Supplementary Materials

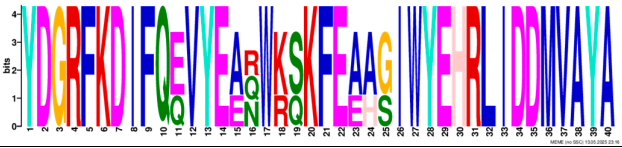
Table S1. List of primers used in this study.

Primer name	Forward primer sequence (5'-3')	Revise primer sequence (5'-3')	Primer purposes
CpNAD-IDH1	ATGTCTCGCCGATCCCTCC	TCAATCCAGATTAGCAATGACTGC	Full-length cloning
CpNAD-IDH2	ATGGCAACGCAGCTGCTGAG	TTAAAGATGATCG-CAGATTGCCTTTG	Full-length cloning
CpNAD-IDH3	ATGGCCCGGCGGTCCCT	TCATTCCAAGGCAGCAATAACAGC	Full-length cloning
CpNADP-IDH1	ATGGCTTTTCAGAAGATCAAGGTC	TCATGCTTTGCCAGAGAGTCTTG	Full-length cloning
CpNADP-IDH2	ATGCTCAGGCTCATCAA-TAGTAGTG	TTACATCGCAAAGCATGTGCCGT	Full-length cloning
CpNADP-IDH3	ATGGAATTCCAGAA-GATCAAGGTGG	TTACAACTTCGCTTTGATAGA-CATTCT	Full-length cloning
CpNAD-IDH1	TATTGCTGGAGGCACTGGTG	ACTTCCCCTCTGCAATTGTG	qRT-PCR
CpNAD-IDH2	CAGCACCTGATATTGCTGGA	CTCTGCAATTGTGCTCAGGA	qRT-PCR
CpNAD-IDH3	AGCAGGAAACGTGGGTAATG	GGCAGCAATAACAGCATCAA	qRT-PCR
CpNADP-IDH1	GAAAATTGGGGATTGGGATT	CAACAGAGGTGCAGCTCAAA	qRT-PCR
CpNADP-IDH2	CAGCGGACATGTGAACAATC	CCGTCCATTTCAACGATAGG	qRT-PCR
CpNADP-IDH3	TACCGGGTTCATCAGAAAGG	AGGCTGCTTCCAGTTTCTCA	qRT-PCR
actin	CCAAGCAGCATGAAGATCAA	ATCTGCTGGAAGGTGCTGAG	qRT-PCR
CpNADP-IDH1	GAGCTCGGTACCCGGG-GATCCATGGCTTTTCAGAAGATC	GAAAGCTCTGCAGCGAC-GCGTTCATGCTTTGCCAGAGAG	Vector construction

Table S3. Physicochemical properties of the IDH gene family.

Gene	No.aa	MW/kDa	PI	No.exon	Chr location	Gravy	Accession
CpNADP-IDH1	414	46.54	7.52	15	3	-0.317	Cs_ont_3g024380.1
CpNADP-IDH2	533	60.05	8.75	16	2	-0.232	Cs_ont_2g028700.1
CpNADP-IDH3	416	46.77	7.46	15	9	-0.279	Cs_ont_9g028630.1
CpNAD-IDH1	359	39.20	8.44	4	8	-0.100	Cs_ont_8g028900.1
CpNAD-IDH2	372	40.78	7.03	7	6	-0.136	Cs_ont_6g020640.1
CpNAD-IDH3	367	39.83	7.99	4	1	-0.100	Cs_ont_1g029210.1

Table S4. Conserved motifs identified from the *CpIDH* gene family.

Motif1		DVWVCPNLDGDVQSDLLAGGFGGLGLMPS
Motif2		YDGRFKDIFQEVYEARWKSKFEAAGIWYEHRLIDDMVAYA
Motif3		EVAIKYPTITPDEVRVDEFCLKLVWKPPN

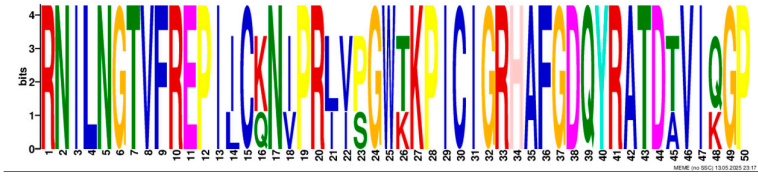
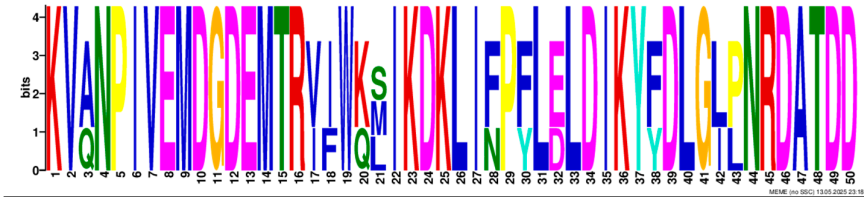
Motif4		RNILNGTVFREPIICKNIPRLVPGWTKPICIGRHAFGDQYRATDTVIQGP
Motif5		HYRVHQKGGZTSANPIALJLAWARGLRHLAKLDKADRLLDA
Motif6		KVANPIVEMDGDEMTRVIWKLIKDKLIFPFLELDIKYFDLGLPNRDATDD

Table S5. The IDH amino acid sequences of different plants.

>ZmIDH1.1
MASAVAPFSTESGETIRATLFPRDGIGPEIAESVKQVFNVAGVPIEWEEHYVG-
TEVDPRTESFLTWESLESVRRNKVGLKGPMATPIGKGHRSLNLTLRKELGLYANVVRGVVESLEIITRQASLRVAEYAFHYAKANGR
ERVSAIHKANIMRKTDGLFLKCCREVAEKYPEIQYEEVIIDNCCMTLVKNPGGICLAEAVHG-
SAPDIAGKNLANPTALMLSAVMLLRHMQFNDKADRIHNAILQTIAEGKYRTADLGGKASTSEFTNAVCDHI
>ZmIDH1.2
MALRRLLQGSVLPRVTGRVSAPAVAPFSTESGETIRATLFPGDGIGPEIAESVKQVFNVAG-
VPIEWEEHYVGTEVDPRTESFLTWESLESVRRNKVGLKGPMATPIGKGHRSLNLTLRKELGLYANVRPCNSLPGYKTRYDDVNLVTI
RENTEGEYSGLEHQVVRGVVESLKIITRQASLRVAEYAFHYAKANGRERVSAIHKANIM-
RKTDGLFLKCCREVAETYPEIQYEEVIIDNCCMTLVKNPGLFDVLVMPNLYGDIISDLCAGLIGGLGLTPSCNIGEGGICLAEAVHGS
APDIAGKNLANPTALMLSAVMMLRHLQFNDKADRIHNAILQTIAGGKYRTADLGGKASTSEFTNAVCDHI
>ZmIDH1.3
MSPPRALSLKPSWEVITKFCSERIAKYAFEYAYLNNRKKVTAVHKANIM-
KLADGLFLESCREVAKKYPGIKYNEIIVDNCCMQLVAKPEQFDVMVTPNLYGNLVANVAAGIAGGTGVMPGGNVGQDHAIFEQ
GASAGNVGNEKIVEKKRANPVALLLSSAMMLRHLQFPSFADRLETAVKRVIAEGKYRTKDLGGTSTTQEVIDAVIAKLG
>ZmIDH1.4
MARRSTPLLRRLLAPSPSPSASTPLAGAVSRRTVTYMPRPGDGAPRGVTLIPGDGIG-
PLVTGAVRQVMEAMHAPVYFETYEVRGDMPTVPAEVIESIRRNKVCLKGGLATPVGGGVSSLNMQLRKELDLYAALVNCFNLPG
LPTRHDNVDIVVIRENTEGEYSGLEHEVVPGVVESLKVITKFCSERIAKYAFEYAFLNNRK-
KVTAVHKANIMKLADGLFLESCREVAKKYPGIQYNEIIVDNCCMQLVAKPEQFDVMVTPNLYGNLVANVAAGIAGGTGVMPGG
NVGQDHAIFEQGASAGNVGNEKIVEKKRANPVALLLSSAMMLRHLQFPSFADRLETAVKR-
VIAEGKYRTKDLGGTSTTQEVTDAVIAKLG
>ZmIDH1.5
MALRRLLQGSVLPRIIGRDLAPAVAPFSTESGETIRATLFPGDGIGPEIAESVKQVFNVAG-
VPIEWEEHYVGTEVDPRTESFLTWESLESVRRNKVGLKGPMATPIGKGHRSLNLTLRKELGLYANVRPCNSLPGYKTRYDDVNLVTI

RENTEGEYSGLEHQVVRGVVESLKIITRQASLRVAEYAFHYAKANGRERVSAIHKANIM-
RKTDGLFLKCCREVSEKYPEIQYEEVIIDNCCMTLVKNPGLFDVLVMPNLYGDIISDLCAGLIGGLGLTPSCNIGEGGICLAEAVHGS
APDIAGKNLANPTALMLSAVMLLRHMQFNDKADRIHNAILQTIAEGKYRTADLGGKASTSEFTNAVCDHI
>ZmIDH1.6
MARRSAPLLRRLVSASSPPALQSLTDHVGVLARRTVTYMPRPGDGAPRAVTLIPGDGIG-
PLVTGAVRQVMEAMHAPVYFETYDVHGDMPTVPPAIIESIRRNKVCIKGGLATPVGGGVSSLNMQLRKELDLYASLVHCSNLPGL
PTRHEGVDIVVIRENTEGEYSGLEHEVVPGVVESLKVITKFCSERIAKYAFEYAYLNNRK-
KVTAVHKANIMKLADGLFLESCREVASKYPGIQYNEMIVDNCSMQLVSKPEQFDVMVTPNLYGNLVANTAAGIVGGTGIMPGG
NVGQDYAIFEQGASAGNVGNENLVEQKKANPVALLLSSAMMLRHLQFPSFADRLETAV-
KRVVAEGTYRTKDLGGSSTTQEVTDAVVANLD
>ZmIDH2.1
MRNLLLPRCLLSAPTTMARASVSGSAAVAKALIPLNPASGGRLPSLLPARLHVPGSSRVLR-
GASLRCYAAAAAAVAEQSRIKVQNPIVEMDGDEMTRVIWKMIKDKLIFPYLELDVKYYDLGILNRDATNDEVTVESAEATLKYNVA
VKCATITPDETRVKEFKLKSMWRSPNGTIRNILNASIP-
WQGLFFVSPSCVKTSQESFLVSWKKPICIGRHAFGDQYRATDMIINGPGKLKMVFVPDGADPMELDVYDFKGPGVALSMYNVD
ESIRAFAESSMAMALSKKWPLYLSTKNTILKKYDGRFKDIFQEVYEEQWKEK-
FEENSIWYEHRLIDDMVAYAVKSDGGYVWACKNYDGDVQSDFLAQGLLKFPSCFGSLGLMTSVLLSSDGKTLEAEAAHGTVTRH
FRLHQKGQETSTNSIASIFAWTR-
GLEHRAKLDKNDSLLDFTHKLESACVETVESGKMTKDLALLIHGPKVTREFYLSTEEFIDAVAQQLRGKIQLPTTV
>ZmIDH2.2
MAFEKIKVSNPIVEMDGDEMTRVFWQSIKDKLIFPFLDLDIKYYDLGILHRDATDDKVTVE-
AAEATLKYNVAIKCATITPDETRVKEFNLKHMWKSPNGTIRNIINGTVFREPIICKNVPRLVPGWTKPICIGRHAFGDQYRATDAVLK
GPGKLKLVFEGKEEQIDLEVFNFTGAGGVALSMYNTDESIRAFAAASMTTAYEKKW-
PLYLSTKNTILKKYDGRFKDIFQEVYEADWKSKFEAAGIWYEHRLIDDMVAYALKSEGGYVWACKNYDGDVQSDFLAQGFGSLGL
MTSVLVCPDGKTIEAEAAHGTVTRHFRVHQKGGETSTNSIASIFAWTRGLAH-
RAKLDDNARLLDFALKLEAACVGAVESGKMTKDLALLVHGSSKVTRSHYLNTEEFIDAVATELRSRLGAN
>ZmIDH2.3
MAFNKIKVSNPVVEMDGDEMTRVFWKSIKDKLIFPFVDLDIKYFDLGLPHRDATDDKVTVE-
AAEATLKYNVAIKCATITPDEARVNEFGLKAMWKSPNGTIRNILNGTVFREPIICKNIPRLVPGWTKPICIGRHAFGDQYRATDAVIK
GPGKLKLVFEGKEEQVELEVFNFTGAGGVALSMYNTDESIHAFADASMATAYEKKW-
PLYLSTKNTILKKYDGRFKDIFQEVYEAGWKTKFEAAGIWYEHRLIDDMVAYALKSEGGYVWACKNYDGDVQSDFLAQGFGSLGL
MTSVLVCPDGKTIEAEAAHGTVTRHYRVHQKGGETSTNSIASIFAWTRGLAH-
RAKLDDNARLLDFTQKLEAACVGAVESGKMTKDLALLVHGSSNITRSHYLNTEEFIDAVADELRSRLAANSNL
>ZmIDH2.4
MAFEKIKVSNPIVEMDGDEMTRVFWQSIKDKLILPFLDLDIKYYDLGILHREATDDKVTVE-
AAEATLKYNVAIKCATITPDETRVKEFNLKHMWKSPNGTIRNIINGTVFREPIICKNVPRLVPGWTKPICIGRHAFGDQYRATDAVLK
GPGKLKLVFEGKEEQIDLEVFNFTGAGGVALSMYNTDESIRAFAEASMTTAYEKKW-
PLYLSTKNTILKKYDGRFKDIFQEVYEADWKSKFEAAGIWYEHRLIDDMVAYALKSEGGYVWACKNYDGDVQSDFLAQGFGSLGL
MTSVLVCPDGKTIEAEAAHGTVTRHFRVHQKGGETSTNSIASIFAWTRGLAH-
RAKLDDNARLLDFALKLEAACVETVESGKMTKDLAILVHGSSSVTRSHYLNTEEFIDAVATELRSRLGAN
>ZmIDH2.5
MTEVSFNWIGFWSAMTSNLMNQSRNVYSKKILADKELLPRI-
ASLPLNFVQLIFPFVDLDIKYFDLGLPHRDATDDKVTVEAAEATLKYNVAIKCATITPDEARVKEFGLKAMWKSPNGTIRNILNGNV
FREPIICRNIPQLVPGWTKPICIGRHAFGDQYRAT-
DAVIKGPGKLKLVFEGKEEQVELEVFNFTGAGGVALSMYNTDESIHAFADASMATAYEKKWPLYLSTKNNILKKYDGMFKDIFQEV
YEAGWKPNLKLPAYGIVSNPVSYPIFFFNKVFWLIGFDDFGTGNCQFSK

>AtICDHa
MLNKLTHGVFTYRASLTAMLSSSTSAGLSSSFVSSRFLSSGIFSSGASRNRVTFPVQFHRAS-
AVRCFASSGGSDRIQVQNPIVEMDGDEMTRVIWSMIKEKLILPYLDLDIKYFDLGILNRDATDDKVTVESAEAALKYNVAIKCATITP
DEGRVKEFGLKSMWRSPNGTIRNILDGTVFREPIMCSNIPRLVPGWEKPICIGRHAF-
GDQYRATDTVIKGPGKLKMVFVPEDGNAPVELDVYDFKGPGVALAMYNVDESIRAFAESSMAMALTKKWPLYLSTKNTILKKYD
GRFKDIFQEVYEANWKQKFEEHSIWYEHRLIDDMVAYAVKSEGGYVWACKNYD-
GDVQSDLLAQGFGSLGLMTSVLLSADGKTLESEAAHGTVTRHFRLHQKGQETSTNSIASIFAWTRGLEHRAKLDKNEKLMDFVKK
LESSCVNTVETGKMTKDLALLIHGPKVSRDLFLNTEEFIDAVASKLKTQFKELPLV
>AtICDHb
MEFEKIKVINPVVEMDGDEMTRVIWKFIKDKLIFPFLELDIKYFDLGLPNRDFTDDKVTIE-
TAEATLKYNVAIKCATITPDEARVREFGLKKMWRSPNGTIRNILNGTVFREPIICRNIPRLVPGWTKPICIGRHAFGDQYRATDLIVNE
PGKLKLVFEPSGSSQKTEFEVFNFTGGGVALAMYNTDESIRAFAESSMYTAYQKKW-
PLYLSTKNTILKIYDGRFKDIFQEVYEANWRSKYEAAGIWYEHRLIDDMVAYAMKSEGGYVWACKNYDGDVQSDFLAQGYGSLG
MMTSVLVCPDGKTIEAEAAHGTVTRHYRVHQKGGETSTNSIASIFAWSRGLAH-
RAKLDSNAALLSYTEKLEAACMGTVESGKMTKDLALLIHGAKVRRDQYVNTEEFIDAVAWELKRRLLGNNSRL
>AtICDHc
MAFEKIKVANPIVEMDGDEMTRVIWKSIKDKLITPFVELD-
IKYFDLGLPHRDATDDKVTIESAEATKKYNVAIKCATITPDEGRVTEFGLKQMWRSPNGTIRNILNGTVFREPIICKNVPKLVPGWTK
PICIGRHAFGDQYRATDAVIKGPGKLTMTFEGKDGKTETEVFTFTGEGGVAMA-
MYNTDESIRAFADASMNTAYEKKWPLYLSTKNTILKKYDGRFKDIFQEVYEASWKSKYDAAGIWYEHRLIDDMVAYALKSEGGYV
WACKNYDGDVQSDFLAQGFGSLGLMTSVLVCPDGKTIEAEAAHGTVTRHFRVHQKG-
GETSTNSIASIFAWTRGLAHRAKLDDNAKLLDFTEKLEAACVGTVESGKMTKDLALIIHGSKLSRDTYLNTEEFIDAVAAELKERLNA
>AtIDH1
MSRRSLTLLKNLARNANGSGIQTRSVTYMPRPGDGAPRAVTLIPGDGIG-
PLVTNAVEQVMEAMHAPIFFEKYDVHGEMSRVPPEVMESIRKNKVCLKGGLKTPVGGGVSSLNVQLRKELDLFASLVNCFNLPGL
PTRHENVDIVVIRENTEGEYAGLEHEVVPGVVESLKVITKFCSERIAKYAFEYAYLNNRK-
KVTAVHKANIMKLADGLFLESCREVAKKYPSITYNEIIVDNCCMQLVAKPEQFDVMVTPNLYGNLVANTAAGIAGGTGVMPGGN
VGADHAVFEQGASAGNVGKDKIVLENKANPVALLLSSAMMLRHLQFPSFADRLETAV-
KKVIAEGKCRTKDLGGTSTTQEVVDAVIAKLD
>AtIDH2
MSRQSFSLLKNLRSIASGSKIQTRSVTYMPRPGDGKPRPVTLIPGDGVG-
PLVTNAVQQVMEAMHAPVYFEPFEVHGDMKSLPEGLLESIKKNKVCLKGGLKTPVGGGVSSLNVNLRKELDLFASLVNCFNLPGL
ASRHENVDIVVIRENTEGEYAGLEHEVVPGVVESLKFCSERIAKYAFEYAYLNNRK-
KVTAVHKANIMKLADGLFLESCQEVAKKYPSIAYNEIIVDNCCMQLVARPEQFDVMVTPNLYGNLVANTAAGIAGGTGVMPGG
NVGAEYAVFEQGASAGNVGKDTTEEQKNANPVALLLSSAMMLRHLQFPSFADRLETAVKR-
VIAEGNCRTEDLGGNSTTQEVVDAVIANLD
>AtIDH3
MARRSVSIFNRLLANPPSPFTSLSRSITYMPRPGDGAPRTVTLIPGDGIG-
PLVTGAVEQVMEAMHAPVHFERYEVLGNMRKVPEEVIESVKRNKVCLKGGLATPVGGGVSSLNMQLRKELDIFASLVNCINVPG
LVTRHENVDIVVIRENTEGEYSGLEHEVVPGVVESLKVITKFCSERIARYAFEYAYLNNRK-
KVTAVHKANIMKLADGLFLESCREVAKHYSGITYNEIIVDNCCMQLVAKPEQFDVMVTPNLYGNLIANTAAGIAGGTGVMPGGN
VGAEHAIFEQGASAGNVGNDKMVEQKKANPVALLLSSAMMLRHLRFPTFADRLETAV-
KQVIKEGKYRTKDLGGDCTTQEVVDAVIAALE
>AtIDH4
MPRPVTVIDSNVTNAVHQVMDAMQAPVYFETYIIKGKNMNHLTWEVVD-
SIRKNKVCLNGRVNNSLCGGARKELDLFASLVDCFNLNGQPSRHENVDIVVIRENTEGEYAGREHEVVPGVIESFQVTMTKFWSD

RIAKYAFEYAHFSKRKKVTAVHNNGKYEKLADAFFLESCQEVAKMYPNITYNEIGINNCCLQLVEKPERFDVIVTPNLYGL
>AtIDH5
MTMAANLARRLIGNRSTQILGAVNSSSGAASSVARAFCSSTTPITATLFPGDGIGPE-
IAESVKKVFTTAGVPIEWEEHYVGTEIDPRTQSFLTWESLESVRRNKVGLKGPMATPIGKGHRSLNLTLRKELNLYANVRPCYSLPGY
KTRYDDVDLITIRENTEGEYSGLEHQVVRGVVESLKIITRQASLRVAEYAFLYAK-
THGRERVSAIHKANIMQKTDGLFLKCCREVAEKYPEITYEEVVIDNCCMMLVKNPALFDVLVMPNLYGDIISDLCAGLVGGLGLTP
SCNIGEDGVALAEAVHGSAPDIAGKNLANPTALLLSGVMMLRHLKFNEQAEQIHSAI-
INTIAEGKYRTADLGGSSTTTEFTKAICDHL
>AtIDH6
MTMTAFLARRLIGNGSSQILGTSSSSSGPFISVSRAFFSSSTPIKATLFPGDGIGPE-
IAESVKQVFTAADVVIDWDEQFVGTEVDPRTNSFLTWDNLQSVLKNKVGLKGPMATPIGKGHRSLNLTLRKELNLYANVRPCYSL
PGYKTRYDDVDLITIRENTEGEYSGLEHQVVKGVVESLKIITRKASMRVAEYAFLYAK-
THGRKKVSAIHKANIMQKTDGLFLQCCDEVAAKYPEIYYEKVVIDNCCMMLVKNPALFDVLVMPNLYGDIISDLCAGLVGGLGLT
PSMNIGEDGIALAEAVHGSAPDIAGMNLANPTALLLSGVMMLRHLKLNKQAEQIHSAI-
INTIAEGKYRTADLGGSSTTTDFTKAICDHL
>OsNADP-IDHa
MAFEKIKVANPIVEMDGDEMTRIFWQSIKDKLIFPFLDLDIKYYDLGVLHRDATDDKVTVE-
AAEATLKYNVAIKCATITPDEARVKEFNLKQMWKSPNGTIRNIINGTVFREPIICKNVPRLVPGWTKPICIGRHAFGDQYRATDAVL
KGPGKLKLVFEGKDEQIDLEVFNFTGAGGVALSMYNTDESIRAFAEASMTTAYEKKW-
PLYLSTKNTILKKYDGRFKDIFQEVYEAGWKSKFEAAGIWYEHRLIDDMVAYALKSEGGYVWACKNYDGDVQSDFLAQGFGSLGL
MTSVLVCPDGKTIEAEAAHGTVTRHFRVHQKGGETSTNSIASIFAWTRGLAH-
RAKLDDNARLLDFALKLEAACVGTVESGKMTKDLALLIHGSSNVTRSHYLNTEEFIDAVAAELRSRLAAN
>OsNADP-IDHb
MASTKIKVANPIVEMDGDEMTRVFWKSIKDKLIFPFLELDIKYFDLGLPYRDQTDDKVTVE-
AAEATLKYNVAIKCATITPDEARVKEFSLKSMWKSPNGTIRNILNGTVFREPIICKNIPRLVPGWTKPICIGRHAFGDQYRATDAVIKG
PGKLKLVYEGKDEEIELEVFNFTGAGGVAQSMYNTDESIRSFAEASMATAYEKKW-
PLYLSTKNTILKKYDGRFKDIFQEVYEAQWKSKFEAAGIWYEHRLIDDMVAYALKSEGGYVWACKNYDGDVQSDFLAQGFGSLGL
MTSVLVCPDGKTIEAEAAHGTVTRHYRVHQKGGETSTNSIASIFAWTRGLAH-
RAKLDDNARLLDFTQKLEAACIGAVESGKMTKDLALLVHGSSNVTRSHYLNTEEFIDAVADELRSRLAAN