Supplementary file 4 SNP and candidate genes significantly associated with flower and leaf traits.

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| Traits | Chr | Position | Allelea | *P* value | R2(%) | Candidate gene | Description |
| APA | Chr 05 | 1332394713323952 | A/CG/C | 1.98×10-7 | 18.71 | DTZ79\_05g05960;DTZ79\_05g05970;DTZ79\_05g05980;DTZ79\_05g05990;DTZ79\_05g06000;DTZ79\_05g06010;DTZ79\_05g06020;DTZ79\_05g06030;DTZ79\_05g06040;DTZ79\_05g06050;DTZ79\_05g06060;DTZ79\_05g06070 | tRNA pseudouridine synthase B;Unknown protein;Genomic DNA, chromosome 3, P1 clone: MMJ24;GHMP kinase ATP-binding protein, putative;Beta-1,4-N-acetylglucosaminyltransferase-like protein;NAC domain protein;NAC domain protein;Kinase family protein;Unknown protein;Ribosomal RNA-processing protein 8;Chalcone-flavonone isomerase family protein;Aldose 1-epimerase, putative |
| APAAPF | Chr 05 | 21860399 | A/T | 1.67×10-72.06×10-7 | 19.4820.54 | DTZ79\_05g11720;DTZ79\_05g11730 | Sieve element occlusion protein;Eukaryotic aspartyl protease family protein |
| PV | Chr 06 | 22519450 | C/T | 8.79×10-7 | 15.32 | DTZ79\_06g14950;DTZ79\_06g14960;DTZ79\_06g14970;DTZ79\_06g14980 | Coffea canephora DH200=94 genomic scaffold, scaffold\_1;Pentatricopeptide repeat-containing protein;Homeobox leucine zipper family protein;Cysteine protease |
| NSF | Chr 13 | 15414747 | T/C | 3.04×10-7 | 20.92 | DTZ79\_13g12560;DTZ79\_13g12570;DTZ79\_13g12580;DTZ79\_13g12590;DTZ79\_13g12600;DTZ79\_13g12610 | Enhanced downy mildew 2, putative;TBC1 domain family member;Unknown protein;Transcription initiation factor TFIID subunit 6;IQ-domain protein;Nuclear ribonuclease Z |
| NPF | Chr 19 | 15281450 | G/T | 6.29×10-8 | 28.19 | DTZ79\_19g06220;DTZ79\_19g06230;DTZ79\_19g06240;DTZ79\_19g06250;DTZ79\_19g06260;DTZ79\_19g06270;DTZ79\_19g06280;DTZ79\_19g06290;DTZ79\_19g06300 | Haloacid dehalogenase-like hydrolase family protein;Unknown protein;Polynucleotidyl transferase, ribonuclease H-like superfamily protein;LOCATED IN: mitochondrion;Importin subunit alpha;Unknown protein;Agenet domain-containing protein, putative;Unknown protein;Neutral/alkaline invertase |
| NPF | Chr 22 | 12323585 | C/T | 7.30×10-8 | 28.82 | DTZ79\_22g04890;DTZ79\_22g04900;DTZ79\_22g04910;DTZ79\_22g04920;DTZ79\_22g04930;DTZ79\_22g04940 | Unknown protein;Nodulin MtN21 /EamA-like transporter family protein;Ras-related protein Rab-8A;Inorganic pyrophosphatase family protein;Coffea canephora DH200=94 genomic scaffold, scaffold\_22;Histone H2A |
| CD | Chr 22 | 21866146 | T/C | 9.72×10-10 | 17.00 | DTZ79\_22g12270;DTZ79\_22g12280;DTZ79\_22g12290;DTZ79\_22g12300;DTZ79\_22g12310;DTZ79\_22g12320;DTZ79\_22g12330;DTZ79\_22g12340;DTZ79\_22g12350;DTZ79\_22g12360 | Coffea canephora DH200=94 genomic scaffold, scaffold\_9;Coffea canephora DH200=94 genomic scaffold, scaffold\_12;Unknown protein;Unknown protein;Unknown protein;Patatin;Chorismate synthase;Unknown protein;Ubiquitin-conjugating enzyme E2;MLO-like protein |
| ACP | Chr 01 | 16955703 | A/G | 9.06×10-8 | 23.74 | DTZ79\_01g09630;DTZ79\_01g09640;DTZ79\_01g09650;DTZ79\_01g09660;DTZ79\_01g09670;DTZ79\_01g09680 | Terpene cyclase/mutase family member;Alkaline alpha-galactosidase seed imbibition protein;Sister chromatid cohesion protein PDS5 like B;Unknown protein;Ribosomal protein S5 family protein;Zinc finger AN1 and C2H2 domain stress-associated protein |
| ACP | Chr 05 | 20301771 | C/T | 1.68×10-7 | 19.53 | DTZ79\_05g10900;DTZ79\_05g10910;DTZ79\_05g10920;DTZ79\_05g10930 | Histone-lysine N-methyltransferase;BEL1-like homeodomain protein 2;5'-3' exonuclease family protein;Flap endonuclease Xni |
| AL | Chr 05 | 19338016 | G/A | 2.57×10-8 | 20.62 | DTZ79\_05g10200;DTZ79\_05g10210;DTZ79\_05g10220;DTZ79\_05g10230 | Heavy metal atpase 1;FAD-dependent oxidoreductase family protein;RP/EB family microtubule-associated protein;Cytochrome P450 |
| AL | Chr 24 | 13872137 | C/T | 2.50×10-9 | 20.25 | DTZ79\_24g08360;DTZ79\_24g08370;DTZ79\_24g08380;DTZ79\_24g08390;DTZ79\_24g08400;DTZ79\_24g08410;DTZ79\_24g08420;DTZ79\_24g08430;DTZ79\_24g08440;DTZ79\_24g08450 | Poly(A) RNA polymerase GLD2-like protein;S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;S-adenosyl-L-methionine-dependent methyltransferases superfamily protein;BTB-POZ and MATH domain protein;Regulator of chromosome condensation (RCC1) family protein;Receptor-like protein kinase;Unknown protein;Eukaryotic translation initiation factor 3 subunit G;Mannose-1-phosphate guanyltransferase, putative;CASP-like protein; |
| TPL | Chr 03 | 19322743 | G/A | 1.81×10-7 | 47.27 | DTZ79\_03g15410;DTZ79\_03g15420 | Nucleolar protein 10;Transcription factor ORG2-like protein |
| TCL | Chr 09 | 4605737 | G/A | 1.04×10-6 | 13.29 | DTZ79\_09g03940;DTZ79\_09g03950;DTZ79\_09g03960;DTZ79\_09g03970;DTZ79\_09g03980;DTZ79\_09g03990;DTZ79\_09g04000;DTZ79\_09g04010;DTZ79\_09g04020;DTZ79\_09g04030;DTZ79\_09g04040;DTZ79\_09g04050;DTZ79\_09g04060 | Zinc finger family protein;Transmembrane and coiled-coil domains protein, putative;Carbon catabolite repressor protein 4 like 2;F-box family protein;Kinase family protein;Thioredoxin;Protein trichome birefringence;Pmr5/Cas1p GDSL/SGNH-like acyl-esterase family protein;Protein trichome birefringence;Homeobox associated leucine zipper protein;Receptor-like kinase;nudix hydrolase homolog 23;Lectin receptor kinase |
| TCL | Chr 12 | 13603928136039501360396313603985 | G/AC/TG/AC/T | 7.90×10-71.04×10-66.64×10-73.04×10-7 | 18.2018.0119.3419.43 | DTZ79\_12g08260;DTZ79\_12g08270;DTZ79\_12g08280;DTZ79\_12g08290 | RING/U-box superfamily protein;Interactor of constitutive active ROPs protein, putative;Coiled-coil domain-containing 94;Gibberellin 2-oxidase 2 |
| TFL | Chr 12 | 16989132 | C/A | 6.05×10-7 | 12.23 | DTZ79\_12g09540;DTZ79\_12g09550;DTZ79\_12g09560;DTZ79\_12g09570;DTZ79\_12g09580;DTZ79\_12g09590 | Coffea canephora DH200=94 genomic scaffold, scaffold\_60;Protein disulfide-isomerase like 2-2;Syntaxin, putative;Syntaxin of plants 122 protein;Isocitrate lyase;Protein yippee-like |
| TFL | Chr 18 | 14479741 | A/G | 5.99×10-7 | 14.45 | DTZ79\_18g06530;DTZ79\_18g06540;DTZ79\_18g06550;DTZ79\_18g06560;DTZ79\_18g06570 | Pentatricopeptide repeat-containing-like protein;WRKY transcription factor;NADH-ubiquinone oxidoreductase-related;UDP-glycosyltransferase;UDP-glycosyltransferase |