Supplementary Material

**Supplementary Table S1 MYB genes used to build phylogenetic tree**

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| --- | --- | --- |
|  | | |
| Gene name | GenBank accession numbers | Protein sequence |
| NtAN2 | ACO52470 | MNICTNKSSSGVKKGAWTEEEDVLLKKCIEKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLRPHIKRGDFSFDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNSHLRKKLIAPHDQKESKQKAKKITIFRPRPRTFSKTNTCVKSNTNTVDKDIEGSSEIIRFNDNLKPTTEELTDDGIQWWADLLANNYNNNGIEEADNSSPTLLHEEMPLLS |
| PhAn2 | AAF66727 | MSTSNASTSGVRKGAWTEEEDLLLRECIDKYGEGKWHLVPVRAGLNRCRKSCRLRWLNYLRPHIKRGDFSLDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLRKKLIAPHDQKQESKNKAVKITENNIIKPRPRTFSRPAMNNFPCWNGKSCNKNTIDKNEGDTEIIKFSDEKQKPEESIDDGLQWWANLLANNIEIEELVSCNSPTLLHEETAPSVNAESSLTQGGGSGLSDFSVDIDDIWDLVS |
| LeANT1 | AAQ55181 | MNSTSMSSLGVRKGSWTDEEDFLLRKCIDKYGEGKWHLVPIRAGLNRCRKSCRLRWLNYLRPHIKRGDFEQDEVDLILRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTNLLRKLNTTKIVPREKINNKCGEISTKIEIIKPQRRKYFSSTMKNVTNNNVILDEEEHCKEIISEKQTPDASMDNVDPWWINLLENCNDDIEEDEEVVINYEKTLTSLLHEEISPPLNIGEGNSMQQGQISHENWGEFSLNLPPMQ |
| IbMYB1 | BAF45114 | MVISSVWSGSSSRVRKGSWSEEEDQLLRECIQKYGEGKWHLIPLRAGLNRCRKSCRLRWLNYLRPDIKRGEFSPDEIDLILRLHRLLGNRWSLIAGRIPGRTANDVKNLWNTHLQKKVSAMASSRQDNYWKGKAPEITENTVVRPRPRRFLKASSSPTTLLTGNATMVAYDGQLQEHMTTQPETTSDLLMENVQQKNLTTTLPSALETTPHDNVKWWEDVLSDKELNEEGQICWSEFPTDIDLLSELLS |
| InMYB2 | BAE94709 | MVNSSSAWPPPSSSRLMRKGAWTEEEDNLLRKCIQKYGEGKWHLVPLRAGLNRCRKSCRLRWLNYLRPDIKRGDFSVDEVDLIMRLHRLLGNRWSLIAGRIPGRTANDVKNYWNTHIQKKVFAMARMQDNWKGKAPEIRENTVVRPRPRRFLNTSLSPTSKTGKATAVTYDAQIQGHTLPQPPEAIITTSDLVMENVQLNNTIATLPSELETTTSDDRVRWWEDLLFDKEFNDDEGNACMHEGQVGWTNLPIDMD |
| VvMYBA1 | BAD18977 | MESLGVRKGAWIQEEDVLLRKCIEKYGEGKWHLVPLRAGLNRCRKSCRLRWLNYLKPDIKRGEFALDEVDLMIRLHNLLGNRWSLIAGRLPGRTANDVKNYWHSHHFKKEVQFQEEGRDKPQTHSKTKAIKPHPHKFSKALPRFELKTTAVDTFDTQVSTSRKPSSTSPQPNDDIIWWESLLAEHAQMDQETDFSASGEMLIASLRTEETATQKKGPMDGMIEQIQGGEGDFPFDVGFWDTPNTQVNHLI |
| VvMYBA2 | BAD18978 | MKSLGVRKGAWTQEEDVLLRKCIEKYGEGKWHLVPLRAGLNRCLKSCRLRWLNYLKPDIKRGEFALDEVDLMIRLHNLLGNRWSLIAGRLPGRTANDVKNYWHGHHLKKKVQFQEEGRKKPQTHSKTKAIKPHPHKFSKALPRFELKTTAVDTFDTQVSTSSKPSSTSPQPNDDIIWWESLLAEHAQMDQETDFSASGEMLIASLWTEETATQKKGTHSKTKAIKPHPHKFSKALPRFELKTTAVDTFDTQVSTS |
| CsRuby | AFB73913 | MADSLGVRKGAWTGEEDDLLRKCIEKYGEAKWHQVPLRAGLHRCRKSCRLRWLNYLNPNIKRGEFAADEVDLILRLHKLLGNRWSLIVGRLPGRTANDVKNFWNTHLRKKVDKCCKNNKEMKAKAEKVEKINIIKPQPRTFAKNSQWLKGKGMTSNNLQLGDYNLGKQSTPSDHHHHHQQQQENETESVWWESFLFGDELDQQGISSSLSRPEEESTTANIFAEKSPVVTKVTENRVIEAGQSCPTDDFAFDAEL |
| AmVENOSA | ABB83828 | MGNNPLGVRKGTWTKEEDILLKQCIEKYGEGKWHQVPIRAGLNRCRKSCRMRWLNYLSPNIKRGSFTRDEVDLIVRLHKLLGNRWSLIAGRLPGRTGNDVKNFWNTHFEKKSGERENTENINPKLINSSNIIKPQPRTFLKLRPKETKKQKNIRNVCTANDDKQQPLSTSGQLEEVNERIRWWSELLDFADYVD |
| AmROSEA1 | ABB83826 | MEKNCRGVRKGTWTKEEDTLLRQCIEEYGEGKWHQVPHRAGLNRCRKSCRLRWLNYLRPNIKRGRFSRDEVDLIVRLHKLLGNKWSLIAGRIPGRTANDVKNFWNTHVGKNLGEDGERCRKNVMNTKTIKLTNIVRPRARTFTGLHVTWPREVGKTDEFSNVRLTTDEIPDCEKQTQFYNDVASPQDEVEDCIQWWSKLLETTEDGELGNLFEEAQQIGN |
| AmROSEA2 | ABB83827 | MQKNPRGVRKGTWTKEEDILLMECIDKYGEGKWHQVPLKAGLNRCRKSCRLRWLNYLRPNIKRGCFSKDEVDLIVRLHKLLGNKWSLIAGRIPGRTANDVKNFWNTHVGKNLGVDGERRKKNVMNTKNSKETNIIRPRARTFNGLHVTWPREHGKNDAFSNVRITSTTENLDYEKQKPFHNNVASTPEEVDESIRWWSNLLETTEDELENLFEDVQQTGKMSEW |
| AtPAP2/MYB90 | AAG42002 | MEGSSKGLRKGAWTAEEDSLLRLCIDKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKRGRLSNDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHESSCCKSKMKKKNIISPPTTPVQKIGVFKPRPRSFSVNNGCSHLNGLPEVDLIPSCLGLKKNNVCENSITCNKDDEKDDFVNNLMNGDNMWLENLLGENQEADAIVPEATTAEHGATLAFDVEQLWSLFDGETVELD |
| AtMYB114 | Q9FNV8 | MEGSSKGLRKGAWTAEEDSLLRQCIGKYGEGKWHQVPLRAGLNRCRKSCRLRWLNYLKPSIKRGKFSSDEVDLLLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKTKIKRINIITPPNTPAQKVDIF |
| AtPAP1/MYB75 | AAG42001 | MEGSSKGLRKGAWTTEEDSLLRQCINKYGEGKWHQVPVRAGLNRCRKSCRLRWLNYLKPSIKRGKLSSDEVDLLLRLHRLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHEPCCKIKMKKRDITPIPTTPALKNNVYKPRPRSFTVNNDCNHLNAPPKVDVNPPCLGLNINNVCDNSIIYNKDKKKDQLVNNLIDGDNMWLEKFLEESQEVDILVPEATTTEKGDTLAFDVDQLWSLFDGETVKFD |
| AtMYB113 | Q9FNV9 | MGESPKGLRKGTWTTEEDILLRQCIDKYGEGKWHRVPLRTGLNRCRKSCRLRWLNYLKPSIKRGKLCSDEVDLVLRLHKLLGNRWSLIAGRLPGRTANDVKNYWNTHLSKKHDERCCKTKMINKNITSHPTSSAQKIDVLKPRPRSFSDKNSCNDVNILPKVDVVPLHLGLNNNYVCESSITCNKDEQKDKLININLLDGDNMWWESLLEADVLGPEATETAKGVTLPLDFEQIWARFDEETLELN |
| GmMYB10 | ACM62751 | MERSSGIRKGTWTVEEDKLLRMCVEKYGEGKWHQIPKKAGLNRCRKSCRLRWLNYLKPNIKRGDFLADEVDLMLKLHKLLGNRWSLIAGRLPGRTANDVKNFWNTHLKKRTVSPPEDEENLKSPTPQKIVTRGNIFKPRPRKFSNCSCPFDASRKKSDIGINSLQSYQLSNNSKSVISLQNHPLVPPISTEENPAWWETMLFEENLEENKLDTKANGWCEQDDQFLTSFFNGEITQGTTVEGSTKNDESGHWPDL |
| MrMYB1 | ADG21957 | MEGSLGVRKGAWTVEEDTLLKLYIEKYGEGKWHQVPPRAGLNRCRKSCRLRWLNYLKPNIKRGEFKADEVDLMIRLHKLLGNRWSMIAGRLPGRTANDVKNYWNTHLRKNAISRIKDGGEKAQQTSKVNIIKPRPRTFAKNLTWFGGKPTIMAASFQPKDNVISDLPPAPLPSENSVKWGENLFDDKEAGDEIGTYDVGGLNEEPIATFRWAEAAPAETVGTPLDEFGPSFWAEFPSNLDVWDFLDP |
| GhMYB10 | CAD87010 | MGAEARSGLRKGAWTAEEDMLLKNCIERYGEGKWHLVPLKAGLNRCRKSCRLRWLNYLRPNIKRGDFGEDEIDLIIRLHKLLGNRWSLIAGRIPGRTANDVKNWWNTHLRSRHQQQQKVHQEDELSQDTTVAIIKPQPRTFSKTLNWFGNRQSVKDHVDINIIKSSSASDTNNISAPPELIASPKILDDAINECRQKLFDGDEKEVDIDGHVRWSFTPADEEPLNIVDQENGHDSLLDFPIDEVVWDLLN |
| LhMYB6 | BAJ05399 | MSPFRVSATSSSFSQMSPSPVLRLVRKGAWTQVEDDLLKRCIERHGVVRWSRVPQLAGLNRCRKSCRLRWLNYLDPRIRRGQFEEDEDDLIIRLHKLLGNRWSLIAGRLPGRTANDVKNYWNSHLSKKLIPQEKKVRACPCIAAPTRPQPRKCSIKTKTSVDDQQVNMSELIPQKKKVRACRIIAAPTRPQPRKCSIETKTSVDEQQVNMSESRPSADTANCAVWQDDLGNVKEMIEQLTEATIPSENTEGFAHE |
| EsMYBA1 | AGT39060 | MKPDFSEMFKSGVRKGAWTKEEDEVLKICVEKYGVGNWHRIPQRAGLNRCRKSCRMRWLNYLNPNINRGVSREDEIDLMLKMHKLLGNRWSLIAGRLPGRTANDVKNFWNTQLRHKSVLNNKDKERILPPKKVQVIKPHPRIFKPVPTRLTGEPAFCNLQEQQQEEGNQHPIAEDTIWWEELLFHDKEMNHGTSVSFGREEVVSTTNSTEEERKAALFSDVDFEFQDFSDLNFWNFE |
| ZmC1 | AAA33482 | MGRRACCAKEGVKRGAWTSKEDDALAAYVKAHGEGKWREVPQKAGLRRCGKSCRLRWLNYLRPNIRRGNISYDEEDLIIRLHRLLGNRWSLIAGRLPGRTDNEIKNYWNSTLGRRAGAGAGAGGSWVVVAPDTGSHATPAATSGACETGQNSAAHRADPDSAGTTTTSAAAVWAPKAVRCTGGLFFFHRDTTPAHAGETATPMAGGGGGGGGEAGSSDDCSSAASVSLRVGSHDEPCFSGDGDGDWMDDVRALAS |
| ZmPl | AAA19819 | MGRRACCAKEGVKRGAWTAKEDDTLAAYVKAHGEGKWREVPQKAGLRRCGKSCRLRWLNYLRPNIKRGNISYDEEDLIVRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNSTLGRRAGGSRVVFAPDTGSHATPAAGSREMTGGQKGAAPRADLGSPASAAVVWAPKAARCTGGLFFHRRDTHTPHAGGTETPTPMMAGGGGGEARSSDDCSSAASVSPLVGSSQHDPCFSGDGDGDWMDDVRALASFLESDEERL |
| LjTT2a | BAG12893 | MGRSPCCSKQGLNRGAWTAQEDQILRDYVHLHGQGKWRNLPQSAGLKRCGKSCRLRWLNYLRPDIKRGNISRDEEELIIRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTNLCKRVQDGVDVGDSKTPSSQEKNNHHDQKAKPQSVTPSVFSSSQPKNNNVIRTKASKCSKVLLRDPLLPCPPMQTQSDDFIAKLLEEAEGEPLLSAVANDFTSGDEDGVLSFDPCGNEKELSTDLLLDLDIGEICLPEFINSDF |
| VvMYBPA2 | ACK56131 | MGRRPCCAKEGLNRGSWSAWEDKILCNYVEVHGEGKWRDLPQRAGLKRCGKSCRLRWLNYLRPDIKRGNISSEEEELIIRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTNLSKRLQASKGQNSPNKKVENPKNQTSGTGKSSAELHTVIRTRAVRCSKVIIPRVQADFDENPSPKMAVPTSEPSSSALEQGETANFFMGFDIGDLLTSDALNSFLDQDEEMGENNSNGVSDHFPPCSDFLAPEIENQEGVSGLL |
| FaMYB11 | AFL02461 | MGRSPCCAKEGLNRGAWTAMEDRTLTEYITTHGEGKWRNLPKRAGLKRCGKSCRLRWLNYLRPDIKRGNITRDEEELIIRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTNIRKKVQDHSSTNSEANITHHKPPNHQTQKKNTNVVRTKASRCTKVFMPHQQSQMDKKGTCNNPTADQQGAAPFLNHDYYDPINYNDDPALRMMGITDTHHQESDDLSPFLNLEIDNENSNSCGFMVDFKMDESFLSEFLNVDFS |
| AtTT2 | NP\_198405 | MGKRATTSVRREELNRGAWTDHEDKILRDYITTHGEGKWSTLPNQAGLKRCGKSCRLRWKNYLRPGIKRGNISSDEEELIIRLHNLLGNRWSLIAGRLPGRTDNEIKNHWNSNLRKRLPKTQTKQPKRIKHSTNNENNVCVIRTKAIRCSKTLLFSDLSLQKKSSTSPLPLKEQEMDQGGSSLMGDLEFDFDRIHSEFHFPDLMDFDGLDCGNVTSLVSSNEILGELVPAQGNLDLNRPFTSCHHRGDDEDWLRD |
| FaMYB9 | AFL02460 | MGRSPCCSKEGLNRGAWTALEDKVLTSYIKAHGEGKWRNLPKRAGLKRCGKSCRLRWLNYLRPDIKRGNISGDEEELIIRLHNLLGNRWSLIAGRLPGRTDNEIKNYWNTTLSKKAKPESHSGSSKETSPGPTRFRPRKASAAATTQPQVIRTKATRLTRMPVPSLPLLIDDCSTSTTALELQVPQTQLVSSLPEDAVNTQVHFQGTDAMNFGCNGFQATAGDDEDAKGDYDIPLDDGMLNDWTGNGNCDLENYG |
| OsMYB3 | BAA23339 | MGRKPCCSKEGLNRGAWTAMEDDILVSYIAKHGEGKWGALPKRAGLKRCGKSCRLRWLNYLRPGIKRGNISGDEEELILRLHTLLGNRWSLIAGRLPGRTDNEIKNYWNSTLSKRVAMQRTAAATSMPAAATTSSNADAAGAAARRRRSPEPRTVVVSPIRTKALRCNNNSSSGIVVVQQAGACSHGGRPPESGAPGDAAADKVATPQAVQQQQQQELAGAEDDDDLPVPAVCIDLDLDDIELGGLDGFLISPWR |
| DkMYB4 | BAI49721 | MGRAPCCSKVGLHRGPWTGKEDGLLTKYIQVHGEGSWRSLPKKAGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIIKMHALLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKRLRSQGTDPNTHKKLSDSHVQEPKKRSSNKKQKNKSKSNLDHTEKLKVHNPKPFRIKSLASFSFSRDSSSFDWTTTTATATPSGSSNHEGERGMLGNNGSNGHEVGFFIGEDGSDHYHHDHMMDDSDLECQSLEKLYEEYL |
| VvMYBPA1 | CAJ90831 | MGRAPCCSKVGLHRGSWTAREDTLLTKYIQAHGEGHWRSLPKKAGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIIRLHSLLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKKLRSQGTDPNTHKKMTEPPEPKRRKNTRTRTNNGGGSKRVKISKDQENSNHKVHLPKPVRVTSLISMSRNNSFESNTVSGGSGSSSGGNGETLPWPSFRDIRDDKVIGVDGVDFFIGDDQGQDLVASSDPESQSHMPPTDN |
| AtMYB32 | EFH43356 | MGRSPCCEKDHTNKGAWTKEEDDKLISYIKSHGEGCWRSLPRSAGLQRCGKSCRLRWINYLRPDLKRGNFTLEEDDLIIKLHSLLGNKWSLIATRLPGRTDNEIKNYWNTHVKRKLLRRGIDPATHRPINKTPQDSSDSSKTEDSLVKILSFGPQLEKIANFGDERNEKEVMCQKERVEYSVVEERCLDLNLELRISPPWQDQLHDEKNLRFGRVKRMCTACRFGFGNGKECSCDNTKSQTEDSSSSSYSSTDFS |
| AtMYB4 | NP\_195574 | MGRSPCCEKAHTNKGAWTKEEDERLVAYIKAHGEGCWRSLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTEEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIRRKLINRGIDPTSHRPIQESSASQDSKPTQLEPVTSNTINISFTSAPKVETFHESISFPGKSEKISMLTFKEEKDECPVQEKFPDLNLELRISLPDDVDRLQGHGKSTTPRCFKCSLGMINGMECRCGRMRCDVVGGSSKGSD |
| AtMYB7 | NP\_179263 | MGRSPCCEKEHMNKGAWTKEEDERLVSYIKSHGEGCWRSLPRAAGLLRCGKSCRLRWINYLRPDLKRGNFTHDEDELIIKLHSLLGNKWSLIAARLPGRTDNEIKNYWNTHIKRKLLSKGIDPATHRGINEAKISDLKKTKDQIVKDVSFVTKFEETDKSGDQKQNKYIRNGLVCKEERVVVEEKIGPDLNLELRISPPWQNQREISTCTASRFYMENDMECSSETVKCQTENSSSISYSSIDISSSNVGYDFLG |
| AtMYB12 | ABB03913 | MGRAPCCEKVGIKRGRWTAEEDQILSNYIQSNGEGSWRSLPKNAGLKRCGKSCRLRWINYLRSDLKRGNITPEEEELVVKLHSTLGNRWSLIAGHLPGRTDNEIKNYWNSHLSRKLHNFIRKPSISQDVSAVIMTNASSAPPPPQAKRRLGRTSRSAMKPKIHRTKTRKTKKTSAPPEPNADVAGADKEALMVESSGAEAELGRPCDYYGDDCNKNLMSINGDNGVLTFDDDIIDLLLDESDPGHLYTNTTCGVM |
| SlMYB12 | ACB46530 | MGRTPCCEKVGIKRGRWTAEEDQILTNYIISNGEGSWRSLPKNAGLLRCGKSCRLRWINYLRSDLKRGNITSQEEDIIIKLHATLGNRWSLIAEHLSGRTDNEIKNYWNSHLSRKVDSLRIPSDEKLPKAVVDLAKKGIPKPIKKSSISRPKNKKSNLLEKEALCCTNMPACDSAMELMQEDLAKIEVPNSWAGPIEAKGSLSSDSDIEWPRLEEIMPDVVIDDEDKNTNFILNCFREEVTSNNVGNSYSCIEEG |
| VvMYBF1 | ACV81697 | MGRAPCCEKVGLKKGRWTAEEDEVLVKYIQANGEGSWRSLPKNAGLLRCGKSCRLRWINYLRADLKRGNFSEEEEEIIIKLHASLGNRWSMIAGQLPGRTDNEIKNYWNSHLSRKVHSFRRLTNEGPSMVIDLAKVTTAHKRKVGRTSRWAMKKNRSDKSIREDVNKSSLEKPKGDDDGNGVIAEKETRSETMTGDLYAQVNEEENPELMASHLLGCGGRMFGEGSETFGPFRVPEVEGLCFSENMESGVLVDGG |
| VvMYB5a | AAS68190 | MRNPASASTSKTPCCTKVGLKRGPWTPEEDELLANYVKREGEGRWRTLPKRAGLLRCGKSCRLRWMNYLRPSVKRGQIAPDEEDLILRLHRLLGNRWSLIAGRIPGRTDNEIKNYWNTHLSKKLISQGIDPRTHKPLNPKPNPSPDVNAPVSKSIPNANPNPSSSRVGEIGSNHEVKEIESNENHKEPPNLDQYHSPLAADSNENWQSADGLVTGLQSTHGTSNDDEDDIGFCNDDTFPSFLNSLINEDVFGNHN |
| VvMYB5b | AAX51291 | MRNASSASAPPSSSSKTPCCIKVGLKRGPWTPEEDEVLANYIKKEGEGRWRTLPKRAGLLRCGKSCRLRWMNYLRPSVKRGQIAPDEEDLILRLHRLLGNRWALIAGRIPGRTDNEIKNYWNTHLSKKLISQGIDPRTHKPLNPNSSSVDVKASSSKAKAVMNPNPNPNPSPSEKAAANKEAGNFKSDNQYQIGAAGNDGSANIQNSDGSGTGLRSSNNEEDDDLNCGTDDVFSSFLNSLINEDVFPGQHHLQQQ |
| DcMYB6 | ARD08871 | MHPKALKNSTNPLKLRKGAWGSDEDALLRKCIEKYGEGKWHLVPRRAGLNRCRKSCRLRWLNYLRPTIKRGDFAADEVDLMMRLHKLLGNRWSLIAGRLPGRTANDVKNFWNTNVQKKLTTSSNHGQTEAVKVQEVVNKNQTSNAGTSAAATHVVVKPLPRTLSKGTSVPCYNPNAIGHKHSPWPGGMVYNKISSSNNNNNSCMVMNKTLSPAAPLPDQDGTEWWKNLFAEIGIQGQEEGSLEGHLVASSSGSEN |
| MDP0000031172 |  | MGRSPCCSKEGLNRGAWTALEDKILTAYIKAHGEGKWRSLPKRAGLKRCGKSCRLRWLNYLRPDIKRGNISGDEEELIVRLHNLLGNRWSLIAGRLPGRTDNEIKNYWNTTLWKKSKADSPSGSSKETSQHPSKSVVKKKDVESKTTSTAAAKPLVIRTKATRLSKILVPQNIPS |
| MDP0000127691 |  | MEGYNENLSVRKGAWTREEDNLLRQCVEIHGEGKWNQVSYKAGLNRCRKSCRQRWLNYLKPNIKRGDFKEDEVDLIIRLHRLLGNRY |
| MDP0000133416 |  | MAGGQHRGWGMINDEGWRKGPWTAEEDGFLIEHVRFHGEGRWNSVARLAGLKRNGKSCRLRWVNYLRPEHKRGQITPHEESLILDLHARWGNRTHFKKEAKMPSDASERAKNHILRRQKFHNQQQQQKNLQVDEEEVKRIMSLLDENETKMPLYWPHAANLR |
| MDP0000159011 |  | MRKPCCEKEGTNKGAWSKQEDQKLIDYIKTHGEGCWRSLPKAAGLHRCGKSCRLRWINYLRPDIKRGNFEQDEEELIIKLHALLGNRWSLIAGRLPGRTDNEVKNYWNSHIRKKLIKMGIDPNNHRLNQIIPRPNPQNDSVSPAATSSGSMSNINACTKTPLKSSDDQIDHRASEAASVLEDETSGPSSRDLNLDLTIAFPEPSLQVEEGMPKLIKGSNTTAREIETNLQHLPTLVLFR |
| MDP0000167107 |  | MSTNTKTLSSNYSGEDDSELRRGQWILEEDSLLIQYIERHGEGQWNLLAKRSGLRRTGKSCRLRWLNYLKPDVKRGNLSPEEQLLILDLHSKMGNRWSKIARYLPGRTDNEIKNYWRTRVHKQARHLNIDTKSREFQNMIRCYWMPRLKQKIGRETSISSAVLNQNPTISQPRENNTFQHFTATISPPPQILVQEEINMSGTMYNLDVEKQNTEADYCRSSFIFPSEPMDMSKTAQFPECPPFYCGDNNGYDMES |
| MDP0000175918 |  | MGRAPCCEKAHTNKGAWTKEEDQRLIDHIRQHGEGCWRSLPKAAGLLRCGKSCRLRWINYLRPDLKRGNFTQEEDELIIKLHSLLGNKWSLIAGRLPGRTDNEIKNYWNTHIKRKLISRGLDPQTHRPLNQTTTAAAAATPASRLDLRNRSSPSSAVFDHKTIKNNKFELLKHPKMEHEYYNYNIESEANCSTTTGSGTTTDEDQKQQNKYKCSDLNLDLSIGLEPFQSEPTRASSGNSAESRLQRIIAPSNSNN |
| MDP0000197283 |  | MGRAPCCDKNGLKKGPWTPEEDQKLMDYIQKHGYGNWRTLPKNAGLQRCGKSCRLRXTNYLRPDIKRGXFSFEEEETIIQLHSILGNKWSAIAARLPGRTDNEIKNYWNTHIRKRLLRMGIDPVTHSPRLDLLDFSSILYNSSHHHHQMNNFSRLLGQPIGLNPELLRLATSLIQSRXENNSNQNFVLQNAQENDYHQICNPQIQPQQPVQDNVPYPNEVSQLMQQQPNVEYPSSLSDFRSQNSQLNEWQSNVGT |
| MDP0000210851 |  | MGRSPCCSKEGLNRGAWTALEDKILSSYIKAHGEGKWRSLPKRAGLKRCGKSCRLRWLNYLRPDIKRGNISGDEEELIVRLHNLLGNRWSLIAGRLPGRTDNEIKNYWNTTLGKKSKVDSFSGSSKETSLNPCKSIAKKKDVESKTSTAAAQPLVIRTKATRLTKILVPQNIPSDENYTAAAANPLELQTQSAEKGGSTEEFPRTNAGDCSNILKNFGCDDDDIDAKGDQYCNEFQLLNSIPLDEAXINDGCWTG |
| MDP0000241185 |  | MSSSSVWNKEEDKEFENAIAMHWIDENSKEMWEKIAELVPSKSMGELKQHYQMLVDDVGAIEAGRVSPPNYAVDEAANTLSSSKDSGHRASSSGASASDKRLNCGHGGGFSGLGHDSAGHGGKGGSRADQERKKGIPWTEEEHRLFLLGLDKFGKGDWRSISRNFVISRTPTQVASHAQKYFIRLNSMNRDRRRSSIHDITSVNNGDVSSHQQPPITGQQTNTYPPSAGTAIRVGGPQTAKHRPQSHMAGLGMYG |
| MDP0000259614 |  | MEGYNENLSVRKGAWTREEDNLLRQCRKSCRQRWLNYLKPNIKRGDFKEDEVDLIIRLHRLLGNRWSLIARRLPGRTANAVKNYWNTRLRIDSRMKTVKNKSQEMRKTNVIRPQPQKFNRSSYYLSSKEPILDHIQSAEDLSTPPQTSSSTKNGNDWWETLLEGEDTFEXAAYPSIELEEELFTSFWFDDRLSPRSCANFPEGQSRSEFSFSTDLWNHSKEE |
| MDP0000261265 |  | MVPVSSRSSKKDVNRGSWTAEEDQKLAQVIEIHGPRRWKSIATKAGLKRCGKSCRLRWMNYLRPNIKRGNISDQEEDLILRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNSHLSKKMKQNRAVSKTVQGSTEQKNIKANDVNALTIEREDAFKLEENFNFGFNGGQFFNCSSSEQGPLNLEWMNKFLEMDESWFTLHDI |
| MDP0000266156 |  | MGRTPCCDKENVKRGPWSPEEDAALKSYLQSHGSDGTASNWIHLPKKAGLRRCGKSCRLRWLNYLRPDIKHGGFTEEEDSIICNLYNQMGSRQYFLTYLHFLNSPNFLRWSVIASYMPGRTDNDVKNYWNTKLKKKLLGGKIKNISSKEPTIANNANFFGIPEAEKPQDSAFSTSEPQVPSTLQMLYDVXSGLSADNQTMSLNPDQLYNPKLSGFSDLGARSRRNYSTTVSLSQEGSSISDSSSMAGNLYLDQDS |
| MDP0000268980 |  | MQEETREIPKPKTSKDDSSKPIPESEDTFLXQRHIXNPIEXSLAEPGLPAKRCHRRXKFFTELNGFPSLAKNHRTDLNKDVDVXSLIAISKGFLVNSLTXXEIEANVVPTIGXVXQANYIVGKNHILSRWRSNVSFWLTRELALESIRSKHKGLVXSAYEFXVEHGYINFGLAPTGNHSGISGTSCHHNSMGLNLNLSSNFGRQPPQSQAAPEYRETEVHRLQRXVFFLAVEQEVLQLQILMHNPELNDLSPASS |
| MDP0000298689 |  | MGAMSSEDRVTGSWNPQEDATLIKLVAQHGPSNWSLISTGIPGRSGKSCRLRWCNQLCPTVQHKPFSPQEDSIIIQAHALHGNKWATIARLLPGRTDNAIKNHWNSTLRRWRRQLAKLSSESSCSDSAAAHGEEPDLKRQCLRASPEHESLKADAGGEGVIVKTSLTLSPPGENAENDVAVKSEEEEHDREAVDNNDDGEKCAVEMDETCLLTIMQRMIAQEVRNYIYGLRPDGGPTFGLHSAHQNENDAQQNME |
| MDP0000317257 |  | MEGCNVNLSVXRKGAWTREEDDLLRQCIEIHGEGKWRQLPNKAGLNTCRKSCRLRWLNYLKPNIKRGDFTEDEVDLTIRLHKLLGNRY |
| MDP0000407613 |  | MVRTPCRDENGMKKGTWTPDEDRKLIAYVTRYGCWNWRQLPKFAGLSRCGKSCRLRWMNYLRPNIKRGNYSTEEEETIVKLHEKLGNRWSAIAAQLPGRTDNEIKNHWHTNLKKRTNNKQCNSSFSSSATNTEETPSYSSLEAAVDQPIKKAIFPNAESTVTPQVTQKTDDRVDNSSQLSPSPQPSSSEVSSMSADNNWVNYVEDINVTSMEAYADSQFIDDFWTEPFLADNSYIPSGFYTPLMDSEFVYPLFGG |
| MDP0000477900 |  | MEALXICSSSASSSDTSSSESSLTRNPNKPERIKGPWSAEEDRVLTRLVERYGPRNWSLISRYIKGRSGKSCRLRWCNQLSPSVQHRSFSQAEDETILAAQARFGNRWATIARLLPGRTDNAVKNHWNSTLKRRVRGDQLTEGGSFLGGGGNVGSNEGMSTNSVSGSLVNGSMEFDPLTELTLAPPGIGSGSGGAMVAEQRRNNESVPAGFWDAMRDVIAREVRDYVATTFSEPSGLL |
| MDP0000573302 |  | MEGYNVNLSVMRKGAWTREEDDLLRRCIETLGEGKWHQVPYKAVTSAYVKRAMPRDLVPHIIVHVERCXXNLGLNRCRKSCRLRWLNYLKPNIKRGDFTEDEVDLIVRLHKLLGNRWSLIAGRLPGRTSNDVKNYWNTQLRIDSGVKTMKNKFQETRKTIAIRPQPQKFIQGSYYLNSKEPILDHIQAAEDLSTLPQTSSSTKNGNDWWXTLLEDEDAFERIACPSLELEEEHFS |
| MDP0000655330 |  | MRNPSSSSKAAAAASAKMQTTITASSSSSKAAGVAGGTKTPCCAKVGLKRGPWTPEEDELLANYIKKEGEGRWRTLPKRAGLLRCGKSCRLRWMNYLRXSVKRGQIAPDEEDLILRLHRLLGNRWSLIAGRIPGRTDNEIKNYWNTHLSKKLISQGIDPRTHKPLNXDHHSAADDXDVDNTNKSTAVASSSKANDRFSNPNPSPPSDRLVHKEGDPNNSRNDGNIAIADHDLGTIVXGFANMITSINNPDASSSA |
| MDP0000693678 |  | MAMKGAXSGEDRVKGSWSPQEDATLIKLVAQHGPRNWSLISTGIPGRSGKSCRLRWCNQLSPTVQHKPFSXQXDSVIIQAHALHGNKWATIARLLPGRTDNAIKNHWNSTLRRGRQRAEXSSTSSGSDLAAAVGDEPDMKRQCLRASPEHESLKANAGGEGVIVETSLTLSPPGEKAENEVVLKSEEEEDGHEAVDNNDDVENCRVETEETSLLKIMHRMIAREVRNYIDSLRENGGPTFGLQSAAHQNDP |
| MDP0000755899 |  | MAFRHLMSDCDGFTRYQDLNFLPPPPVSNQLSLSNIFGGSSTSAMGVVPFSPSSSQQTNKPWSFQALENGGPKNISDLGVLSGVDQKRPTPLNLNLVGEEDDDEGRSPAGGRTSAKSCIRGHWRPAEDSKLKELVGQYGPQNWNVIAEHLDGRSGKSCRLRWFNQLDPRINRGAFSEEEEERLLAAHRLYGNKWAMIARLFPGRTDNAVKNHWHVIMARRHREQSNVFKRRKPSSPPPPSPLPHVVANFPKNPST |
| MDP0000764760 |  | MPVQSKFCLISYSQELVDGQPLYASSNCLPVKALNREPAGHSFHAVALKLRGCVEENKEVEDEKVVNNKEQTSIPSFDSYSSKGKKKSGGEGKEQDHYALLGLSHLRYLATEEQIRKSYRETALKYHPDKQAALLLNEVTEAAKQTKKDEIESHFKSIQEAYEVLIDPVKRRIYDSTDEFDDEIPTECAPQDFFRVFSPAFMRNGRWSVSQPIPFLGDESTPLKEVDDFYDFWYTFKSWREFPHADEFDLEQAES |
| MDP0000787808 |  | MGRQPCCDKLGVKKGPWTAEEDKKLVNFLLTHGQCCWRAVPKLAGLRRCGKSCRLRWINYLRPDLKRGLLNDAEEQLVIDLHARLGNRWSKIAARLPGRTDNEIKNHWNTHIKKKLVKMGIDPITHEPLHKQVTTXQEMPCEASNQPANSDMSIQQMNTNIPEHGISTNSDGNSTSENSPSNDSEPAEPNPNYSEEEDPLVSFILSDTFLEDLTWDFSTSSEYSSADNPTEENSLAWFMDCNDFGVEDFEL |
| MDP0000819856 |  | MDGEKLRKGPWLEEEDERLTTVVNLKGNRRWDAXAKESGLRRSGRSCRMRWLNYLRPNIKHGQITIIEEKTILQLHQRWGNKWSKIARALPGRTDNEIKNYWRTHLKKKTQIPDGNFQCTLNKNGRGLFCQEGDMNNEKYDFDQDHDSVKNSWETKVTSSDDLGLSDFAVTNSPYETQLSDWISELSSEQNGTAYNQDCNSVESDLCHLTWTPDDSDTWDCPSFLWDMN |
| MDP0000887107 |  | MGRSPCCAKEGLNRGAWTAHEDKVLTQYIKLHGEGRWRNLPKKAGLKRCGKSCRLRWLNYLRPDIKRGNISPDEEELIIRLHKLLGNRWSLIAGRLPGRTDNEIKNYWNTNLGKKVPDRQQQRSASNLKHHKNGEPNSKKAKSMDMASPSSLVYRTKAVKCTQVFINPQPHKVLLGHDHQHCTEETNTVLMFDGKPAAMDDDHINRTLSFSSFSNINADQENSTSDFLVDFDMNEISIASLLNSDFPEINRDYLN |
| MDP0000915330 |  | MGRAPCCSKVGLHRGPWTPREDTLLTKYIEAHGEGHWRSLPKKAGLLRCGKSCRLRWMNYLRPDIKRGNITPDEDDLIIRLHSLLGNRWSLIAGRLPGRTDNEIKNYWNTHLSKRLRNEGTDPNTHKKLSEPIARENKRRKNQRSKSNNNKKEMVMTKDKNNKTAQHVEPQKPKVHLPKPTRFTSFLSLPRNDSFTSSTTVTTGSSSQDLNGGGGRGGGGGGFGVNTWCNNGGLVFCVGDEDQDHDPINSSADGG |
| MDP0000932804 |  | MGRHSCCYKQKLRKGLWSPEEDEKLLNYITKHGHGCWSSVPKLAGLQRCGKSCRLRWINYLRPDLKRGPFSQQEENLIVELHAVLGNRWSQIAAQLPGRTDNEIKNLWNSCIKKKLRQRGIDPNTHKLLSEVLNQNIDTETNNNNNINLSPTYKSNEKASEGSNELSLVEAVSXKHPPSASENRFNPVEVSSTSKLISSKSLTHEGSXSSCRPCDFVGYFSFPHHNNQNNYGSSSDMGLQAVNQNTTFSFLNQNP |

**Supplementary Table S2 Sequences of 21 MdMATE members of clade I and 24 different known MATEs**

|  |  |
| --- | --- |
| Gene ID | Protein sequence |
| VvAM1  [*Vitis vinifera*] | METPLLNSGAEEGYSGPDGDYQPLRSWREVRSMVWKETVKLWRVAGPLAFQILCQFGTNSMTSVFVGHIGNLQLSAVSISLSVIGTFSFGFMLGMGSALETLCGQAYGAGQVHLLGVYLQRSWIILLVTCVILSPVYVFATPILKVLGQEDAIADLAGQFTIETIPQLFSLAIIFPTQKFLQAQSKVNVQATIAFVALILHIGMLSVFIFVFGWGTTGAAIAYDISNWVIAVSQVVYAIGWCKEGWTGLTWSAFR |
| VvAM3  [*Vitis vinifera*] | METPLLKSGAERGYGGEGGDYPPLTTWREVRSMLWRETVKVWRVAGPLAFQILCQFGTNLVTTVFVGHIGNLELSAVSISVSVIGTFSFGFMLGMGSALETLCGQAYGAGQVQLLGVYLQRSWIILLVSCIILLPIYIFATPILKALGQEDEIADLAGQFTLETIPQLFSLAIIFPTQKFLQAQSKVNVQATICFVALILDIGMLAVFIFVFGWGTTGAAIAYDISSWVTAVAQVVYAISWCKEGWTGLTWSAFR |
| MtMATE2  [*Medicago truncatula*] | MDSHTPLLNTTAATSSSSELLELDGGDYLEVKGFKQARKVFAIETLRIWKIALPIVFNILCQYGVNSITNIFVGHLGDIQLSAISLINSVIGTFAFGFMLGMGSATETLCGQAFGAGQVHMLGVYMQRSWIILFVTSIILLPIYIFAAPILKLLGQQEDMADLAGSFALLVIPQFLSLSFNFPTQKFLQSQSKVNVIAWIGLVALIVHIGLLWLLIYVLDLGLTGAAIAFDVTSWGITLAQLVYVVIWCKDCWNG |
| SlMTP77  [*Solanum lycopersicum*] | METPLLNGYSGSGERNDLIGADGDYRPAKSTKDWWAIFCVETLKLWRIGGPIAFNIICQYGVNSLTNIFVGHLGNVELSAISIAQTVISTFSFGFMMGMGSALETLCGQAYGAGQVHMLGVYMQRSIIILLATCVFLLPIYLFTTPLLVLLGQETAIADLSGRYTMLLIPQLFSLAINFPTSKFLQAQSKVDVLAGIGFAAVLVHALFLWLFIYTLEWGTNGAAIAFDLTNWLTAMAQLAYVVGWCKDGWKGLSW |
| GhTT12  [*Gossypium hirsutum*] | MGSAAPEYQPLLLGLDSHSRIPDLSSVAIEEFLQHRPIALRWWPRLVAWESRLLWLLSGSSIVLSIFNYMLSFVTLMFTGHLGALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKQYSAMGIICQRAIILHLGAAVLLTFLYWFSGDVLQAIGQTESIAQQGQVFSRGLIPQIYAFAISCPMQRFLQAQNIVNPLAFMSIGIFLVHVLLTWLVVNVLGCGLLGAALTLSLSWWFLVVINGLYIVLSP |
| AtDTX35 (AtFFT)  [*Arabidopsis thaliana*] | MDPTAPLLTHGGEVEEDYAPARSWTDVKRVLSTESAKLWMIAAPVGFNIICQYGVSSVTNIFVGHIGEVELSAVSISLSVIGTFSFGFLLGMGSALETLCGQAYGAGQVNMLGVYMQRSWIILFVSYFFLLPIYIFATPVLRLLGQAEEIAVPAGQFTLLTIPQLFSLAFNFPTSKFLQAQSKVVAIAWIGFVALSLHVIMLWLFIIEFGWGTNGAALAFNITNWGTAIAQIVYVIGWCNEGWTGLSWLAFKEIW |
| MtMATE1  [*Medicago truncatula*] | MENQPFLVGLDSHSHTHIADLSSDAIEEFLEHRPIGLRWWLKLVAWESRLLWILSGASIVVYLCNFMLSFVTMMFCGHLGSLELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKKHAAMCITLQRAIILHFGAAVILTFLYWFSGDFLKVIGQTESIAVQGQVFARGLIPQLYAFAFSCPMQRFLQAQNIVNPLAYMAVGVLLLHALLSWLVVVVLGYGLLGAALTLSFSWWILVFLNALYIIFSPKCK |
| AtTT12  [*Arabidopsis thaliana*] | MSSTETYEPLLTRLHSDSQITERSSPEIEEFLRRRGSTVTPRWWLKLAVWESKLLWTLSGASIVVSVLNYMLSFVTVMFTGHLGSLQLAGASIATVGIQGLAYGIMLGMASAVQTVCGQAYGARQYSSMGIICQRAMVLHLAAAVFLTFLYWYSGPILKTMGQSVAIAHEGQIFARGMIPQIYAFALACPMQRFLQAQNIVNPLAYMSLGVFLLHTLLTWLVTNVLDFGLLGAALILSFSWWLLVAVNGMYILMS |
| VvMATE1  [*Vitis vinifera*] | MASAAEDGEPLLLGHSSAGIHELSSSAVEELLLHKPVPGRWWPRLFGWESRLLWVLSGSAIVSSVFNYMLSFITLMFAGQLGALELAGASIASVGIQGLAYGLMLGMASAVQTVCGQAYGAKKYAAMGIICQRAIVLHLGAAILLTFLYWYSGAFLKAIGQSESIAVQGQIFARGLILQVYAFALSCPMQRFLQAQNIVNPLAYIAVGVTLLHILLTWLVVNVLDSGLLGIALTLSLSWWLLVFSIALYILLSPS |
| VvMATE2  [*Vitis vinifera*] | MGSEEYQPLLLGLNSHARIPDLSSFAVEEFLAHKPVAVRWWPRLFGWESRLLWLLSGSSIVASIFNYMLSFVTLMFTGHLGALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKKYKAMGIICQRAIILHLGAAVLLTFLYWFSGPFLRAIGQSDSISAQGQIFARGLILQLYAFAISCPMQRFLQAQNIVNPLAYMAVGVFFLHVLLTWLVVYVLDYGLLGAALTLSFSWWILVVVIALYILLSPSC |
| VcMATE2  [*Vaccinium corymbosum*] | MAAAEEYHPLLPGILQEESLASAEVEEILMQKPVAASRYIKLFGWESKLLWILSWASIVVSICNYMLSFVTLTFSGHLGALDLAGASIAMVGAQGLAYGIMLGMASAVQTVCGQAYGAKQYGAMGIICQRAIILHLGMAILLTFLYVYFGEVLKIIGQAEDIAEKGQIFARGMIPQLYAFSISCPLQRFLQAQNIANPLAYMSLSVFLVHIFLSWLVVYHFDFGLLGAALTLSLSWWILVVLQGLYILLSPSCKN |
| FaTT12-1  [*Fragaria x ananassa*] | MGSSEQYQPLLLGLDSHSRIPDLSSAVIEEFLEQSPVAVRWWPRLVAWESRLLWILSGSSILVSVFNYMLSFVTLMFCGHLSALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKHLSAMGIICQRAIVLHLGAAVLLTFLYWFSGPILVAMGQSESIAEQGQIFARGLIPQLYAFAINCPQQRFLQAQNIVNPLAYMSIGVFLVHTLLTWVVVYVVDYGLIGAALTLSFSWYLLVITNGIYILVSPN |
| DkMATE1  [*Diospyros kaki*] | MGSEEYQTLLLRLDSHLSLSSSGVEGLLSQSQPTSLNWYLRLAGWESRLLWQLSGASIAVSIFNYMLSFVTLTFTGHLGALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKRYGALGVICQRAVVLHVGAAVLLTFLYWFAGPILKAIGQSDSIADEGQVFARGLIPQLYAFSISCPLQRFLQAQNIVNPLAYMSVGVFLLHILITWLAVYVLNYGLIGAALTLSLSWWLLVILQSLYILLSPSCAQ |
| Nt-JAT1  [*Nicotiana tabacum*] | MVEELPQSLKEKKWQINWDAVSQELKKTSRFMAPMVAVTVFQYLLQVVSVMMVGHLGELALSSVAIATSLTNVTGFSLLTGLVGGMETLCGQAYGAQQYHKLSTYTYTAIISLFLVCIPICVLWCFMDKLLILTGQDHSISVEARKYSLWVIPAIFGGAISKPLSRYSQAQSLILPMLLSSFAVLCFHLPISWALIFKLELGNIGAAIAFSISSWLYVLFLASYVKLSSSCEKTRAPFSMEAFLCIRQFFRLAVP |
| NtMATE1  [*Nicotiana tabacum*] | MGKSMKSEVEQPLLIAAHGGSSELEEVLSDTQLPYFRRLRYASWIEFQLLYRLAAPSVAVYMINNAMSMSTRIFSGQLGNLQLAAASLGNQGIQLFAYGLMLGMGSAVETLCGQAYGAHRYEMLGVYLQRATVVLSVTGIPLTVVYLFSKNILLALGESKLVASAAAVFVYGLIPQIFAYAVNFPIQKFLQAQSIVAPSAFISLGTLFVHILLSWVVVYKIGLGLLGASLVLSFSWWIIVVAQFIYIIKSERCKA |
| AtEDS5  [*Arabidopsis thaliana*] | MLIKSQRLTLFSPLLSKTRRIPVNSHQTLVAESVITRRTLGAITATPSFHKNPVVIRRRIKLERVTRNCVRIDREIDEEEEEEEKERGDLVKQSIWEQMKEIVKFTGPAMGMWICGPLMSLIDTVVIGQGSSIELAALGPGTVLCDHMSYVFMFLSVATSNMVATSLAKQDKKEAQHQISVLLFIGLVCGLMMLLLTRLFGPWAVTAFTRGKNIEIVPAANKYIQIRGLAWPFILVGLVAQSASLGMKNSWGPLK |
| VcMATE3  [*Vaccinium corymbosum*] | MGTADTTPLLLNNNNLQEGGGGDLQGKAVAVARAFGTESKRLWKIAGPAILTAICQYSLGALTQTFAGFVGDLELAAVSVENSVVAGLAFGVMLGMGSALETLCGQAYGAGQVRMLGVYMQRSWVILLVTACLLVPVYVFSPPILELAGETTEISEAAGKFAIKMLPQLFAYALNFPIQKFLQAQRKVLVMTWVSAIVLVIHVVFSWLLMLKLGWGLTGAAIVLNTSWWLIVIGQLLYIFVTTSDGAWSGFSWLA |
| VcMATE8  [*Vaccinium corymbosum*] | MDNNIEHRLLGSEEEDPTDLKLRVWVESKKIWRVAAPGILARVSQFGLMVVTQSFIGHISEFDLAAYALVQTLTVRFANGILLGMSSATETLCGQAFGAGQHHMMGIYLQRSWIVDFVTATILLPLFIWTTQIFELLGEDTAISILAEKISIWFIPFLYNFVFTLTIQMYLQAQLKNMIVAWLATVSFIFHLVVSWLFVSELDLGIPGAMGALSISSWLVAVGEFVYIFGGWCPLSWKGFSKAAFSDLWPLIKLS |
| VcMATE9  [*Vaccinium corymbosum*] | MVTNIETQPDDELHQPILHSTPLPPPPPPPPPPQPPSTATYQPSTELEGVLSDTQLPLFNRLRLASWIELRLLFRLAGPAVMMYLINNAMSVSTRIYCGHLGNLELAAASLGNQGIQLFVYGLMLGMGSAVETLCGQAYGAHKYEMLGVYLQRSTVVLTLTGIPLTVIYILSKKILLLLGESSAVSSEAAVFVYGLIPQIFAYAINFPIQKFLQSQSIVAPSAYISASTLVLHLVLSWVVVYKLGLGLIGASLVL |
| RsMATE2  [*Raphanus sativus*] | MDSSQNDGAYQPLLQPQLSQATEWNNGELERVLSDVETPVFARLRKATMIESKLLFKLAAPAVIVYMINYLMSMSTQIFSGHLGNLELAAASLGNTGIQVFAYGLMLGMGSAVETLCGQAFGGKKYDMLGVYLQRSAVLLTLTGVLLTFIYVFSEPILLFLGESPEIASAASLFVYGLIPQIFAYAMNFPIQKFLQAQSIVAPSAYIATATLFVHLLLSWLAVYKLGMGLLGASLVLSLSWWIIVAAQFVYIVTS |
| RsMATE3  [*Raphanus sativus*] | MEKDNSFMDPFLSSTEDLDPTTQKALMDYLGVGSPASSLVSFCSTAVDIPPISNVGDFVREFRIESKKLWKLAGPAIFTSMAQFSLGAITQVFAGHISTIALAAVSIENSVIAGFSFGIMLGMGSALETLCGQAFGAGQASLLGVYLQRSWVILSATALMLSLLYIFAAPILTFIGQTATISAMAGLFSIFMIPQIFAYAINYPTAKFLQSQSKIMVMAGISGVALVIHTLLTWLVMSKFHWGLPGLAFVLNTSW |
| RsMATE5  [*Raphanus sativus*] | MDHTSPLLPHGGEVEEDYAPARTWSDVRRVLCTESAKMWLIAAPVGFNVICQYGVSSVTNIFVGHIGEIELSAVSISLSVIGTFSFGFLLGMGSALETLCGQAFGAGQFHMLGVYMQRSWIILFVSCLFLLPIYIFATPVLRLLGQAEEIAVPAGQFTLLTIPQLFSMAFNFPTSKFLQAQSKVTVIASIGFIALLLHVGMLWLFIIVFGLGTNGAALAFNITNWGIAISQIVYVIGWCNDGWTGLSWLAFKEIW |
| RsMATE7  [*Raphanus sativus*] | MSEDIGYNKETACDFPRNPLCIFLSDFKSVLIFDELGLEIARIALPAALALTADPIASLVDTAFIGQIGPVELAAVGVSIALFNQVSRIAIFPLVSITTSFVAEEDACSSQETTVQDHKECIETGINNAKEETQELIPDNNTDSISNESKISSSIFSVSESPVKKRNIPSVSSALIIGAILGLLQAAFLISTARPLLSFMGIKHDSPMLGPAQRYLSLRSLGAPAVLLSLATQGVFRGFKDTTTPLYATVVGDAT |
| RsMATE8  [*Raphanus sativus*] | MEPTTPLLDHGGGDEVKEDYSPARTLSDVKRVLSMESAKLWKIAAPIGFNIICQYGVTSFTNIFVGHIGEIGLSAVSISLSVIGTFSFGFLLGMGSALETLCGQAFGAGQVHMLGVYMQRSWIILFVSCIFLLPIYIFATPVLRFLGQAEEIAVAAGEFTLLTIPQLFSMAFTFPTSKFLQAQSKVIAIAWIGFVALIMHVAMLWLFIVVFGWGTNGAALAFSITNWGTAISQIVYVIGWCNEGWTGLTWLAFKE |
| MdMATE4 | MEKPLLHTAGDGDVELSYKPLLYEGTNEDYAPVRSFDALRRMFWIETVKLWQIAGSTVITMVCMYGNTAVVVLFAGHLGTIELSAISISLTVISIFSFGVMLGMGSALETLCGQAFGAGQVHMLGIYMQRSCIILFVTNIFLLPTYIFATPILKWLGQEDDIANLAGKFSLQIIPHLFSLAVIFPTQKFLQSQRKVKVLAWIAVLALIVEIGMLGLFIYVFDWGTTGAAVAFNVTRWGMAITQVVYIMGWCREGW |
| MdMATE8 | MEEPLLDTAAGGTTEYSNKQLMYEGESEDYAPVRSFGELRQMFWIETVKLWQIGGSAVITIMCMYGTNSVIVLFAGHLGTIELSAISISLSVISTFTYGFMLGMGSALETLCGQAFGAGQVHMLGIYMQRSCIILFVTSFLLLPIYIFATPVLKWLGQEDDIANEAGKFTLQIIPQLFSLAINFPAQKFLKAQRKVKVLAWIAVLALLIHIGMLALFIYVFDWGTSGAAVSFNITRWGISIAQVVYIMGWCYEGW |
| MdMATE7 | MEEPLLHTAAAGADELSNRPPLYEGGNEDYAPVRSFDAFQRMFWIETVKLWQIGVSSVITIICMYGTNAVILLFAGHLGTIQLSAISISLAVISTFTDGLMLGMGSALETLCGQAFGAGQVHMLGIYLQRSWIILFVTTLFLLPVYIFAVPILKWLGQEDDIANLAGKFTLQIIPQIFSLAIYFPAQKFLQAQRKVKVLAWIAFLGLVIHIGMLGLFMYEFDWGTLGAAVSFNITRWGMAIAQVVYIMGWCKEGW |
| MdMATE23 | MEEQEPPLHTAAAGATELSNKPPLYVGGNEDYAQVKSFDALRSMFWIETVKLWQMAGSAVITIICMYGTNAVILLFAGHLGTIQLSAISISLAVISTFTDGLMLGMASALETLCGQAFGAGQVHMLGIYLQRSWIILFVTTLFILPIYIFAAPILKLLGQEDDIANLAGKFTLQIIPQLFSLAINFPAQKFLQAQRKVKMLAWIAMLALVIHIGMIALFMYVFNWGTLGAAVSFNITRWAIAIAQVVYIMGWCKE |
| MdMATE6 | METPLLHGVSDGEFHDYEPVRSFKDARSVAWTETKKLWKIAGPIAFTIICNYGTNTASTMFVGHLGNLELSAVSISLSVISTFSFGFMLGMGSALETLCGQAFGAGRVHMLGVYMQRSWIILFTSCVILTPLYVFSGPILKLLGQEDDVANLAGSFTRYCIPQLFSLAFNFPAQKFLQSQSKVLVLMWIGFIALVVHIGWLFLFVYVFDWGIYGIGIAFSLTGWETVIAQNIYIMNWCKEGWTGFSWLAFKDIWA |
| MdMATE21 | MVTPVPLLHAVNGGEFHDYEPVRNFRDARSVAWNETKKLWKIAGPIAFTIICNFGNNTATTMFVGHLGNLQLSAVSISLSVICTFSFGFMLGMGSALETLCGQAFGAGHVNMLGVYMQRSWIILFTSCVILTPIYIFSAPILKLLGQDDDVANLAGTFTIYCIPQLFSLAFNFPAQKFLQAQSKVLVLAWIGFISLLVQIGMLSLFIYVFDWGIYGAGIAFGITGWVIVIAQNIYIMKWCKEGWTGFSWLAFKDI |
| MdMATE22 | METPLLTIKAEAAAAADYAPVRSFGEAMKVSWKEAVKLWRVATLVACTSLFQYLVQSITTVFVGHLGDVELSAVSLSLGVICNIPFGFLLGMATALGTLCGQAYGAGQVGQLGIYMQRSWIVLFIACIILSPVFIFAAPILKFLGQEHGIADPAGVYSLKIIPQMFSYAINLPTQRFLQAQSKVLVITLIAFAALIIQTGLLHLFINVFGLGTTGAAVAYDITNWGVAIGQVGYVMVCCKEEWTGFSWLAFREIW |
| MdMATE20 | MVQSPTLMIDGEDDAVSTFEPADLHHAPPAFIGSSDGDYPVIRSFQDAKSICFVESTKLWSIAGPIAFNILCNYGVNSFTNIFVGHIGNVELSAVAISLSVISNFSFGFLLGMASALETLCGQAFGAGQVDMLGVYMQRSWIMLFAACIAILPLYIYSTPVLKLLGQEDDIADLAGKFSIQTIPQMVSLAINFPTQKFLQAQSKVGVLAWIGFITLIAHVGILFLFIKVFGWGTSGAAAAYNISAWGMALAQVVY |
| MdMATE24 | MEIGNDQNTPLLVSNHSGHEDGGEEKVGFVKQYGIESKKLWKIAGPAIFTSLCQYSLGALTQTFAGFVGDLELAAVSIENSVIAGLAFGVMLGMGSALETLCGQAYGAGQIRMLGVYMQRSWIILLVTACAMVPIYVWSPPILKLFGETTEISEAAGRFALLMLPQLFAYALNFPIQKFLQAQRKVSVIAWISGAVLVEHAVLSWLLMIKLGWGLTGAAITLNASWWLIIIGQLLYIFITKSDGAWSGFSWLAFS |
| MdMATE49 | MPTTSRMAIVQEDDPVVVHAGDIPPIVSFRGFSRQFYKETKKLWYLAGPAIFTSLSQYSIGAITQIFAGHVGTLELATVSVENSVIAGFSFGFMYGMGSALETLCGQAFGAGQLDMLGIYMQRSWVILNATAVLLSFLYIFAEQLLKMIGQPDDISKAAGQFAIWMIPQLFAYAMNFPLAKFLQSQSKIMVMAAISAVALVLHTLFSWLLTLKLGWGLVGAAVVLNTSWWFIVLAQLVYIFSGTCGRAWAGFSWK |
| MdMATE3 | MASNSALVEAEVPLLDDLASTVRLKREHNDDENQATTLVRRSWIESKKLWHIVGPAIFSRVASYSMLVITQAFAGHLGDLELAAISIANNVIVGFDFGLLLGMASALETLCGQAYGAKKYYMLGVYMQRSWIVLFLCCILLLPIYLFASPFLKLLGQPAEVAELSGVVSMVMIPLHFSFAFQFPLQRFLQSQLKTAVIAWVSLVSLAVHVFVSWLFVYRLQFGVIGTAITINFSWWVLVFGLLGYTLFGGCPLTW |
| MdMATE25 | MKGSVEEKVMDRQKYSLLAIESSSTSEMKKIATDFLSRVWIESKKLWHIVGPDIINRLAGYSMTVITQAFAGHLGDVELASISMANNIIVGFGYGLLLGMASALATLCGQTFGAKRYHMLGIYMQRSWIVLFSCCILLLPVYLYASPILKLIGQSDEVAEQSGALALWLIPLHFSYAFQFPLQRFLQCQLKNFVTLWVSLAVLVLHSVTTWILVSVLDFGVVGAAIALDISCWACGLGLFWYVVSGGCPLSWVGF |
| MdMATE43 | MLFTDSFNNSYFTKIPNCYVTPRANSLSLSLSLSTNIGSQQTRVQFLISLMGNRNSDQDGDLTQSLLPEALPQNSAANDRDQKTDLSLRVWLETKKLWKIVGPAIFSRVATFSMNVITQAFAGHLGEVELASVSIGITLVIGFNFGLLLGMASALETLCGQAFGAKRYHMLGIYLQRSWTVLFLCCIALLPVYIFVTPILKLLGQSDDVAALSGAVALWLIPLHFSFAFYFPLTRFLQSQLQNIVIAWVSLVALL |
| MdMATE32 | MGEEIKGSLLVKETGVGEEEARIIDGDEELSLKRRVWIETKKMWVVAGPAIFTRVASFGTNVISQAFIGHIGSAQLAAFSLVFTVLVRFANGILLGMASALETLCGQSYGAKQYNMLGIHLQRSWIVLFVSTCLLIPLFVFTTPIFEALGQAENISEIAGHISLWVIPVLFAFVVSFTCQMYLQAQSKNMIIAYVSAISIGIHIFLCWLLSVKLKFGVPGVMVSTLIAYWLPNLGQLLFVLCGGCPETWTGFSML |
| MdMATE40 | MGEDIKRSLLVKETSAGEEETRVIDGEEELSLKRRVWIEIKKMWLVAGPAIFTRVASFGTNVVSQAFIGHIGSLELAAFSLVFTVLVRFGNGILLGMASALETLCGQSYGAKQYNMLGIHLQRSWIVLCVGTLFLIPLFVFTTPIFEALGQADNISEVAGYISLWVIPVLFAFVVSFTCQMYLQAQSKNMIVAYVSAVSIGIHIFLCWLLSVKFKFGVPGVLVSTIISYWLPNVGQLLFILCGGCPETWTGFSML |
| MdMATE1 | MGSQEEYQPLLIRLDSYSQIPNLSSSAIEEFLEHKPVAVRWWPKLVAWESRLLWILSGSSIAVSIFNYMLSFVTLMFCGHLGALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKQLPAMGIICQRAIILHLGAAVLLTFVYWWSGPILIAIGQTEDIAEQGQVFARGIIPQLYAFAINCPQQRFLQAQNIVNPLAYMSFGVFLVHILLTWVVVYVVDYGLMGAALTLSLSWWLLVITYGIYILVSPM |
| MdMATE52 | MGSVEEIQQPLLLGFDTHSRLADLSSPAVEEFLGHRPVALWWWPRLVVWESRLLWILSGSSIIVSVFNYMLSFVTLMFCGHLSALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGAKQLPAMGIICQRAIILHLGAAILLSFVYWWSGPILVAIGQSEEIAEQGQIFARGIIPQLFAFAINCPQQRFLQAQNIVNPLAYMSVGVFILHILLNWVVVFVVDYGLIGAALTLSFSWWLLVIIYGLYILLSP |
| MdMATE2 | MGTAEEYQPLLNGLDSHSRIPDLSSTAVEEFLEHKPVAVRWWLRLVAWESRLLWTLSGSSIIVSIFNYMLSFTTLMFCGHLSALELAGASIASVGIQGLAYGIMLGMASAVQTVCGQAYGARQYPAMGIICQRAIVLHLGAAVLLTFLYWWSGPILIAIGQTEEIAEQGQVFARGIVPQLYAFAINCPQQRFLQAQNIVNPLAFMSFGVFLVHILLSWVVVYVADYGLTGAALTLSFSWWLLVIVYGIYIVVSPK |
| MdMATE17 | MEYSSDSDLSEPMLVPKTSSLQQIVSSELEDTLNNTDLSNFQRLRTATWLETKTLYRLAAPAVVVYLLNNVISMSTQILCGHLGNLELAASSLGNTGIQVFAYGLMLGMGSAVETLCGQAYGAHKYEMLGIYMQRSTILLVATGIPLTIVYIFSKPLLLALGESASISAAAAVFVYGLIPQIFAYACNFPIQKFLQAQSIVFPSAYISAGALVVHIVLSWVVVYKLDWGLLGAALMLSFSWWIIVVAQFVYIVWT |
| MdMATE51 | MANNELQHPLLESYHPLPPTSTQSSKHSHDEDASRELEQVLSDTDKPFSQRLKPALWIESKLLVILAAPAIIVYVINYVMSMSTQIFSGHLGNLELAASSLGNNGIQMFAYGLLLGMGSAVETLCGQAYGAQKYEMLGIYLQRSTVLLFFPGVLLTIIYIFSEPILLLLGESPSIASSAAVYVYGLIPQIFAYVVNFPIQKFMQAQSIVAPSAYISTGTLVIHIVLSWVAVYTLGLGLLGASLVLSLSWWITVVA |
| MdMATE16 | MPKSTYVHGQRVKYIRSLTWTSYIINAASYFQNSKHQFLSMHRTVAHFCHTPHHLFGPKMGSQHPLHQPILHSEPEPVAQASSDGDGVDFLLEKVLSDTQLPSFKRFRSATWIELKLLFRLAAPAVLVYVINNSMSLSARVFAGHLGNLELAAASLGNNGIQLLAYGLMLGMGSAVETLCGQAYGAQKYDMLSIYLQRATIVLSLTGLPLLAIFLLTKPMLILLGEPPAVASAAAVFVYGLIPQIFAYAVNFPIQ |

**Supplementary Table S3 Primer sequences used in the study**

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
|  | Primer name | Genebank | Froward primer | Reverse primer |
| CDS amplification | MdMYB10(OE) | MDP0000259614 | CGGGATCCATGGAGGGATATAACGAAAACCTGAG | CGGGATCCATTCTTCTTTTGAATGATTCCAAAGGTCCG |
| MdMYB10(i) | MDP0000259614 | GGGGACAAGTTTGTACAAAAAAGCAGGCAGGTGGTCATTGATTGCT | GGGGACCACTTTGTACAAGAAAGCTGGGTATTCCAAAGGTCCGTGCTA |
| MdMYB9(OE) | MDP0000210851 | GCTCTAGAATGGGAAGGAGTCCGTGTTG | CGAGCTCTTAGACTACAACATTTTCTTGGGAAGGC |
| MdMYB9(i) | MDP0000210851 | GGGGACAAGTTTGTACAAAAAAGCAGGCTGGGAAGGAGTCCGTGTTG | GGGGACCACTTTGTACAAGAAAGCTGGGTCAGCGGCAGTTGATGTTT |
| MdMATE8(i) | MDP0000210851 | GGGGACAAGTTTGTACAAAAAAGCAGGACACTCCAAATCATCCCTCAA | GGGGACCACTTTGTACAAGAAAGCTGGGTTCCAACCCTCATAACACCAAC |
| qRT-PCR | *MdUBQ* | DQ438989 | CTCCGTGGTGGTTTTTAAGT | GGAGGCAGAAACAGTACCAT |
| *MdMYB10* | MDP0000259614 | TGCCTGGACTCGAGAGGAAGACA | CCTGTTTCCCAAAAGCCTGTGAA |
| *MdMYB9* | MDP0000210851 | CCGCAAACCCATTAGAGC | GTCCAGCAGCCGTCATTT |
| *MdbHLH* | MDP0000225680 | CCTACAAGCCACGATTACTACAA | TGAACGCAATGAGGAATACAA |
| *MdbZIP* | MDP0000265875 | TCCAATAGGGAATCGGCACG | AATCCTTCACCTCCACCAA |
| *MdCHS* | MDP0000686666 | GGAGACAACTGGAGAAGGACTGGAA | CGACATTGATACTGGTGTCTTC |
| *MdCHS* | MDP0000575740 | CGTTCCTGGGCTTATTTCC | CAGCAGACTTCCTCCTCACTT |
| *MdF3'H* | MDP0000286933 | TTCAACATCGGCGACTTCA | TTCAACAATGGCGGTCAAG |
| *MdDFR* | MDP0000494976 | ACATTATGGCATCATCAAGCA | TCAAACCCTATCTCCCTCAACT |
| *MdLDOX* | MDP0000360447 | AAGCGTGACTTGTCTATTTG | ACTTCTTTCTCCAGCCTCC |
| *MdLODX* | MDP0000788934 | CCAAGTGAAGCGGGTTGTGCT | CAAAGCAGGCGGACAGGAGTAGC |
| *MdUFGT* | MDP0000543445 | CCACCGCCCTTCCAAACACTCT | CACCCTTATGTTACGCGGCATGT |
| *MdGST* | MDP0000252292 | AGTTGTAGAAGATGGTGACT | CAGGTCGTTGAAGTTGTG |
| *MdMATE* | MDP0000175055 | CTTCTTACTGTTGCCGATT | TCTGAGCCTGGAGGAACTTTT |
| Y1H | MdMYB10-pGADT7 | MDP0000259614 | CGGGATCCATGGAGGGATATAACGAAAACCTGAG | CCGCTCGAGATGATTCCAAAGGTCCGTGCT |
| MdMYB9-pGADT7 | MDP0000210851 | CGAGCTCGCTCTAGAATGGGAAGGAGTCCGTG | CCGCTCGAGGCTCTAGAGACTACAACATTTTCTTGGGAAG |
| MdMATE8-pHIS2 | MDP0000175055 | GAGCTCATTAGCCGGTTGACTTTCAAAA | GAATTCTTAGTTAGGCGTAAGATTTAAGTTTTG |

**Supplementary Table S4.** **Summary of the sequencing results and correlation coefficient values.**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TABLE4 | Summary of the sequencing results.** | | | | | | | | | | | |
| **Sample name** | | **Raw reads** | **Clean reads** | **Clean reads rate (%)** | **Mapping to genome** | | **Mapped position (%)** | | | **Q30 (%)** |
|  | **Rate (%)** | **Exon** | **Intron** | **Intergenic** |
| Control-24 | C1 | 33763726 | 32022902 | 94.84 | 29041737 | 90.69 | 83.8 | 1.8 | 14.3 | 90.82 |
| C2 | 27497162 | 26395420 | 95.99 | 24058541 | 91.15 | 84.2 | 2 | 13.8 | 91.65 |
| C3 | 27168760 | 26082490 | 96 | 23644410 | 90.65 | 84.4 | 1.8 | 13.8 | 91.17 |
| ALA-24 | T4 | 27298414 | 26275352 | 96.25 | 23692171 | 90.17 | 83.6 | 1.9 | 14.5 | 91.22 |
| T5 | 26376820 | 25078268 | 95.08 | 22636521 | 90.26 | 83 | 2.2 | 14.8 | 91.5 |
| T6 | 29591274 | 28299616 | 95.64 | 25447680 | 89.92 | 83.5 | 2.1 | 14.4 | 91.06 |
| Control-48 | C7 | 28636090 | 27085828 | 94.59 | 24533552 | 90.58 | 84.1 | 2 | 13.9 | 91.52 |
| C8 | 30744152 | 29388298 | 95.59 | 26789159 | 91.16 | 84.8 | 1.9 | 13.3 | 91.6 |
| C9 | 28614420 | 27468658 | 96 | 24894274 | 90.63 | 84.9 | 1.8 | 13.3 | 91.52 |
| ALA-48 | T10 | 31803012 | 30571964 | 96.13 | 27715364 | 90.66 | 83.7 | 2 | 14.3 | 91.41 |
| T11 | 27520458 | 26492144 | 96.26 | 23978432 | 90.51 | 83.7 | 2 | 14.3 | 91.69 |
| T12 | 25503524 | 24457092 | 95.9 | 22301014 | 91.18 | 83.9 | 2.1 | 14 | 91.16 |
| Control-72 | C13 | 29788534 | 28481664 | 95.61 | 25810073 | 90.62 | 84.8 | 1.9 | 13.3 | 91.17 |
| C14 | 31353898 | 30074766 | 95.92 | 27346568 | 90.93 | 84.9 | 1.9 | 13.2 | 91.53 |
| C15 | 28556660 | 26791794 | 93.82 | 24254091 | 90.53 | 84.1 | 2.1 | 13.8 | 89.2 |
| ALA-72 | T16 | 27268836 | 26004326 | 95.36 | 23611323 | 90.8 | 84 | 1.9 | 14.1 | 90.94 |
| T17 | 24099168 | 22679590 | 94.11 | 20466525 | 90.24 | 84.2 | 1.9 | 13.9 | 90.5 |
| T18 | 28898534 | 27497178 | 95.15 | 24866350 | 90.43 | 84 | 2 | 14.1 | 90.7 |
| Total | -- | 514483442 | 491147350 | -- | 445087785 | -- | -- | -- | -- | -- |
| Mean | -- | 28582413 | 27285964 | 95.46 | 24727099 | 90.62 | -- | -- | -- | -- |

**Supplementary Table S4. Summary of the sequencing results and correlation coefficient values.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| **TABLE 4 | Correlation coefficient vlaues** | | | | | | | | | | | | | | | | | | |
| **Sample** | **C1** | **C2** | **C3** | **T4** | **T5** | **T6** | **C7** | **C8** | **C9** | **T10** | **T11** | **T12** | **C13** | **C14** | **C15** | **T16** | **T17** | **T18** |
| **C1** | 1 | 0.968 | 0.966 | 0.947 | 0.946 | 0.942 | 0.96 | 0.954 | 0.96 | 0.951 | 0.951 | 0.942 | 0.951 | 0.938 | 0.946 | 0.957 | 0.953 | 0.947 |
| **C2** | 0.968 | 1 | 0.97 | 0.943 | 0.943 | 0.94 | 0.961 | 0.954 | 0.959 | 0.947 | 0.944 | 0.94 | 0.951 | 0.94 | 0.948 | 0.951 | 0.948 | 0.942 |
| **C3** | 0.966 | 0.97 | 1 | 0.944 | 0.944 | 0.941 | 0.957 | 0.95 | 0.954 | 0.947 | 0.943 | 0.94 | 0.946 | 0.936 | 0.945 | 0.949 | 0.945 | 0.942 |
| **T4** | 0.947 | 0.943 | 0.944 | 1 | 0.968 | 0.967 | 0.941 | 0.932 | 0.942 | 0.968 | 0.964 | 0.966 | 0.942 | 0.945 | 0.948 | 0.955 | 0.951 | 0.965 |
| **T5** | 0.946 | 0.943 | 0.944 | 0.968 | 1 | 0.967 | 0.937 | 0.928 | 0.939 | 0.966 | 0.962 | 0.964 | 0.935 | 0.938 | 0.942 | 0.953 | 0.951 | 0.963 |
| **T6** | 0.942 | 0.94 | 0.941 | 0.967 | 0.967 | 1 | 0.935 | 0.928 | 0.936 | 0.963 | 0.961 | 0.962 | 0.932 | 0.936 | 0.939 | 0.953 | 0.95 | 0.963 |
| **C7** | 0.96 | 0.961 | 0.957 | 0.941 | 0.937 | 0.935 | 1 | 0.968 | 0.969 | 0.949 | 0.947 | 0.942 | 0.964 | 0.948 | 0.958 | 0.958 | 0.956 | 0.944 |
| **C8** | 0.954 | 0.954 | 0.95 | 0.932 | 0.928 | 0.928 | 0.968 | 1 | 0.968 | 0.94 | 0.942 | 0.934 | 0.96 | 0.938 | 0.95 | 0.958 | 0.957 | 0.939 |
| **C9** | 0.96 | 0.959 | 0.954 | 0.942 | 0.939 | 0.936 | 0.969 | 0.968 | 1 | 0.949 | 0.949 | 0.944 | 0.963 | 0.949 | 0.957 | 0.958 | 0.956 | 0.946 |
| **T10** | 0.951 | 0.947 | 0.947 | 0.968 | 0.966 | 0.963 | 0.949 | 0.94 | 0.949 | 1 | 0.968 | 0.968 | 0.95 | 0.951 | 0.955 | 0.96 | 0.956 | 0.967 |
| **T11** | 0.951 | 0.944 | 0.943 | 0.964 | 0.962 | 0.961 | 0.947 | 0.942 | 0.949 | 0.968 | 1 | 0.964 | 0.949 | 0.942 | 0.948 | 0.964 | 0.961 | 0.968 |
| **T12** | 0.942 | 0.94 | 0.94 | 0.966 | 0.964 | 0.962 | 0.942 | 0.934 | 0.944 | 0.968 | 0.964 | 1 | 0.946 | 0.948 | 0.952 | 0.956 | 0.953 | 0.966 |
| **C13** | 0.951 | 0.951 | 0.946 | 0.942 | 0.935 | 0.932 | 0.964 | 0.96 | 0.963 | 0.95 | 0.949 | 0.946 | 1 | 0.963 | 0.968 | 0.956 | 0.953 | 0.948 |
| **C14** | 0.938 | 0.94 | 0.936 | 0.945 | 0.938 | 0.936 | 0.948 | 0.938 | 0.949 | 0.951 | 0.942 | 0.948 | 0.963 | 1 | 0.969 | 0.945 | 0.941 | 0.949 |
| **C15** | 0.946 | 0.948 | 0.945 | 0.948 | 0.942 | 0.939 | 0.958 | 0.95 | 0.957 | 0.955 | 0.948 | 0.952 | 0.968 | 0.969 | 1 | 0.953 | 0.95 | 0.952 |
| **T16** | 0.957 | 0.951 | 0.949 | 0.955 | 0.953 | 0.953 | 0.958 | 0.958 | 0.958 | 0.96 | 0.964 | 0.956 | 0.956 | 0.945 | 0.953 | 1 | 0.967 | 0.962 |
| **T17** | 0.953 | 0.948 | 0.945 | 0.951 | 0.951 | 0.95 | 0.956 | 0.957 | 0.956 | 0.956 | 0.961 | 0.953 | 0.953 | 0.941 | 0.95 | 0.967 | 1 | 0.961 |
| **T18** | 0.947 | 0.942 | 0.942 | 0.965 | 0.963 | 0.963 | 0.944 | 0.939 | 0.946 | 0.967 | 0.968 | 0.966 | 0.948 | 0.949 | 0.952 | 0.962 | 0.961 | 1 |

**Supplementary Table S5.** **Gene expression quantification**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| FPKM Interval | Control-24\_1 | Control-24\_2 | Control-24\_3 | ALA-24\_1 | ALA-24\_2 | ALA-24\_3 | Control-48\_1 | Control-48\_2 | Control-48\_3 | ALA-48\_1 | ALA-48\_2 | ALA-48\_3 | Control-72\_1 | Control-72\_2 | Control-72\_3 | ALA-72\_1 | ALA-72\_2 | ALA-72\_3 |
| 0~1 | 34805  (54.80%) | 34490  (54.30%) | 34720  (54.66%) | 34078  (53.65%) | 34097  (53.68%) | 34159  (53.78%) | 34515  (54.34%) | 34947  (55.02%) | 34377  (54.12%) | 34060  (53.63%) | 34169  (53.80%) | 33915  (53.40%) | 34107  (53.70%) | 33870  (53.33%) | 33694  (53.05%) | 34442  (54.23%) | 34548  (54.39%) | 33947  (53.45%) |
| 1~3 | 6407  (10.09%) | 6374  (10.04%) | 6426  (10.12%) | 6262  (9.86%) | 6319  (9.95%) | 6314  (9.94%) | 6464  (10.18%) | 6446  (10.15%) | 6375  (10.04%) | 6230  (9.81%) | 6349  (10.00%) | 6197  (9.76%) | 6304  (9.93%) | 6189  (9.74%) | 6344  (9.99%) | 6397  (10.07%) | 6355  (10.01%) | 6349  (10.00%) |
| 3~15 | 11609  (18.28%) | 11852  (18.66%) | 11733  (18.47%) | 11782  (18.55%) | 11858  (18.67%) | 11796  (18.57%) | 11797  (18.57%) | 11716  (18.45%) | 11880  (18.70%) | 11865  (18.68%) | 11841  (18.64%) | 11946  (18.81%) | 11982  (18.86%) | 11863  (18.68%) | 12030  (18.94%) | 11863  (18.68%) | 11825  (18.62%) | 11811  (18.60%) |
| 15~60 | 7570  (11.92%) | 7532  (11.86%) | 7364  (11.59%) | 8312  (13.09%) | 8150  (12.83%) | 8127  (12.80%) | 7593  (11.95%) | 7295  (11.49%) | 7682  (12.09%) | 8250  (12.99%) | 8122  (12.79%) | 8367  (13.17%) | 8017  (12.62%) | 8390  (13.21%) | 8258  (13.00%) | 7760  (12.22%) | 7758  (12.21%) | 8343  (13.14%) |
| >60 | 3124  (4.92%) | 3267  (5.14%) | 3272  (5.15%) | 3081  (4.85%) | 3091  (4.87%) | 3119  (4.91%) | 3146  (4.95%) | 3111  (4.90%) | 3201  (5.04%) | 3110  (4.90%) | 3034  (4.78%) | 3090  (4.86%) | 3105  (4.89%) | 3203  (5.04%) | 3189  (5.02%) | 3053  (4.81%) | 3029  (4.77%) | 3065  (4.83%) |

**Supplementary Table S6.** **DEGs between ALA-treated and control calli.**

|  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Gene\_id | 24h | 48h | 72h | Gene\_id | 24h | 48h | 72h | Gene\_id | 24h | 48h | 72h | Gene\_id | 24h | 48h | 72h |
| MDP0000014856 | 1.0332 |  |  | MDP0000196672 | -2.1984 |  |  | MDP0000273384 | 1.0429 |  |  | MDP0000535947 |  | 1.7024 |  |
| MDP0000022760 | -1.6192 |  |  | MDP0000196740 | 1.1987 |  |  | MDP0000273828 | 1.2145 |  |  | MDP0000538331 | -2.0873 |  |  |
| MDP0000031172 | 1.9155 |  |  | MDP0000196862 |  | 1.0859 |  | MDP0000274409 |  |  | 1.089 | MDP0000541805 |  |  | -1.0151 |
| MDP0000032171 |  | -1.5745 |  | MDP0000196876 |  | 1.4136 |  | MDP0000274423 |  |  | 1.0277 | MDP0000542815 |  | -2.3481 |  |
| MDP0000044356 |  | 1.5905 |  | MDP0000196922 | -1.4873 |  |  | MDP0000274441 | 1.9352 |  |  | MDP0000542944 | 3.2861 | 1.8143 |  |
| MDP0000059789 | 1.0107 |  |  | MDP0000197025 |  |  | -1.0249 | MDP0000274766 | -1.8905 |  |  | MDP0000543445 | 2.8258 | 1.9941 | 1.4211 |
| MDP0000064909 |  | 1.2131 |  | MDP0000197224 |  | -1.2237 |  | MDP0000274908 |  | -2.4928 |  | MDP0000543718 |  | -1.4561 |  |
| MDP0000065186 |  | -1.1354 |  | MDP0000197283 | 2.0613 | 1.34 |  | MDP0000275026 | -1.4827 |  |  | MDP0000544274 | -1.502 |  |  |
| MDP0000073873 | -1.0923 |  |  | MDP0000197297 | -1.2886 |  |  | MDP0000275151 | 1.1569 |  |  | MDP0000544533 |  |  | 1.3327 |
| MDP0000091523 |  | 2.0758 |  | MDP0000197360 | 1.2838 |  |  | MDP0000275985 |  | -1.5429 |  | MDP0000545463 | -2.3867 |  |  |
| MDP0000094767 |  | 1.1035 |  | MDP0000197977 |  | 1.4563 |  | MDP0000276215 |  | -2.0055 |  | MDP0000545558 |  | -1.4983 |  |
| MDP0000096349 |  | -1.2632 |  | MDP0000198054 |  | -5.5322 |  | MDP0000276431 | -1.8997 |  |  | MDP0000546099 |  |  | -2.1407 |
| MDP0000103621 | -1.2585 |  |  | MDP0000198217 | -1.5064 |  |  | MDP0000276889 | 1.6929 |  |  | MDP0000547254 |  |  | -1.4215 |
| MDP0000119262 |  | -1.2071 |  | MDP0000198843 |  |  | 1.4934 | MDP0000277088 |  |  | -1.2258 | MDP0000547283 |  | 1.7022 |  |
| MDP0000119275 |  | 1.0831 |  | MDP0000199052 | 1.0302 |  |  | MDP0000277457 | -1.2242 |  |  | MDP0000547655 |  |  | -2.1372 |
| MDP0000119425 | 1.0309 |  |  | MDP0000199202 | -1.2191 |  |  | MDP0000277477 |  | 2.59 |  | MDP0000551192 | -1.963 |  |  |
| MDP0000119931 | 1.8971 |  |  | MDP0000199698 | 1.1042 |  |  | MDP0000277525 |  | 1.3147 |  | MDP0000552015 |  |  | 1.244 |
| MDP0000119961 | -1.033 |  |  | MDP0000199827 | 1.4709 |  |  | MDP0000277906 | 1.049 |  |  | MDP0000554480 | -4.0854 |  |  |
| MDP0000120120 | 1.1115 |  |  | MDP0000199837 |  |  | -1.314 | MDP0000277990 | -2.7494 |  |  | MDP0000554950 | -1.3377 |  |  |
| MDP0000120125 | -1.3762 |  |  | MDP0000200231 |  | 1.0363 |  | MDP0000278249 | -1.1605 |  |  | MDP0000555486 | 1.6084 |  |  |
| MDP0000120180 |  | -1.729 |  | MDP0000200564 | -2.1941 | -2.061 |  | MDP0000278259 | -1.0135 |  |  | MDP0000556996 | 1.0073 |  |  |
| MDP0000120214 |  |  | 1.1816 | MDP0000200635 |  | -1.5497 |  | MDP0000278762 | -2.2637 |  |  | MDP0000557169 |  | -1.179 |  |
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| MDP0000185406 | 1.244 |  | 1.2827 | MDP0000263680 | -2.0406 |  |  | MDP0000460074 |  | 3.0507 |  | MDP0000915330 | 1.288 |  |  |
| MDP0000186135 | -2.9251 |  |  | MDP0000263736 | 1.6137 |  |  | MDP0000460502 |  | -1.0024 |  | MDP0000915991 | 1.1914 |  |  |
| MDP0000186322 | 1.1972 |  |  | MDP0000263835 |  | 1.3506 |  | MDP0000463045 | -2.4276 |  |  | MDP0000916623 | 1.6234 |  |  |
| MDP0000186494 | -1.4794 |  |  | MDP0000264409 | 1.4608 | 1.0208 |  | MDP0000463117 |  | -1.011 |  | MDP0000916647 |  |  | 1.1922 |
| MDP0000186587 |  |  | 1.2568 | MDP0000264424 | -1.7122 |  |  | MDP0000463624 | 1.2328 |  |  | MDP0000916930 |  |  | -1.079 |
| MDP0000187482 | -1.4934 |  |  | MDP0000264731 |  |  | 1.3584 | MDP0000465335 |  |  | 2.2259 | MDP0000917496 | 3.4996 |  |  |
| MDP0000187617 | 1.3892 |  |  | MDP0000264936 |  | 1.2499 |  | MDP0000465844 |  | -1.9578 | -2.2069 | MDP0000917582 |  | 1.1299 |  |
| MDP0000187703 | 2.0759 |  | -1.7292 | MDP0000265094 | -1.2248 |  |  | MDP0000466825 |  |  | 1.4186 | MDP0000918133 | 1.0408 |  |  |
| MDP0000187851 | -3.9879 |  |  | MDP0000265157 |  | 1.0457 |  | MDP0000468391 |  | -2.3154 |  | MDP0000918738 |  |  | 1.4443 |
| MDP0000187900 | -1.7772 | -1.4842 |  | MDP0000265372 |  |  | -1.0231 | MDP0000469664 |  | 1.4894 |  | MDP0000919471 |  |  | -1.6572 |
| MDP0000187921 |  | -1.2351 |  | MDP0000265423 |  |  | 1.6887 | MDP0000470297 | 1.069 | 2.5946 |  | MDP0000920069 | -1.1951 |  |  |
| MDP0000188093 |  |  | 1.0902 | MDP0000265560 | 1.0974 | 1.2067 |  | MDP0000472943 |  |  | 1.4861 | MDP0000920189 |  |  | 1.369 |
| MDP0000188275 | -3.5499 |  |  | MDP0000265654 |  | 1.3227 | 1.0845 | MDP0000475144 |  | -1.9707 | -2.6494 | MDP0000920266 | -1.5944 |  |  |
| MDP0000188310 |  | -1.3447 | -1.477 | MDP0000265806 | -1.0667 |  |  | MDP0000475658 |  | -1.6484 |  | MDP0000920792 | 2.753 |  |  |
| MDP0000188909 |  | -2.7534 |  | MDP0000265817 |  |  | -1.1224 | MDP0000476095 |  | -1.0727 |  | MDP0000920996 | 2.5992 |  |  |
| MDP0000189281 |  |  | 2.1348 | MDP0000265875 | 1.0644 |  |  | MDP0000477900 | -1.6694 |  |  | MDP0000921871 | -3.541 |  |  |
| MDP0000189486 |  |  | -1.4066 | MDP0000266004 |  | 1.3965 |  | MDP0000479094 | -2.0888 |  |  | MDP0000923711 |  |  | -1.1234 |
| MDP0000189901 |  | -1.852 |  | MDP0000266107 |  | -1.5587 |  | MDP0000479177 |  |  | -2.3778 | MDP0000924327 |  | 1.7822 |  |
| MDP0000190029 | -1.6662 |  |  | MDP0000266156 | -1.5818 |  |  | MDP0000480293 |  |  | 2.7068 | MDP0000925058 | -2.8797 |  |  |
| MDP0000190452 | -1.4054 |  |  | MDP0000267047 | -3.1442 |  |  | MDP0000480581 | -3.8837 |  |  | MDP0000928620 |  | -1.1907 |  |
| MDP0000190460 | 1.12 |  |  | MDP0000267128 |  | 1.3786 |  | MDP0000480605 | 1.1829 | 1.537 |  | MDP0000928643 |  |  | -1.2273 |
| MDP0000190785 | 1.1341 |  |  | MDP0000267178 |  | 1.6551 |  | MDP0000482092 |  |  | -1.2676 | MDP0000929213 | 1.8698 | 1.8087 |  |
| MDP0000190809 | -1.7551 |  |  | MDP0000267249 |  |  | 4.0528 | MDP0000482268 |  | 1.815 |  | MDP0000930268 | 1.1271 |  |  |
| MDP0000191472 |  | 1.5742 |  | MDP0000267662 | 1.5725 |  |  | MDP0000486046 |  | 1.4401 |  | MDP0000930655 | -3.4974 |  |  |
| MDP0000191620 |  |  | 1.1233 | MDP0000267894 | 1.1105 |  |  | MDP0000487271 |  |  | 1.3284 | MDP0000931334 |  |  | 1.1333 |
| MDP0000191851 | -2.4117 | -1.9169 |  | MDP0000268423 |  |  | -1.4433 | MDP0000487488 |  |  | -1.3402 | MDP0000932449 |  | 1.4005 |  |
| MDP0000191921 | -1.1864 |  |  | MDP0000268505 |  |  | -1.4963 | MDP0000487946 | -1.3902 |  |  | MDP0000932804 | -2.583 |  |  |
| MDP0000191939 | 1.3693 |  | 1.1078 | MDP0000268589 |  | 1.3801 |  | MDP0000491872 |  | -1.0239 |  | MDP0000933711 |  |  | 1.2977 |
| MDP0000192000 | 1.0924 |  |  | MDP0000268890 | 1.3427 |  |  | MDP0000494976 | 2.5743 | 1.3714 | 1.2547 | MDP0000934489 |  |  | 1.0824 |
| MDP0000192210 |  |  | -1.5381 | MDP0000268980 | 1.822 | 1.8662 |  | MDP0000495801 | -2.2145 |  |  | MDP0000935120 | 1.2207 |  |  |
| MDP0000192374 |  | 1.414 | 1.082 | MDP0000269628 | 1.2342 |  |  | MDP0000496370 |  |  | 1.0235 | MDP0000935925 | 1.3975 |  |  |
| MDP0000192586 |  |  | -1.4857 | MDP0000269735 |  | -1.8353 |  | MDP0000498615 | -2.636 |  |  | MDP0000936591 |  |  | 1.7724 |
| MDP0000192960 |  | 1.8204 |  | MDP0000270189 | 1.5276 |  |  | MDP0000499282 | -2.3776 | -2.6286 |  | MDP0000937996 |  | 2.9467 |  |
| MDP0000193181 |  | 1.285 |  | MDP0000270365 | -2.3191 |  |  | MDP0000501816 |  | 1.5739 |  | MDP0000939379 | 1.7674 |  | -1.8536 |
| MDP0000193206 |  |  | 1.2994 | MDP0000270618 | 1.0658 |  |  | MDP0000502306 |  |  | 1.8529 | MDP0000939502 |  | -1.2556 |  |
| MDP0000193325 | 1.0388 |  |  | MDP0000270938 |  | 1.403 |  | MDP0000505556 | 1.9485 |  |  | MDP0000940411 |  |  | 1.103 |
| MDP0000193385 |  | -2.0556 |  | MDP0000270966 |  |  | 1.1265 | MDP0000512219 | -7.08 |  |  | MDP0000940828 |  | -1.2369 |  |
| MDP0000193734 | 1.859 |  |  | MDP0000270977 |  |  | 1.3021 | MDP0000514153 | 1.6613 | 1.2437 |  | MDP0000943292 | -1.5178 |  |  |
| MDP0000193947 |  |  | 1.1381 | MDP0000271115 | -1.6787 |  |  | MDP0000516194 | 1.0789 |  |  | MDP0000943413 | 1.6719 |  |  |
| MDP0000194255 |  | -1.1269 |  | MDP0000271480 |  | -1.3856 |  | MDP0000516287 | -1.3932 |  |  | MDP0000943529 |  | 1.8479 |  |
| MDP0000194319 | -2.3466 |  |  | MDP0000271527 | -1.5747 |  |  | MDP0000517257 | 1.339 |  |  | MDP0000943790 | 1.0926 | 1.464 |  |
| MDP0000194613 |  |  | -1.0306 | MDP0000271554 |  |  | 1.1875 | MDP0000517262 | 1.0052 |  |  | MDP0000944210 |  | 1.0158 |  |
| MDP0000194772 |  |  | 1.0214 | MDP0000271872 |  |  | -2.1928 | MDP0000519318 | -2.581 |  |  | MDP0000944576 | -1.0886 |  |  |
| MDP0000195256 | 1.0679 |  |  | MDP0000272336 | 1.731 |  |  | MDP0000519389 | 1.1464 |  |  | MDP0000945035 |  | -1.6362 |  |
| MDP0000195390 | 1.5266 |  |  | MDP0000272499 | -2.8553 |  |  | MDP0000521662 | 1.9764 |  |  | MDP0000946489 |  |  | 1.1731 |
| MDP0000195397 | -2.5355 |  |  | MDP0000272549 | 1.3255 |  |  | MDP0000523477 |  |  | 1.4004 | MDP0000949258 |  | 1.7374 |  |
| MDP0000195801 | 1.129 |  |  | MDP0000272597 | -2.9016 |  |  | MDP0000523942 |  |  | 1.0572 | MDP0000950137 | 1.0858 |  |  |
| MDP0000195855 | -2.1906 |  |  | MDP0000272612 |  |  | 1.098 | MDP0000525641 |  | 1.3318 |  | MDP0000950422 |  |  | 1.0911 |
| MDP0000196399 |  | -1.0822 |  | MDP0000272674 |  | 1.4082 |  | MDP0000532061 | 1.1491 |  |  | MDP0000950554 | -2.516 |  |  |
| MDP0000196402 | 1.1533 | 1.1451 |  | MDP0000272843 |  |  | 1.538 | MDP0000532338 |  |  | 1.6287 | MDP0000951795 | 2.6377 |  |  |
| MDP0000196404 | 2.2895 | 1.7838 |  | MDP0000272901 |  |  | 1.2623 | MDP0000533075 | -2.4589 |  | -1.0355 | MDP0000951863 |  |  | -1.3128 |
| MDP0000196639 |  |  | -1.8409 | MDP0000273148 | 1.751 |  |  | MDP0000535805 |  |  | 1.0148 | MDP0000951897 |  |  | 1.0223 |

**Supplementary Table S7. GO Annotation of DEGs**

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Class | GO\_Name | GO\_ID | GO\_Level | P\_value | Enrichment Score | Hits Genes Counts In Selected Set | Hits Genes Counts In Background | All Genes Counts In Selected Set | All Genes Counts In Background | corrected p-value |
| Molecular function | sequence-specific DNA binding | GO:0043565 | 6 | 0 | 2.587697 | 113 | 2544 | 1130 | 65831 | 0 |
| sequence-specific double-stranded DNA binding | GO:1990837 | 7 | 4.88E-15 | 2.571074 | 85 | 1926 | 1130 | 65831 | 2.48E-12 |
| double-stranded DNA binding | GO:0003690 | 6 | 1.73E-14 | 2.433029 | 90 | 2155 | 1130 | 65831 | 5.86E-12 |
| protein kinase activity | GO:0004672 | 6 | 7.72E-13 | 1.912204 | 133 | 4052 | 1130 | 65831 | 1.96E-10 |
| DNA-binding transcription factor activity | GO:0003700 | 3 | 1.40E-12 | 2.019263 | 114 | 3289 | 1130 | 65831 | 2.84E-10 |
| transcription regulator activity | GO:0140110 | 2 | 4.11E-12 | 1.943537 | 120 | 3597 | 1130 | 65831 | 6.95E-10 |
| transcription regulatory region sequence-specific DNA binding | GO:0000976 | 8 | 6.74E-12 | 2.408412 | 74 | 1790 | 1130 | 65831 | 9.77E-10 |
| regulatory region nucleic acid binding | GO:0001067 | 5 | 6.74E-12 | 2.408412 | 74 | 1790 | 1130 | 65831 | 9.77E-10 |
| protein serine/threonine kinase activity | GO:0004674 | 7 | 7.72E-12 | 1.905765 | 123 | 3760 | 1130 | 65831 | 8.71E-10 |
| kinase activity | GO:0016301 | 5 | 5.89E-11 | 1.757824 | 141 | 4673 | 1130 | 65831 | 5.98E-09 |
| phosphotransferase activity, alcohol group as acceptor | GO:0016773 | 5 | 1.13E-10 | 1.766966 | 135 | 4451 | 1130 | 65831 | 1.05E-08 |
| small molecule binding | GO:0036094 | 3 | 4.97E-09 | 1.318923 | 346 | 15283 | 1130 | 65831 | 4.20E-07 |
| microtubule binding | GO:0008017 | 6 | 7.01E-09 | 3.745126 | 27 | 420 | 1130 | 65831 | 5.48E-07 |
| anion binding | GO:0043168 | 4 | 2.13E-08 | 1.306222 | 340 | 15164 | 1130 | 65831 | 1.55E-06 |
| tubulin binding | GO:0015631 | 5 | 5.04E-08 | 3.40466 | 27 | 462 | 1130 | 65831 | 3.41E-06 |
| carbohydrate derivative binding | GO:0097367 | 3 | 8.62E-08 | 1.31072 | 311 | 13823 | 1130 | 65831 | 5.47E-06 |
| microtubule motor activity | GO:0003777 | 9 | 2.74E-07 | 5.170786 | 15 | 169 | 1130 | 65831 | 1.64E-05 |
| protein binding | GO:0005515 | 3 | 3.27E-07 | 1.42549 | 190 | 7765 | 1130 | 65831 | 1.85E-05 |
| nucleotide binding | GO:0000166 | 5 | 3.31E-07 | 1.284506 | 322 | 14604 | 1130 | 65831 | 1.77E-05 |
| nucleoside phosphate binding | GO:1901265 | 4 | 3.31E-07 | 1.284506 | 322 | 14604 | 1130 | 65831 | 1.77E-05 |
| flavonol synthase activity | GO:0045431 | 6 | 3.47E-07 | 29.12876 | 5 | 10 | 1130 | 65831 | 1.67E-05 |
| motor activity | GO:0003774 | 8 | 5.46E-07 | 4.343763 | 17 | 228 | 1130 | 65831 | 2.31E-05 |
| purine nucleotide binding | GO:0017076 | 6 | 9.69E-07 | 1.28547 | 300 | 13596 | 1130 | 65831 | 3.94E-05 |
| cytoskeletal protein binding | GO:0008092 | 4 | 1.26E-06 | 2.520045 | 34 | 786 | 1130 | 65831 | 4.93E-05 |
| hydrolase activity, acting on glycosyl bonds | GO:0016798 | 4 | 1.68E-06 | 1.865389 | 65 | 2030 | 1130 | 65831 | 6.30E-05 |
| DNA primase activity | GO:0003896 | 9 | 1.70E-06 | 22.40674 | 5 | 13 | 1130 | 65831 | 6.15E-05 |
| purine ribonucleotide binding | GO:0032555 | 7 | 2.51E-06 | 1.273646 | 297 | 13585 | 1130 | 65831 | 8.77E-05 |
| ribonucleotide binding | GO:0032553 | 6 | 2.67E-06 | 1.271274 | 299 | 13702 | 1130 | 65831 | 9.04E-05 |
| DNA binding | GO:0003677 | 5 | 2.71E-06 | 1.349669 | 213 | 9194 | 1130 | 65831 | 8.89E-05 |
| oxidoreductase activity | GO:0016491 | 3 | 3.49E-06 | 1.501056 | 127 | 4929 | 1130 | 65831 | 1.11E-04 |
| protein heterodimerization activity | GO:0046982 | 5 | 4.22E-06 | 3.426913 | 19 | 323 | 1130 | 65831 | 1.30E-04 |
| L-ascorbic acid binding | GO:0031418 | 6 | 5.71E-06 | 6.990903 | 9 | 75 | 1130 | 65831 | 1.70E-04 |
| adenyl ribonucleotide binding | GO:0032559 | 8 | 7.92E-06 | 1.267945 | 280 | 12865 | 1130 | 65831 | 2.30E-04 |
| adenyl nucleotide binding | GO:0030554 | 7 | 8.31E-06 | 1.267157 | 280 | 12873 | 1130 | 65831 | 2.34E-04 |
| polysaccharide binding | GO:0030247 | 4 | 9.92E-06 | 4.403185 | 13 | 172 | 1130 | 65831 | 2.72E-04 |
| organic acid binding | GO:0043177 | 4 | 1.33E-05 | 3.426913 | 17 | 289 | 1130 | 65831 | 3.54E-04 |
| carboxylic acid binding | GO:0031406 | 5 | 1.33E-05 | 3.426913 | 17 | 289 | 1130 | 65831 | 3.54E-04 |
| carbohydrate binding | GO:0030246 | 3 | 1.44E-05 | 2.02512 | 43 | 1237 | 1130 | 65831 | 3.66E-04 |
| naringenin 3-dioxygenase activity | GO:0045486 | 6 | 1.85E-05 | 14.56438 | 5 | 20 | 1130 | 65831 | 4.58E-04 |
| chalcone isomerase activity | GO:0045430 | 5 | 3.05E-05 | 13.24035 | 5 | 22 | 1130 | 65831 | 7.37E-04 |
| chitinase activity | GO:0004568 | 6 | 4.07E-05 | 6.29811 | 8 | 74 | 1130 | 65831 | 9.61E-04 |
| transferase activity, transferring glycosyl groups | GO:0016757 | 4 | 5.70E-05 | 1.784094 | 52 | 1698 | 1130 | 65831 | 0.001314 |
| dioxygenase activity | GO:0051213 | 4 | 7.88E-05 | 2.375919 | 25 | 613 | 1130 | 65831 | 0.001778 |
| calcium ion binding | GO:0005509 | 6 | 8.03E-05 | 2.326721 | 26 | 651 | 1130 | 65831 | 0.001773 |
| DNA replication origin binding | GO:0003688 | 8 | 8.39E-05 | 6.685289 | 7 | 61 | 1130 | 65831 | 0.001812 |
| drug binding | GO:0008144 | 3 | 9.08E-05 | 1.236246 | 265 | 12488 | 1130 | 65831 | 0.00192 |
| S-adenosylmethionine-dependent methyltransferase activity | GO:0008757 | 6 | 1.13E-04 | 2.543468 | 21 | 481 | 1130 | 65831 | 0.002344 |
| protein dimerization activity | GO:0046983 | 4 | 1.15E-04 | 1.609589 | 67 | 2425 | 1130 | 65831 | 0.002342 |
| oxidoreductase activity, acting on single donors with incorporation of molecular oxygen, incorporation of two atoms of oxygen | GO:0016702 | 5 | 1.22E-04 | 4.315372 | 10 | 135 | 1130 | 65831 | 0.002422 |
| active transmembrane transporter activity | GO:0022804 | 4 | 1.47E-04 | 1.716369 | 52 | 1765 | 1130 | 65831 | 0.002878 |
| purine ribonucleoside triphosphate binding | GO:0035639 | 5 | 1.50E-04 | 1.225031 | 268 | 12745 | 1130 | 65831 | 0.002877 |
| oxidoreductase activity, acting on CH or CH2 groups | GO:0016725 | 4 | 1.73E-04 | 9.396375 | 5 | 31 | 1130 | 65831 | 0.003196 |
| monosaccharide binding | GO:0048029 | 4 | 2.25E-04 | 4.406031 | 9 | 119 | 1130 | 65831 | 0.004078 |
| intramolecular lyase activity | GO:0016872 | 4 | 3.13E-04 | 8.322503 | 5 | 35 | 1130 | 65831 | 0.005289 |
| ATPase-coupled xenobiotic transmembrane transporter activity | GO:0008559 | 7 | 3.23E-04 | 6.473058 | 6 | 54 | 1130 | 65831 | 0.005374 |
| xyloglucan:xyloglucosyl transferase activity | GO:0016762 | 7 | 3.94E-04 | 6.241877 | 6 | 56 | 1130 | 65831 | 0.006457 |
| ATP binding | GO:0005524 | 9 | 4.09E-04 | 1.21602 | 251 | 12025 | 1130 | 65831 | 0.006586 |
| hydrolase activity, hydrolyzing O-glycosyl compounds | GO:0004553 | 5 | 4.26E-04 | 1.899702 | 33 | 1012 | 1130 | 65831 | 0.00675 |
| glucosyltransferase activity | GO:0046527 | 6 | 5.38E-04 | 2.16816 | 23 | 618 | 1130 | 65831 | 0.008402 |
| protein homodimerization activity | GO:0042803 | 5 | 5.90E-04 | 1.955403 | 29 | 864 | 1130 | 65831 | 0.009071 |
| transferase activity, transferring hexosyl groups | GO:0016758 | 5 | 6.20E-04 | 1.771029 | 38 | 1250 | 1130 | 65831 | 0.009385 |
| oxidoreductase activity, acting on single donors with incorporation of molecular oxygen | GO:0016701 | 4 | 7.34E-04 | 3.447191 | 10 | 169 | 1130 | 65831 | 0.010955 |
| 2-oxoglutarate-dependent dioxygenase activity | GO:0016706 | 5 | 7.68E-04 | 3.426913 | 10 | 170 | 1130 | 65831 | 0.011297 |
| methyltransferase activity | GO:0008168 | 5 | 8.35E-04 | 1.937305 | 28 | 842 | 1130 | 65831 | 0.012107 |
| hydrolase activity, hydrolyzing N-glycosyl compounds | GO:0016799 | 5 | 8.84E-04 | 1.838502 | 32 | 1014 | 1130 | 65831 | 0.012286 |
| nucleoside-triphosphatase activity | GO:0017111 | 7 | 0.001026 | 1.509388 | 62 | 2393 | 1130 | 65831 | 0.013887 |
| transferase activity, transferring one-carbon groups | GO:0016741 | 4 | 0.001177 | 1.868881 | 29 | 904 | 1130 | 65831 | 0.015722 |
| transmembrane transporter activity | GO:0022857 | 3 | 0.001372 | 1.412732 | 80 | 3299 | 1130 | 65831 | 0.01786 |
| pyrophosphatase activity | GO:0016462 | 6 | 0.001413 | 1.473439 | 65 | 2570 | 1130 | 65831 | 0.01815 |
| signaling receptor activity | GO:0038023 | 3 | 0.001553 | 1.812993 | 30 | 964 | 1130 | 65831 | 0.019459 |
| cis-regulatory region sequence-specific DNA binding | GO:0000987 | 9 | 0.001577 | 3.115376 | 10 | 187 | 1130 | 65831 | 0.019521 |
| xenobiotic transmembrane transporter activity | GO:0042910 | 4 | 0.001586 | 3.361011 | 9 | 156 | 1130 | 65831 | 0.01939 |
| hydrolase activity, acting on acid anhydrides, in phosphorus-containing anhydrides | GO:0016818 | 5 | 0.001683 | 1.462626 | 65 | 2589 | 1130 | 65831 | 0.020097 |
| transporter activity | GO:0005215 | 2 | 0.001877 | 1.386686 | 83 | 3487 | 1130 | 65831 | 0.022147 |
| transmembrane receptor protein kinase activity | GO:0019199 | 7 | 0.001887 | 2.132742 | 19 | 519 | 1130 | 65831 | 0.022016 |
| ubiquitin-like protein transferase activity | GO:0019787 | 4 | 0.002295 | 1.713457 | 33 | 1122 | 1130 | 65831 | 0.025877 |
| sucrose synthase activity | GO:0016157 | 8 | 0.00233 | 5.394215 | 5 | 54 | 1130 | 65831 | 0.025987 |
| hydrolase activity, acting on acid anhydrides | GO:0016817 | 4 | 0.002343 | 1.442018 | 65 | 2626 | 1130 | 65831 | 0.02585 |
| identical protein binding | GO:0042802 | 4 | 0.002357 | 1.607374 | 41 | 1486 | 1130 | 65831 | 0.025721 |
| ubiquitin-protein transferase activity | GO:0004842 | 5 | 0.002612 | 1.715033 | 32 | 1087 | 1130 | 65831 | 0.027616 |
| secondary active transmembrane transporter activity | GO:0015291 | 5 | 0.002612 | 1.715033 | 32 | 1087 | 1130 | 65831 | 0.027616 |
| protein disulfide oxidoreductase activity | GO:0015035 | 6 | 0.002631 | 3.401899 | 8 | 137 | 1130 | 65831 | 0.02725 |
| RNA polymerase II cis-regulatory region sequence-specific DNA binding | GO:0000978 | 10 | 0.002631 | 3.401899 | 8 | 137 | 1130 | 65831 | 0.02725 |
| molecular transducer activity | GO:0060089 | 2 | 0.0027 | 1.74598 | 30 | 1001 | 1130 | 65831 | 0.027408 |
| hormone binding | GO:0042562 | 3 | 0.002752 | 3.377248 | 8 | 138 | 1130 | 65831 | 0.027654 |
| disulfide oxidoreductase activity | GO:0015036 | 5 | 0.00307 | 3.048359 | 9 | 172 | 1130 | 65831 | 0.029395 |
| enzyme regulator activity | GO:0030234 | 3 | 0.003118 | 1.694764 | 32 | 1100 | 1130 | 65831 | 0.029579 |
| organic anion transmembrane transporter activity | GO:0008514 | 6 | 0.003124 | 2.263893 | 15 | 386 | 1130 | 65831 | 0.029362 |
| oxidoreductase activity, acting on paired donors, with incorporation or reduction of molecular oxygen | GO:0016705 | 4 | 0.003127 | 1.679038 | 33 | 1145 | 1130 | 65831 | 0.029117 |
| NAD+ nucleotidase, cyclic ADP-ribose generating | GO:0061809 | 7 | 0.003155 | 1.765379 | 28 | 924 | 1130 | 65831 | 0.029108 |
| NAD(P)+ nucleosidase activity | GO:0050135 | 6 | 0.003155 | 1.765379 | 28 | 924 | 1130 | 65831 | 0.029108 |
| NAD+ nucleosidase activity | GO:0003953 | 6 | 0.003155 | 1.765379 | 28 | 924 | 1130 | 65831 | 0.029108 |
| RNA polymerase II transcription regulatory region sequence-specific DNA binding | GO:0000977 | 9 | 0.003277 | 2.252224 | 15 | 388 | 1130 | 65831 | 0.029438 |
| proton-exporting ATPase activity, phosphorylative mechanism | GO:0008553 | 10 | 0.003973 | 4.775207 | 5 | 61 | 1130 | 65831 | 0.035067 |
| chitin binding | GO:0008061 | 4 | 0.003973 | 4.775207 | 5 | 61 | 1130 | 65831 | 0.035067 |
| ATPase-coupled transmembrane transporter activity | GO:0042626 | 6 | 0.004351 | 1.935466 | 20 | 602 | 1130 | 65831 | 0.037428 |
| oxidoreductase activity, acting on a sulfur group of donors | GO:0016667 | 4 | 0.005258 | 2.493513 | 11 | 257 | 1130 | 65831 | 0.044104 |
| enzyme inhibitor activity | GO:0004857 | 4 | 0.005657 | 2.062213 | 16 | 452 | 1130 | 65831 | 0.047068 |
| inorganic molecular entity transmembrane transporter activity | GO:0015318 | 4 | 0.006105 | 1.436116 | 53 | 2150 | 1130 | 65831 | 0.048789 |
| Cellular component | cell periphery | GO:0071944 | 3 | 1.58E-08 | 1.308467 | 344 | 11592 | 1181 | 52073 | 6.75E-06 |
| protein-DNA complex | GO:0032993 | 3 | 1.28E-06 | 3.416746 | 21 | 271 | 1181 | 52073 | 2.73E-04 |
| microtubule | GO:0005874 | 7 | 1.60E-06 | 2.44569 | 35 | 631 | 1181 | 52073 | 2.28E-04 |
| polymeric cytoskeletal fiber | GO:0099513 | 6 | 2.44E-06 | 2.365607 | 36 | 671 | 1181 | 52073 | 2.60E-04 |
| alpha DNA polymerase:primase complex | GO:0005658 | 9 | 2.45E-06 | 20.04195 | 5 | 11 | 1181 | 52073 | 2.10E-04 |
| supramolecular fiber | GO:0099512 | 5 | 2.95E-06 | 2.314064 | 37 | 705 | 1181 | 52073 | 2.10E-04 |
| supramolecular polymer | GO:0099081 | 4 | 2.95E-06 | 2.314064 | 37 | 705 | 1181 | 52073 | 2.10E-04 |
| kinesin complex | GO:0005871 | 4 | 8.12E-06 | 3.913517 | 15 | 169 | 1181 | 52073 | 4.34E-04 |
| intrinsic component of membrane | GO:0031224 | 3 | 8.73E-06 | 1.219718 | 361 | 13050 | 1181 | 52073 | 4.14E-04 |
| plasma membrane | GO:0005886 | 4 | 8.90E-06 | 1.260652 | 289 | 10108 | 1181 | 52073 | 3.80E-04 |
| nuclear replisome | GO:0043601 | 5 | 1.83E-05 | 6.916438 | 8 | 51 | 1181 | 52073 | 7.12E-04 |
| replisome | GO:0030894 | 4 | 2.12E-05 | 6.78343 | 8 | 52 | 1181 | 52073 | 7.56E-04 |
| membrane | GO:0016020 | 3 | 3.83E-05 | 1.149977 | 506 | 19401 | 1181 | 52073 | 0.001257 |
| integral component of membrane | GO:0016021 | 4 | 7.92E-05 | 1.198237 | 341 | 12548 | 1181 | 52073 | 0.002417 |
| microtubule associated complex | GO:0005875 | 3 | 9.31E-05 | 2.814402 | 18 | 282 | 1181 | 52073 | 0.002649 |
| DNA packaging complex | GO:0044815 | 3 | 9.87E-05 | 3.318775 | 14 | 186 | 1181 | 52073 | 0.002633 |
| supramolecular complex | GO:0099080 | 3 | 1.31E-04 | 1.84818 | 42 | 1002 | 1181 | 52073 | 0.003294 |
| microtubule cytoskeleton | GO:0015630 | 7 | 1.44E-04 | 1.872284 | 40 | 942 | 1181 | 52073 | 0.003412 |
| nuclear replication fork | GO:0043596 | 4 | 2.06E-04 | 4.968146 | 8 | 71 | 1181 | 52073 | 0.004619 |
| nucleosome | GO:0000786 | 4 | 2.48E-04 | 3.391715 | 12 | 156 | 1181 | 52073 | 0.005297 |
| cell wall | GO:0005618 | 4 | 4.13E-04 | 1.552204 | 64 | 1818 | 1181 | 52073 | 0.008407 |
| external encapsulating structure | GO:0030312 | 3 | 4.19E-04 | 1.551351 | 64 | 1819 | 1181 | 52073 | 0.00814 |
| plant-type vacuole membrane | GO:0009705 | 7 | 7.94E-04 | 2.42579 | 17 | 309 | 1181 | 52073 | 0.014735 |
| plant-type vacuole | GO:0000325 | 7 | 0.001934 | 1.995947 | 22 | 486 | 1181 | 52073 | 0.030582 |
| replication fork | GO:0005657 | 3 | 0.002116 | 2.979209 | 10 | 148 | 1181 | 52073 | 0.032272 |
| cytoskeleton | GO:0005856 | 6 | 0.002271 | 1.54484 | 48 | 1370 | 1181 | 52073 | 0.033442 |
| secretory vesicle | GO:0099503 | 8 | 0.003714 | 2.150844 | 16 | 328 | 1181 | 52073 | 0.049554 |
| DNA polymerase complex | GO:0042575 | 6 | 0.003776 | 4.792641 | 5 | 46 | 1181 | 52073 | 0.04886 |
| Biological process | response to abiotic stimulus | GO:0009628 | 3 | 0 | 1.927861 | 171 | 5111 | 1110 | 63960 | 0 |
| response to hormone | GO:0009725 | 5 | 0 | 2.053938 | 166 | 4657 | 1110 | 63960 | 0 |
| regulation of biological process | GO:0050789 | 3 | 0 | 1.688157 | 429 | 14643 | 1110 | 63960 | 0 |
| response to stimulus | GO:0050896 | 2 | 0 | 1.760801 | 523 | 17115 | 1110 | 63960 | 0 |
| response to organic substance | GO:0010033 | 4 | 0 | 1.893668 | 189 | 5751 | 1110 | 63960 | 0 |
| cellular response to stimulus | GO:0051716 | 3 | 0 | 1.798795 | 269 | 8617 | 1110 | 63960 | 0 |
| response to stress | GO:0006950 | 3 | 0 | 1.702526 | 335 | 11338 | 1110 | 63960 | 0 |
| biological regulation | GO:0065007 | 2 | 0 | 1.643712 | 466 | 16336 | 1110 | 63960 | 0 |
| response to endogenous stimulus | GO:0009719 | 3 | 1.11E-16 | 1.997613 | 168 | 4846 | 1110 | 63960 | 3.59E-14 |
| flavonoid metabolic process | GO:0009812 | 4 | 1.11E-16 | 6.05027 | 42 | 400 | 1110 | 63960 | 3.59E-14 |
| response to chemical | GO:0042221 | 3 | 2.22E-16 | 1.795575 | 242 | 7766 | 1110 | 63960 | 5.87E-14 |
| flavonoid biosynthetic process | GO:0009813 | 5 | 2.22E-16 | 6.599124 | 41 | 358 | 1110 | 63960 | 5.87E-14 |
| regulation of cellular process | GO:0050794 | 4 | 3.33E-16 | 1.695556 | 373 | 12676 | 1110 | 63960 | 7.46E-14 |
| anatomical structure development | GO:0048856 | 3 | 9.99E-16 | 1.634702 | 253 | 8918 | 1110 | 63960 | 2.08E-13 |
| developmental process | GO:0032502 | 2 | 1.67E-15 | 1.61946 | 260 | 9251 | 1110 | 63960 | 3.23E-13 |
| response to oxygen-containing compound | GO:1901700 | 4 | 2.66E-15 | 1.932356 | 155 | 4622 | 1110 | 63960 | 4.85E-13 |
| cell cycle | GO:0007049 | 3 | 3.44E-15 | 2.516351 | 89 | 2038 | 1110 | 63960 | 5.89E-13 |
| signal transduction | GO:0007165 | 5 | 1.03E-14 | 1.807697 | 177 | 5642 | 1110 | 63960 | 1.67E-12 |
| signaling | GO:0023052 | 2 | 1.25E-14 | 1.798465 | 178 | 5703 | 1110 | 63960 | 1.92E-12 |
| cellular response to chemical stimulus | GO:0070887 | 4 | 2.08E-14 | 1.927276 | 147 | 4395 | 1110 | 63960 | 3.02E-12 |
| defense response | GO:0006952 | 4 | 2.10E-14 | 1.757788 | 187 | 6130 | 1110 | 63960 | 2.91E-12 |
| multicellular organismal process | GO:0032501 | 2 | 3.50E-14 | 1.610333 | 239 | 8552 | 1110 | 63960 | 4.63E-12 |
| response to biotic stimulus | GO:0009607 | 3 | 4.87E-14 | 1.881118 | 152 | 4656 | 1110 | 63960 | 6.17E-12 |
| response to acid chemical | GO:0001101 | 4 | 7.23E-14 | 2.028359 | 125 | 3551 | 1110 | 63960 | 8.76E-12 |
| response to chitin | GO:0010200 | 6 | 8.14E-14 | 5.284823 | 31 | 338 | 1110 | 63960 | 9.47E-12 |
| hormone-mediated signaling pathway | GO:0009755 | 6 | 1.84E-13 | 2.163128 | 105 | 2797 | 1110 | 63960 | 2.06E-11 |
| cell communication | GO:0007154 | 3 | 1.96E-13 | 1.699701 | 192 | 6509 | 1110 | 63960 | 2.11E-11 |
| cellular response to hormone stimulus | GO:0032870 | 6 | 1.97E-13 | 2.106026 | 111 | 3037 | 1110 | 63960 | 2.05E-11 |
| multicellular organism development | GO:0007275 | 4 | 3.09E-13 | 1.634928 | 213 | 7507 | 1110 | 63960 | 3.10E-11 |
| response to external biotic stimulus | GO:0043207 | 4 | 5.45E-13 | 1.856697 | 145 | 4500 | 1110 | 63960 | 5.28E-11 |
| response to other organism | GO:0051707 | 5 | 5.45E-13 | 1.856697 | 145 | 4500 | 1110 | 63960 | 5.28E-11 |
| response to external stimulus | GO:0009605 | 3 | 6.16E-13 | 1.745491 | 171 | 5645 | 1110 | 63960 | 5.60E-11 |
| cellular response to endogenous stimulus | GO:0071495 | 4 | 1.90E-12 | 2.015865 | 113 | 3230 | 1110 | 63960 | 1.67E-10 |
| regulation of metabolic process | GO:0019222 | 4 | 3.56E-12 | 1.607503 | 207 | 7420 | 1110 | 63960 | 3.04E-10 |
| response to drug | GO:0042493 | 4 | 7.68E-12 | 2.577705 | 65 | 1453 | 1110 | 63960 | 6.38E-10 |
| biosynthetic process | GO:0009058 | 3 | 1.71E-11 | 1.392491 | 334 | 13821 | 1110 | 63960 | 1.38E-09 |
| organic substance biosynthetic process | GO:1901576 | 4 | 3.38E-11 | 1.392797 | 326 | 13487 | 1110 | 63960 | 2.66E-09 |
| regulation of cellular metabolic process | GO:0031323 | 5 | 3.75E-11 | 1.626921 | 182 | 6446 | 1110 | 63960 | 2.87E-09 |
| anthocyanin-containing compound biosynthetic process | GO:0009718 | 6 | 4.08E-11 | 7.515864 | 18 | 138 | 1110 | 63960 | 3.04E-09 |
| mitotic cell cycle | GO:0000278 | 4 | 4.82E-11 | 2.958115 | 48 | 935 | 1110 | 63960 | 3.51E-09 |
| regulation of biosynthetic process | GO:0009889 | 5 | 4.88E-11 | 1.724854 | 150 | 5011 | 1110 | 63960 | 3.46E-09 |
| regulation of cellular macromolecule biosynthetic process | GO:2000112 | 7 | 5.24E-11 | 1.755475 | 142 | 4661 | 1110 | 63960 | 3.63E-09 |
| regulation of cellular biosynthetic process | GO:0031326 | 6 | 5.32E-11 | 1.730519 | 148 | 4928 | 1110 | 63960 | 3.60E-09 |
| anthocyanin-containing compound metabolic process | GO:0046283 | 5 | 6.65E-11 | 6.402402 | 20 | 180 | 1110 | 63960 | 4.40E-09 |
| regulation of macromolecule biosynthetic process | GO:0010556 | 6 | 1.02E-10 | 1.73832 | 142 | 4707 | 1110 | 63960 | 6.62E-09 |
| cellular response to hypoxia | GO:0071456 | 7 | 2.10E-10 | 4.125993 | 29 | 405 | 1110 | 63960 | 1.33E-08 |
| cellular response to oxygen levels | GO:0071453 | 5 | 2.49E-10 | 4.095654 | 29 | 408 | 1110 | 63960 | 1.54E-08 |
| cellular response to decreased oxygen levels | GO:0036294 | 6 | 2.49E-10 | 4.095654 | 29 | 408 | 1110 | 63960 | 1.54E-08 |
| regulation of transcription, DNA-templated | GO:0006355 | 10 | 3.25E-10 | 1.779055 | 126 | 4081 | 1110 | 63960 | 1.93E-08 |
| regulation of nucleic acid-templated transcription | GO:1903506 | 9 | 3.67E-10 | 1.775575 | 126 | 4089 | 1110 | 63960 | 2.13E-08 |
| regulation of RNA biosynthetic process | GO:2001141 | 8 | 4.39E-10 | 1.770379 | 126 | 4101 | 1110 | 63960 | 2.50E-08 |
| cellular response to organic substance | GO:0071310 | 5 | 4.40E-10 | 1.834366 | 114 | 3581 | 1110 | 63960 | 2.46E-08 |
| regulation of primary metabolic process | GO:0080090 | 5 | 6.17E-10 | 1.606977 | 168 | 6024 | 1110 | 63960 | 3.39E-08 |
| secondary metabolic process | GO:0019748 | 3 | 6.47E-10 | 2.887644 | 44 | 878 | 1110 | 63960 | 3.49E-08 |
| response to hypoxia | GO:0001666 | 6 | 7.76E-10 | 3.690641 | 31 | 484 | 1110 | 63960 | 4.11E-08 |
| regulation of nitrogen compound metabolic process | GO:0051171 | 5 | 1.07E-09 | 1.611933 | 162 | 5791 | 1110 | 63960 | 5.55E-08 |
| response to decreased oxygen levels | GO:0036293 | 5 | 1.39E-09 | 3.601351 | 31 | 496 | 1110 | 63960 | 7.12E-08 |
| response to oxygen levels | GO:0070482 | 4 | 1.53E-09 | 3.586888 | 31 | 498 | 1110 | 63960 | 7.70E-08 |
| cell cycle process | GO:0022402 | 3 | 2.08E-09 | 2.399147 | 57 | 1369 | 1110 | 63960 | 1.03E-07 |
| RNA biosynthetic process | GO:0032774 | 8 | 2.58E-09 | 1.697421 | 131 | 4447 | 1110 | 63960 | 1.25E-07 |
| regulation of RNA metabolic process | GO:0051252 | 7 | 2.69E-09 | 1.696277 | 131 | 4450 | 1110 | 63960 | 1.28E-07 |
| proanthocyanidin biosynthetic process | GO:0010023 | 7 | 3.12E-09 | 20.0423 | 8 | 23 | 1110 | 63960 | 1.47E-07 |
| aromatic compound biosynthetic process | GO:0019438 | 5 | 3.44E-09 | 1.515523 | 191 | 7262 | 1110 | 63960 | 1.59E-07 |
| reproductive process | GO:0022414 | 2 | 3.46E-09 | 1.651016 | 141 | 4921 | 1110 | 63960 | 1.57E-07 |
| organic cyclic compound biosynthetic process | GO:1901362 | 5 | 3.61E-09 | 1.496665 | 200 | 7700 | 1110 | 63960 | 1.62E-07 |
| regulation of macromolecule metabolic process | GO:0060255 | 5 | 3.95E-09 | 1.54367 | 177 | 6607 | 1110 | 63960 | 1.74E-07 |
| cell division | GO:0051301 | 3 | 4.00E-09 | 2.399083 | 55 | 1321 | 1110 | 63960 | 1.74E-07 |
| regulation of nucleobase-containing compound metabolic process | GO:0019219 | 6 | 4.17E-09 | 1.668222 | 135 | 4663 | 1110 | 63960 | 1.78E-07 |
| reproduction | GO:0000003 | 2 | 4.41E-09 | 1.644666 | 141 | 4940 | 1110 | 63960 | 1.86E-07 |
| defense response to other organism | GO:0098542 | 6 | 5.53E-09 | 1.738007 | 117 | 3879 | 1110 | 63960 | 2.30E-07 |
| transcription, DNA-templated | GO:0006351 | 10 | 5.93E-09 | 1.682098 | 129 | 4419 | 1110 | 63960 | 2.43E-07 |
| cellular component organization | GO:0016043 | 4 | 6.57E-09 | 1.494774 | 195 | 7517 | 1110 | 63960 | 2.66E-07 |
| nucleic acid-templated transcription | GO:0097659 | 9 | 6.59E-09 | 1.679058 | 129 | 4427 | 1110 | 63960 | 2.63E-07 |
| mitotic cell cycle process | GO:1903047 | 4 | 9.93E-09 | 2.984717 | 36 | 695 | 1110 | 63960 | 3.91E-07 |
| interspecies interaction between organisms | GO:0044419 | 2 | 1.02E-08 | 1.573594 | 157 | 5749 | 1110 | 63960 | 3.94E-07 |
| positive regulation of anthocyanin biosynthetic process | GO:0031542 | 8 | 1.33E-08 | 17.07307 | 8 | 27 | 1110 | 63960 | 5.09E-07 |
| pigment biosynthetic process | GO:0046148 | 4 | 1.37E-08 | 3.431267 | 29 | 487 | 1110 | 63960 | 5.16E-07 |
| DNA replication | GO:0006260 | 7 | 1.45E-08 | 3.184615 | 32 | 579 | 1110 | 63960 | 5.42E-07 |
| cell wall organization | GO:0071555 | 6 | 1.87E-08 | 2.233993 | 58 | 1496 | 1110 | 63960 | 6.90E-07 |
| cellular component organization or biogenesis | GO:0071840 | 3 | 1.89E-08 | 1.4448 | 212 | 8455 | 1110 | 63960 | 6.86E-07 |
| cell wall organization or biogenesis | GO:0071554 | 3 | 1.89E-08 | 2.091359 | 67 | 1846 | 1110 | 63960 | 6.79E-07 |
| regulation of gene expression | GO:0010468 | 6 | 1.98E-08 | 1.577234 | 150 | 5480 | 1110 | 63960 | 7.03E-07 |
| regulation of anthocyanin biosynthetic process | GO:0031540 | 7 | 2.94E-08 | 12.64865 | 9 | 41 | 1110 | 63960 | 1.03E-06 |
| post-embryonic development | GO:0009791 | 3 | 3.19E-08 | 1.65711 | 123 | 4277 | 1110 | 63960 | 1.11E-06 |
| cellular response to stress | GO:0033554 | 4 | 3.46E-08 | 1.756022 | 102 | 3347 | 1110 | 63960 | 1.19E-06 |
| response to fungus | GO:0009620 | 6 | 6.86E-08 | 2.020224 | 67 | 1911 | 1110 | 63960 | 2.32E-06 |
| positive regulation of biological process | GO:0048518 | 4 | 7.58E-08 | 1.619524 | 126 | 4483 | 1110 | 63960 | 2.53E-06 |
| positive regulation of anthocyanin metabolic process | GO:0031539 | 7 | 7.58E-08 | 13.96888 | 8 | 33 | 1110 | 63960 | 2.51E-06 |
| defense response to fungus | GO:0050832 | 7 | 8.30E-08 | 2.090969 | 61 | 1681 | 1110 | 63960 | 2.71E-06 |
| system development | GO:0048731 | 4 | 8.37E-08 | 1.557633 | 144 | 5327 | 1110 | 63960 | 2.71E-06 |
| external encapsulating structure organization | GO:0045229 | 5 | 8.81E-08 | 2.134134 | 58 | 1566 | 1110 | 63960 | 2.82E-06 |
| regulation of flavonoid biosynthetic process | GO:0009962 | 6 | 9.63E-08 | 8.23166 | 11 | 77 | 1110 | 63960 | 3.05E-06 |
| pigment metabolic process | GO:0042440 | 3 | 1.05E-07 | 3.048763 | 30 | 567 | 1110 | 63960 | 3.28E-06 |
| response to abscisic acid | GO:0009737 | 6 | 1.05E-07 | 2.091529 | 60 | 1653 | 1110 | 63960 | 3.25E-06 |
| heterocycle biosynthetic process | GO:0018130 | 5 | 1.10E-07 | 1.469855 | 178 | 6978 | 1110 | 63960 | 3.36E-06 |
| microtubule-based process | GO:0007017 | 3 | 1.12E-07 | 2.912941 | 32 | 633 | 1110 | 63960 | 3.39E-06 |
| response to organonitrogen compound | GO:0010243 | 5 | 1.44E-07 | 2.597416 | 38 | 843 | 1110 | 63960 | 4.31E-06 |
| phenylpropanoid metabolic process | GO:0009698 | 5 | 1.51E-07 | 3.066105 | 29 | 545 | 1110 | 63960 | 4.49E-06 |
| cellular biosynthetic process | GO:0044249 | 4 | 1.75E-07 | 1.310482 | 298 | 13103 | 1110 | 63960 | 5.15E-06 |
| gametophyte development | GO:0048229 | 5 | 2.35E-07 | 2.412869 | 42 | 1003 | 1110 | 63960 | 6.83E-06 |
| response to alcohol | GO:0097305 | 5 | 2.53E-07 | 2.0373 | 60 | 1697 | 1110 | 63960 | 7.28E-06 |
| phenol-containing compound biosynthetic process | GO:0046189 | 6 | 2.71E-07 | 7.456916 | 11 | 85 | 1110 | 63960 | 7.73E-06 |
| DNA-dependent DNA replication | GO:0006261 | 8 | 3.45E-07 | 3.469365 | 23 | 382 | 1110 | 63960 | 9.75E-06 |
| syncytium formation | GO:0006949 | 4 | 4.01E-07 | 14.40541 | 7 | 28 | 1110 | 63960 | 1.12E-05 |
| macromolecule modification | GO:0043412 | 5 | 4.57E-07 | 1.443841 | 175 | 6984 | 1110 | 63960 | 1.27E-05 |
| positive regulation of flavonoid biosynthetic process | GO:0009963 | 7 | 5.04E-07 | 9.260618 | 9 | 56 | 1110 | 63960 | 1.38E-05 |
| leading strand elongation | GO:0006272 | 10 | 6.03E-07 | 18.1963 | 6 | 19 | 1110 | 63960 | 1.64E-05 |
| response to nitrogen compound | GO:1901698 | 4 | 6.66E-07 | 2.346064 | 41 | 1007 | 1110 | 63960 | 1.79E-05 |
| DNA replication initiation | GO:0006270 | 8 | 6.83E-07 | 6.815461 | 11 | 93 | 1110 | 63960 | 1.82E-05 |
| nuclear DNA replication | GO:0033260 | 10 | 7.98E-07 | 8.789739 | 9 | 59 | 1110 | 63960 | 2.11E-05 |
| response to salicylic acid | GO:0009751 | 6 | 8.93E-07 | 2.752625 | 30 | 628 | 1110 | 63960 | 2.34E-05 |
| cell cycle DNA replication initiation | GO:1902292 | 9 | 1.12E-06 | 24.00901 | 5 | 12 | 1110 | 63960 | 2.90E-05 |
| nuclear cell cycle DNA replication initiation | GO:1902315 | 10 | 1.12E-06 | 24.00901 | 5 | 12 | 1110 | 63960 | 2.90E-05 |
| mitotic DNA replication initiation | GO:1902975 | 11 | 1.12E-06 | 24.00901 | 5 | 12 | 1110 | 63960 | 2.90E-05 |
| microtubule-based movement | GO:0007018 | 4 | 1.14E-06 | 4.348802 | 16 | 212 | 1110 | 63960 | 2.89E-05 |
| developmental process involved in reproduction | GO:0003006 | 3 | 1.32E-06 | 1.593292 | 109 | 3942 | 1110 | 63960 | 3.31E-05 |
| regulation of anthocyanin metabolic process | GO:0031537 | 6 | 1.41E-06 | 8.23166 | 9 | 63 | 1110 | 63960 | 3.52E-05 |
| cellular protein modification process | GO:0006464 | 7 | 1.46E-06 | 1.476181 | 146 | 5699 | 1110 | 63960 | 3.60E-05 |
| protein modification process | GO:0036211 | 6 | 1.46E-06 | 1.476181 | 146 | 5699 | 1110 | 63960 | 3.60E-05 |
| nucleobase-containing compound biosynthetic process | GO:0034654 | 6 | 1.48E-06 | 1.449254 | 158 | 6282 | 1110 | 63960 | 3.58E-05 |
| reproductive system development | GO:0061458 | 5 | 1.79E-06 | 1.639987 | 96 | 3373 | 1110 | 63960 | 4.31E-05 |
| reproductive structure development | GO:0048608 | 4 | 1.79E-06 | 1.639987 | 96 | 3373 | 1110 | 63960 | 4.31E-05 |
| response to jasmonic acid | GO:0009753 | 6 | 2.11E-06 | 2.588797 | 31 | 690 | 1110 | 63960 | 4.99E-05 |
| phenylpropanoid biosynthetic process | GO:0009699 | 6 | 2.22E-06 | 3.111027 | 23 | 426 | 1110 | 63960 | 5.21E-05 |
| organonitrogen compound metabolic process | GO:1901564 | 4 | 2.58E-06 | 1.285806 | 279 | 12503 | 1110 | 63960 | 6.01E-05 |
| macromolecule biosynthetic process | GO:0009059 | 5 | 2.63E-06 | 1.363426 | 202 | 8537 | 1110 | 63960 | 6.08E-05 |
| regulation of response to stimulus | GO:0048583 | 4 | 3.09E-06 | 1.736417 | 76 | 2522 | 1110 | 63960 | 7.09E-05 |
| protein phosphorylation | GO:0006468 | 8 | 3.39E-06 | 1.787721 | 69 | 2224 | 1110 | 63960 | 7.72E-05 |
| response to radiation | GO:0009314 | 4 | 3.60E-06 | 1.897816 | 58 | 1761 | 1110 | 63960 | 8.11E-05 |
| secondary metabolite biosynthetic process | GO:0044550 | 4 | 3.67E-06 | 2.789874 | 26 | 537 | 1110 | 63960 | 8.22E-05 |
| response to antibiotic | GO:0046677 | 4 | 4.21E-06 | 2.315154 | 36 | 896 | 1110 | 63960 | 9.35E-05 |
| response to lipid | GO:0033993 | 5 | 4.45E-06 | 1.781842 | 68 | 2199 | 1110 | 63960 | 9.81E-05 |
| carbohydrate metabolic process | GO:0005975 | 4 | 6.20E-06 | 1.619596 | 90 | 3202 | 1110 | 63960 | 1.36E-04 |
| seed development | GO:0048316 | 5 | 6.51E-06 | 1.896582 | 55 | 1671 | 1110 | 63960 | 1.41E-04 |
| mitotic DNA replication | GO:1902969 | 11 | 8.12E-06 | 16.94754 | 5 | 17 | 1110 | 63960 | 1.75E-04 |
| tissue development | GO:0009888 | 4 | 9.41E-06 | 1.859833 | 56 | 1735 | 1110 | 63960 | 2.01E-04 |
| cellular macromolecule biosynthetic process | GO:0034645 | 6 | 1.01E-05 | 1.343884 | 195 | 8361 | 1110 | 63960 | 2.14E-04 |
| regulation of signaling | GO:0023051 | 4 | 1.03E-05 | 2.118442 | 40 | 1088 | 1110 | 63960 | 2.16E-04 |
| response to light stimulus | GO:0009416 | 5 | 1.07E-05 | 1.863133 | 55 | 1701 | 1110 | 63960 | 2.25E-04 |
| negative regulation of cellular process | GO:0048523 | 5 | 1.24E-05 | 1.734344 | 67 | 2226 | 1110 | 63960 | 2.57E-04 |
| DNA strand elongation involved in DNA replication | GO:0006271 | 9 | 1.34E-05 | 7.317031 | 8 | 63 | 1110 | 63960 | 2.76E-04 |
| fruit development | GO:0010154 | 5 | 1.37E-05 | 1.823672 | 57 | 1801 | 1110 | 63960 | 2.81E-04 |
| regulation of signal transduction | GO:0009966 | 6 | 1.38E-05 | 2.114058 | 39 | 1063 | 1110 | 63960 | 2.81E-04 |
| DNA strand elongation | GO:0022616 | 8 | 1.50E-05 | 7.202703 | 8 | 64 | 1110 | 63960 | 3.04E-04 |
| glucosamine-containing compound catabolic process | GO:1901072 | 7 | 1.59E-05 | 6.173745 | 9 | 84 | 1110 | 63960 | 3.19E-04 |
| amino sugar catabolic process | GO:0046348 | 6 | 1.59E-05 | 6.173745 | 9 | 84 | 1110 | 63960 | 3.19E-04 |
| chitin metabolic process | GO:0006030 | 7 | 1.59E-05 | 6.173745 | 9 | 84 | 1110 | 63960 | 3.19E-04 |
| chitin catabolic process | GO:0006032 | 8 | 1.59E-05 | 6.173745 | 9 | 84 | 1110 | 63960 | 3.19E-04 |
| regulation of cell communication | GO:0010646 | 5 | 1.62E-05 | 2.076455 | 40 | 1110 | 1110 | 63960 | 3.15E-04 |
| phenol-containing compound metabolic process | GO:0018958 | 5 | 1.64E-05 | 3.935135 | 14 | 205 | 1110 | 63960 | 3.18E-04 |
| positive regulation of macromolecule metabolic process | GO:0010604 | 6 | 1.89E-05 | 1.744432 | 63 | 2081 | 1110 | 63960 | 3.63E-04 |
| positive regulation of metabolic process | GO:0009893 | 5 | 1.91E-05 | 1.680138 | 71 | 2435 | 1110 | 63960 | 3.66E-04 |
| aminoglycan catabolic process | GO:0006026 | 6 | 2.11E-05 | 5.960857 | 9 | 87 | 1110 | 63960 | 4.02E-04 |
| abscisic acid-activated signaling pathway | GO:0009738 | 7 | 2.40E-05 | 2.287158 | 31 | 781 | 1110 | 63960 | 4.53E-04 |
| megagametogenesis | GO:0009561 | 3 | 2.70E-05 | 4.005781 | 13 | 187 | 1110 | 63960 | 5.07E-04 |
| negative regulation of biological process | GO:0048519 | 4 | 2.93E-05 | 1.540774 | 93 | 3478 | 1110 | 63960 | 5.46E-04 |
| RNA metabolic process | GO:0016070 | 7 | 2.93E-05 | 1.336111 | 182 | 7849 | 1110 | 63960 | 5.44E-04 |
| cellular response to acid chemical | GO:0071229 | 5 | 2.97E-05 | 1.817825 | 53 | 1680 | 1110 | 63960 | 5.47E-04 |
| positive regulation of cellular process | GO:0048522 | 5 | 3.16E-05 | 1.525559 | 96 | 3626 | 1110 | 63960 | 5.78E-04 |
| positive regulation of nitrogen compound metabolic process | GO:0051173 | 6 | 3.22E-05 | 1.748804 | 59 | 1944 | 1110 | 63960 | 5.85E-04 |
| phosphorelay signal transduction system | GO:0000160 | 7 | 3.59E-05 | 2.443984 | 26 | 613 | 1110 | 63960 | 6.49E-04 |
| regulation of auxin mediated signaling pathway | GO:0010928 | 7 | 3.88E-05 | 4.495304 | 11 | 141 | 1110 | 63960 | 6.97E-04 |
| glucosamine-containing compound metabolic process | GO:1901071 | 6 | 3.94E-05 | 5.516964 | 9 | 94 | 1110 | 63960 | 7.03E-04 |
| response to auxin | GO:0009733 | 6 | 3.99E-05 | 2.013659 | 39 | 1116 | 1110 | 63960 | 7.07E-04 |
| response to karrikin | GO:0080167 | 4 | 4.53E-05 | 3.402852 | 15 | 254 | 1110 | 63960 | 7.98E-04 |
| positive regulation of gene expression | GO:0010628 | 7 | 4.58E-05 | 1.823469 | 50 | 1580 | 1110 | 63960 | 8.03E-04 |
| positive regulation of cellular metabolic process | GO:0031325 | 6 | 4.89E-05 | 1.680084 | 64 | 2195 | 1110 | 63960 | 8.53E-04 |
| growth | GO:0040007 | 2 | 5.33E-05 | 1.717008 | 59 | 1980 | 1110 | 63960 | 9.23E-04 |
| positive regulation of RNA metabolic process | GO:0051254 | 8 | 5.56E-05 | 1.877605 | 45 | 1381 | 1110 | 63960 | 9.57E-04 |
| ethylene-activated signaling pathway | GO:0009873 | 8 | 5.84E-05 | 2.473916 | 24 | 559 | 1110 | 63960 | 1.00E-03 |
| maintenance of seed dormancy | GO:0010231 | 5 | 7.58E-05 | 11.08108 | 5 | 26 | 1110 | 63960 | 0.00129 |
| maintenance of dormancy | GO:0097437 | 4 | 7.58E-05 | 11.08108 | 5 | 26 | 1110 | 63960 | 0.00129 |
| positive regulation of transcription, DNA-templated | GO:0045893 | 11 | 7.58E-05 | 1.882773 | 43 | 1316 | 1110 | 63960 | 0.001276 |
| cellular response to ethylene stimulus | GO:0071369 | 7 | 7.67E-05 | 2.430437 | 24 | 569 | 1110 | 63960 | 0.001282 |
| cellular response to abscisic acid stimulus | GO:0071215 | 7 | 7.69E-05 | 2.146959 | 31 | 832 | 1110 | 63960 | 0.001279 |
| response to water | GO:0009415 | 5 | 7.73E-05 | 2.062248 | 34 | 950 | 1110 | 63960 | 0.001278 |
| cellular response to alcohol | GO:0097306 | 6 | 7.86E-05 | 2.144382 | 31 | 833 | 1110 | 63960 | 0.001292 |
| positive regulation of macromolecule biosynthetic process | GO:0010557 | 7 | 8.00E-05 | 1.820038 | 47 | 1488 | 1110 | 63960 | 0.001308 |
| photomorphogenesis | GO:0009640 | 7 | 8.08E-05 | 3.601351 | 13 | 208 | 1110 | 63960 | 0.001313 |
| positive regulation of nucleobase-containing compound metabolic process | GO:0045935 | 7 | 9.00E-05 | 1.824222 | 46 | 1453 | 1110 | 63960 | 0.001455 |
| positive regulation of nucleic acid-templated transcription | GO:1903508 | 10 | 9.57E-05 | 1.862955 | 43 | 1330 | 1110 | 63960 | 0.001538 |
| positive regulation of RNA biosynthetic process | GO:1902680 | 9 | 9.73E-05 | 1.861555 | 43 | 1331 | 1110 | 63960 | 0.001555 |
| stomatal movement | GO:0010118 | 3 | 1.07E-04 | 2.625131 | 20 | 439 | 1110 | 63960 | 0.001698 |
| response to inorganic substance | GO:0010035 | 4 | 1.07E-04 | 1.633932 | 64 | 2257 | 1110 | 63960 | 0.001698 |
| cellular water homeostasis | GO:0009992 | 8 | 1.10E-04 | 10.28958 | 5 | 28 | 1110 | 63960 | 0.001731 |
| cellular response to auxin stimulus | GO:0071365 | 7 | 1.16E-04 | 2.195109 | 28 | 735 | 1110 | 63960 | 0.001817 |
| response to water deprivation | GO:0009414 | 6 | 1.29E-04 | 2.031532 | 33 | 936 | 1110 | 63960 | 0.002007 |
| response to ethylene | GO:0009723 | 6 | 1.39E-04 | 2.10554 | 30 | 821 | 1110 | 63960 | 0.002159 |
| anatomical structure morphogenesis | GO:0009653 | 3 | 1.51E-04 | 1.537908 | 77 | 2885 | 1110 | 63960 | 0.002324 |
| response to UV-B | GO:0010224 | 7 | 1.59E-04 | 3.841441 | 11 | 165 | 1110 | 63960 | 0.002442 |
| cell cycle DNA replication | GO:0044786 | 9 | 1.68E-04 | 3.8183 | 11 | 166 | 1110 | 63960 | 0.002562 |
| cell volume homeostasis | GO:0006884 | 7 | 1.82E-04 | 9.29381 | 5 | 31 | 1110 | 63960 | 0.002761 |
| regulation of developmental growth | GO:0048638 | 5 | 1.85E-04 | 2.76714 | 17 | 354 | 1110 | 63960 | 0.002788 |
| response to organic cyclic compound | GO:0014070 | 5 | 1.87E-04 | 1.885979 | 38 | 1161 | 1110 | 63960 | 0.002807 |
| aminoglycan metabolic process | GO:0006022 | 5 | 1.88E-04 | 4.509518 | 9 | 115 | 1110 | 63960 | 0.002812 |
| plant organ development | GO:0099402 | 4 | 1.89E-04 | 1.552098 | 72 | 2673 | 1110 | 63960 | 0.002804 |
| positive regulation of cellular biosynthetic process | GO:0031328 | 7 | 1.90E-04 | 1.740615 | 48 | 1589 | 1110 | 63960 | 0.002802 |
| regulation of response to stress | GO:0080134 | 5 | 2.21E-04 | 1.777946 | 44 | 1426 | 1110 | 63960 | 0.003245 |
| positive regulation of biosynthetic process | GO:0009891 | 6 | 2.22E-04 | 1.717433 | 49 | 1644 | 1110 | 63960 | 0.003246 |
| movement of cell or subcellular component | GO:0006928 | 3 | 2.32E-04 | 2.713484 | 17 | 361 | 1110 | 63960 | 0.003382 |
| embryo sac development | GO:0009553 | 6 | 2.40E-04 | 2.705988 | 17 | 362 | 1110 | 63960 | 0.003475 |
| regulation of stomatal movement | GO:0010119 | 5 | 2.46E-04 | 3.055692 | 14 | 264 | 1110 | 63960 | 0.003545 |
| cellular response to jasmonic acid stimulus | GO:0071395 | 7 | 2.56E-04 | 2.69112 | 17 | 364 | 1110 | 63960 | 0.003668 |
| embryo development ending in seed dormancy | GO:0009793 | 6 | 2.65E-04 | 1.870175 | 37 | 1140 | 1110 | 63960 | 0.003782 |
| anatomical structure formation involved in morphogenesis | GO:0048646 | 3 | 2.74E-04 | 2.230514 | 24 | 620 | 1110 | 63960 | 0.003894 |
| cellular response to oxygen-containing compound | GO:1901701 | 5 | 2.84E-04 | 1.596239 | 61 | 2202 | 1110 | 63960 | 0.004006 |
| amino sugar metabolic process | GO:0006040 | 5 | 2.94E-04 | 4.250775 | 9 | 122 | 1110 | 63960 | 0.004126 |
| nuclear division | GO:0000280 | 7 | 2.99E-04 | 2.426174 | 20 | 475 | 1110 | 63960 | 0.004189 |
| double-strand break repair | GO:0006302 | 9 | 3.00E-04 | 2.752077 | 16 | 335 | 1110 | 63960 | 0.004175 |
| pollen development | GO:0009555 | 6 | 3.28E-04 | 2.125053 | 26 | 705 | 1110 | 63960 | 0.00452 |
| organelle organization | GO:0006996 | 5 | 3.30E-04 | 1.392012 | 109 | 4512 | 1110 | 63960 | 0.004524 |
| regulation of multicellular organismal process | GO:0051239 | 4 | 3.82E-04 | 1.666328 | 50 | 1729 | 1110 | 63960 | 0.005219 |
| karyogamy | GO:0000741 | 7 | 3.90E-04 | 5.238329 | 7 | 77 | 1110 | 63960 | 0.005297 |
| polar nucleus fusion | GO:0010197 | 8 | 3.90E-04 | 5.238329 | 7 | 77 | 1110 | 63960 | 0.005297 |
| phosphorylation | GO:0016310 | 6 | 3.96E-04 | 1.511938 | 72 | 2744 | 1110 | 63960 | 0.005339 |
| auxin-activated signaling pathway | GO:0009734 | 7 | 4.24E-04 | 2.124691 | 25 | 678 | 1110 | 63960 | 0.00568 |
| plant-type cell wall organization | GO:0009664 | 7 | 4.31E-04 | 2.571043 | 17 | 381 | 1110 | 63960 | 0.005729 |
| chromosome organization | GO:0051276 | 6 | 4.38E-04 | 1.665758 | 49 | 1695 | 1110 | 63960 | 0.005797 |
| mitotic nuclear division | GO:0140014 | 8 | 4.51E-04 | 3.020488 | 13 | 248 | 1110 | 63960 | 0.005938 |
| response to UV | GO:0009411 | 6 | 4.61E-04 | 2.870828 | 14 | 281 | 1110 | 63960 | 0.006037 |
| jasmonic acid mediated signaling pathway | GO:0009867 | 7 | 4.99E-04 | 2.626627 | 16 | 351 | 1110 | 63960 | 0.00651 |
| regulation of growth | GO:0040008 | 4 | 5.00E-04 | 1.902881 | 32 | 969 | 1110 | 63960 | 0.006497 |
| water homeostasis | GO:0030104 | 6 | 5.06E-04 | 5.960857 | 6 | 58 | 1110 | 63960 | 0.006542 |
| regulation of DNA replication | GO:0006275 | 8 | 5.24E-04 | 3.928747 | 9 | 132 | 1110 | 63960 | 0.006746 |
| regulation of microtubule cytoskeleton organization | GO:0070507 | 8 | 5.55E-04 | 5.859826 | 6 | 59 | 1110 | 63960 | 0.007113 |
| negative regulation of cellular macromolecule biosynthetic process | GO:2000113 | 8 | 5.89E-04 | 1.906372 | 31 | 937 | 1110 | 63960 | 0.007519 |
| negative regulation of transcription, DNA-templated | GO:0045892 | 11 | 5.94E-04 | 2.010057 | 27 | 774 | 1110 | 63960 | 0.007552 |
| cellular nitrogen compound biosynthetic process | GO:0044271 | 5 | 6.00E-04 | 1.255271 | 187 | 8584 | 1110 | 63960 | 0.007597 |
| cellular response to lipid | GO:0071396 | 6 | 6.12E-04 | 1.757031 | 39 | 1279 | 1110 | 63960 | 0.007706 |
| organelle fission | GO:0048285 | 6 | 6.36E-04 | 2.14103 | 23 | 619 | 1110 | 63960 | 0.007944 |
| meiotic cell cycle | GO:0051321 | 4 | 6.66E-04 | 2.334351 | 19 | 469 | 1110 | 63960 | 0.008278 |
| cellular developmental process | GO:0048869 | 3 | 6.68E-04 | 1.542308 | 61 | 2279 | 1110 | 63960 | 0.008266 |
| response to bacterium | GO:0009617 | 6 | 6.89E-04 | 1.631115 | 49 | 1731 | 1110 | 63960 | 0.008499 |
| negative regulation of macromolecule biosynthetic process | GO:0010558 | 7 | 7.36E-04 | 1.880284 | 31 | 950 | 1110 | 63960 | 0.009036 |
| negative regulation of RNA biosynthetic process | GO:1902679 | 9 | 7.46E-04 | 1.979369 | 27 | 786 | 1110 | 63960 | 0.009126 |
| negative regulation of nucleic acid-templated transcription | GO:1903507 | 10 | 7.46E-04 | 1.979369 | 27 | 786 | 1110 | 63960 | 0.009126 |
| negative regulation of cellular biosynthetic process | GO:0031327 | 7 | 7.49E-04 | 1.85689 | 32 | 993 | 1110 | 63960 | 0.009086 |
| gene expression | GO:0010467 | 5 | 7.59E-04 | 1.240326 | 197 | 9152 | 1110 | 63960 | 0.009159 |
| polysaccharide metabolic process | GO:0005976 | 5 | 7.70E-04 | 1.684385 | 43 | 1471 | 1110 | 63960 | 0.009253 |
| shoot system development | GO:0048367 | 5 | 7.89E-04 | 1.498117 | 67 | 2577 | 1110 | 63960 | 0.009445 |
| inflorescence development | GO:0010229 | 7 | 7.89E-04 | 5.487773 | 6 | 63 | 1110 | 63960 | 0.009411 |
| negative regulation of biosynthetic process | GO:0009890 | 6 | 8.13E-04 | 1.847587 | 32 | 998 | 1110 | 63960 | 0.00966 |
| mitotic spindle organization | GO:0007052 | 9 | 8.15E-04 | 4.636222 | 7 | 87 | 1110 | 63960 | 0.009645 |
| carbohydrate derivative catabolic process | GO:1901136 | 5 | 8.16E-04 | 3.169189 | 11 | 200 | 1110 | 63960 | 0.009614 |
| response to salt stress | GO:0009651 | 5 | 8.27E-04 | 1.728649 | 39 | 1300 | 1110 | 63960 | 0.009699 |
| regulation of biological quality | GO:0065008 | 3 | 8.30E-04 | 1.41088 | 88 | 3594 | 1110 | 63960 | 0.009697 |
| response to temperature stimulus | GO:0009266 | 4 | 9.01E-04 | 1.670755 | 43 | 1483 | 1110 | 63960 | 0.010363 |
| response to osmotic stress | GO:0006970 | 4 | 9.53E-04 | 1.654929 | 44 | 1532 | 1110 | 63960 | 0.010914 |
| methylation | GO:0032259 | 3 | 9.78E-04 | 1.807522 | 33 | 1052 | 1110 | 63960 | 0.011159 |
| phosphate ion transport | GO:0006817 | 8 | 9.97E-04 | 4.481682 | 7 | 90 | 1110 | 63960 | 0.011333 |
| macromolecule methylation | GO:0043414 | 6 | 0.001086 | 2.095332 | 22 | 605 | 1110 | 63960 | 0.012251 |
| protein metabolic process | GO:0019538 | 5 | 0.001098 | 1.236655 | 190 | 8853 | 1110 | 63960 | 0.012337 |
| developmental growth | GO:0048589 | 3 | 0.001106 | 1.714661 | 38 | 1277 | 1110 | 63960 | 0.012376 |
| negative regulation of response to stimulus | GO:0048585 | 5 | 0.001108 | 1.90036 | 28 | 849 | 1110 | 63960 | 0.01235 |
| cell growth | GO:0016049 | 3 | 0.001129 | 1.741711 | 36 | 1191 | 1110 | 63960 | 0.012541 |
| response to red or far red light | GO:0009639 | 6 | 0.001131 | 2.178511 | 20 | 529 | 1110 | 63960 | 0.012513 |
| transmembrane transport | GO:0055085 | 5 | 0.001132 | 1.620168 | 46 | 1636 | 1110 | 63960 | 0.012478 |
| DNA repair | GO:0006281 | 8 | 0.001146 | 1.828322 | 31 | 977 | 1110 | 63960 | 0.01259 |
| drug catabolic process | GO:0042737 | 5 | 0.001163 | 2.010057 | 24 | 688 | 1110 | 63960 | 0.012719 |
| negative regulation of nucleobase-containing compound metabolic process | GO:0045934 | 7 | 0.001171 | 1.869158 | 29 | 894 | 1110 | 63960 | 0.012767 |
| regulation of molecular function | GO:0065009 | 3 | 0.001184 | 1.824587 | 31 | 979 | 1110 | 63960 | 0.012852 |
| cytoskeleton-dependent cytokinesis | GO:0061640 | 5 | 0.001259 | 3.003971 | 11 | 211 | 1110 | 63960 | 0.013617 |
| root system development | GO:0022622 | 5 | 0.001339 | 1.696066 | 38 | 1291 | 1110 | 63960 | 0.014329 |
| root development | GO:0048364 | 5 | 0.001339 | 1.696066 | 38 | 1291 | 1110 | 63960 | 0.014329 |
| double-strand break repair via homologous recombination | GO:0000724 | 10 | 0.001357 | 2.975764 | 11 | 213 | 1110 | 63960 | 0.014415 |
| cell surface receptor signaling pathway | GO:0007166 | 6 | 0.001366 | 2.810811 | 12 | 246 | 1110 | 63960 | 0.01445 |
| drug metabolic process | GO:0017144 | 4 | 0.001446 | 1.582287 | 48 | 1748 | 1110 | 63960 | 0.015243 |
| spindle organization | GO:0007051 | 8 | 0.001515 | 3.13161 | 10 | 184 | 1110 | 63960 | 0.015915 |
| response to nematode | GO:0009624 | 6 | 0.001517 | 2.934434 | 11 | 216 | 1110 | 63960 | 0.015878 |
| regulation of cell size | GO:0008361 | 6 | 0.001545 | 4.158261 | 7 | 97 | 1110 | 63960 | 0.016113 |
| embryo sac central cell differentiation | GO:0009559 | 5 | 0.001545 | 4.158261 | 7 | 97 | 1110 | 63960 | 0.016113 |
| response to wounding | GO:0009611 | 4 | 0.001593 | 2.07201 | 21 | 584 | 1110 | 63960 | 0.0165 |
| cellular response to DNA damage stimulus | GO:0006974 | 5 | 0.001632 | 1.750933 | 33 | 1086 | 1110 | 63960 | 0.016839 |
| negative regulation of RNA metabolic process | GO:0051253 | 8 | 0.00166 | 1.872183 | 27 | 831 | 1110 | 63960 | 0.017007 |
| multidimensional cell growth | GO:0009825 | 4 | 0.001667 | 3.658516 | 8 | 126 | 1110 | 63960 | 0.017017 |
| cellular protein metabolic process | GO:0044267 | 6 | 0.001691 | 1.234355 | 179 | 8356 | 1110 | 63960 | 0.017201 |
| response to heat | GO:0009408 | 5 | 0.00173 | 2.018592 | 22 | 628 | 1110 | 63960 | 0.017544 |
| positive regulation of transcription from RNA polymerase II promoter in response to stress | GO:0036003 | 13 | 0.001893 | 5.649179 | 5 | 51 | 1110 | 63960 | 0.018866 |
| positive regulation of transcription from RNA polymerase II promoter in response to heat stress | GO:0061408 | 14 | 0.001893 | 5.649179 | 5 | 51 | 1110 | 63960 | 0.018866 |
| fluid transport | GO:0042044 | 5 | 0.001963 | 4.60973 | 6 | 75 | 1110 | 63960 | 0.019362 |
| water transport | GO:0006833 | 6 | 0.001963 | 4.60973 | 6 | 75 | 1110 | 63960 | 0.019362 |
| negative regulation of cellular metabolic process | GO:0031324 | 6 | 0.002006 | 1.669538 | 37 | 1277 | 1110 | 63960 | 0.019656 |
| embryo development | GO:0009790 | 5 | 0.002015 | 1.656295 | 38 | 1322 | 1110 | 63960 | 0.019678 |
| organic hydroxy compound biosynthetic process | GO:1901617 | 5 | 0.002151 | 2.061596 | 20 | 559 | 1110 | 63960 | 0.02073 |
| defense response to bacterium | GO:0042742 | 7 | 0.002166 | 1.614823 | 41 | 1463 | 1110 | 63960 | 0.020801 |
| anion transport | GO:0006820 | 6 | 0.002168 | 1.861071 | 26 | 805 | 1110 | 63960 | 0.020748 |
| recombinational repair | GO:0000725 | 9 | 0.002239 | 2.792237 | 11 | 227 | 1110 | 63960 | 0.021358 |
| microtubule cytoskeleton organization involved in mitosis | GO:1902850 | 8 | 0.002303 | 3.878378 | 7 | 104 | 1110 | 63960 | 0.021898 |
| cellular homeostasis | GO:0019725 | 5 | 0.002394 | 1.847302 | 26 | 811 | 1110 | 63960 | 0.02269 |
| cell wall macromolecule metabolic process | GO:0044036 | 6 | 0.002475 | 2.248649 | 16 | 410 | 1110 | 63960 | 0.023385 |
| mitotic cytokinesis | GO:0000281 | 6 | 0.002499 | 3.142998 | 9 | 165 | 1110 | 63960 | 0.023537 |
| glycosinolate metabolic process | GO:0019757 | 7 | 0.002567 | 3.414615 | 8 | 135 | 1110 | 63960 | 0.024101 |
| glucosinolate metabolic process | GO:0019760 | 8 | 0.002567 | 3.414615 | 8 | 135 | 1110 | 63960 | 0.024101 |
| S-glycoside metabolic process | GO:0016143 | 6 | 0.002567 | 3.414615 | 8 | 135 | 1110 | 63960 | 0.024101 |
| cellular response to heat | GO:0034605 | 6 | 0.002603 | 3.124064 | 9 | 166 | 1110 | 63960 | 0.024198 |
| regulation of cell cycle | GO:0051726 | 5 | 0.002977 | 1.868809 | 24 | 740 | 1110 | 63960 | 0.027154 |
| regulation of developmental process | GO:0050793 | 4 | 0.003037 | 1.448993 | 60 | 2386 | 1110 | 63960 | 0.027615 |
| cell differentiation | GO:0030154 | 4 | 0.003182 | 1.478882 | 54 | 2104 | 1110 | 63960 | 0.028847 |
| meristem development | GO:0048507 | 5 | 0.003183 | 1.858762 | 24 | 744 | 1110 | 63960 | 0.028769 |
| defense response to Gram-negative bacterium | GO:0050829 | 8 | 0.003275 | 4.165418 | 6 | 83 | 1110 | 63960 | 0.029506 |
| cytokinesis by cell plate formation | GO:0000911 | 5 | 0.003353 | 3.269312 | 8 | 141 | 1110 | 63960 | 0.030117 |
| amine metabolic process | GO:0009308 | 5 | 0.003409 | 2.408621 | 13 | 311 | 1110 | 63960 | 0.030519 |
| mitotic cell cycle phase transition | GO:0044772 | 5 | 0.003426 | 2.640991 | 11 | 240 | 1110 | 63960 | 0.030586 |
| homeostatic process | GO:0042592 | 4 | 0.003495 | 1.52684 | 46 | 1736 | 1110 | 63960 | 0.031105 |
| regulation of multicellular organismal development | GO:2000026 | 5 | 0.00357 | 1.559348 | 42 | 1552 | 1110 | 63960 | 0.031387 |
| regulation of jasmonic acid mediated signaling pathway | GO:2000022 | 7 | 0.003664 | 3.569481 | 7 | 113 | 1110 | 63960 | 0.032119 |
| positive regulation of response to stimulus | GO:0048584 | 5 | 0.004197 | 1.748072 | 27 | 890 | 1110 | 63960 | 0.036454 |
| microtubule cytoskeleton organization | GO:0000226 | 7 | 0.004472 | 2.114555 | 16 | 436 | 1110 | 63960 | 0.038614 |
| protein ubiquitination | GO:0016567 | 10 | 0.00463 | 1.554191 | 40 | 1483 | 1110 | 63960 | 0.039864 |
| regulation of meristem development | GO:0048509 | 5 | 0.00467 | 2.319136 | 13 | 323 | 1110 | 63960 | 0.040091 |
| phloem or xylem histogenesis | GO:0010087 | 5 | 0.004912 | 2.400901 | 12 | 288 | 1110 | 63960 | 0.041919 |
| regulation of catalytic activity | GO:0050790 | 4 | 0.004996 | 1.791346 | 24 | 772 | 1110 | 63960 | 0.04251 |
| organic hydroxy compound metabolic process | GO:1901615 | 4 | 0.005123 | 1.684503 | 29 | 992 | 1110 | 63960 | 0.043336 |
| regulation of microtubule-based process | GO:0032886 | 5 | 0.00515 | 3.799228 | 6 | 91 | 1110 | 63960 | 0.043442 |
| negative regulation of nitrogen compound metabolic process | GO:0051172 | 6 | 0.005239 | 1.621069 | 33 | 1173 | 1110 | 63960 | 0.04406 |
| cellular response to radiation | GO:0071478 | 6 | 0.005299 | 2.204106 | 14 | 366 | 1110 | 63960 | 0.044441 |
| cellular response to blue light | GO:0071483 | 8 | 0.005459 | 4.432432 | 5 | 65 | 1110 | 63960 | 0.045648 |
| meiotic cell cycle process | GO:1903046 | 4 | 0.005681 | 2.186186 | 14 | 369 | 1110 | 63960 | 0.04683 |
| chromatin organization involved in negative regulation of transcription | GO:0097549 | 7 | 0.005689 | 2.466295 | 11 | 257 | 1110 | 63960 | 0.046767 |
| regulation of meristem growth | GO:0010075 | 6 | 0.006073 | 3.252833 | 7 | 124 | 1110 | 63960 | 0.048283 |
| regulation of mitotic cell cycle | GO:0007346 | 6 | 0.006084 | 2.168556 | 14 | 372 | 1110 | 63960 | 0.048242 |
| positive regulation of growth | GO:0045927 | 5 | 0.006136 | 2.954955 | 8 | 156 | 1110 | 63960 | 0.048518 |
| negative regulation of cell cycle | GO:0045786 | 6 | 0.006335 | 2.560961 | 10 | 225 | 1110 | 63960 | 0.049827 |
| positive regulation of catalytic activity | GO:0043085 | 5 | 0.006346 | 2.092795 | 15 | 413 | 1110 | 63960 | 0.049778 |
| nucleus organization | GO:0006997 | 6 | 0.006369 | 2.936134 | 8 | 157 | 1110 | 63960 | 0.049824 |

**Supplementary Table S8. The DEGs significantly enriched in KEGG pathway after ALA treatment**

|  |  |  |  |
| --- | --- | --- | --- |
| Illumination Time (h) | ID | Pathway | DEGs |
| 24 | mdm00941 | Flavonoid biosynthesis | MDP0000686666|MDP0000729533|MDP0000686661|MDP0000264424|MDP0000759336|MDP0000575740|MDP0000183682|MDP0000494976|MDP0000140621|MDP0000636927|MDP0000294667|MDP0000286933|MDP0000225491|MDP0000240641|MDP0000688415|MDP0000252589|MDP0000134791|MDP0000240643|MDP0000788934|MDP0000271527|MDP0000361449 |
|  | mdm03430 | Mismatch repair | MDP0000184480|MDP0000125070|MDP0000568341|MDP0000208491|MDP0000248100|MDP0000786815|MDP0000245551|MDP0000321215 |
|  | mdm03030 | DNA replication | MDP0000184480|MDP0000125070|MDP0000195390|MDP0000208491|MDP0000196740|MDP0000786815|MDP0000568341|MDP0000321215|MDP0000131617 |
|  | mdm04712 | Circadian rhythm - plant | MDP0000686666|MDP0000686661|MDP0000575740|MDP0000252999|MDP0000287992|MDP0000241199 |
| 48 | mdm00941 | Flavonoid biosynthesis | MDP0000686666|MDP0000286933|MDP0000686661|MDP0000494976|MDP0000575740|MDP0000183682|MDP0000759336|MDP0000170162|MDP0000294667|MDP0000360447|MDP0000788934|MDP0000688415|MDP0000252589|MDP0000240643|MDP0000134791 |
| 72 | mdm00941 | Flavonoid biosynthesis | MDP0000686666|MDP0000286933|MDP0000686661|MDP0000494976|MDP0000575740|MDP0000183682|MDP0000205890|MDP0000294667|MDP0000523477|MDP0000360447|MDP0000788934|MDP0000688415|MDP0000252589|MDP0000240643 |
|  | mdm01110 | Biosynthesis of secondary metabolites | MDP0000286933|MDP0000307964|MDP0000280527|MDP0000332597|MDP0000788934|MDP0000271872|MDP0000252589|MDP0000523942|MDP0000171795|MDP0000183682|MDP0000198843|MDP0000494976|MDP0000251253|MDP0000303739|MDP0000294667|MDP0000293578|MDP0000523477|MDP0000360447|MDP0000194772|MDP0000248777|MDP0000176374|MDP0000240643|MDP0000800945|MDP0000272901|MDP0000274409|MDP0000238942|MDP0000130459|MDP0000223309|MDP0000575740|MDP0000397367|MDP0000205890|MDP0000874800|MDP0000931334|MDP0000680997|MDP0000754054|MDP0000280662|MDP0000263180|MDP0000686666|MDP0000686661|MDP0000547655|MDP0000634676|MDP0000442206|MDP0000272843|MDP0000688415|MDP0000296410 |
|  | mdm01100 | Metabolic pathways | MDP0000286933|MDP0000307964|MDP0000297138|MDP0000280527|MDP0000270977|MDP0000788934|MDP0000271872|MDP0000252589|MDP0000523942|MDP0000575740|MDP0000194772|MDP0000183682|MDP0000126946|MDP0000209143|MDP0000198843|MDP0000494976|MDP0000251253|MDP0000303739|MDP0000332597|MDP0000293578|MDP0000156131|MDP0000523477|MDP0000360447|MDP0000171795|MDP0000248777|MDP0000176374|MDP0000252292|MDP0000240643|MDP0000800945|MDP0000272901|MDP0000274409|MDP0000238942|MDP0000233546|MDP0000130459|MDP0000223309|MDP0000939379|MDP0000787842|MDP0000397367|MDP0000205890|MDP0000157447|MDP0000874800|MDP0000931334|MDP0000680997|MDP0000448896|MDP0000754054|MDP0000280662|MDP0000263180|MDP0000686885|MDP0000686666|MDP0000686661|MDP0000127757|MDP0000547655|MDP0000634676|MDP0000239530|MDP0000442206|MDP0000272843|MDP0000210077|MDP0000294667|MDP0000296410|MDP0000146639 |
|  | mdm00592 | alpha-Linolenic acid metabolism | MDP0000296410|MDP0000874800|MDP0000272843|MDP0000680997|MDP0000523942|MDP0000272901 |
|  | mdm03030 | DNA replication | MDP0000125070|MDP0000144558|MDP0000313603|MDP0000770205|MDP0000210654|MDP0000231390 |
|  | mdm04712 | Circadian rhythm - plant | MDP0000139278|MDP0000234215|MDP0000686666|MDP0000575740|MDP0000686661 |
|  | mdm00944 | Flavone and flavonol biosynthesis | MDP0000286933|MDP0000319451 |
|  | mdm00350 | Tyrosine metabolism | MDP0000296410|MDP0000680997|MDP0000523942|MDP0000272901 |
|  | mdm00010 | Glycolysis / Gluconeogenesis | MDP0000238942|MDP0000198843|MDP0000296410|MDP0000680997|MDP0000523942|MDP0000800945|MDP0000272901 |
|  | mdm03430 | Mismatch repair | MDP0000313603|MDP0000210654|MDP0000248100|MDP0000125070 |
|  | mdm00071 | Fatty acid degradation | MDP0000296410|MDP0000680997|MDP0000523942|MDP0000272901 |

**Supplementary Table S9. Differentially expressed transcription factors related to anthocyanin metabolism in apple calli**

|  |  |  |
| --- | --- | --- |
| Type of TFs | Number of DEGs | Description |
| AP2-EREBP | 18 | Ethylene-responsive transcription factor |
| ARF | 2 | Auxin response factor |
| bHLH | 12 | Basic helix-loop-helix protein |
| bZIP | 2 | Basic Leucine Zipper Domain transcription factor |
| C2C2-Dof | 3 | Zinc finger protein |
| C2H2 | 7 | Zinc finger C2H2 domain-containing protein |
| C3H | 3 | Zinc finger CCCH domain-containing protein |
| CCAAT | 7 | Zinc finger CCCH domain-containing protein |
| GRAS | 3 | Scarecrow-like protein |
| HB | 6 | Homeobox-leucine zipper protein |
| HSF | 5 | Heat stress transcription factor |
| LOB | 4 | LOB domain-containing protei |
| MADS | 5 | MADS-box protein |
| MYB | 27 | Myb (Myeloblastosis) -related protein |
| NAC | 7 | NAC domain-containing protein |
| Orphans | 8 | Orphan Transcription Factor |
| TIFY | 2 | TIFY protein |
| Trihelix | 3 | Trihelix transcription factor |
| WRKY | 13 | WRKY transcription factor |
| Other TFs | 34 |  |
| Total TFs | 171 |  |

**Supplementary Table S10. Correlations between the relative expressions of MdMYB10 and MdMYB9 and anthocyanin metabolism genes under ALA treatment**

|  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- |
|  | Gene | *MdCHS* | *MdF3’H* | *MdDFR* | *MdANS* | *MdUFGT* | *MdGST* | *MdMATE* |
| Correlations | *MdMYB10* | 0.96\*\* | 0.97\*\* | 0.99\*\* | 0.98\*\* | 0.98\*\* | 0.88\*\* | 0.92\*\* |
| *MdMYB9* | 0.99\*\* | 0.98\*\* | 0.96\*\* | 0.99\*\* | 0.98\*\* | 0.85\*\* | 0.94\*\* |
| Note: Pearson correlation test, \*\* represent correlation between MYB genes of apple and anthocyanin biosynthesis and transport genes is significant at the  *P* = 0.01 level. | | | | | | | | |



**Supplementary Figure 1.** Principal component analysis (PCA) showing the divergence of the respective transcriptomes in response to ALA treatment. The PCA was conducted with the using the internal steps of the *R* package version 3.5.3 (http://www.Bioconductor.org).



**Supplementary Figure 2.** qRT-PCR analysis of the relative expression of target genes in transgenic calli. Relative expression level was calculated using the 2-ΔΔCT method with three replicates. The different letters in each gene represent significant differences (*P* < 0.05).



**Supplementary Figure 3.** Chromosomal location of MdMATEs and phylogenetic analysis of MdMATEs proteins and MATE proteins from other species. The phylogenetic tree was generated with MEGA X software using the maximum likelihood (ML) method. Bootstrap values from 1000 replicates are indicated at each branch.



**Supplementary Figure 4.** Screening of the optimal concentration of 3-AT used for yeast one hybrid assay. The yeast strain Y187 transformed with the pHIS2-MdMATE8pro vectors were grown on -Trp/-His medium containing different concentrations of 3-AT.