Figure S1

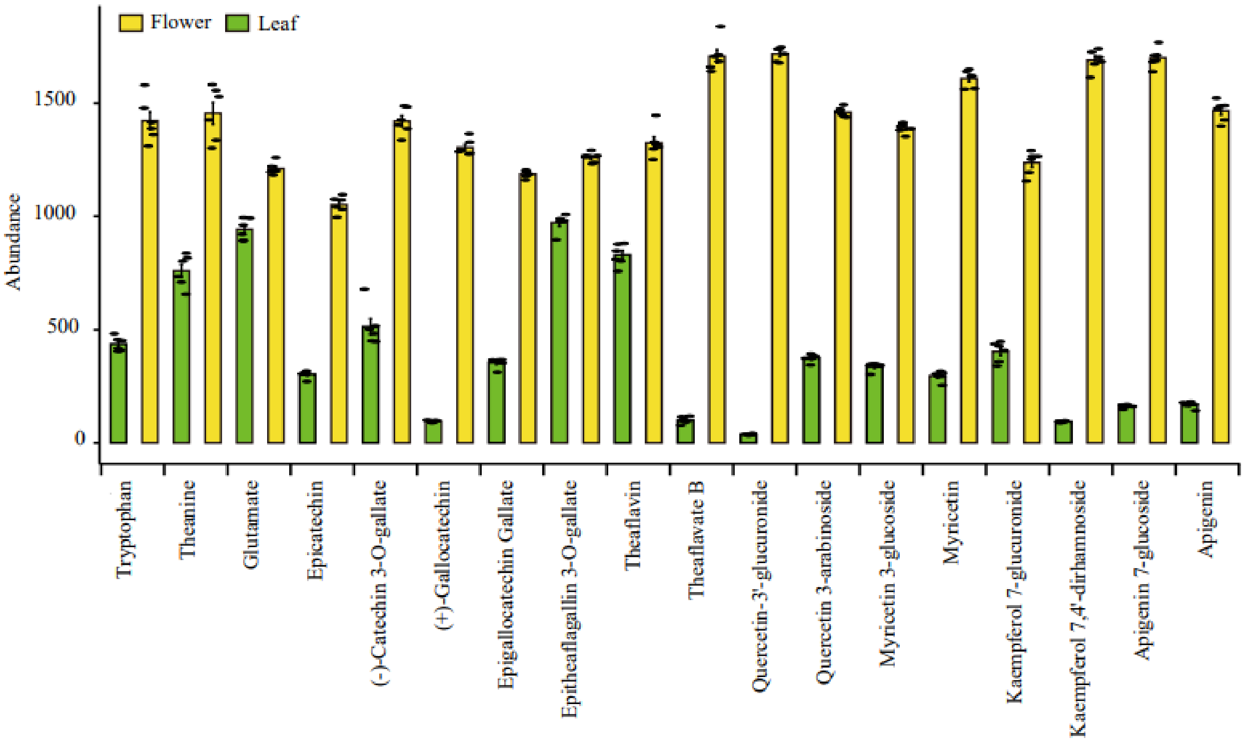


Figure S1. Differences in key metabolites between tea flowers and leaves.

Figure S2

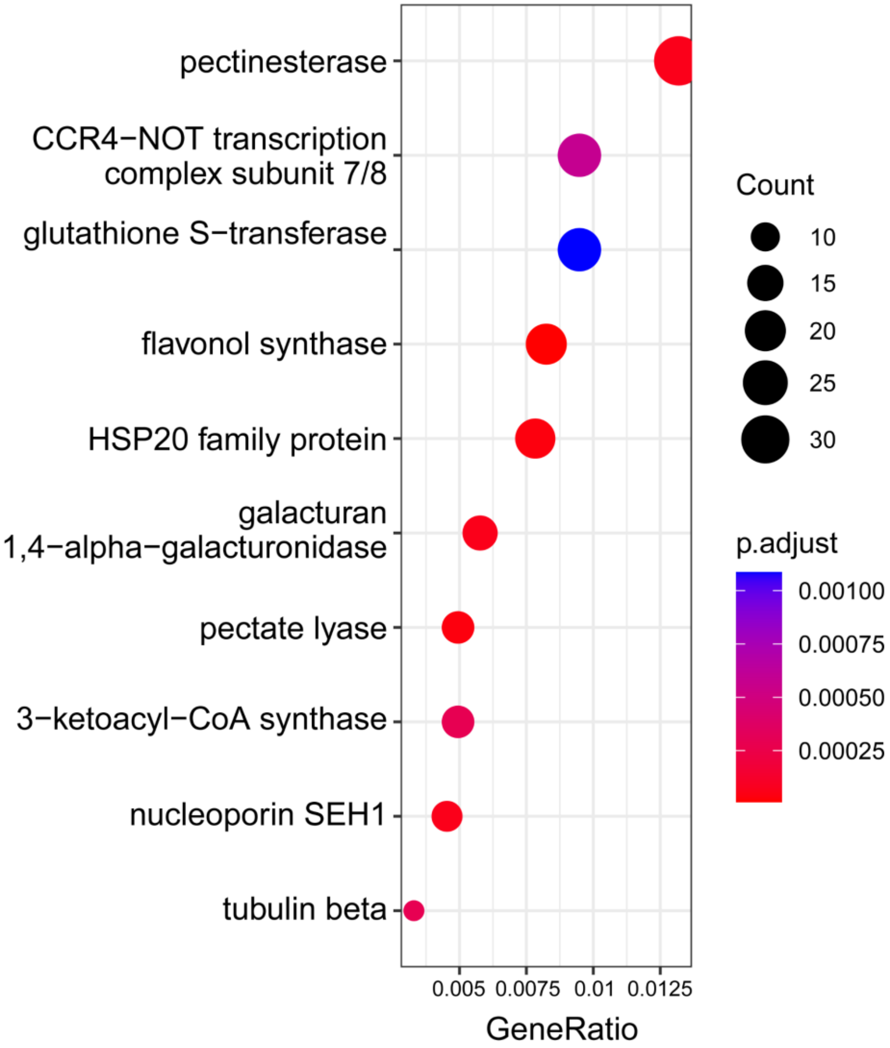


Figure S2. KEGG pathway analysis of different expression genes in developing tea flowers.

Figure S3

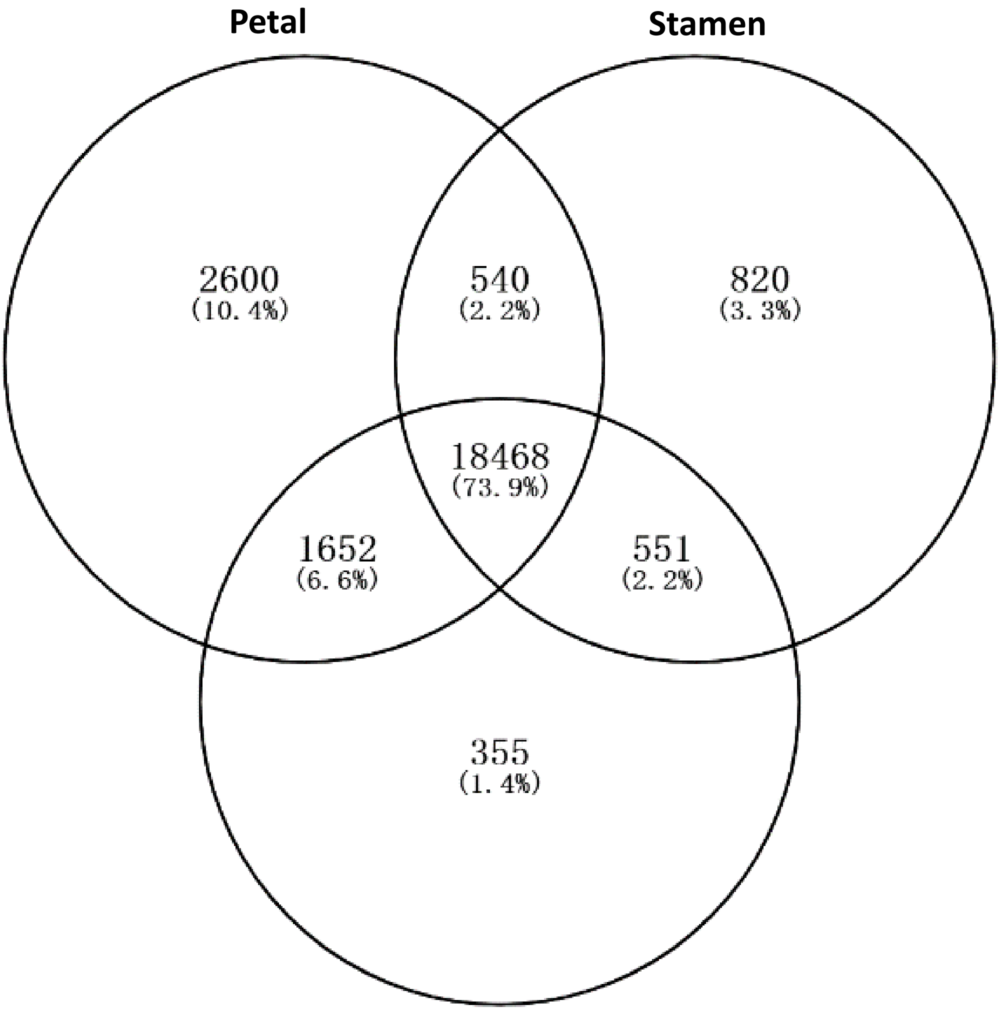


Figure S3. Venn showing the number of expression genes in petal, stamen and receptacle.

Figure S4

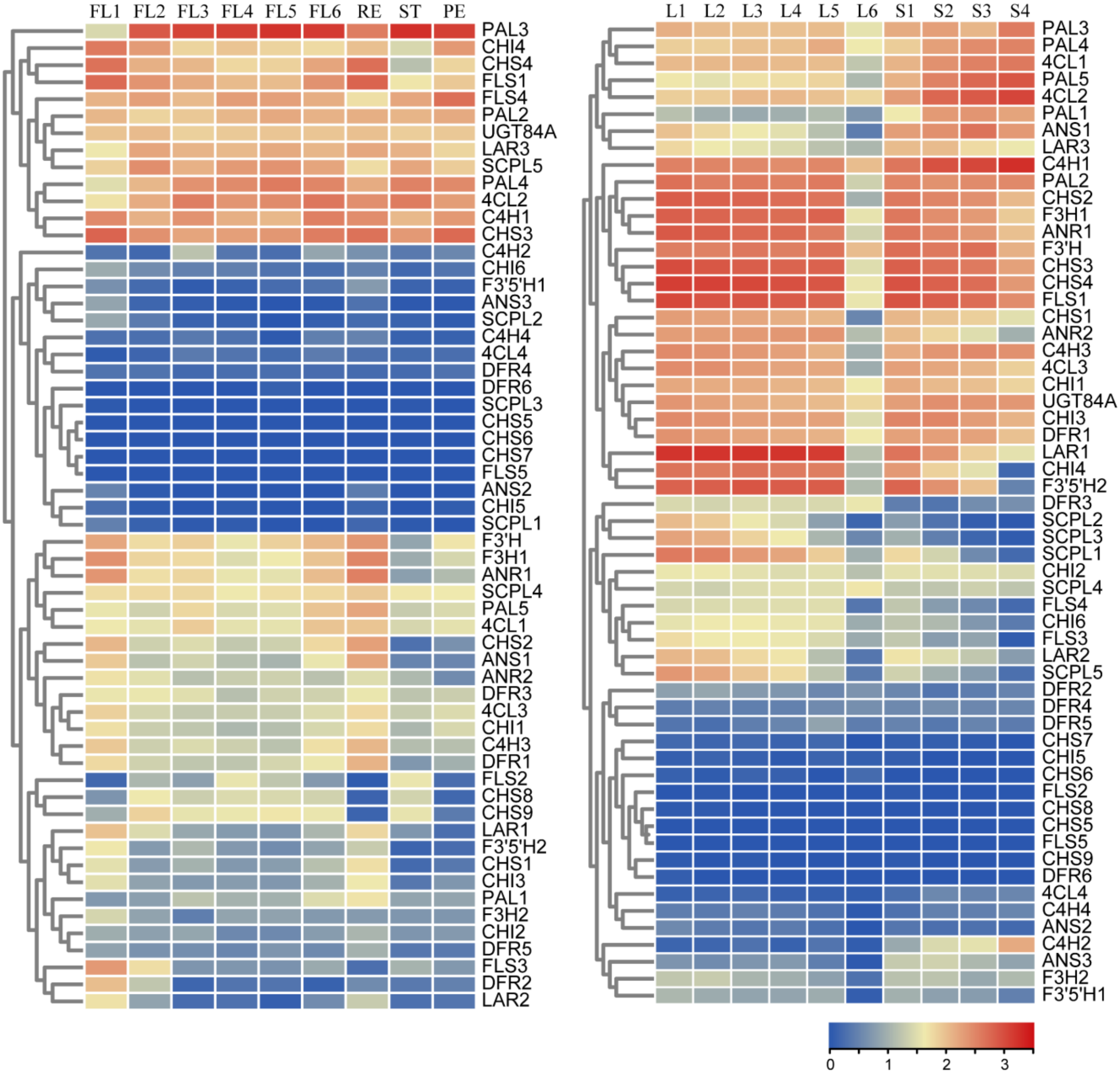
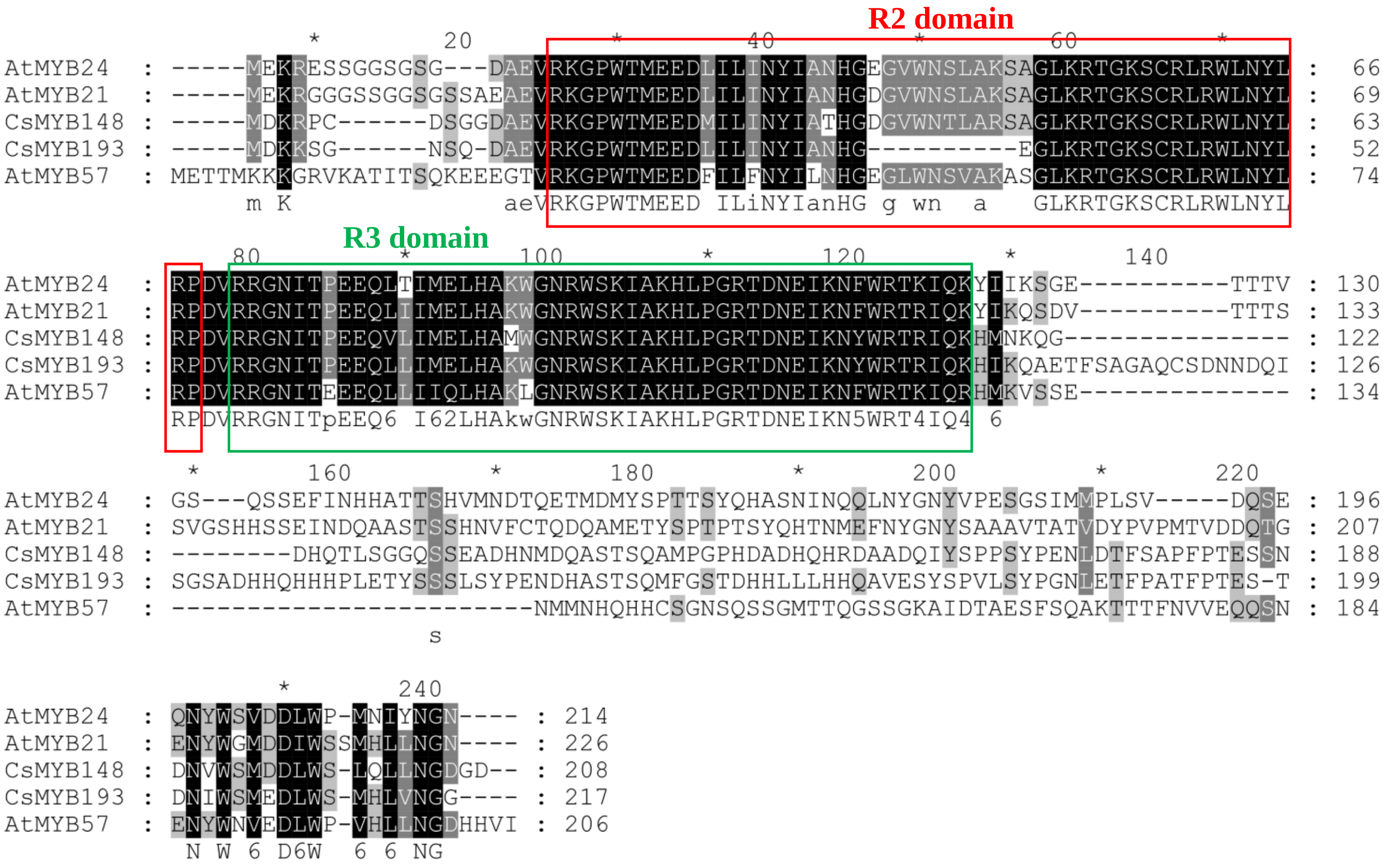


Figure S4. Heat map expression analysis of genes involved in flavonoid biosynthesis in tea flowers and leaves. The expression level (log10(FPKM)) of each gene is shown in the heatmap boxes.

Figure S5



```
                    *          20          *         40          *         60          *
AtMYB24  : -----MEKRESSGGSGSG---DAEVRKGPWTMEEDLILINYIANHGEGVWNSLAKSAGLKRTGKSCRLRWLNYL :  66
AtMYB21  : -----MEKRGGGSSGGSGSSAEAEVRKGPWTMEEDLILINYIANHGDGVWNSLAKSAGLKRTGKSCRLRWLNYL :  69
CsMYB148 : -----MDKRPC------DSGGDAEVRKGPWTMEEDMILINYIATHGDGVWNTLARSAGLKRTGKSCRLRWLNYL :  63
CsMYB193 : -----MDKKSG------NSQ-DAEVRKGPWTMEEDLILINYIANHG----------EGLKRTGKSCRLRWLNYL :  52
AtMYB57  : METTMKKKGRVKATITSQKEEEGTVRKGPWTMEEDFILFNYILNHGEGLWNSVAKASGLKRTGKSCRLRWLNYL :  74
                m K              aeVRKGPWTMEED ILiNYIanHG g wn  a   GLKRTGKSCRLRWLNYL

               80         *       100         *       120         *       140
AtMYB24  : RPDVRRGNITPEEQLTIMELHAKWGNRWSKIAKHLPGRTDNEIKNFWRTKIQKYIIKSGE----------TTTV : 130
AtMYB21  : RPDVRRGNITPEEQLIIMELHAKWGNRWSKIAKHLPGRTDNEIKNFWRTRIQKYIKQSDV----------TTTS : 133
CsMYB148 : RPDVRRGNITPEEQVLIMELHAMWGNRWSKIAKHLPGRTDNEIKNYWRTRIQKHMNKQG--------------- : 122
CsMYB193 : RPDVRRGNITPEEQLLIMELHAKWGNRWSKIAKHLPGRTDNEIKNYWRTRIQKHIKQAETFSAGAQCSDNNDQI : 126
AtMYB57  : RPDVRRGNITEEEQLLIIQLHAKLGNRWSKIAKHLPGRTDNEIKNFWRTKIQRHMKVSSE-------------- : 134
           RPDVRRGNITpEEQ6 I62LHAkwGNRWSKIAKHLPGRTDNEIKN5WRT4IQ4 6

            *       160         *       180         *       200         *       220
AtMYB24  : GS---QSSEFINHHATTSHVMNDTQETMDMYSPTTSYQHASNINQQLNYGNYVPESGSIMMPLSV-----DQSE : 196
AtMYB21  : SVGSHHSSEINDQAASTSSHNVFCTQDQAMETYSPTPTSYQHTNMEFNYGNYSAAAVTATVDYPVPMTVDDQTG : 207
CsMYB148 : --------DHQTLSGGQSSEADHNMDQASTSQAMPGPHDADHQHRDAADQIYSPPSYPENLDTFSAPFPTESSN : 188
CsMYB193 : SGSADHHQHHHPLETYSSSLSYPENDHASTSQMFGSTDHHLLLHHQAVESYSPVLSYPGNLETFPATFPTES-T : 199
AtMYB57  : ------------------------NMMNHQHHCSGNSQSSGMTTQGSSGKAIDTAESFSQAKTTTFNVVEQQSN : 184
                            s

                  *       240
AtMYB24  : QNYWSVDDLWP-MNIYNGN---- : 214
AtMYB21  : ENYWGMDDIWSSMHLLNGN---- : 226
CsMYB148 : DNVWSMDDLWS-LQLLNGDGD-- : 208
CsMYB193 : DNIWSMEDLWS-MHLVNGG---- : 217
AtMYB57  : ENYWNVEDLWP-VHLLNGDHHVI : 206
            N W 6 D6W  6 6 NG
```

Figure S5. Alignment of tea MYB148 and MYB193 and related MYBs involved in regulating the flavonol biosynthesis in flowers. The R2R3 domain of those MYB proteins were remarked by rectangles.

Figure S6

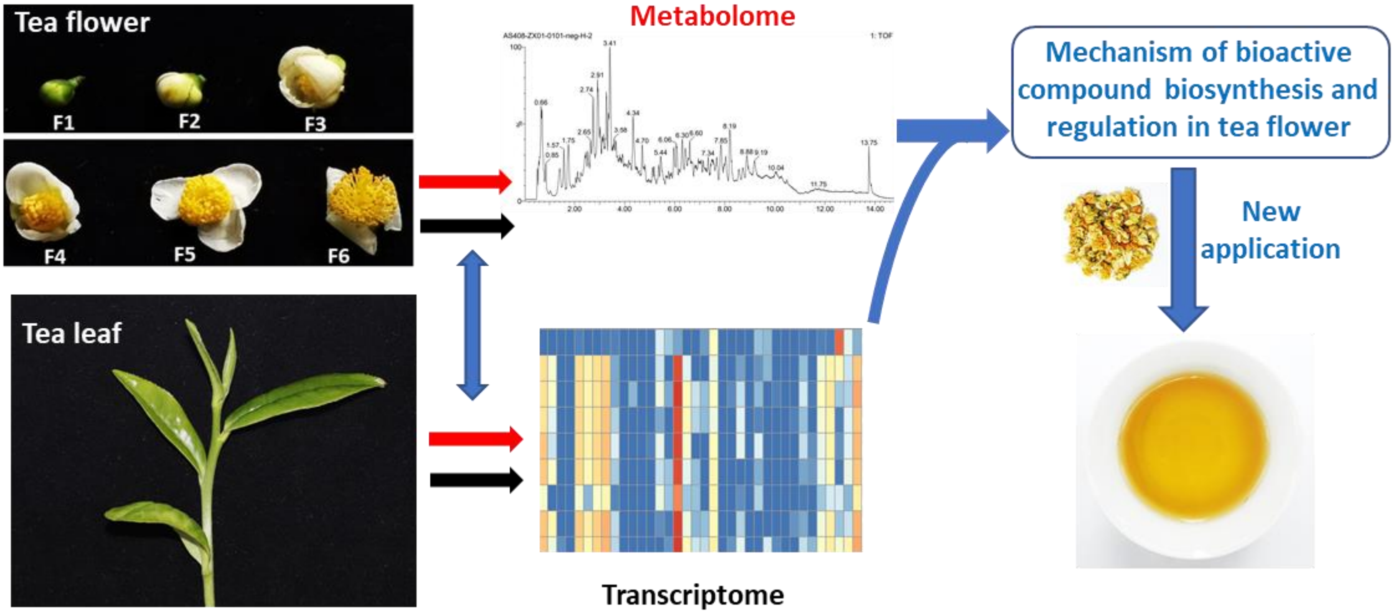


Figure S6. A summary of this study on tea flowers.