

Table 1 Suppl. Primers used for real-time PCR analysis of *Populus histone deacetylase* genes in a reduced potassium dependency 3 / histone deacetylase 1 family.

Genes	Forward primer (5'-3')	Reverse primer (5'-3')	Amplicon size [bp]
<i>HDA901</i>	CAGCTGGAGCAGGACTAACC	GCCCTTTTGGGAATAGCATGA	120
<i>HDA902</i>	CCCGGCACAGGAGATATACGTGAC	CTCATCGTCAATTCCATCATCCAAT	89
<i>HDA903</i>	GCAAGCCATTACCAGGCAGAGTC	CACTTGCAATTCTCGGCTATTGTTGT	125
<i>HDA904</i>	ATTCAACTTGCCCTTGTTGG	CTGGAATCTCATTGGGCAGT	119
<i>HDA905</i>	GTTTCATGGGGTCCATCTCAC	ATATCCCCTATCGCCTGTCC	116
<i>HDA906</i>	TTGGAATGATTCTCGGGTCT	CGTACCTGGTCCTTCTCCAA	112
<i>HDA907</i>	TAATCTTGCGGATGGTGTC	TGCGTCTTGTGATGAAGGAG	100
<i>HDA908</i>	TGATGAAGATGAGAAACCTGGACCTA	CACAACCCTGGATGCTCTTTCTTGT	117
<i>HDA909</i>	CAGCAGGTCCTGAAGACATAGGGTG	CATGTGCCGGATCACTCGCT	96
<i>HDA910</i>	TCTTTACCCATTTGCAAGC	GTGATGGAAACCTCCTCCAA	100
<i>HDA912</i>	CTGCTGGGTATGATGGTCCT	TCCTCCCTCCAAGAAAAACA	104
<i>18S rRNA</i>	TCAACTTTCGATGGTAGGATAGAG	CCGTGTCAGGATTGGGTAATTT	145

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      10      20      30      40      50      60      70      80
HDA902 : -RKVCYFDPEVGNYYGQGHMPKPHRIRMTALLAHYGLLQHMQL-KPFPARDRLCRFHADDYVSFIRSITPETQQD-Q : 79
HDA903 : -RKVCYFDPEVGNYYGQGHMPKPHRIRMTALLAHYGLLQHMQL-KPFPARDRLCRFHADDYVSFIRSITPETQQD-Q : 79
HDA908 : -----FYEPTIGDYGGQGHMPKPHRIRMAHNLIVHYALHRRMEIN-RPFPAGPTDIRKFSHDEYVEFISVSPQSVGDPAF : 76
HDA909 : -----FYEPTIGDYGGQGHSMKPHRIRMAHNLIVHYALHRRMEIN-RPFPAGPEDIGWFHSDDYVEFISVSPQASDPAH : 76
HDA904 : -RIAYFYDGDVGSVYFGPNHMPKPHRIRMTTHLLVLSYELHKKMEIYVRPHKAYVELAQFHSDEYVEFHRIITPDITQHL-F : 79
HDA901 : -----HPESYLVRPAIVSALEKAELETSKFRGEIIEIQDFKPASLDDIANVHARAYVAGLEKAMDQASEQGI : 67
HDA912 : ----- : -
HDA906 : -----YDEKMKCHHTPDGSDHPENPNRIRVIWNKLLAN-NIPQRCVVLSGKEADKYLMVHSEHNILIRNISSKQFDSRRN : 77
HDA907 : -----HPERSDRIRAIASLATAGLPGRCPYISAREITREELQMVHSEHIDQY-ELTSHIFSSYFT : 62
HDA905 : -IDVFWHEGMLNHETGKGVFDGTPGFIDVLEKHPENSRIKMMVSLQKGPISPIYSWQGRPAQVPELDSFHAPEYIDELV : 83
HDA910 : -----HPFDSKSGWGRICRFLIVDGVLDK-NSIIIEPLEASKDDLVLVHITESYISIKSSANVAMIIEVP : 62

      90      100      110      120      130      140      150      160
HDA902 : LRQLKRFN-VGEDCPVFDGLYSFCQTYAGGSVGGAVKLNHN-----LCDIATNWAGELHHAHKKCEASGFCYVNDIVLAIL- : 153
HDA903 : LRQLKRFN-VGEDCPVFDGLYSFCQTYAGGSVGGAVKLNHN-----LCDIATNWAGELHHAHKKCEASGFCYVNDIVLAIL- : 153
HDA908 : GRQLKRFN-VGEDCPVFDGLFQCQASAGGSVGAAVKLNRG-----DADIALNWAGELHHAHKKSEASGFCYVNDIVLAIL- : 150
HDA909 : GRQLKRFN-IGEDCPVYGLFQCQASAGGSVGAAVKLNRG-----DADIALNWAGELHHAHKKSEASGFCYVNDIVLAIL- : 150
HDA904 : AGELARYN-LGEDCPVFENLFECQIYAGCTIDAAHRNNQ-----LCDIATNWAGELHHAHKKCGASGFCYVNDIVLAIL- : 153
HDA901 : IYIDG-----SGPTYATATTFRESLVAGAGITLVDVSVMSQPGIQNPPTGFALIRPPG-HHAIPKGPMSFCVFGNVTIAAH- : 143
HDA912 : -----GFALEKPPG-HHAIPKGPMSFCVFGNVTIAAH- : 31
HDA906 : RIASK-----LNSIYFNEGSSEAAHYAGSVLELAERIAKAG-DLNSGAAIVRPPG-HHAIEYDEAMGFCFLNVAIAASF : 149
HDA907 : -----PDYANEHSACAARLANGLCADLASTIFSG-----RVKNGFAMVRPPG-HHAGVREAGFCFLHNAIAA- : 126
HDA905 : EAGKQGGKMICAGTFLNPGSWDAALLAAGTTISAMKHLIDG-HGKLAYALVRPPG-HHAQPKQADGFCFLNVAIAVQ- : 159
HDA910 : PVALLP-----NCLVQKQVLYPFRKQVGGTILAAKLAKER-----GWAIVNGGEPHHCSSERGGFCAYADTISLCTH- : 129
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      170      180      190      200      210      220      230      240      25
HDA902 : ---ELLKVHERVLYVDIDVHEDGVVEEAYTTDRVITVSFKFGD-YFPG-TQDTRDITGFSKCKYYSLNVLDDG-IDDE : 227
HDA903 : ---ELLKVHERVLYVDIDVHEDGVVEEAYTTDRVITVSFKFGD-YFPG-TQDTRDITGFSKCKYYSLNVLDDG-IDDE : 227
HDA908 : ---ELLKVHERVLYVDIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TCHIKDTAGCKYSALNINPLKDG-MDDE : 224
HDA909 : ---ELLKVHERVLYVDIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TCHIKDTAGCKYSALNINPLKDG-MDDE : 224
HDA904 : ---ELLKHARVLYVDIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TQDKELGEGREKFYAINVPLKDG-IDDT : 228
HDA901 : -HAQLVHGLKRVFIIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TCHIKDTAGCKYSALNINPLKDG-MDDE : 218
HDA912 : -HAQSCAWIKTIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TQDKELGEGREKFYAINVPLKDG-IDDT : 101
HDA906 : LLDERPELGVKITIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TQDKELGEGREKFYAINVPLKDG-IDDT : 232
HDA907 : -LAAQ-AAGAKKVLIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TCHIKDTAGCKYSALNINPLKDG-MDDE : 205
HDA905 : -LALDGGCKKVTIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TQDKELGEGREKFYAINVPLKDG-IDDT : 238
HDA910 : -YAFNRDISKVMITIDVHEDGVVEEAYTTDRVITVSFKYGD-FEPC-TQDKELGEGREKFYAINVPLKDG-IDDT : 197
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      0      260      270      280      290      300      310      320      330
HDA902 : SYHFLKPKITGKVMVEIKPGAVILQCCADSLSGDRICCFNLSIK-----HAECVKYMRSFNVPLILGGGGYITRNVARCWC : 305
HDA903 : SYHFLKPKITGKVMVEIKPGAVILQCCADSLSGDRICCFNLSIK-----HAECVKYMRSFNVPLILGGGGYITRNVARCWC : 305
HDA908 : NERGLRPLITGKVMVEIKPGAVILQCCADSLSGDRICCFNLSVK-----HADCLRFLRSYNVPLILGGGGYITRNVARCWC : 302
HDA909 : CERLRPLITGKVMVEIKPGAVILQCCADSLSGDRICCFNLSVK-----HADCLRFLRSYNVPLILGGGGYITRNVARCWC : 302
HDA904 : SIFRLKPKITGKVMVEIKPGAVILQCCADSLSGDRICCFNLSID-----HAECVRFVKKFNLPLVLTGGGGYITRNVARCWC : 306
HDA901 : SMRTVDEYIVPSAQRKPDITISAGYDAHVLPGLSLQFTTGTYYTLASNIKELAKDLGGRCVFFLEGGYNDSSYSVT : 301
HDA912 : AISTVDEYIVPSAQRKPDITISAGYDAHVLPGLSLQFTTGTYYTLASNIKELAKDLGGRCVFFLEGGYNDSSYSVA : 171
HDA906 : DYLAVIDHILIPYAKKIDPDITISAGYDAHVLPGLSLQFTTGTYYTLASNIKELAKDLGGRCVFFLEGGYNDSSYSVA : 311
HDA907 : DYLAVIDHILIPYAKKIDPDITISAGYDAHVLPGLSLQFTTGTYYTLASNIKELAKDLGGRCVFFLEGGYNDSSYSVA : 284
HDA905 : GYGYAMKKIIVPAVHKIDPDITISAGYDAHVLPGLSLQFTTGTYYTLASNIKELAKDLGGRCVFFLEGGYNDSSYSVA : 321
HDA910 : EYLVKLDIAVAVAGMKIDPDITISAGYDAHVLPGLSLQFTTGTYYTLASNIKELAKDLGGRCVFFLEGGYNDSSYSVA : 278

      340      350      360      370      380      390      400
HDA902 : YETGVALGIEVDDKMPQHEYYEYFGPDYTLHVAPSNMENKNSFQLLEEIRSKLLDNLQKHPASVQFQERPP- : 378
HDA903 : YETGVALGIEVDDKMPQHEYYEYFGPDYTLHVAPSNMENKNSHQLLEEIRCKLLDNLQKHPASVQFQERVPD : 379
HDA908 : YETAVA----- : 308
HDA909 : YETAVA----- : 308
HDA904 : VETGVLLDTLPNEIPENEYIKYFAPDYSLSKSPGGLMENLNSKSYLSTIKMQVLENLRCIQHPASVQMQ- : 375
HDA901 : DSFRAPFL----- : 308
HDA912 : GYFHAF----- : 177
HDA906 : ACMKVLLLEDKPVSGSVEAYPFESTWRVIQAVRKKLSPYWPALA- : 354
HDA907 : SVIKVLL----- : 291
HDA905 : AILEGVLDLPQLLCDPIATYPE----- : 344
HDA910 : DSIANL----- : 284

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Fig. 1 Suppl. The multiple sequence alignment of histone deacetylases (HDACs) in *Populus trichocarpa*. Amino acid sequences of HDAC domains of *Populus* reduced potassium dependency 3 / histone deacetylase 1 proteins were aligned. Black boxes indicate residues conserved in all sequences, and gray boxes indicate amino acid identity in 80 % of the proteins. Amino acids with asterisks are predicted histone deacetylase catalytic residues.