

Analysis of Terpene Synthase Family Genes in *Camellia sinensis* with an Emphasis on Abiotic Stress Conditions

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Supplementary Information

Supplementary Table S1 Primer for tea TPS genes analysis

| Gene Name | Primer for qRT-PCR |
|-----------|--|
| CsTPS01 | F:CATCCTACCATTTGGGGAGATCATT R:GCTGATCATTAGCTGCCACTAGCAT |
| CsTPS02 | F:TCACTCGACGCTCAGCCAATTATCA R:TGGATTGCATCGATGAAGTTCAGTT |
| CsTPS03 | F:CACATCTCAGGATGCGAGGAGAAGA R:AATGGATGGGCTGATTCAGAGCATG |
| CsTPS22 | F:AGGAATGCCCAGATTAGAGGCCAGG R:TGGTGCAACCTTTGTAAAAGATTGA |
| CsTPS23 | F:TGAGGTGAGAGGGATGCTACGTGAT R:TCATCATCATCACCACCACCACCAC |
| CsTPS29 | F:CCTACTCGCCACTTGGCCAAATTTC R:CGGCTACCACCATGCTCCTCACTTG |
| CsTPS42 | F:TAGAGAAGCTGGAGGAGCCATTGGA R:GCGCCAATTCATTTTGTGATCAATA |
| CsTPS43 | F:TTCAAGTGAATCCACGACGATCAGC R:ATTCAACTCTTCTAATTTGGTCCCA |
| CsTPS51 | F:CTTTAGGCTCCTCAGGCAGCATGGA R:AGGCTTCAAGAAGCTCAAGCATTGC |
| CsTPS73 | F:TTTCCCCATCTGCCTATGACACTGC R:ACCATCATTGCCAACTTCACCCCAA |
| CsTPS76 | F:TAACGGTTTGATGCCACATCTTTCT R:CCGTGTCTTTCCACCACTTTGATAC |
| CsTPS77 | F:GCAAGAAGGGTACAATGTGCCCGCG R:CTGCGGCTTGATCAAGAATGTCTTC |
| CsTPS78 | F:AGGCATTGATTACCACTTCCGGGAG R:GCACATTGTAGCCTTGTTGCCTCAA |
| CsTPS79 | F:CATGATCGATGCCCTCCAACG R:GTTGCCTCAACAGACGAAAGCGA |

Supplementary Table S2. Identification of tea TPS gene family in CSS genome

| NO. | Name | Gene ID | Location | Protein(aa) | Nucleotide(bp) | Exon | Pfam analysis | SWISS PROT Annotation | TPS sub-family |
|-----|---------|-------------|--------------------------------|-------------|----------------|------|-------------------|--|----------------|
| 1 | CsTPS01 | TEA032539.1 | Scaffold2014:1796883:1802367:- | 567 | 1704 | 7 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 2 | CsTPS02 | TEA029356.1 | Scaffold559:448741:453375:+ | 537 | 1614 | 7 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 3 | CsTPS03 | TEA014184.1 | Scaffold2694:466713:471430:- | 569 | 1710 | 7 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 4 | CsTPS04 | TEA031969.1 | Scaffold982:939616:948654:+ | 1042 | 3129 | 8 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 5 | CsTPS05 | TEA031966.1 | Scaffold982:979330:981825:+ | 441 | 1326 | 5 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 6 | CsTPS06 | TEA025177.1 | Scaffold7725:83168:89037:+ | 624 | 1875 | 9 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 7 | CsTPS07 | TEA010895.1 | Scaffold1955:1632511:1641345:+ | 559 | 1680 | 8 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 8 | CsTPS08 | TEA005128.1 | Scaffold1857:381589:396451:- | 265 | 798 | 4 | PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 9 | CsTPS09 | TEA017888.1 | Scaffold5016:408273:412431:- | 373 | 1122 | 5 | PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 10 | CsTPS10 | TEA032538.1 | Scaffold2014:1849901:1856947:- | 432 | 1299 | 6 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 11 | CsTPS11 | TEA005117.1 | Scaffold1857:396807:397525:- | 195 | 588 | 1 | PF01397 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 12 | CsTPS12 | TEA022784.1 | Scaffold1059:445091:449726:- | 385 | 1158 | 6 | PF01397 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 13 | CsTPS13 | TEA021924.1 | Scaffold1039:738385:745242:+ | 301 | 906 | 6 | PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 14 | CsTPS14 | TEA017878.1 | Scaffold5016:412689:414195:- | 280 | 843 | 3 | PF01397 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 15 | CsTPS15 | TEA002287.1 | Scaffold569:2037188:2039624:+ | 315 | 948 | 4 | PF01397 / PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 16 | CsTPS16 | TEA017309.1 | Scaffold4032:135383:138230:- | 207 | 624 | 3 | PF03936 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 17 | CsTPS17 | TEA033098.1 | Scaffold5126:880963:886581:- | 185 | 558 | 3 | PF01397 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 18 | CsTPS18 | TEA029355.1 | Scaffold559:506685:510183:+ | 207 | 624 | 2 | PF01397 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |
| 19 | CsTPS19 | TEA031961.1 | Scaffold982:978097:979246:+ | 186 | 561 | 2 | PF01397 | TPSGD_VITVI, (-)- germacrene D synthase | TPS-a |

| | | | | | | | | | |
|----|---------|-------------|--------------------------------|-----|------|----|-------------------|--|-------|
| 20 | CsTPS20 | TEA029353.1 | Scaffold559:545565:545945:+ | 126 | 381 | 1 | PF03936 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 21 | CsTPS21 | TEA029348.1 | Scaffold559:382474:391211:+ | 730 | 2193 | 10 | PF01397 / PF03936 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 22 | CsTPS22 | TEA012463.1 | Scaffold1840:218881:222925:- | 547 | 1644 | 7 | PF01397 / PF03936 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 23 | CsTPS23 | TEA023168.1 | Scaffold485:499764:506329:+ | 540 | 1623 | 7 | PF01397 / PF03936 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 24 | CsTPS24 | TEA017886.1 | Scaffold5016:315868:326381:- | 527 | 1584 | 7 | PF01397 / PF03936 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 25 | CsTPS25 | TEA010551.1 | Scaffold1188:1285004:1291162:- | 839 | 2520 | 7 | PF01397 / PF03936 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 26 | CsTPS26 | TEA003774.1 | Scaffold5587:3985:6273:- | 367 | 1104 | 5 | PF03936 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 27 | CsTPS27 | TEA005096.1 | Scaffold1857:406724:409024:- | 131 | 396 | 2 | PF01397 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 28 | CsTPS28 | TEA005082.1 | Scaffold10509:51897:63536:- | 399 | 1356 | 6 | PF01397 / PF03936 | TPSGD_VITVI, (-)-germacrene D synthase | TPS-a |
| 29 | CsTPS29 | TEA024081.1 | Scaffold1689:579330:586136:- | 541 | 1626 | 7 | PF01397 / PF03936 | TPS32_SOLLC, Viridiflorene synthase | TPS-a |
| 30 | CsTPS30 | TEA007878.1 | Scaffold23:868027:874480:+ | 487 | 1464 | 6 | PF01397 / PF03936 | TPS32_SOLLC, Viridiflorene synthase | TPS-a |
| 31 | CsTPS31 | TEA027025.1 | Scaffold228:1416204:1431743:- | 338 | 1017 | 5 | PF01397 | TPS32_SOLLC, Viridiflorene synthase | TPS-a |
| 32 | CsTPS32 | TEA021499.1 | Scaffold626:560395:570357:+ | 435 | 1308 | 7 | PF01397 / PF03936 | TPS32_SOLLC, Viridiflorene synthase | TPS-a |
| 33 | CsTPS33 | TEA010904.1 | Scaffold1955:1784442:1785892:+ | 285 | 855 | 5 | PF01397 / PF03936 | TPSVS_VITVI, Valencene synthase | TPS-a |
| 34 | CsTPS34 | TEA017307.1 | Scaffold4032:138287:144440:- | 223 | 672 | 3 | PF01397 / PF03936 | TPSVS_VITVI, Valencene synthase | TPS-a |
| 35 | CsTPS35 | TEA027070.1 | Scaffold228:1596311:1599132:- | 186 | 561 | 5 | PF01397 | 5EAS4_NICAT, Probable 5-epi-aristolochene synthase 4 | TPS-a |
| 36 | CsTPS36 | TEA027061.1 | Scaffold228:1547137:1548048:- | 174 | 525 | 3 | PF03936 | TPS1_RICCO, Alpha-copaene synthase | TPS-a |
| 37 | CsTPS37 | TEA009449.1 | Scaffold1786:1345647:1360438:- | 595 | 1788 | 7 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 38 | CsTPS38 | TEA023157.1 | Scaffold2616:240593:250372:- | 500 | 1503 | 6 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 39 | CsTPS39 | TEA009450.1 | Scaffold1786:1406070:1450966:- | 236 | 711 | 3 | PF03936 | TPS10_RICCO, Terpene synthase 10 | TPS-b |
| 40 | CsTPS40 | TEA017654.1 | Scaffold285:1744284:1744859:+ | 153 | 462 | 3 | PF01397 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 41 | CsTPS41 | TEA032709.1 | Scaffold1618:391002:404626:+ | 599 | 1800 | 8 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |

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|----|---------|-------------|--------------------------------|-----|------|---|-------------------|---|-------|
| 42 | CsTPS42 | TEA002963.1 | Scaffold2253:770954:781331:+ | 568 | 1707 | 7 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 43 | CsTPS43 | TEA014987.1 | Scaffold5359:390672:398897:+ | 607 | 1824 | 7 | PF01397 / PF03936 | TPS9_RICCO, Probable terpene synthase 9 | TPS-b |
| 44 | CsTPS44 | TEA032731.1 | Scaffold1618:216308:232484:+ | 583 | 1752 | 7 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 45 | CsTPS45 | TEA030379.1 | Scaffold300:536240:539893:- | 473 | 1472 | 6 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 46 | CsTPS46 | TEA020730.1 | Scaffold281:289297:2893962:+ | 243 | 732 | 3 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 47 | CsTPS47 | TEA022294.1 | Scaffold881:746241:773646:- | 547 | 1644 | 9 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 48 | CsTPS48 | TEA014219.1 | Scaffold2428:561525:589292:+ | 558 | 1677 | 8 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 49 | CsTPS49 | TEA023784.1 | Scaffold4432:595162:597357:- | 303 | 912 | 4 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 50 | CsTPS50 | TEA007029.1 | Scaffold4476:460151:468825:- | 390 | 1173 | 5 | PF01397 / PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-b |
| 51 | CsTPS51 | TEA033306.1 | Scaffold596:223621:233875:+ | 528 | 1587 | 7 | PF01397 / PF03936 | TPS7_RICCO, Alpha-farnesene synthase | TPS-b |
| 52 | CsTPS52 | TEA009170.1 | Scaffold1816:859236:866711:+ | 454 | 1365 | 7 | PF01397 / PF03936 | TPS7_RICCO, Alpha-farnesene synthase | TPS-b |
| 53 | CsTPS53 | TEA026271.1 | Scaffold3165:1751525:1755140:- | 334 | 1005 | 5 | PF01397 / PF03936 | TPS7_RICCO, Alpha-farnesene synthase | TPS-b |
| 54 | CsTPS54 | TEA012490.1 | Scaffold6781:57499:58656:- | 188 | 567 | 2 | PF03936 | AFS1_MALDO, (E,E)-alpha-farnesene synthase | TPS-b |
| 55 | CsTPS55 | TEA009866.1 | Scaffold4688:2601:3839:- | 182 | 549 | 2 | PF03936 | AFS1_MALDO, (E,E)-alpha-farnesene synthase | TPS-b |
| 56 | CsTPS56 | TEA004653.1 | Scaffold3940:666045:676363:+ | 136 | 411 | 2 | PF03936 | TPS7_RICCO, Alpha-farnesene synthase | TPS-b |
| 57 | CsTPS57 | TEA004606.1 | Scaffold10585:153621:173467:- | 521 | 1566 | 7 | PF01397 / PF03936 | SAUBS_SANAS, Beta-bisabolene synthase | TPS-b |
| 58 | CsTPS58 | TEA031754.1 | Scaffold2326:935654:955868:+ | 560 | 1683 | 8 | PF01397 / PF03936 | SAUBS_SANAS, Beta-bisabolene synthase | TPS-b |
| 59 | CsTPS59 | TEA026152.1 | Scaffold11662:400841:404486:+ | 188 | 567 | 3 | PF01397 | SAUBS_SANAS, Beta-bisabolene synthase | TPS-b |
| 60 | CsTPS60 | TEA014989.1 | Scaffold5359:1062848:1075257:- | 451 | 1356 | 6 | PF01397 / PF03936 | TPS2_LOTJA, Tricyclene synthase EBOS, chloroplastic | TPS-b |
| 61 | CsTPS61 | TEA014996.1 | Scaffold5359:1134064:1143428:- | 371 | 1116 | 7 | PF01397 / PF03936 | TPS4_MEDTR, Tricyclene synthase TPS4, chloroplastic | TPS-b |
| 62 | CsTPS62 | TEA016812.1 | Scaffold4385:22190:22783:+ | 150 | 477 | 2 | PF03936 | TPS4_MEDTR, Tricyclene synthase TPS4, chloroplastic | TPS-b |
| 63 | CsTPS63 | TEA031457.1 | Scaffold1399:777225:788144:- | 500 | 1500 | 7 | PF01397 / PF03936 | TPS12_RICCO, Probable terpene synthase 12 | TPS-b |

| | | | | | | | | | |
|----|---------|-------------|--------------------------------|-----|------|----|-------------------|--|-------|
| 64 | CsTPS64 | TEA031444.1 | Scaffold1399:767017:769790:- | 430 | 1293 | 6 | PF03936 | ISPS_POPTM, Isoprene synthase, chloroplastic | TPS-b |
| 65 | CsTPS65 | TEA031453.1 | Scaffold1399:675106:678765:- | 398 | 1197 | 6 | PF01397 / PF03936 | ISPS_POPTM, Isoprene synthase, chloroplastic | TPS-b |
| 66 | CsTPS66 | TEA020739.1 | Scaffold281:320490:329627:- | 296 | 891 | 6 | PF01397 / PF03936 | ATESY_MAGGA, Alpha-terpineol synthase, chloroplastic | TPS-b |
| 67 | CsTPS67 | TEA000496.1 | Scaffold682:1760053:1779446:+ | 723 | 2172 | 11 | PF01397 / PF03936 | KSA_PEA, Ent-copalyl diphosphate synthase, chloroplastic | TPS-c |
| 68 | CsTPS68 | TEA024173.1 | Scaffold2697:535837:540208:+ | 274 | 825 | 5 | PF03936 | KSB_ARATH, Ent-kaur-16-ene synthase, chloroplastic | TPS-e |
| 69 | CsTPS69 | TEA017740.1 | Scaffold1561:239440:241090:- | 297 | 894 | 6 | PF01397 / PF03936 | KSB_ARATH, Ent-kaur-16-ene synthase, chloroplastic | TPS-e |
| 70 | CsTPS70 | TEA024176.1 | Scaffold2697:527999:534944:+ | 454 | 1365 | 7 | PF01397 / PF03936 | KSB_CUCMA, Ent-kaur-16-ene synthase, chloroplastic | TPS-e |
| 71 | CsTPS71 | TEA008638.1 | Scaffold217:754423:765133:- | 202 | 609 | 3 | PF03936 | KSB_CUCMA, Ent-kaur-16-ene synthase, chloroplastic | TPS-e |
| 72 | CsTPS72 | TEA007033.1 | Scaffold4476:490748:497232:- | 426 | 1281 | 9 | PF03936 | ATESY_VITVI, (-)-alpha-terpineol synthase | TPS-e |
| 73 | CsTPS73 | TEA019347.1 | Scaffold1889:780853:787842:- | 801 | 2430 | 13 | PF01397 / PF03936 | GES_ARATH, (E,E)-geranylinalool synthase | TPS-f |
| 74 | CsTPS74 | TEA005451.1 | Scaffold1133:280712:284333:- | 565 | 1698 | 9 | PF01397 / PF03936 | GES_ARATH, (E,E)-geranylinalool synthase | TPS-f |
| 75 | CsTPS75 | TEA005162.1 | Scaffold5444:588299:592626:- | 500 | 1503 | 7 | PF03936 | GES_ARATH, (E,E)-geranylinalool synthase | TPS-f |
| 76 | CsTPS76 | TEA007191.1 | Scaffold4183:109141:116548:- | 557 | 1674 | 7 | PF01397 / PF03936 | NES1_FRAAN, (3S,6E)-nerolidol synthase 1 | TPS-g |
| 77 | CsTPS77 | TEA004822.1 | Scaffold1497:1131549:1136588:+ | 557 | 1674 | 7 | PF01397 / PF03936 | NES1_FRAAN, (3S,6E)-nerolidol synthase 1 | TPS-g |
| 78 | CsTPS78 | TEA019472.1 | Scaffold161:572157:579727:+ | 534 | 1605 | 7 | PF01397 / PF03936 | NES1_FRAAN, (3S,6E)-nerolidol synthase 1 | TPS-g |
| 79 | CsTPS79 | TEA004657.1 | Scaffold3940:831501:836109:+ | 598 | 1797 | 7 | PF01397 / PF03936 | TPS13_RICCO, Probable terpene synthase 13 | TPS-g |
| 80 | CsTPS80 | TEA018721.1 | Scaffold3180:769431:773238:- | 450 | 1356 | 7 | PF01397 / PF03936 | TPS13_RICCO, Probable terpene synthase 13 | TPS-g |

Supplementary Table S3. Identification of tea TPS gene family in CSA genome

| CSA | | | | | Blast against CSS | | | | |
|-----|-------------|-----------------------|--|-----------------|-------------------|-----------------------|--------------------|----------------|-----------------------|
| NO. | Gene ID | Predicted protein(aa) | SWISS PROT(HMMER) | Pfam | Gene ID | Predicted protein(aa) | Protein Similarity | CDS similarity | Coverage (nucleotide) |
| 1 | CSA000384.1 | 433 | LINS_ARATH S-(+)-linalool synthase, chloroplastic | PF03936 | TEA004657.1 | 598 | 99% | 99% | 100% |
| 2 | CSA012738.1 | 103 | TPSGD_VITVI, (-)-germacrene D synthase | PF01397 | TEA029355.1 | 207 | 100% | 100% | 91% |
| 3 | CSA009231.1 | 213 | TPSGD_VITVI, (-)-germacrene D synthase | PF01397 | TEA032539.1 | 567 | 99% | 99% | 99% |
| 4* | CSA006772.1 | 544 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936/PF01397 | TEA014184.1 | 569 | 99% | 99% | 93% |
| 5 | CSA019627.1 | 166 | RLC1_CITSI, (R)-limonene synthase 1, chloroplastic | PF01397 | TEA023157.1 | 500 | 98% | 98% | 100% |
| 6 | CSA025505.1 | 250 | VTSS2_HYOMU, Vetispiradiene synthase 2 (Fragment) | PF03936 | TEA024081.1 | 541 | 99% | 99% | 100% |
| 7 | CSA035357.1 | 147 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936 | TEA010904.1 | 284 | 99% | 99% | 100% |
| 8 | CSA018887.1 | 185 | TPS10_RICCO, Terpene synthase 10 | PF03936 | TEA020730.1 | 243 | 99% | 99% | 96% |
| 9 | CSA019813.1 | 151 | TPS12_RICCO, Probable terpene synthase 12 | PF03936 | TEA014989.1 | 451 | 99% | 99% | 92% |
| 10 | CSA009230.1 | 166 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936 | TEA032539.1 | 567 | 98% | 98% | 100% |
| 11 | CSA022343.1 | 413 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF03936/PF01397 | TEA009449.1 | 595 | 98% | 98% | 100% |
| 12 | CSA026804.1 | 519 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936/PF01397 | TEA012463.1 | 547 | 98% | 98% | 100% |
| 13 | CSA016735.1 | 482 | TPS13_RICCO, Probable terpene synthase 13 | PF03936/PF01397 | TEA004657.1 | 598 | 98% | 98% | 100% |
| 14 | CSA018886.1 | 96 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA032731.1 | 583 | 98% | 98% | 96% |
| 15 | CSA019812.1 | 130 | ATESY_MAGGA, Alpha-terpineol synthase, chloroplastic | PF01397 | TEA014996.1 | 371 | 98% | 98% | 92% |
| 16 | CSA005676.1 | 101 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936 | TEA031966.1 | 441 | 96% | 96% | 96% |
| 17 | CSA026262.1 | 84 | LABER_LAVAN, Exo-alpha-bergamotene synthase | PF01397 | TEA007033.1 | 426 | 96% | 96% | 98% |
| 18 | CSA025571.1 | 213 | TPSGD_VITVI, (-)-germacrene D synthase | PF01397 | TEA029348.1 | 730 | 95% | 95% | 99% |
| 19 | CSA025572.1 | 169 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936 | TEA029356.1 | 537 | 96% | 96% | 97% |
| 20 | CSA014761.1 | 63 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA030379.1 | 473 | 93% | 93% | 100% |
| 21 | CSA020011.1 | 281 | TPS9_RICCO, Probable terpene synthase 9 | PF03936/PF01397 | TEA014987.1 | 607 | 99% | 99% | 97% |
| 22 | CSA018130.1 | 75 | ISPS_POPCN, Isoprene synthase, chloroplastic | PF01397 | TEA014989.1 | 451 | 98% | 98% | 90% |
| 23 | CSA029044.1 | 238 | NES1_FRAAN, (3S,6E)-nerolidol synthase 1 | PF01397 | TEA019472.1 | 534 | 95% | 95% | 91% |
| 24 | CSA034089.1 | 411 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936/PF01397 | TEA029356.1 | 537 | 95% | 95% | 94% |
| 25 | CSA025246.1 | 127 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA030379.1 | 473 | 95% | 95% | 91% |
| 26 | CSA005369.1 | 335 | NES1_FRAAN, (3S,6E)-nerolidol synthase | PF01397 | TEA004822.1 | 557 | 98% | 98% | 90% |
| 27 | CSA008212.1 | 600 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF03936/PF01397 | TEA030379.1 | 473 | 95% | 95% | 99% |
| 28 | CSA005041.1 | 114 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA017654.1 | 153 | 97% | 97% | 93% |
| 29 | CSA001660.1 | 366 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF03936 | TEA009449.1 | 595 | 84% | 84% | 100% |
| 30 | CSA001659.1 | 63 | LABER_LAVAN, Exo-alpha-bergamotene synthase | PF01397 | TEA030379.1 | 473 | 99% | 99% | 88% |
| 31 | CSA003199.1 | 145 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA030379.1 | 473 | 98% | 98% | 88% |

| | | | | | | | | | | |
|---------|-------------|-----|---|-----------------|-------------|-----|------|------|-----|-----|
| 32 | CSA033064.1 | 145 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA030379.1 | 473 | 98% | 98% | 88% | |
| 33 | CSA032703.1 | 157 | NES2_FRAAN, (3S,6E)-nerolidol synthase 2 | PF03936 | TEA007191.1 | 557 | 83% | 83% | 87% | |
| 34 | CSA032320.1 | 140 | TPS10_RICCO, Terpene synthase 10 | PF01397 | TEA017654.1 | 153 | 93% | 93% | 86% | |
| 35 | CSA003009.1 | 223 | NES1_FRAAN, (3S,6E)-nerolidol synthase | PF03936 | TEA004657.1 | 598 | 91% | 91% | 85% | |
| 36 | CSA014760.1 | 66 | LABER_LAVAN, Exo-alpha-bergamotene synthase | PF01397 | TEA030379.1 | 473 | 99% | 99% | 84% | |
| 37 | CSA032393.1 | 173 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA007033.1 | 426 | 98% | 98% | 84% | |
| 38 | CSA005131.1 | 165 | TPSGD_VITVI, (-)-germacrene D synthase | PF01397 | TEA032539.1 | 567 | 92% | 92% | 83% | |
| 39 | CSA018895.1 | 296 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936 | TEA029348.1 | 730 | 97% | 97% | 83% | |
| 40 | CSA020936.1 | 502 | NES1_FRAAN, (3S,6E)-nerolidol synthase 1 | PF03936/PF01397 | TEA019472.1 | 534 | 99% | 99% | 83% | |
| 41 | CSA005675.1 | 299 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936 | TEA017888.1 | 373 | 99% | 99% | 82% | |
| 42 | CSA033119.1 | 294 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA030379.1 | 473 | 77% | 77% | 82% | |
| 43 | CSA003008.1 | 229 | NES1_FRAAN, (3S,6E)-nerolidol synthase | PF01397 | TEA004657.1 | 598 | 99% | 99% | 80% | |
| 44 | CSA012357.1 | 256 | NES1_FRAAN, (3S,6E)-nerolidol synthase 1 | PF03936 | TEA004657.1 | 598 | 98% | 98% | 78% | |
| 45 | CSA030979.1 | 316 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF03936 | TEA007029.1 | 390 | 91% | 91% | 77% | |
| 46 | CSA003485.1 | 99 | SPIBS_SANSP, Alpha-bisabolol synthase | PF01397 | TEA007033.1 | 426 | 97% | 97% | 76% | |
| 47 | CSA029126.1 | 80 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA002963.1 | 568 | 95% | 95% | 76% | |
| 48 | CSA022871.1 | 108 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA030379.1 | 473 | 92% | 92% | 75% | |
| 49 | CSA014975.1 | 116 | LABER_LAVAN, Exo-alpha-bergamotene synthase | PF01397 | TEA007033.1 | 426 | 96% | 96% | 73% | |
| 50 | CSA019490.1 | 808 | NES1_FRAVE, (3S,6E)-nerolidol synthase 1, chloroplastic | PF03936/PF01397 | TEA004657.1 | 598 | 96% | 96% | 69% | |
| 51 | CSA019811.1 | 98 | ISPS_POPTM, Isoprene synthase, chloroplastic | PF01397 | TEA014989.1 | 451 | 100% | 100% | 69% | |
| 52 | CSA004219.1 | 262 | TPSGD_VITVI, (-)-germacrene D synthase | PF01397 | TEA022784.1 | 385 | 100% | 100% | 68% | |
| 53 | CSA036842.1 | 843 | KSA_PEA, Ent-copalyl diphosphate synthase | PF03936/PF01397 | TEA000496.1 | 723 | 99% | 99% | 66% | |
| 54 | CSA036823.1 | 513 | LIS_CLABR, S-linalool synthase | PF03936 | TEA005451.1 | 565 | 82% | 82% | 64% | |
| 55 | CSA018888.1 | 169 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF03936 | TEA023784.1 | 303 | 98% | 98% | 59% | |
| 56 | CSA022342.1 | 164 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA009449.1 | 595 | 100% | 100% | 54% | |
| 57 | CSA030850.1 | 138 | ATESY_VITVI, (-)-alpha-terpineol synthase | PF01397 | TEA007033.1 | 426 | 94% | 94% | 52% | |
| 58 | CSA029009.1 | 209 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936 | TEA014184.1 | 569 | 98% | 98% | 49% | |
| 59 | CSA011050.1 | 202 | TPS10_RICCO, Terpene synthase 10 | PF01397 | TEA014219.1 | 558 | 99% | 99% | 48% | |
| 60 | CSA004334.1 | 287 | TPSGD_VITVI, (-)-germacrene D synthase | PF03936/PF01397 | TEA021924.1 | 301 | 93% | 93% | 26% | |
| Average | | | | | | | | 96% | 96% | 84% |

*, the highlighted eight TPS genes from both "Yunkang10" and "Shu-Cha-Zao" share similar protein sequence length (90-110%), high identity at both cDNA and protein levels (>90%).

Supplementary Table S4. Identification of putative functional tea TPS gene

| Identified in genome | | | | | | | Verified in the full-length transcripts | | | |
|----------------------|-------------|-------------|-------|-------|---------|-------|---|-------------------|-----------------------------------|------------|
| Name | Gene ID | Protein(aa) | exons | DDXXD | NSE/DTE | RRX8W | Transcripts ID | coverage/identity | Reference | Annotation |
| CsTPS01 | TEA032539.1 | 567 | 7 | YES | YES | YES | CssPBTTrans029702/PB.8683.1 | 1702/1704 (99%) | Xia et al.,2019/ Qiao et al.,2019 | full |
| CsTPS02 | TEA029356.1 | 537 | 7 | YES | YES | YES | CssPBTTrans041118/PB.24310.30 | 1462/1480 (99%) | Xia et al.,2019/ Qiao et al.,2019 | full |
| CsTPS03 | TEA014184.1 | 569 | 7 | YES | YES | NO | CssPBTTrans068400/PB.13101.1 | 1592/1593(99%) | Xia et al.,2019/ Qiao et al.,2019 | full |
| CsTPS04 | TEA031969.1 | 1042 | 8 | YES | YES | YES | PB.31351.2 | 1653/1682(98%) | Qiao et al.,2019 | full |
| CsTPS05 | TEA031966.1 | 441 | 5 | NO | NO | NO | PB.31351.8 | 1281/1306(98%) | Qiao et al.,2019 | full |
| CsTPS21 | TEA029348.1 | 730 | 10 | YES | YES | YES | CssPBTTrans020115 | 1645/1648 (99%) | Xia et al.,2019 | full |
| CsTPS22 | TEA012463.1 | 547 | 7 | YES | YES | NO | PB.22660.1 | 1535/1571(98%) | Qiao et al.,2019 | full |
| CsTPS23 | TEA023168.1 | 540 | 7 | YES | YES | YES | CssPBTTrans024950 | 1649/1649(100%) | Xia et al.,2019 | full |
| CsTPS25 | TEA010551.1 | 839 | 7 | YES | YES | NO | CssPBTTrans026737/PB.1889.1 | 1369/1397 (98%) | Xia et al.,2019/ Qiao et al.,2019 | full |
| CsTPS29 | TEA024081.1 | 541 | 7 | YES | NO | NO | No hits found | | | full |
| CsTPS42 | TEA002963.1 | 568 | 7 | YES | YES | YES | CssPBTTrans058925 | 1704/1707 (99%) | Xia et al.,2019 | full |
| CsTPS43 | TEA014987.1 | 607 | 7 | YES | YES | YES | No hits found | | | full |
| CsTPS45 | TEA030379.1 | 473 | 6 | YES | NO | YES | CssPBTTrans048789 | 1098/1123 (98%) | Xia et al.,2019 | full |
| CsTPS47 | TEA022294.1 | 547 | 8 | NO | YES | NO | PB.21690.2 | 1004/1007(99%) | Qiao et al.,2019 | full |
| CsTPS51 | TEA033306.1 | 528 | 7 | YES | YES | NO | PB.25018.1 | 1251/1265(99%) | Qiao et al.,2019 | full |
| CsTPS57 | TEA004606.1 | 521 | 7 | YES | YES | NO | CssPBTTrans046146/PB.522.1 | 1517/1536 (99%) | Xia et al.,2019/ Qiao et al.,2019 | full |
| CsTPS63 | TEA031457.1 | 500 | 7 | YES | YES | NO | PB.3574.1 | 1494/1503(99%) | Qiao et al.,2019 | full |
| CsTPS70 | TEA024176.1 | 454 | 7 | YES | NO | NO | CssPBTTrans055745 | 1290/1308(98%) | Xia et al.,2019 | full |
| CsTPS73 | TEA019347.1 | 801 | 13 | YES | NO | NO | No hits found | | | full |
| CsTPS76 | TEA007191.1 | 557 | 7 | YES | YES | NO | PB.20489.1 | 1517/1530 (99%) | Qiao et al.,2019 | full |
| CsTPS77 | TEA004822.1 | 557 | 7 | YES | YES | NO | PB.4391.1 | 1528/1530 (99%) | Qiao et al.,2019 | full |
| CsTPS78 | TEA019472.1 | 534 | 7 | YES | YES | NO | PB.5304.3 | 1538/1546(99%) | Qiao et al.,2019 | full |
| CsTPS79 | TEA004657.1 | 598 | 7 | YES | YES | NO | PB.19331.4 | 1516/1547 (98%) | Qiao et al.,2019 | full |

| Identified in genome | | | | | | | Verified in the full-length transcripts | | | |
|----------------------|-------------|-------------|-------|-------|---------|-------|---|-------------------|-----------------------------------|------------|
| Name | Gene ID | Protein(aa) | exons | DDXXD | NSE/DTE | RRX8W | Transcripts ID | coverage/identity | Reference | Annotation |
| CsTPS06 | TEA025177.1 | 624 | 9 | YES | YES | YES | CssPBTTrans041118/PB.31351.8 | 1077/1145 (94%) | Xia et al.,2019/ Qiao et al.,2019 | full? |
| CsTPS07 | TEA010895.1 | 559 | 8 | YES | YES | NO | CssPBTTrans041118/PB.24310.21 | 1287/1361 (95%) | Xia et al.,2019/ Qiao et al.,2019 | full? |
| CsTPS24 | TEA017886.1 | 527 | 7 | YES | YES | NO | CssPBTTrans024950/PB.22660.1 | 1180/1230 (95%) | Xia et al.,2019/ Qiao et al.,2019 | full? |
| CsTPS37 | TEA009449.1 | 595 | 7 | YES | YES | NO | CssPBTTrans048789 | 1328/1555 (85%) | Xia et al.,2019 | full? |
| CsTPS41 | TEA032709.1 | 599 | 8 | YES | YES | YES | CssPBTTrans058925 | 639/648 (99%) | Xia et al.,2019 | full? |
| CsTPS44 | TEA032731.1 | 583 | 7 | YES | NO | NO | CssPBTTrans058925 | 639/648 (99%) | Xia et al.,2019 | full? |

| | | | | | | | | | | |
|---------|-------------|-----|----|-----|-----|----|------------------------------|---------------|-----------------------------------|-------|
| CsTPS48 | TEA014219.1 | 558 | 8 | NO | YES | NO | PB.21690.2 | 585/599(98%) | Qiao et al.,2019 | full? |
| CsTPS58 | TEA031754.1 | 560 | 8 | YES | YES | NO | CssPBTTrans026173/PB.522.2 | 850/851 (99%) | Xia et al.,2019/ Qiao et al.,2019 | full? |
| CsTPS67 | TEA000496.1 | 723 | 11 | NO | NO | NO | CssPBTTrans065569/PB.30438.1 | 482/485 (99%) | Xia et al.,2019/ Qiao et al.,2019 | full? |

| Identified in genome | | | | Verified in the full-length transcripts | | | | | | | |
|----------------------|--|--|--|---|--|--|--|--|--|--|--|
|----------------------|--|--|--|---|--|--|--|--|--|--|--|

| Name | Gene ID | Protein(aa) | exons | DDXXD | NSE/DTE | RRX8W | Transcripts ID | coverage/identity | Reference | Annotation |
|---------|-------------|-------------|-------|-------|---------|-------|-------------------------------|-------------------|-----------------------------------|------------|
| CsTPS08 | TEA005128.1 | 265 | 4 | NO | NO | NO | CssPBTTrans029702/PB.24310.11 | 769/798 (96%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS09 | TEA017888.1 | 373 | 5 | NO | NO | NO | CssPBTTrans029702/PB.31351.8 | 683/741 (92%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS10 | TEA032538.1 | 432 | 6 | YES | NO | NO | CssPBTTrans057668/PB.24310.16 | 727/767 (95%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS11 | TEA005117.1 | 195 | 1 | NO | NO | NO | CssPBTTrans057668/PB.24310.21 | 353/355 (99%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS12 | TEA022784.1 | 385 | 6 | NO | NO | NO | CssPBTTrans033837/PB.13101.1 | 560/584 (96%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS13 | TEA021924.1 | 301 | 6 | NO | YES | NO | CssPBTTrans029702 | 280/313 (89%) | Xia et al.,2019 | partial |
| CsTPS14 | TEA017878.1 | 280 | 3 | NO | NO | YES | CssPBTTrans078631/PB.8683.4 | 367/378 (97%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS15 | TEA002287.1 | 315 | 4 | YES | NO | YES | CssPBTTrans049906/PB.24310.23 | 390/404 (97%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS16 | TEA017309.1 | 207 | 3 | NO | NO | NO | CssPBTTrans046143/PB.31351.8 | 523/601 (87%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS17 | TEA033098.1 | 185 | 3 | NO | NO | NO | CssPBTTrans070005/PB.18777.3 | 82/83 (99%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS18 | TEA029355.1 | 207 | 2 | NO | NO | NO | CssPBTTrans072461 | 273/286 (95%) | Xia et al.,2019 | partial |
| CsTPS19 | TEA031961.1 | 186 | 2 | NO | NO | YES | CssPBTTrans036197/PB.31351.2 | 402/434 (93%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS20 | TEA029353.1 | 126 | 1 | NO | NO | NO | CssPBTTrans072461/PB.24310.26 | 359/378 (95%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS26 | TEA003774.1 | 367 | 5 | YES | NO | NO | CssPBTTrans024950/PB.22660.1 | 797/817 (98%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS27 | TEA005096.1 | 131 | 2 | NO | NO | NO | CssPBTTrans026737/PB.22660.1 | 191/199 (96%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS28 | TEA005082.1 | 399 | 6 | NO | NO | NO | CssPBTTrans032981/PB.31165.4 | 643/677 (95%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS30 | TEA007878.1 | 487 | 6 | NO | NO | NO | CssPBTTrans032981 | 1081/1136 (95%) | Xia et al.,2019 | partial |
| CsTPS31 | TEA027025.1 | 338 | 5 | NO | NO | YES | CssPBTTrans024114/PB.24110.1 | 616/647 (95%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS32 | TEA021499.1 | 435 | 7 | NO | NO | YES | CssPBTTrans032981 | 396/398 (99%) | Xia et al.,2019 | partial |
| CsTPS33 | TEA010904.1 | 285 | 5 | YES | NO | NO | CssPBTTrans057668/PB.31351.9 | 309/322 (96%) | Xia et al.,2019/ Qiao et al.,2019 | partial |

| | | | | | | | | | | |
|---------|-------------|-----|---|-----|-----|-----|------------------------------|-----------------|-----------------------------------|---------|
| CsTPS34 | TEA017307.1 | 223 | 3 | YES | NO | NO | CssPBTrans072461/PB.24310.26 | 313/329 (95%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS35 | TEA027070.1 | 186 | 5 | NO | NO | NO | CssPBTrans024114 | 361/380 (95%) | Xia et al.,2019 | partial |
| CsTPS36 | TEA027061.1 | 174 | 3 | NO | NO | NO | CssPBTrans032981/PB.4785.11 | 225/230 (98%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS38 | TEA023157.1 | 500 | 6 | YES | NO | YES | No hits found | | | partial |
| CsTPS39 | TEA009450.1 | 236 | 3 | NO | YES | YES | CssPBTrans058925 | 534/572 (93%) | Xia et al.,2019 | partial |
| CsTPS40 | TEA017654.1 | 153 | 3 | NO | NO | YES | CssPBTrans058211 | 266/319 (83%) | Xia et al.,2019 | partial |
| CsTPS46 | TEA020730.1 | 243 | 3 | YES | NO | NO | CssPBTrans048789/PB.21573.8 | 697/716 (97%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS49 | TEA023784.1 | 303 | 4 | YES | NO | NO | CssPBTrans052197/PB.21573.5 | 345/359 (96%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS50 | TEA007029.1 | 390 | 5 | NO | YES | NO | CssPBTrans035865/PB.22991.1 | 138/148 (93%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS52 | TEA009170.1 | 454 | 7 | YES | NO | YES | PB.25018.1 | 1326/1346 (98%) | Qiao et al.,2019 | partial |
| CsTPS53 | TEA026271.1 | 334 | 5 | YES | NO | NO | PB.25018.1 | 947/963 (98%) | Qiao et al.,2019 | partial |
| CsTPS54 | TEA012490.1 | 188 | 2 | NO | YES | NO | PB.7071.2 | 548/550 (99%) | Qiao et al.,2019 | partial |
| CsTPS55 | TEA009866.1 | 182 | 2 | NO | YES | NO | PB.7071.1 | 99/100 (99%) | Qiao et al.,2019 | partial |
| CsTPS56 | TEA004653.1 | 136 | 2 | NO | YES | NO | PB.7071.1 | 262/262 (100%) | Qiao et al.,2019 | partial |
| CsTPS59 | TEA026152.1 | 188 | 3 | NO | NO | NO | CssPBTrans072185/PB.1592.8 | 595/609 (98%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS60 | TEA014989.1 | 451 | 6 | YES | NO | NO | CssPBTrans026167/PB.23856.1 | 351/362 (97%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS61 | TEA014996.1 | 371 | 7 | YES | NO | NO | CssPBTrans026167 | 351/362 (97%) | Xia et al.,2019 | partial |
| CsTPS62 | TEA016812.1 | 150 | 2 | NO | YES | NO | PB.3574.1 | 349/360 (96%) | Qiao et al.,2019 | partial |
| CsTPS64 | TEA031444.1 | 430 | 6 | YES | NO | NO | PB.3574.1 | 475/505 (90%) | Qiao et al.,2019 | partial |
| CsTPS65 | TEA031453.1 | 398 | 6 | YES | NO | NO | No hits found | | | partial |
| CsTPS66 | TEA020739.1 | 296 | 6 | YES | NO | NO | CssPBTrans026167/PB.13892.1 | 322/333 (97%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS68 | TEA024173.1 | 274 | 5 | NO | NO | NO | CssPBTrans038300/PB.13128.1 | 275/294 (94%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS69 | TEA017740.1 | 297 | 6 | YES | NO | NO | CssPBTrans056949/PB.13127.2 | 699/704 (99%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS71 | TEA008638.1 | 202 | 3 | NO | NO | NO | CssPBTrans022223/PB.13127.7 | 419/425 (99%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS72 | TEA007033.1 | 426 | 9 | NO | NO | NO | No hits found | | | partial |
| CsTPS74 | TEA005451.1 | 565 | 9 | NO | YES | NO | CssPBTrans050478/PB.24009.1 | 1646/1689 (97%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS75 | TEA005162.1 | 500 | 7 | YES | YES | NO | CssPBTrans050478/PB.24009.1 | 726/736 (99%) | Xia et al.,2019/ Qiao et al.,2019 | partial |
| CsTPS80 | TEA018721.1 | 450 | 7 | NO | YES | NO | CssPBTrans038907/PB.19331.5 | 628/647 (97%) | Xia et al.,2019/ Qiao et al.,2019 | partial |

Supplementary Table S5 Identification of transposable elements in tea TPS genes

| Name | gene ID | Gene location | Transposon ID | Location | Class | Number |
|----------|--------------------------------|--------------------------------|---------------|--------------------------------|-------------------|--------|
| CsTPS10 | TEA032538.1 | Scaffold2014:1849901:1856947:- | TE311378 | Scaffold2014:1853913:1854085:- | LINE/L1 | 1 |
| CsTPS13 | TEA021924.1 | Scaffold1039:738385:745242:+ | TE164009 | Scaffold1039:744626:744733:+ | LTR/Copia | 1 |
| CsTPS24 | TEA017886.1 | Scaffold5016:315868:326381:- | TE546805 | Scaffold5016:318934:319633:- | LTR/Copia | 1 |
| CsTPS28 | TEA005082.1 | Scaffold10509:51897:63536:- | TE625680 | Scaffold10509:62665:63201:- | LTR/Copia | 1 |
| CsTPS35 | TEA027070.1 | Scaffold228:1596311:1599132:- | TE529858 | Scaffold228:1597128:1597212:- | DNA/hAT | 1 |
| CsTPS37 | TEA009449.1 | Scaffold1786:1345647:1360438:- | TE273709 | Scaffold1786:1354512:1355716:- | LINE/L1 | 4 |
| | | | TE273710 | Scaffold1786:1355117:1355781:- | LINE/L1 | |
| | | | TE273711 | Scaffold1786:1355956:1356223:- | LINE/L1 | |
| | | | TE273712 | Scaffold1786:1358305:1358729:- | LINE/L1 | |
| CsTPS39 | TEA009450.1 | Scaffold1786:1406070:1450966:- | TE273720 | Scaffold1786:1407859:1410112:- | LTR/Copia | 11 |
| | | | TE273721 | Scaffold1786:1400171:1412454:- | LTR/Copia | |
| | | | TE273722 | Scaffold1786:1405810:1426929:- | LTR/Gypsy | |
| | | | TE273723 | Scaffold1786:1407158:1428929:- | LTR/Gypsy | |
| | | | TE273724 | Scaffold1786:1401045:1441905:- | LTR/Gypsy | |
| | | | TE273725 | Scaffold1786:1401897:1442588:- | LTR/Gypsy | |
| | | | TE273726 | Scaffold1786:1402899:1443119:- | LTR/Gypsy | |
| | | | TE273727 | Scaffold1786:1403567:1444499:- | LTR/Gypsy | |
| | | | TE273728 | Scaffold1786:1404517:1444957:- | LTR/Gypsy | |
| | | | TE273729 | Scaffold1786:1405238:1445603:- | LTR/Gypsy | |
| TE273730 | Scaffold1786:1407440:1447470:- | LTR/Gypsy | | | | |
| CsTPS41 | TEA032709.1 | Scaffold1618:391002:404626:+ | TE250880 | Scaffold1618:395563:398333:+ | LTR/Copia | 1 |
| CsTPS44 | TEA032731.1 | Scaffold1618:216308:232484:+ | TE250838 | Scaffold1618:220936:221017:+ | LTR/Copia | 5 |
| | | | TE250839 | Scaffold1618:221146:222249:+ | LTR/Copia | |
| | | | TE250840 | Scaffold1618:222352:222567:+ | LTR/Copia | |
| | | | TE250841 | Scaffold1618:222394:222565:+ | LTR/Copia | |
| | | | TE250842 | Scaffold1618:222593:224090:+ | LTR/Copia | |
| CsTPS48 | TEA014219.1 | Scaffold2428:561525:589292:+ | TE359549 | Scaffold2428:577278:577358:+ | LTR/Copia | 4 |
| | | | TE359550 | Scaffold2428:577884:577986:+ | LTR/Copia | |
| | | | TE359551 | Scaffold2428:578397:579225:+ | LTR/Copia | |
| | | | TE359552 | Scaffold2428:579654:581275:+ | LTR/Copia | |
| CsTPS50 | TEA007029.1 | Scaffold4476:460151:468825:- | TE522179 | Scaffold4476:466233:466387:- | LTR/Gypsy | 1 |
| CsTPS53 | TEA026271.1 | Scaffold3165:1751525:1755140:- | TE429535 | Scaffold3165:1754459:1754549:- | DNA/PIF-Harbinger | 1 |
| CsTPS57 | TEA004606.1 | Scaffold10585:153621:173467:- | TE626080 | Scaffold10585:157007:157243:- | LINE/L1 | 1 |
| CsTPS58 | TEA031754.1 | Scaffold2326:935654:955868:+ | TE348377 | Scaffold2326:951961:952698:+ | LINE/L1 | 2 |
| | | | TE348378 | Scaffold2326:953063:953147:+ | LINE/L1 | |
| CsTPS60 | TEA014989.1 | Scaffold5359:1062848:1075257:- | TE554481 | Scaffold5359:1063890:1065716:- | LTR/Copia | 4 |
| | | | TE554482 | Scaffold5359:1066183:1066496:- | LTR/Copia | |
| | | | TE554483 | Scaffold5359:1066771:1066902:- | LTR/Copia | |
| | | | TE554484 | Scaffold5359:1067345:1067448:- | LTR/Copia | |
| CsTPS63 | TEA031457.1 | Scaffold1399:777225:788144:- | TE214393 | Scaffold1399:785957:786101:- | LTR/Copia | 1 |

| | | | | | | |
|---------|-------------|-------------------------------|----------|-------------------------------|-------------------|---|
| CsTPS67 | TEA000496.1 | Scaffold682:1760053:1779446:+ | TE089287 | Scaffold682:1760606:1761229:+ | LTR/Gypsy | 3 |
| | | | TE089288 | Scaffold682:1761433:1762666:+ | LTR/Gypsy | |
| | | | TE089289 | Scaffold682:1763042:1763096:+ | LTR/Gypsy | |
| CsTPS70 | TEA024176.1 | Scaffold2697:527999:534944:+ | TE389462 | Scaffold2697:530047:533222:+ | LINE/RTE- BovB | 1 |
| CsTPS72 | TEA007033.1 | Scaffold4476:490748:497232:- | TE522189 | Scaffold4476:496274:496317:- | LINE/L1 | 1 |

Supplementary Table S6 TPM value of tea TPS genes in transcriptome of eight tea organs

| Name | Gene ID | Apical bud | Young leaf | Mature leaf | Old leaf | Stem | Flower | Fruit | Root |
|---------|-------------|------------|------------|-------------|-----------|-----------|-----------|-----------|-----------|
| CsTPS01 | TEA032539 | 31.3278 | 23.1825 | 0.918775 | 0.12187 | 5.48689 | 42.9248 | 0.0639724 | 0.127303 |
| CsTPS02 | TEA029356 | 77.7795 | 79.3262 | 1.30856 | 0.043525 | 2.30623 | 0.903892 | 0.0274167 | 0.019585 |
| CsTPS03 | TEA014184 | 0.149306 | 1.89402 | 4.79805 | 0 | 0.115311 | 0.0602595 | 0.438668 | 0.019585 |
| CsTPS04 | TEA031969 | 10.2933 | 7.82464 | 0.49187 | 0.0870501 | 0.586166 | 22.3462 | 0.630585 | 0.11751 |
| CsTPS05 | TEA031966 | 0 | 0.0257107 | 0.3341 | 0.05223 | 1.05702 | 1.91826 | 0.776807 | 0 |
| CsTPS06 | TEA025177 | 0.500613 | 0.591347 | 0.0185611 | 0 | 0.124921 | 0 | 0.0182778 | 0 |
| CsTPS07 | TEA010895 | 1.83558 | 1.33696 | 0.139208 | 0 | 0.0480464 | 0.080346 | 0 | 0 |
| CsTPS08 | TEA005128 | 0.0263481 | 0.0514215 | 0 | 0 | 0 | 10.3445 | 0.0913891 | 0.0587551 |
| CsTPS09 | TEA017888.1 | | | | | | | | |
| CsTPS10 | TEA032538 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0.0293775 |
| CsTPS11 | TEA005117 | 28.6843 | 30.9557 | 2.58928 | 0 | 0.701477 | 0.150649 | 0.0822502 | 0.0783401 |
| CsTPS12 | TEA022784 | 0.0263481 | 0.068562 | 0.0742445 | 0 | 0 | 0 | 0 | 0.0293775 |
| CsTPS13 | TEA021924.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| CsTPS14 | TEA017878 | 21.7547 | 17.329 | 0.872372 | 0 | 0.509291 | 0.100432 | 0.0548335 | 0 |
| CsTPS15 | TEA002287 | 0.0878269 | 0.454223 | 0 | 0.10446 | 0.0960927 | 0.080346 | 0.1645 | 0 |
| CsTPS16 | TEA017309.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| CsTPS17 | TEA033098 | 3.22325 | 2.35682 | 4.50107 | 2.41129 | 4.09355 | 5.34301 | 4.79793 | 2.03684 |
| CsTPS18 | TEA029355 | 44.9586 | 16.9605 | 1.03942 | 0.0783451 | 0.836007 | 0.974195 | 0 | 0.0783401 |
| CsTPS19 | TEA031961 | 0.0878269 | 1.01986 | 0.204172 | 0 | 0.201795 | 0.451946 | 0.146223 | 0 |
| CsTPS20 | TEA029353 | 12.6734 | 13.5838 | 0 | 0 | 0.643821 | 2.4606 | 0 | 0 |
| CsTPS21 | TEA029348 | 4.11908 | 5.63922 | 0.194892 | 0.0783451 | 0.52851 | 322.228 | 0.173639 | 1.51784 |
| CsTPS22 | TEA012463 | 0.237133 | 0.171405 | 0.603236 | 0.957551 | 0.595775 | 0.0703027 | 0.219334 | 0 |
| CsTPS23 | TEA023168 | 0.307394 | 0.0428512 | 3.18323 | 8.07825 | 5.06409 | 1.31567 | 0.703696 | 0 |
| CsTPS24 | TEA017886 | 0.149306 | 0.111413 | 0.0742445 | 0.391725 | 0.192185 | 0.040173 | 0.155361 | 0.019585 |
| CsTPS25 | TEA010551 | 0.245915 | 0.145694 | 0 | 0.03482 | 0 | 0 | 0 | 0 |
| CsTPS26 | TEA003774 | 0 | 0 | 0 | 0.774746 | 0 | 0 | 0 | 0 |
| CsTPS27 | TEA005096.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| CsTPS28 | TEA005082 | 0.0614788 | 0 | 0 | 0 | 0 | 2.55098 | 0 | 0.0293775 |
| CsTPS29 | TEA024081 | 0 | 0 | 0 | 0 | 0.0480464 | 23.7222 | 0 | 0.303568 |
| CsTPS30 | TEA007878 | 0 | 0.0257107 | 0 | 0 | 0 | 11.3589 | 0.0274167 | 0.0293775 |
| CsTPS31 | TEA027025 | 0 | 0 | 0 | 0 | 0 | 22.2759 | 0 | 0.15668 |
| CsTPS32 | TEA021499 | 0 | 0.0257107 | 0 | 0 | 0.0576556 | 17.3447 | 0.0274167 | 0.0979251 |
| CsTPS33 | TEA010904.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| CsTPS34 | TEA017307 | 0.254698 | 0.0171405 | 0 | 0 | 0.0768742 | 0.0602595 | 0 | 0 |
| CsTPS35 | TEA027070 | 0 | 0 | 0 | 0 | 0 | 1.84796 | 0 | 0 |
| CsTPS36 | TEA027061 | 0 | 0 | 0 | 0 | 0 | 67.2596 | 0.109667 | 0.881326 |
| CsTPS37 | TEA009449 | 0.0526961 | 0.582777 | 1.47561 | 0.757336 | 0.230623 | 0.0200865 | 0.0456945 | 1.79203 |
| CsTPS38 | TEA023157 | 0 | 0 | 0 | 0 | 0 | 0.0703027 | 0 | 1.6941 |
| CsTPS39 | TEA009450 | 0 | 0 | 0.0742445 | 0 | 4.29534 | 0 | 8.01482 | 0 |
| CsTPS40 | TEA017654 | 0.237133 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | | | |
|---------|-------------|----------|-----------|-----------|----------|-----------|-----------|-----------|-----------|
| CsTPS41 | TEA032709 | 0 | 0 | 0 | 0 | 0.66304 | 0 | 0.237612 | 1.08697 |
| CsTPS42 | TEA002963 | 0 | 0 | 0.0278417 | 0 | 0.201795 | 0 | 1.06925 | 3.11402 |
| CsTPS43 | TEA014987 | 2.44159 | 0.557066 | 5.98596 | 0 | 21.4479 | 3.62561 | 0.0182778 | 0.176265 |
| CsTPS44 | TEA032731 | 0 | 0 | 0 | 0 | 0.0480464 | 0 | 0.0822502 | 0.146888 |
| CsTPS45 | TEA030379 | 1.12418 | 12.0155 | 34.6072 | 21.5101 | 3.99746 | 0.100432 | 1.08753 | 4.72978 |
| CsTPS46 | TEA020730 | 2.45915 | 27.7333 | 84.351 | 57.2528 | 8.85975 | 0.451946 | 0.42039 | 0.949874 |
| CsTPS47 | TEA022294 | 0.974878 | 0.137124 | 0 | 0.01741 | 0.211404 | 0.190822 | 0 | 0.421078 |
| CsTPS48 | TEA014219 | 0.632353 | 0.0942727 | 0 | 0 | 0.182576 | 0.160692 | 0 | 0.23502 |
| CsTPS49 | TEA023784 | 0.904617 | 7.79035 | 13.6981 | 11.6212 | 1.78732 | 0.331427 | 0.0456945 | 0.0489626 |
| CsTPS50 | TEA007029 | 0.509396 | 0.325669 | 0 | 0 | 0.144139 | 0.522249 | 0 | 0.323153 |
| CsTPS51 | TEA033306 | 4.44404 | 1.85974 | 4.48251 | 0 | 1.9699 | 0 | 5.82149 | 0 |
| CsTPS52 | TEA009170 | 3.23203 | 1.1227 | 1.82827 | 0 | 0.52851 | 0.0301297 | 1.87348 | 0 |
| CsTPS53 | TEA026271 | 1.67749 | 0.265678 | 0 | 0 | 0.211404 | 0 | 0 | 0 |
| CsTPS54 | TEA012490 | 16.8188 | 6.71907 | 16.3895 | 0 | 1.13389 | 0 | 10.985 | 0 |
| CsTPS55 | TEA009866 | 10.1177 | 3.48809 | 5.79107 | 0 | 4.68932 | 0 | 8.91958 | 0 |
| CsTPS56 | TEA004653 | 0.755311 | 1.21698 | 0 | 0 | 0 | 0 | 0 | 0 |
| CsTPS57 | TEA004606 | 104.347 | 50.2216 | 2.32942 | 0.45266 | 30.0001 | 2.35012 | 11.6795 | 0.949874 |
| CsTPS58 | TEA031754 | 19.6205 | 6.04202 | 0.389783 | 0.05223 | 9.0135 | 0.944065 | 9.2303 | 0.166473 |
| CsTPS59 | TEA026152 | 20.3758 | 7.13902 | 0.714603 | 0.1741 | 13.6644 | 1.01437 | 8.06966 | 0.254605 |
| CsTPS60 | TEA014989 | 7.32476 | 5.75921 | 3.71222 | 4.97926 | 1.84498 | 1.4864 | 1.10581 | 0.0783401 |
| CsTPS61 | TEA014996 | 0.500613 | 0.617058 | 0.937336 | 0 | 0.249841 | 0 | 0.137084 | 0 |
| CsTPS62 | TEA016812 | 0.219567 | 0.128554 | 0 | 0 | 0 | 0 | 0 | 0 |
| CsTPS63 | TEA031457 | 6.92954 | 5.72493 | 0.0278417 | 0.026115 | 0 | 0 | 0 | 0 |
| CsTPS64 | TEA031444 | 0.606005 | 0.35995 | 0.250575 | 0.15669 | 0.288278 | 0.160692 | 0.246751 | 0.11751 |
| CsTPS65 | TEA031453.1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| CsTPS66 | TEA020739 | 0.13174 | 0.111413 | 0 | 0 | 0.0960927 | 0 | 0 | 0 |
| CsTPS67 | TEA000496 | 28.008 | 33.0726 | 0.380503 | 0.12187 | 12.0692 | 0.100432 | 0.0365556 | 5.20962 |
| CsTPS68 | TEA024173 | 0.711398 | 0.462793 | 0.631078 | 0.29597 | 0.778351 | 0.331427 | 0.594029 | 0.401493 |
| CsTPS69 | TEA017740 | 5.18179 | 4.58508 | 6.5892 | 3.37754 | 6.77454 | 2.93263 | 9.3491 | 5.15086 |
| CsTPS70 | TEA024176 | 3.09151 | 3.05101 | 4.19481 | 2.10661 | 5.46768 | 3.32432 | 7.50305 | 4.20099 |
| CsTPS71 | TEA008638 | 7.6585 | 7.00189 | 9.51257 | 5.17948 | 11.5792 | 4.4592 | 16.2398 | 7.91235 |
| CsTPS72 | TEA007033 | 0.58844 | 0.145694 | 0 | 0 | 0.153748 | 0 | 0.0913891 | 0.293775 |
| CsTPS73 | TEA019347 | 0 | 0 | 0 | 0 | 0 | 0 | 0.0456945 | 0 |
| CsTPS74 | TEA005451 | 1.09784 | 1.44837 | 3.60086 | 0.01741 | 1.22999 | 21.8642 | 0 | 0.137095 |
| CsTPS75 | TEA005162 | 2.71385 | 2.75105 | 9.46617 | 0.026115 | 3.68035 | 28.9848 | 0.0274167 | 0.254605 |
| CsTPS76 | TEA007191 | 21.4034 | 41.4543 | 4.39898 | 1.01849 | 2.26779 | 16.7923 | 0 | 0.0881326 |
| CsTPS77 | TEA004822 | 27.3844 | 55.1753 | 7.99984 | 2.91618 | 4.78542 | 2.57107 | 0.0639724 | 0.146888 |
| CsTPS78 | TEA019472 | 3.53942 | 3.24812 | 0.278417 | 0.513595 | 5.41002 | 119.635 | 0.0822502 | 0.519003 |
| CsTPS79 | TEA004657 | 69.6028 | 41.8485 | 3.97208 | 5.15336 | 19.2762 | 1378.65 | 12.301 | 7.53044 |
| CsTPS80 | TEA018721 | 2.90707 | 3.53951 | 1.11367 | 0.609351 | 0 | 14.0605 | 0 | 0.35253 |

Supplementary Fig S1. The structure analysis of *CsTPS67* with three retrotransposons inserted in the first intron. (A), loss of 89 amino acids of *CsTPS67* due to the insertion of retrotransposons compared to other *CPS* genes identified in GenBank (B); Phylogenetic analysis of *CsTPS67* with *CPS* genes of other species.

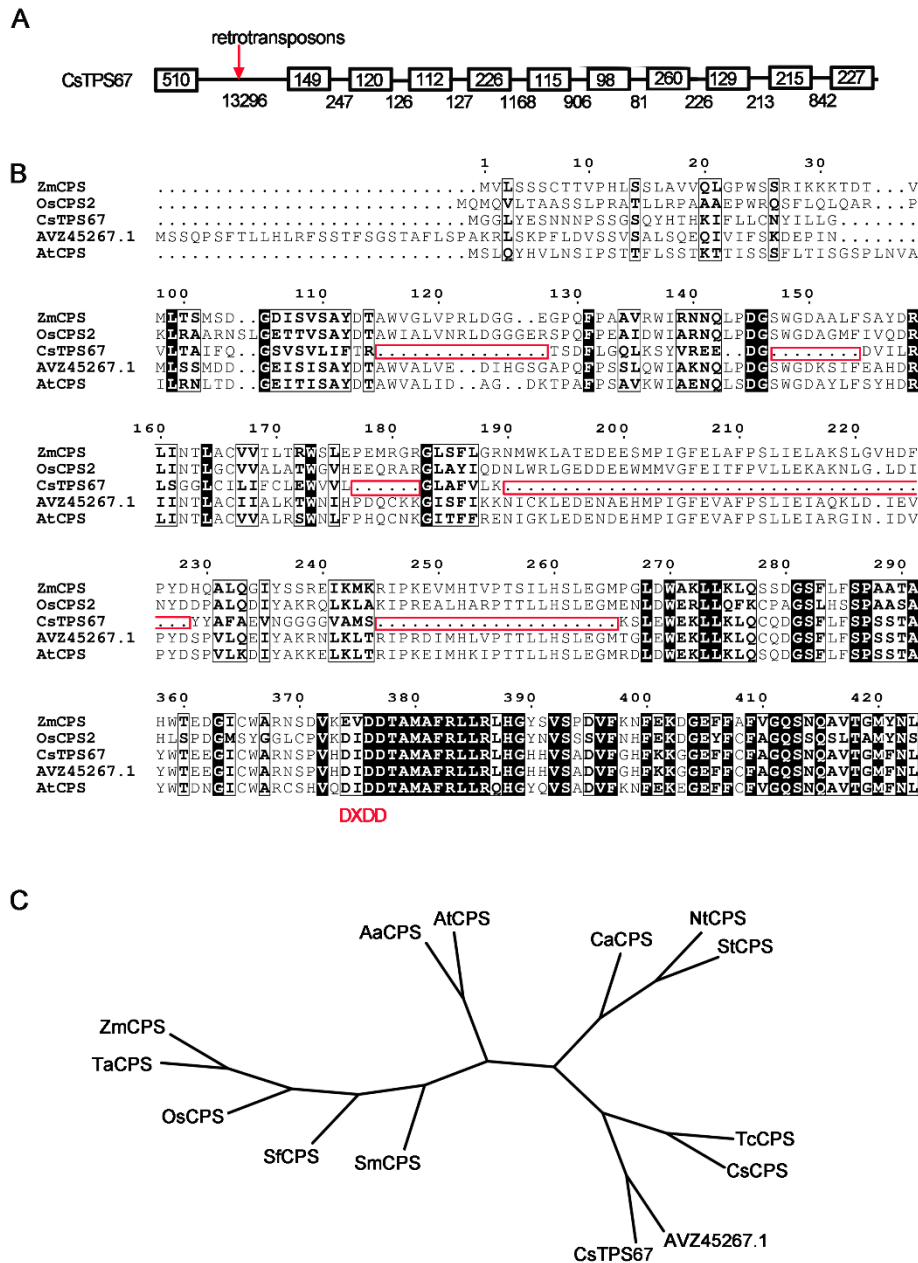


Fig S1

Supplementary Fig S2. Tempo-spatial expression patterns of 80 *CsTPS* genes in tea apical buds (B), young leaves (YL), mature leaves (ML), old leaves (OL), immature stems (S), flowers (FL), young fruits (FR) and roots (R).

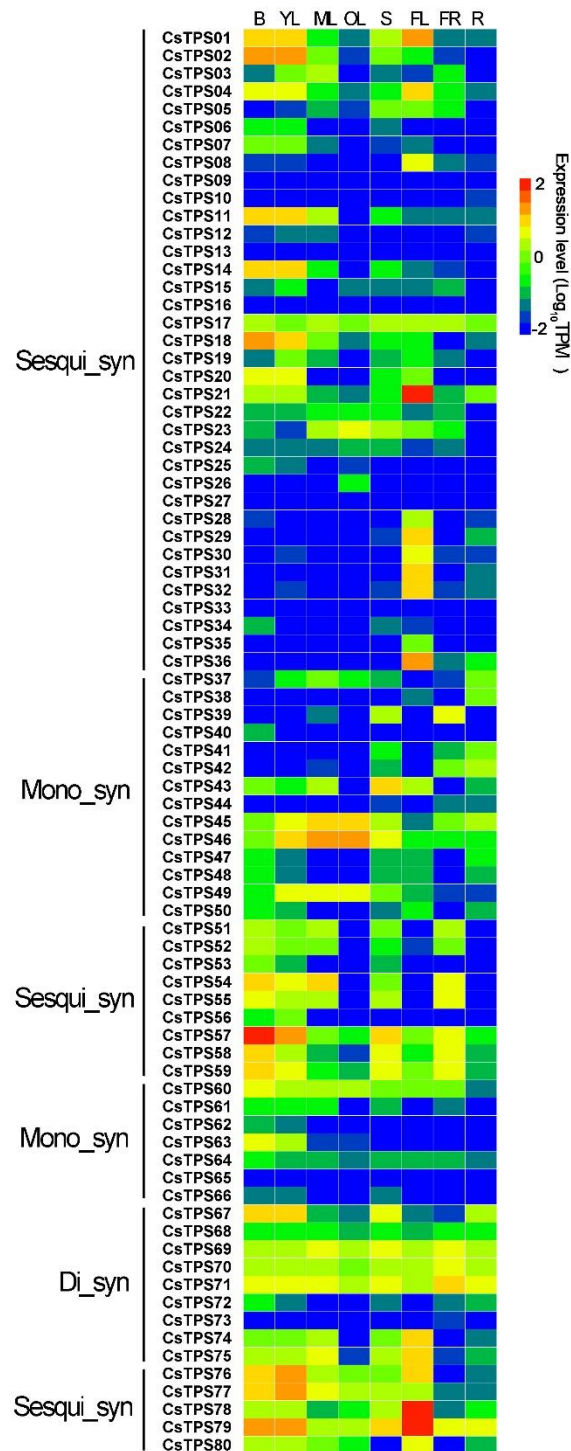


Fig S2

