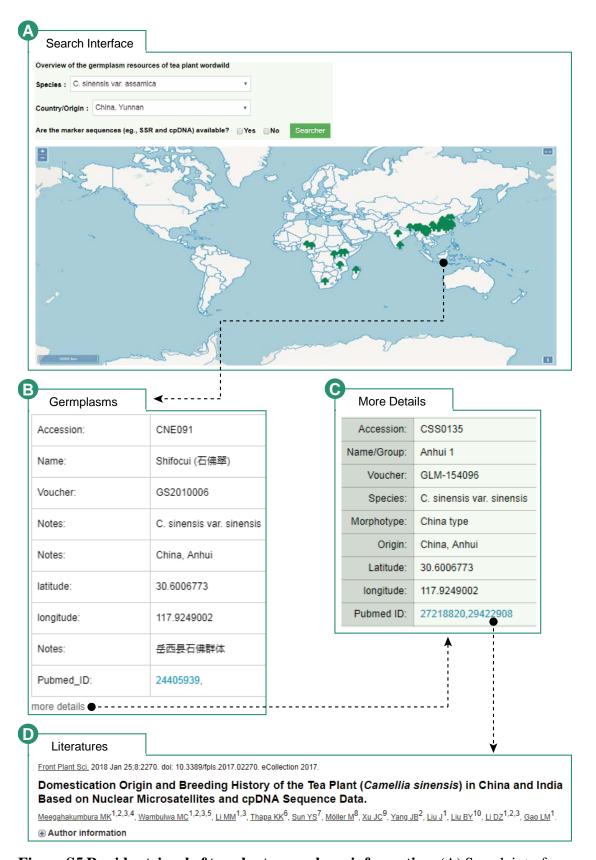


Figure S5 Rapid retrieval of tea plant germplasm information. (A) Search interface;

(B) Searched germplasms; (C) Details of the search results; and (D) Related literatures.