

| | | |
|---------------------|---|-----|
| AtHDA8_AT1G08460.1_ |MVTNRVDVFWHEGMLRHDAVEGVFDTGYDPGFLLVLEKHFENADRVRNMLISIL | 53 |
| Pm001496 | MAASTATAFTDRIDVFWDSGMLNHNNSGNGVFDTCMDPGFLLVLEKHPENS DRVKNMVISIL | 60 |
| Pm017060 | MAASTATAFTDRIDVFWDSGMLNHNNSGNGVFDTCMDPGFLLVLEKHPENS DRVKNMVISIL | 60 |
| Consensus | t r dvfw gml h gvfdtg dpgfldvlekhpen drv nm sil | |
| AtHDA8_AT1G08460.1_ | RRGPTAFHVNVFTICLFAIVSELI MEHTSEYIEKLVEADKSGERCEIAAGTFMSPGSWEEAA | 113 |
| Pm001496 | KRGPTISFYISWLPGRPMLISELISFHSSEYINELVEADRDGGK.MLCSGTFLNPGSWDAS | 119 |
| Pm017060 | KRGPTISFYISWLPGRPMLISELISFHSSEYINELVEADRDGGK.MLCSGTFLNPGSWDAS | 119 |
| Consensus | rgpi p w g p sell fh seyi lvead g gtf pgsw a | |
| AtHDA8_AT1G08460.1_ | LLAAGTTLSAMQHILDCCHKIAYAIIVREPGHHSOPTQADGYCFINNAALAVKIALNSGSC | 173 |
| Pm001496 | LLAAGTTLSAMKHVLEGHGKIAYAIIVREPGHHAQPTRADGYCFINNAGLAVQFALNSGAC | 178 |
| Pm017060 | LLAAAYS.....SRWILLP.....DNAGLAVQIALNSGAC | 148 |
| Consensus | llaa l p na lav alnsg c | |
| AtHDA8_AT1G08460.1_ | SRVAVIDIDVHYGNGTAEFCFVTSCKVLTIVSLHMHGSWGSSHPQKGSIDELCEIDVGLCYN | 233 |
| Pm001496 | AKVAVIDIDVHYGNGTAEFCFYRSCKVLTISLHMHGSWGSSHPQNGSVDELCEAEFCGYN | 238 |
| Pm017060 | AKVAVIDIDVHYGNGTAEFCFYRSCKVLTISLHMHGSWGSSHPQNGSIDELCEGEGENYN | 208 |
| Consensus | vavididvhyngtae fy sdkvlt slhm hsgwg shpq gs del e g yn | |
| AtHDA8_AT1G08460.1_ | LNIPLENGTGDRGYEYAMNELVVFVAVRFEEDMVLVVGQDSSAVSS.....FFAQ | 284 |
| Pm001496 | LNIPLENGTGDRGYRHAMTELVVEMIQKFEEMVVIIGQDSSAFDPNGRQCLTMEGYQE | 298 |
| Pm017060 | LNIPLENGTGDRGYKHDTELVVEMIQKFEEMVVLVAGQDSSAGSKGR.....FAQSSD | 264 |
| Consensus | ln plp gtgdrgy m elvvp f p m vlv gqdssa | |
| AtHDA8_AT1G08460.1_ | IR..VDYLTEHLLR.....VLFATIVLVTSKSLMYAAPIWICCDKSA..... | 324 |
| Pm001496 | IGRIVRSLADRHCSGRLLIVQEGGYHTYSAYCLHATLEGVINLPTSLLSDPIAYYPEDE | 358 |
| Pm017060 | VGLCASCDDDTCL.....LCFRFGSSELRQVVVPSEHPLLAGRKTCLPWCS | 312 |
| Consensus | | |
| AtHDA8_AT1G08460.1_ | | 324 |
| Pm001496 | ALAVEVIKSIKKFQKDNVFFLK | 381 |
| Pm017060 | ITLG..... | 316 |
| Consensus | | |

Figure S1 Sequences alignment of HDA8 homologous proteins in *Arabidopsis* and mei.

| | | |
|------------|---|-----|
| PQP91789.1 | MELLTVSFSSSLAGNALFLARQHLCWKWNSRFDLEAKFVRNRI LNKSRLRGRRC LSEKREASISCSCTGTGEDPLIPV NK | 80 |
| PQP94174.1 | | 0 |
| PQP91793.1 | | 0 |
| Consensus | | |
| PQP91789.1 | KLSDARVIYAVAPAMGHNQESHPE SHFRVPAIVNALEKWELSEKFRGLEVIELENFNAASSNDIASVHTRAYVSGLEKAM | 160 |
| PQP94174.1 |MGHNQESHPE SHFRVPAIVNALEKWELSEKFRGLEVIELENFNAASSNDIASVHTRAYVSGLEKAM | 66 |
| PQP91793.1 |MANEQTLSEIDSSIDSTQVTLLKNLEAGRHPILVQ....AM | 37 |
| Consensus | p e v am | |
| PQP91789.1 | DQASKQGIILIEGSGPTYATVDTERESLVAAGAGISLIDAVV.....AESKISKSPPVGFALIRPPGHH | 224 |
| PQP94174.1 | DQASKQGIILIEGSGPTYATVDTERESLVAAGAGIALIDAVV.....AESKISKSPPVGFALIRPPGHH | 130 |
| PQP91793.1 | DQASKQGIILIEGSGPTYATVDTERESLVAAGAGIALIDAVILFEVVSFFNTSEFIARVAESKISKSPPVGFALIRPPGHH | 117 |
| Consensus | dqaskqgiiliegs gptyatvdtf eslvaagagi lidav aeskiskspvpgfalirppghh | |
| PQP91789.1 | AIPKGPMSGFCVFGNVAVAARYAQRSHGLKRVFIIDFDVHHGNGTNDAFYDDPDIFFLSTHQDGSYPGCKFEEVGHGDGE | 304 |
| PQP94174.1 | AIPKGPMSGFCVFGNVAVAARYAQRSHGLKRVFIIDFDVHHGNGTNDAFYDDPDIFFLSTHQDGSYPGCKFEEVGHGDGE | 210 |
| PQP91793.1 | AIPKGPMSGFCVFGNVAVAARYAQRSHGLKRVFIIDFDVHHGNGTNDAFYDDPDIFFLSTHQ..VWICGGLV..... | 186 |
| Consensus | aipkgpmgfcvfgnvavaaryaq shglkrvfiidfdvhhgngtndafyddpdifflsthq g g | |
| PQP91789.1 | GTTLNLPLPGSGDTAMRTVFDEIIVPCAQRFPDIILVSAGYDAHVLDPLASLQFTTGTYYMLASYIQQLANDLCGGRC | 384 |
| PQP94174.1 | GTTLNLPLPGSGDTAMRTVFDEIIVPCAQRFPDIILVSAGYDAHVLDPLASLQFTTGTYYMLASYIQQLANDLCGGRC | 290 |
| PQP91793.1 | | 186 |
| Consensus | | |
| PQP91789.1 | VFFLEGGYNLKSLSYSVADSFR AFLGEP SLASEFDNPAILHEEPSTRVRQA IERVKHIHS | 444 |
| PQP94174.1 | VFFLEGGYNLKSLSYSVADSFR AFLGEP SLASEFDNPAILYEEPSTRVRQA IERVKHIHS | 350 |
| PQP91793.1 | | 186 |
| Consensus | | |

Figure S2 Sequences alignment of three PyHDA14 homologous proteins in Somei-Yoshino.

| | | |
|------------|--|-----|
| HF10663-RA | MDTGGSNLSVSGPDGVKRVSYFYDPEVGNYYYGGQHPMKPHRIRMTHALLAHYGLLQNMQVLKPYPARDRDLRCRFHADDY | 80 |
| HF36232-RA | MDTGGSNLSVSGPDGVKRVSYFYDPEVGNYYYGGQHPMKPHRIRMTHALLAHYGLLQNMQVLKPYPARDRDLRCRFHADDY | 80 |
| HF10684-RA | MDTGGSNLSVSGPDGVKRVSYFYDPEVGNYYYGGQHPMKPHRIRMTHALLAHYGLLQNMQVLKPYPAR...DLRCRFHA... | 75 |
| Consensus | mdtggsnsl sgpdgvkrkvsyfydpevgnnyyggqghpmkphrirmthallahyglqlqnmqvlkpypar dlcrfha | |
| HF10663-RA | VAFRLRNITFEQQDQLRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGAVKLNHGICDISINWAGGLHHAKECEASGFCY | 160 |
| HF36232-RA | VAFRLRNITFEQQDQLRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGAVKLNHGICDISINWAGGLHHAKECEASGFCY | 160 |
| HF10684-RA |ETQQDQLRQLKRFNVGEDCPVFDGLYSFCQTYAGGSVGGAVKLNHGICDISINWAGGLHHAKECEASGFCY | 146 |
| Consensus | etqqdqlrqlkrfnvgedcpvfdglysfcqtyaggsvggavklnhgicdisinwagglhha keasgfcy | |
| HF10663-RA | VNDIVLAILELLKQHERVLYVDIDIHGHDGVEEAFYTDRVMTVSFHKFGDYFPGTGDIRDIGYGKGKYYSLNVPLDDGI | 240 |
| HF36232-RA | VNDIVLAILELLKQHERVLYVDIDIHGHDGVEEAFYTDRVMTVSFHKFGDYFPGTGDIRDIGYGKGKYYSLNVPLDDGI | 240 |
| HF10684-RA | VNDIVLAILELLK..... | 159 |
| Consensus | vndivlailellk | |
| HF10663-RA | DDESYHYLFKPIIGKVMEIFKPGVVLQCGADSLSGDRLGCFNLSIKGHAECVRYMRSFNVPLLLGGGGYTIRNVARCW | 320 |
| HF36232-RA | DDESYHYLFKPIIGKVMEIFKPGVVLQCGADSLSGDRLGCFNLSIKGHAECVRYMRSFNVPLLLGGGGYTIRNVARCW | 320 |
| HF10684-RA |LGCFNLSIKGHAECVRYMRSFNVPLLLGGGGYTIRNVARCW | 201 |
| Consensus | lgcfnlslkghaecvrymrsfnvpllllggggytirnvarcw | |
| HF10663-RA | CYETGVALGAEIEDKMPQHEYYEYFGPDYTLHVAPSNMENKNSHMLLEEIRSKLLENLSRLQHAPSVQFCRRPPDTELPE | 400 |
| HF36232-RA | CYETGVALGAEIEDKMPQHEYYEYFGPDYTLHVAPSNMENKNSHMLLEEIRSKLLENLSRLQHAPSVQFCRRPPDTELPE | 400 |
| HF10684-RA | CYETGVALGAEIEDKMPQHEYYEYFGPDYTLHVAPSNMENKNSHMLLEEIRSKLLENLSRLQHAPSVQFCRRPPDTELPE | 281 |
| Consensus | cyetgvalgaeiedkmpqheyyeyfgpdytlhvapsnmknshmlleeirskllenls lqhapsvqfq rppdtelpe | |
| HF10663-RA | ENEEQDDPDERWDPDSMEVDDERKPLPSRVKKEIVEPEVKDPKGTSENARSSGYDPAVDEITTCALDMSGSGSVDEPT | 480 |
| HF36232-RA | ENEEQDDPDERWDPDSMEVDDERKPLPSRVKKEIVEPEVKDPKGTSENARSSGYDPAVDEITTCALDMSGSGSADEFA | 480 |
| HF10684-RA |DDPDERWDPDSMEVDDERKPLPSRVKKEIVEPEVKDPKGTSENARSSGYDPAVDEITTCALDMSGSGSVDEPT | 356 |
| Consensus | ddpderwdpsdsmevdderkplpsrvkkeivepevkdpkgtsenarssgydpavdeittg kaldmsgsgs dep | |
| HF10663-RA | VKVEQDTMKNPADQ | 494 |
| HF36232-RA | VKVEQDTMKNPADQ | 494 |
| HF10684-RA | VKVEQDTMKNPADQ | 370 |
| Consensus | vkveq t nkpdaq | |

Figure S3 Sequences alignment of three MdHDA1 homologous proteins in apple.

| | | |
|-------------|--|-----|
| RC2G0299600 | MFFLKFGFSLMYHFVYCKDSEDNCSGLGNVLFLARQRCFNWKSPELRLHDAIFATDGILYKNLRRGRGCFSKTTEASSSF | 80 |
| RC6G0022900 | | 0 |
| RC1G0265100 | | 0 |
| RC6G0533000 | | 0 |
| Consensus | | |
| RC2G0299600 | SNGTEESPYIPVNTKPSDARIYAVAPAMGHNQEAHPESHFRVPAIVQALDKLELTPKFRGSKVIELQNFRPASVDDITS | 160 |
| RC6G0022900 | | 0 |
| RC1G0265100 | | 0 |
| RC6G0533000 | | 0 |
| Consensus | | |
| RC2G0299600 | VHTQSYVSGLEKAMDQASKDGLIFIEGTGPTYATVETFQESLIAAGAGIALIDSVAESKNSRDPPTGFALIRPPGHAI | 240 |
| RC6G0022900 | | 0 |
| RC1G0265100 | | 0 |
| RC6G0533000 | | 0 |
| Consensus | | |
| RC2G0299600 | PKGPMGFCVFGNIAIAAHYAQRAGHLKRVFIIDFDVHHGNGTNDAFYEDDIFFLSTHQDGSYPGTGKFDEIGRGDGEET | 320 |
| RC6G0022900 | ...MGFCVFGNIAIAAHYAQRAGHLKRVFIIDFDVHHGNGTNDAFYEDDIFFLSTHQI..... | 56 |
| RC1G0265100 | ...MGFCVFGNIAIAAHYAQRAGHLKRVFIIDFDVHHGNGTNDAFYEDDIFFLSTHQVT.....IFDTLSVQIYLYV | 70 |
| RC6G0533000 | ...MGFCVFGNIAIAAHYAQRAGHLKRVFIIDFDVHHGNGTNDAFYEDDIFFLSTHQI..... | 56 |
| Consensus | mgfcvfgniaiaa yaq a glk vfiidfdvhhgngtndafy d diffflsthq | |
| RC2G0299600 | TLNLPLPGSGDTAMRTVFDDVIVPCAQRFKPDIIILVSAGYDAHALDPLASLQFTTGTYMLASSIQQLAKDICGGRCVF | 400 |
| RC6G0022900 | | 56 |
| RC1G0265100 | LVMIV..... | 75 |
| RC6G0533000 | | 56 |
| Consensus | | |
| RC2G0299600 | FLEGGYNLDSLSYSVADSFR AFLKEPSLASTFDNPAMLYEEPSMKIKQAIQRVKHLHS | 458 |
| RC6G0022900 | | 56 |
| RC1G0265100 | | 75 |
| RC6G0533000 | | 56 |
| Consensus | | |

Figure S4 Sequences alignment of the four RcHDA14 homologous proteins in rose.

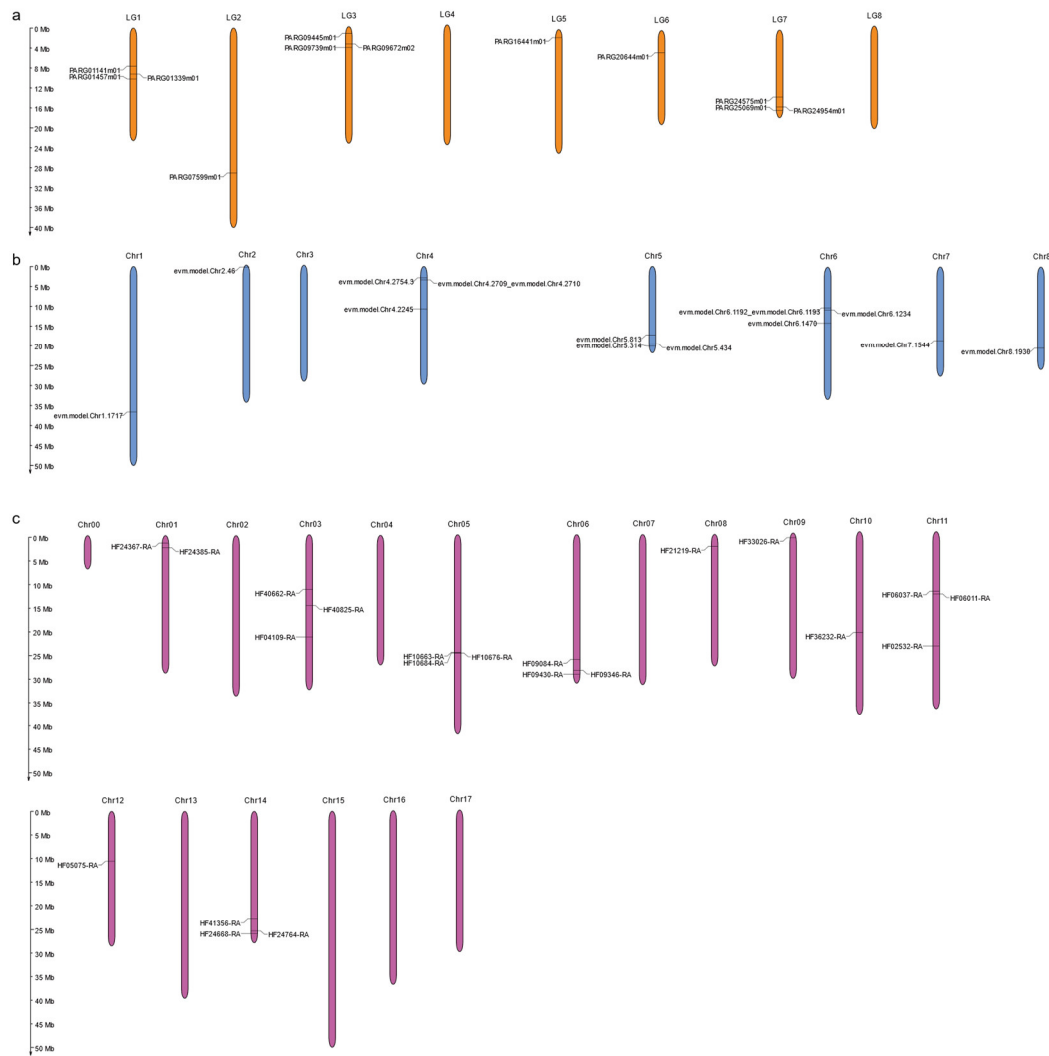


Figure S6 Gene locations of *HDACs* on the chromosome. a.The *ParHDACs* genes of *P. armeniaca* b.The *PyHDACs* genes of *P. yedoensis* c.The *MdHDACs* genes of *M. domenstica*

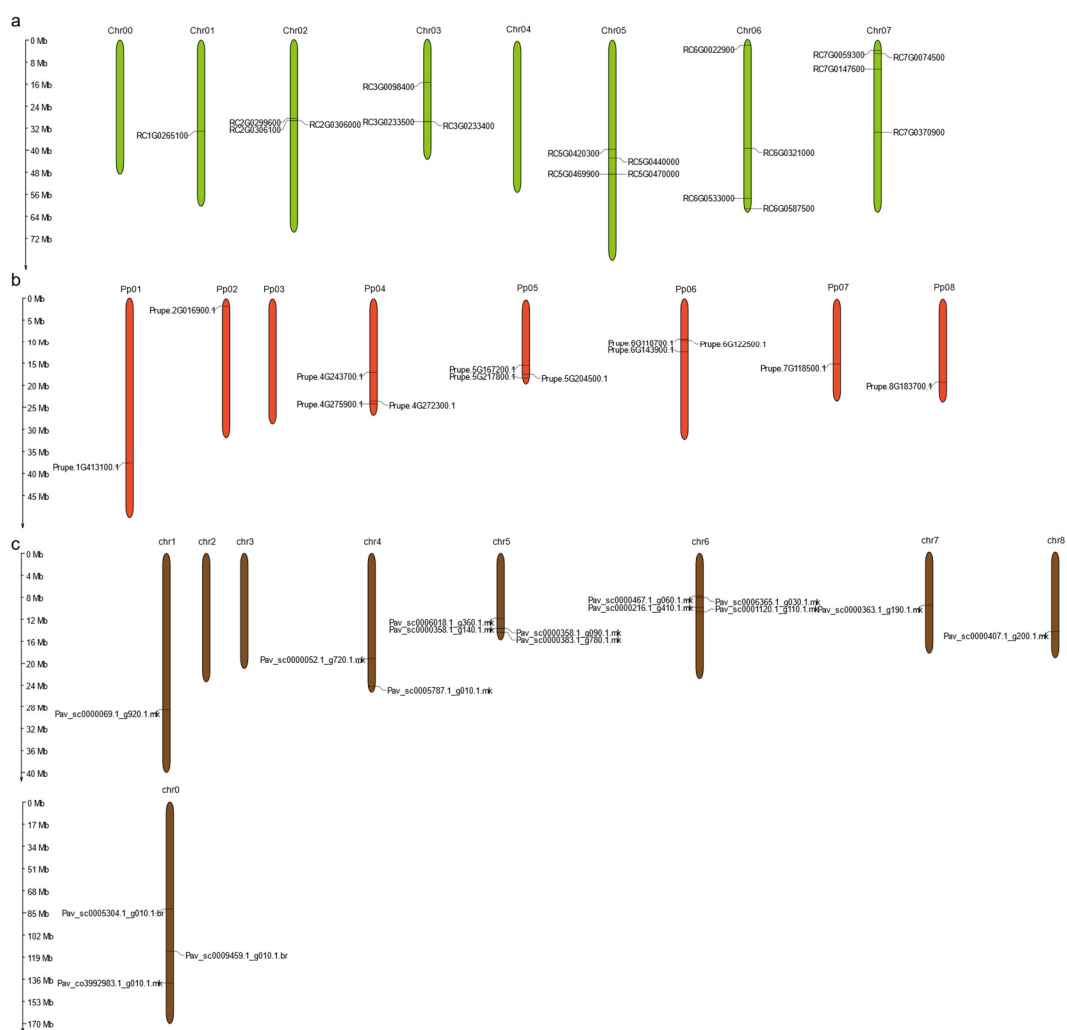


Figure S7 Gene locations of *HDACs* on the chromosome. a.The *RcHDACs* genes of *R. chinensis* b.The *PpHDACs* genes of *P.persica* c.The *PavHDACs* genes of *P.avium*.

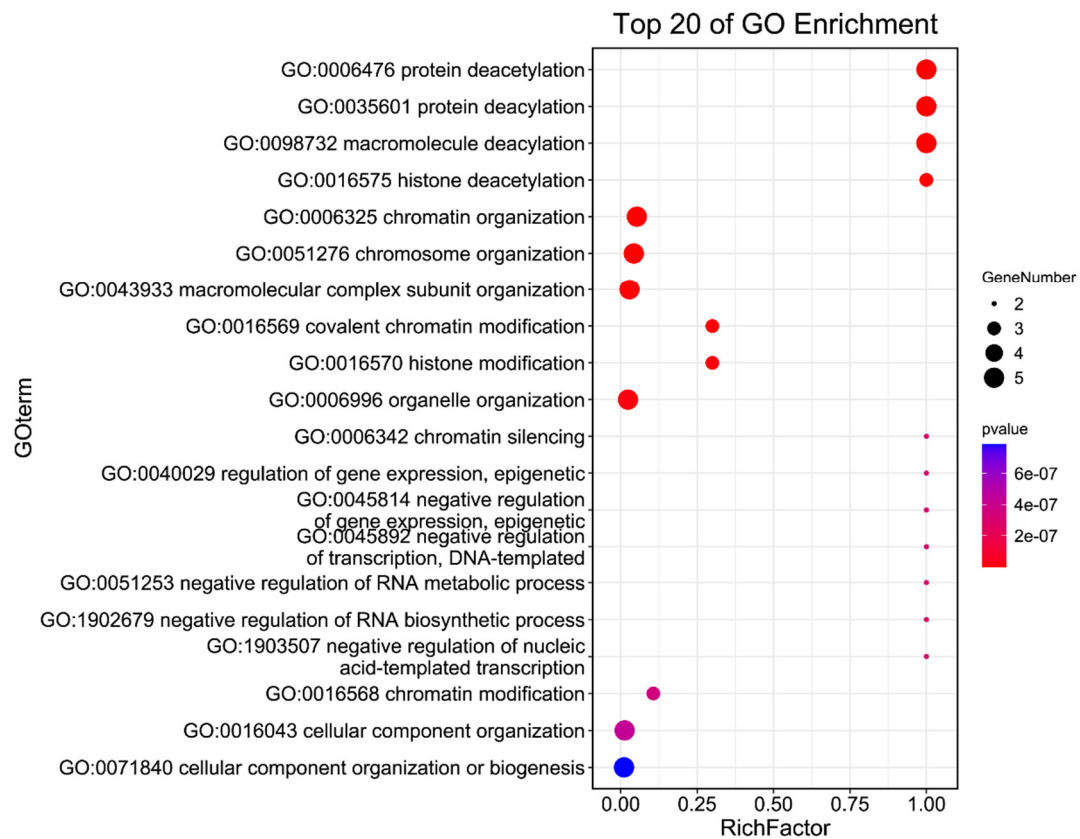


Figure S8 Dot plot of PmHDACs GO enrichment analysis.

| | | |
|-----------|---|-----|
| AtHDT1 | MEFWGIEVKSQKPVTVTEEGILTHVSOALGECNKKKEGFVPLHVKVGNNQNLVGLTLSTENIPQLFCDLVFDKEFELSHTWGRKGSVYVGV | 92 |
| AtHDT2 | MEFWGVAITPKNATKVTEEDSLVHISQASILDCTVKSGESVVLSTVVGAKLVLGTLSDKFPQISFDLVFDKEFELSHSGTKANVHFVGY | 91 |
| AtHDT3 | MEFWGVEVKNKGKPLHLDELGLDRLVHISQALGESKNNVTEPQLYVTVGSDKLVLGTLSHKFPQLSTELVLERNPALSHTWKNGSVFFSGY | 92 |
| PtHDT903 | MEFWGVEVKGEPKLVESGDGFLHLHISQACIGAKKDKGNEVCLFVNFDQKLVLGTLSEHKFPQLPFDLVFEKDFELSHNLKNGSVFFSGY | 93 |
| PtHDT902 | MSSMEFWGVEVKGEPKLVESGDGFLHISQALGESKKNESVPLFLKLDEKKLVLGTLSPDKPQLSFDLVFEKDFELSHNLKNGSVFFSGY | 95 |
| PtHDT901 | MSSMEFWGVEVKGEPKLVESGDGFLHISQALGESKKNESVPLFLKLDEKKLVLGTLSPENIPQLSFDLVFEKDFELSHNLKNGSVFFSGY | 94 |
| MdHDT1-2 | MEFWGVEVKGEPKLVESGDGFLHISQALGESKKNESVPLFLKLDEKKLVLGTLSPDKPQLSFDLVFEKDFELSHNLKNGSVFFSGY | 91 |
| MdHDT1-3 | MEFWGVEVKGEPKLVESGDGFLHISQALGESKKNESVPLFLKLDEKKLVLGTLSPDKPQLSFDLVFEKDFELSHNLKNGSVFFSGY | 108 |
| MdHDT1-1 | MISMSVSGLRCDAINVCCSLNNDVSFVGLGVKVEKAGEPLKVVVEESYVHLSHATLGELKKGGDQCVIHVKVGDNKLVLANLSSDKPQLSFDLVFEKDFELSHNLKNGSVFFSGY | 108 |
| PmHDT1 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 89 |
| PmHDT3 | MEFWGVEVKSQGSVSVEEKNKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 92 |
| ParHDT1 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 91 |
| PpHDT1 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 113 |
| PpHDT3 | MEFWGVEVKSQGSVSVEEKNKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 92 |
| PsHDT1 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 91 |
| PsHDT3 | MEFWGVEVKSQGSVSVEEKNKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 92 |
| PyHDT1 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 91 |
| PavHDT1 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 14 |
| PavHDT2 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 0 |
| PyHDT1 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 7 |
| RcHDT1-2 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 0 |
| RcHDT3-1 | MEFWGVEVKGAGEPVKYVEVDGKVVHLSQACIGETKKGADQGVISVKIDDKKFLVGLTSSDKFPQLFLDLVFEKDFELSHNLKNGSVFFSGY | 0 |
| AtHDT4 | MEFWGIEIKPKKPKVIQKDGFMVHASQVITGDEVKVKKDETFAVYVIRIGDDENGFMIGNLSQKFPQFSIDLYLGHFEISHNLSTSSVYIIGY | 93 |
| RcHDT1-1 | MEFWGVEVKGAGEPLSVFEDQGNVVLHISQACIGESKKNESVPLFLKLDEKKLVLGTLSPDKPQLSFDLVFEKDFELSHNLKNGSVFFSGY | 91 |
| RcHDT3-2 | MANMKFWGVEVKSQGSVSVEEGLTLVHLSQACIGEVKKKGSDSISLFLVKTGDQKLVLGTLSPDKPQLSFDLVFEKDFELSHNLKNGSVFFSGY | 96 |
| Consensus | | |
| AtHDT1 | KTPNIEPQGYSEEEEEEEVPA.....GNA.....AKAVAKPKPAEVKPAVD.....DEEEDSDSG. | 147 |
| AtHDT2 | KSPNIEQDDFT.....SSDEDVPEAVPA.....ATAVTANGNAGA.....KADTKPKPAEVKPAEEK.....PESEDEESDDEDE | 165 |
| AtHDT3 | KVDASD.....PEPDELIDQLLEAQAAPKSAQKQVNFQLPNEDVKAQKQDADGSGEE.....DSSDDDS.....E | 156 |
| PtHDT903 | KVAQPESSDSE.....FISGDEELLPVVDNCKEEAKQKPEPENAAKPDSSKQKVIKEPNKDGPKPENDDSSDEESSDSDGE | 173 |
| PtHDT902 | QAAI.....PENISDFSDGDGE.....IPFEKVENVKFATGTDKAAPKPKKAN.....PVVPSKDDSDDDSD | 155 |
| PtHDT901 | QVIP.....DDASDFSGDEEL.....FEFADAKIMKAATAKDKAAPKPKAT.....LVEPSIDDDSDSD | 153 |
| MdHDT1-2 | QTYIANESDEDDQSPD.....SSESEELPLNPFNGNGINEAKAPPPKTNIVKPESSGKQKVIKEPKD.....EDSDSDSD.....E | 164 |
| MdHDT1-3 | LLCSAATESDEEDQSGKPYIILPFCFLFSVVMNLLFNLSYGVNFCMYYSSEELPLNPFNGNGINEAKAPPPKTNIVKPESSGKQKVIKEPKD.....EDSDSDSDSD | 219 |
| MdHDT1-1 | TTCCFCCHRRIGRPI.....CSESEELPLNPFNGNGINEAKAPPPKTNIVKPESSGKQKVIKEPKD.....EDSDSDSDSD.....E | 180 |
| PmHDT1 |EFDSSDEDVMEITQNG.....APSKTNIVKPEASEKQKVIKEPSND.....DDSDSDSD.....E | 139 |
| PmHDT3 | KLSLKYFCFDCN.....SSESEEDVLTVDNG.....KPVISGPKPLSTEDTKKAIKSEKQKASS.....DDSDSDSDSDVADGQTK | 162 |
| ParHDT1 | QTLIGEDEEGDS.....EFDSSDEDVMEITQNG.....MPAPSKTNIVKPEASEKQKVIKEPTND.....DDSDSDSD.....E | 156 |
| PpHDT1 | QTLIGEYFPNNCANWLFFS.....AYVEFDSSDEDVMEITQNG.....MPAPSKTNIVKPEASEKQKVIKEPSND.....DDSDSDSD.....E | 188 |
| PpHDT3 | KLSLNL.....SSESEEDVLTVDNG.....KPVISGPKPLSTEDTKKAIKSEKQKASS.....DDSDSDSDSDVADGQTK | 160 |
| PsHDT1 | QTLIGEDEEGDS.....EFDSSDEDVMEITQNG.....IPAPSKTNIVKPEASEKQKVIKEPSND.....DDSDSDSD.....E | 156 |
| PsHDT3 | KLSLNL.....SSESEEDVLTVDNG.....KPVISGPKPLSTEDTKKAIKSEKQKASS.....DDSDSDSDSDVADGQTK | 160 |
| PyHDT1 | KLSLNL.....SSESEEDVLTVDNG.....KPVISGPKPLSTEDTKKAIKSEKQKASS.....DDSDSDSDSDVADGQTK | 160 |
| PavHDT1 | QTLIGEYFPNDS.NRLFFS.....AYVEFDSSDEDVMEITQNG.....IPAPSKTNIVKPEASEKQKVIKEPSND.....DDSDSDSD.....E | 122 |
| PavHDT2 |TGDN.....SSESEEDVLTVDNG.....KPVISGPKPLSTEDTKKAIKSEKQKASS.....DDSDSDSDSDVADGQTK | 77 |
| PyHDT1 | NRMFPESES.....SEELPMIAENKGVENAKPAIAKQNAVKPESSGKQKVIKEPKD.....EADSDSDA.....S | 0 |
| RcHDT1-2 |MMAN.....LKQSKELIRSVKMAVMMK..... | 71 |
| RcHDT3-1 |ARDELDEEDSD.....SELCEYMEQQAALFQNEINPEED.....DESDESD.....E | 25 |
| AtHDT4 | RTED.....GDEYP.....STIFLYFSVIDGSFY..... | 140 |
| RcHDT1-1 | QSVN.....IANTG.....YFPC..... | 115 |
| RcHDT3-2 | | 105 |
| Consensus | | |
| AtHDT1 | MEEDSDSG.....EDSE.....EETPTPKPKASKKKANITTPKAPVSAKKA.....VAVTPORTDEKKKGK.....AANGSPKSA | 216 |
| AtHDT2 | SEDDSDSEKGMVDVEDSDSDDEEDSEDEEETPTPKPEPINKKRNESVSKTPVSGKKAAPAAAPASTPKTEKKKGKHTATPHPAKKGKSE.....VNANGSPKSG | 271 |
| AtHDT3 | NSGDDEEEKVTAESDSEEDSDSDDEEDSS.....EETPTPKPEPEPKKRSAPNNSKNPASNKKA.....FVT.....PDKTSGKKPHVHTATPHPSQAQKNGSGGSGTETSQOQTPKSA | 265 |
| PtHDT903 | SDDQAMMMANDEDESEDEDESDSDSDGDKPKKAEVKKKRSAPNNSKNPASNKKA.....FVT.....PDKTSGKKPHVHTATPHPSQAQKNGSGGSGTETSQOQTPKSA | 280 |
| PtHDT902 | DSDEEDSDSGSGMSLEEDLDESDSDSEDEETPTPKAEVKKKRSAPNNSKNPASNKKA.....FVT.....PDKTSGKKPHVHTATPHPSQAQKNGSGGSGTETSQOQTPKSA | 251 |
| PtHDT901 | DDSDDEEDSDSGSGMSLEEDLDESDSDSEDEETPTPKAEVKKKRSAPNNSKNPASNKKA.....FVT.....PDKTSGKKPHVHTATPHPSQAQKNGSGGSGTETSQOQTPKSA | 247 |
| MdHDT1-2 | DDSDDEEDSDSDSGSGMSLEEDLDESDSDSEDEETPTPKAEVKKKRSAPNNSKNPASNKKA.....FVT.....PDKTSGKKPHVHTATPHPSQAQKNGSGGSGTETSQOQTPKSA | 257 |
| MdHDT1-3 | DDSDDEEDSDSDSGSGMSLEEDLDESDSDSEDEETPTPKAEVKKKRSAPNNSKNPASNKKA.....FVT.....PDKTSGKKPHVHTATPHPSQAQKNGSGGSGTETSQOQTPKSA | 320 |
| MdHDT1-1 | DDSDDEEDSDSDSGSGMSLEEDLDESDSDSEDEETPTPKAEVKKKRSAPNNSKNPASNKKA.....FVT.....PDKTSGKKPHVHTATPHPSQAQKNGSGGSGTETSQOQTPKSA | 273 |
| PmHDT1 | SSDEGLGGF.....EDSSIE.....ASKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 218 |
| PmHDT3 | VKFEEGSSDEDESDSDSDSDSDDEEDSEETPKKADVSKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 266 |
| ParHDT1 | SSDEGLGGF.....EDSSIE.....ASKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 256 |
| PpHDT1 | SSDEGLGGF.....EDSSIE.....ASKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 290 |
| PpHDT3 | VKFEEGSSDEDESDSDSDSDSDDEEDSEETPKKADVSKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 267 |
| PsHDT1 | SSDEGLGGF.....EDSSIE.....ASKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 258 |
| PsHDT3 | VKIEEGSSDEDESDSDSDSDSDDEEDSEETPKKADVSKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 267 |
| PyHDT1 | SSDEGLGGF.....EDSSIE.....ASKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 189 |
| PavHDT1 | SSDEGLGGF.....EDSSIE.....ASKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 244 |
| PavHDT2 | VKFEEGSSDEDESDSDSDSDSDDEEDSEETPKKADVSKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 184 |
| PyHDT1 |MRMSRWKSHR.....M.....ASKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 75 |
| RcHDT1-2 | DMDSDDLIL.....EDSSIE.....ASKKRPNSASKTEPVPAKKKA.....QYLRIFIGDKKAAHTATPHPAKKGKTEMTGDKPKFOTPKSGG | 175 |
| RcHDT3-1 |KAVMMMMMMVVG.....SNKRAAESKTPVQKKKA.....FVT.....PEKTSKKKGAVHTATPHPSQAQKNGSGGSGTETSQOQTPKSA | 99 |
| AtHDT4 |MGLDEEDSDSD.....EEDVEAEAPLKVAFPSKKMEN.....GAFELAKGG.....KKNKSSGSK.....KRCFPCG | 198 |
| RcHDT1-1 | | 115 |
| RcHDT3-2 | | 105 |
| Consensus | | |
| AtHDT1 | Q.VSCG.SCKTNSGALSHNKAKHAK..... | 245 |
| AtHDT2 | Q.SSGGNNNKKPNSGKFGSGNNKSGNKGGKGR..... | 305 |
| AtHDT3 |AFGCKSTRITTSKGLSHTKAKHSA..... | 294 |
| PtHDT903 |CNSCNRSFGSNGALSHSKAKHSA..... | 305 |
| PtHDT902 |NFSCKSCERSFGSGALSHSKAKHGD..... | 279 |
| PtHDT901 |NFSCKSCDKAFSGGALSHSKAKHGD..... | 275 |
| MdHDT1-2 | G.DHSCKTCSKSNFGSNGALSHSHNKAKHGA..... | 286 |
| MdHDT1-3 | G.DHSCKCPNKSNSNGALSHSHNKAKHGA..... | 349 |
| MdHDT1-1 | G.DHSCKTCSKSNFGSNGALSHSHNKAKHGA..... | 302 |
| PmHDT1 |EHSCKPCKSNFGSNGALSHSHNKAKHSA..... | 246 |
| PmHDT3 |TFNQCSCNRSNSNGALSHTKAKHSA..... | 295 |
| ParHDT1 |EHSCKPCKSNFGSNGALSHSHNKAKHSA..... | 286 |
| PpHDT1 |EHSCKPCKSNFGSNGALSHSHNKAKHSA..... | 318 |
| PpHDT3 |TFNQCSCNRSNSNGALSHTKAKHSA..... | 296 |
| PsHDT1 |EHSCKPCKSNFGSNGALSHSHNKAKHSA..... | 286 |
| PsHDT3 |AFNQCSCNRSNSNGALSHTKAKHSA..... | 296 |
| PyHDT1 |TFNQCSCNRSNSNGALSHTKAKHSA..... | 218 |
| PavHDT1 |EHSCKPCKSNFGSNGALSHSHNKAKHSA..... | 272 |
| PavHDT2 |TFNQCSCNRSNSNGALSHTKAKHSA..... | 213 |
| PyHDT1 |EHSCKPCKSNFGSNGALSHSHNKAKHSA..... | 103 |
| RcHDT1-2 | G.NFSQSCSKSPGSGNGALSHSHNKAKHSA..... | 205 |
| RcHDT3-1 | GGTFPCDPNRSNSNGALSHTKAKHGA..... | 130 |
| AtHDT4 |PSCKK..... | 203 |
| RcHDT1-1 | | 115 |
| RcHDT3-2 | | 105 |
| Consensus | | |

Figure S9 Sequences alignment of all HD2 family proteins in *Arabidopsis*, *P. trichocarpa* and 8

Rosaceae plants.

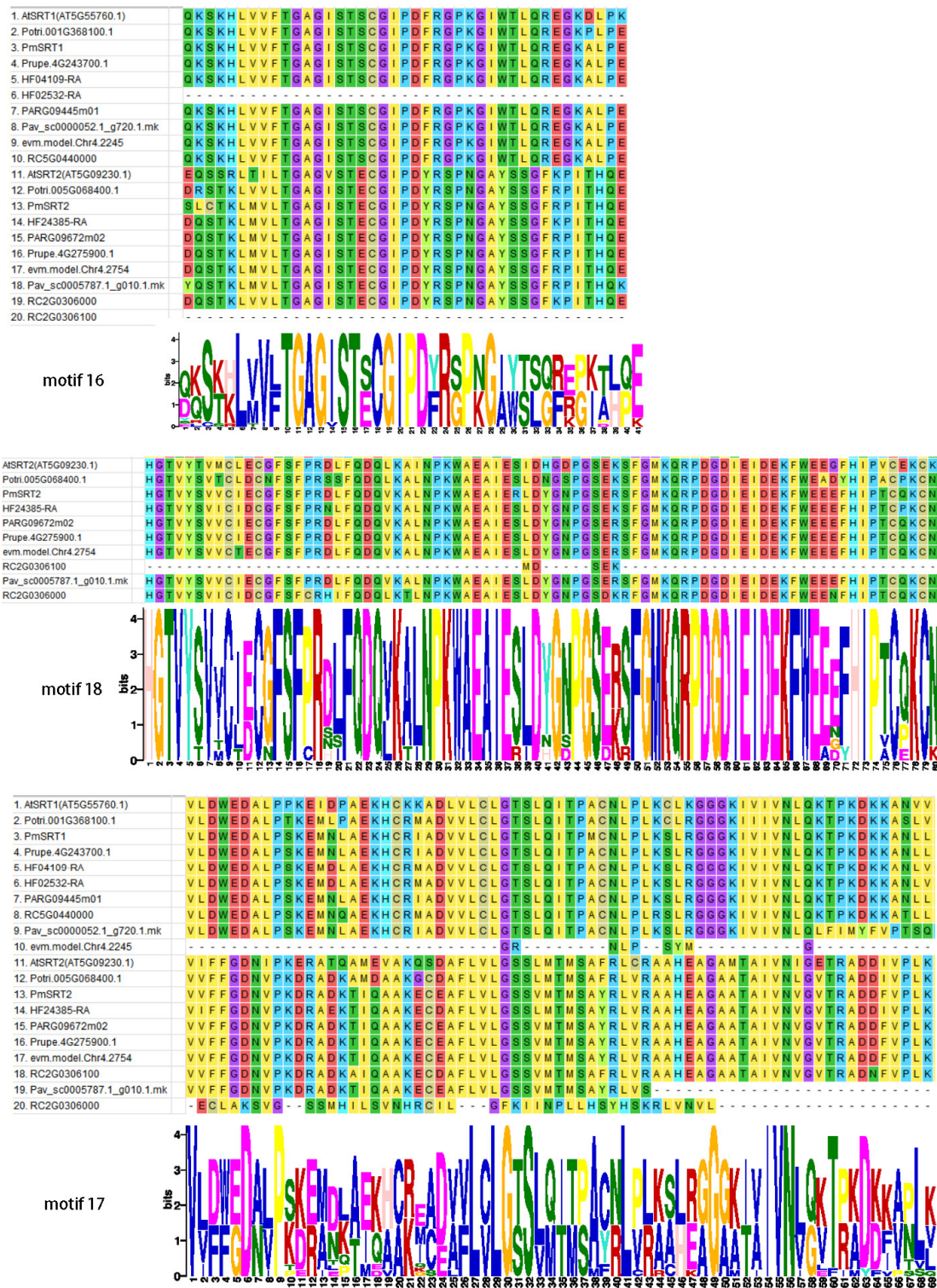


Figure S10 Motif and sequences analysis of *SIR2* genes in 10 plants.