

Gp dh N

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TaGAPDH1  EARLKVAINGFGRIGRNFLRCWHGRGSSPLEVIAINDTGG-VKQASHLLKYDSTLGIFFDADVKPVGNNASISVDG-KVIKVVSDRNEENLFWGEMGIDLIEGTGVFVDRAGKHLLEAGAKKVLITAPGKG-DIFTYVCGVNAADLYTHADT-IIISNASCTTNCL
TaGAPDH2  EARLKVAINGFGRIGRNFLRCWHGRGSSPLEVIAINDTGG-VKQASHLLKYDSTLGIFFDADVKPVGNNASISVDG-KVIKVVSDRNEENLFWGEMGIDLIEGTGVFVDRAGKHLLEAGAKKVLITAPGKG-DIFTYVCGVNAADLYTHADT-IIISNASCTTNCL
TaGAPDH3  MDGELLCAAGFGRIGRLVAVVALQSPD---VELVAVNDFEITTDYMTYMFKYDITVHGQWKHHEVVKVSKTLLFGQKQEVAVFGCRNEEIPWAAAAGAEYVVESTGVFTDKDKAAAHKGGAKKVVISAPSK--DAFMFVCGVNEKEYKSDID-IVSNASCTTNCL
TaGAPDH4  MAPIKIGINGFGRIGRLVAVVALQSPD---VELVAVNDFEITTDYMTYMFKYDITVHGQWKHHEVVKVSKTLLFGQKQEVAVFGCRNEEIPWAAAAGAEYVVESTGVFTDKDKAAAHKGGAKKVVISAPSK--DAFMFVCGVNEKEYKSDID-IVSNASCTTNCL
TaGAPDH5  GEKTKVINGFGRIGRLVLAIAISRDD---IEVVAVNDFFIDAKYMAVMFYDSTHGPFRRG-SINVVVDSLEINGKRIITTSKRDEAEIPWGNFGADYVVESTGVFTTIDKASVHLKGGAKKVVISAPSA--DAFMFVGVNEMSYDFKMN-VVSNASCTTNCL
TaGAPDH6  MAPIKIGINGFGRIGRLVAVVALQSPD---VELVAVNDFEITTDYMTYMFKYDITVHGQWKHHEVVKVSKTLLFGQKQEVAVFGCRNEEIPWAAAAGAEYVVESTGVFTDKDKAAAHKGGAKKVVISAPSK--DAFMFVCGVNEKEYKSDID-IVSNASCTTNCL
TaGAPDH7  GEKTKVINGFGRIGRLVLAIAISRDD---IEVVAVNDFFIDAKYMAVMFYDSTHGPFRRG-SINVVVDSLEINGKRIITTSKRDEAEIPWGNFGADYVVESTGVFTTIDKASVHLKGGAKKVVISAPSA--DAFMFVGVNEMSYDFKMN-VVSNASCTTNCL
TaGAPDH8  MAPIKIGINGFGRIGRLVAVVALQSPD---VELVAVNDFEITTDYMTYMFKYDITVHGQWKHHEVVKVSKTLLFGQKQEVAVFGCRNEEIPWAAAAGAEYVVESTGVFTDKDKAAAHKGGAKKVVISAPSK--DAFMFVCGVNEKEYKSDID-IVSNASCTTNCL
TaGAPDH9  REKTKVINGFGRIGRLVLAIAISRDD---IEVVAVNDFFIDAKYMAVMFYDSTHGPFRRG-TITVLESTLEINGKRVSVTSKRDESDIPWGNFGAEYVVESTGVFTTVEKASAHKGGAKKVVISAPSA--DAFMFVGVNEMSYDFKMN-VVSNASCTTNCL
TaGAPDH10  MGKIKIGINGFGRIGRLVAVVALQSPD---VELVAVNDFEITTEYMTYMFKYDITVHGHWKHSIDIKLKDITLLFGKPVTVFGVRNEEIPWGEAGADYVVESTGVFTDKDKAAAHKGGAKKVVISAPSK--DAFMFVGVNEMSYDFKMN-VVSNASCTTNCL
TaGAPDH11  GEKTKVINGFGRIGRLVLAIAISRDD---IEVVAVNDFFIDAKYMAVMFYDSTHGPFRRG-TITVLESTLEINGKRVSVTSKRDESDIPWGNFGAEYVVESTGVFTTVEKASAHKGGAKKVVISAPSA--DAFMFVGVNEMSYDFKMN-VVSNASCTTNCL
TaGAPDH12  MGKIKIGINGFGRIGRLVAVVALQSPD---VELVAVNDFEITTEYMTYMFKYDITVHGHWKHSIDIKLKDITLLFGKPVTVFGVRNEEIPWGEAGADYVVESTGVFTDKDKAAAHKGGAKKVVISAPSK--DAFMFVGVNEMSYDFKMN-VVSNASCTTNCL
TaGAPDH13  GEKTKVINGFGRIGRLVLAIAISRDD---IEVVAVNDFFIDAKYMAVMFYDSTHGPFRRG-TIIVLESTLEINGKRVSVTSKRDESDIPWGNFGAEYVVESTGVFTTVEKASAHKGGAKKVVISAPSA--DAFMFVGVNEMSYDFKMN-VVSNASCTTNCL
Consensus  gfgigrgr r d e a n d k y d g d k r p p w g v e g v f a h g a k k v i a p d p v g n y s n a s c t t n c l

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Gp dh C

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TaGAPDH1  AFVAVVLDQKFGIIGKMTTTHSYGDRLLD-ASHRLRRAAALNIVPTSTGAAKAVLVLPNLRKGLNGIALRVPTPNVSVVDLTVVQVSKTLAEEVNCAFRRD-----AAANEKGLLDVCDPLVSVDFRCSIVSSTIDAS
TaGAPDH2  AFVAVVLDQKFGIIGKMTTTHSYGDRLLD-ASHRLRRAAALNIVPTSTGAAKAVLVLPNLRKGLNGIALRVPTPNVSVVDLTVVQVSKTLAEEVNCAFRRD-----AAANEKGLLDVCDPLVSVDFRCSIVSSTIDAS
TaGAPDH3  AFLAKVINDRFVIGELMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ATYDQIKAAIKE-----ESEGNLKGILGYVDEDLVSTDFQGDNRSSIFDAK
TaGAPDH4  AFLAKVINDRFVIGELMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ATYDQIKAAIKE-----ESEGNLKGILGYVDEDLVSTDFQGDNRSSIFDAK
TaGAPDH5  AFLAKVVHEEFGILEGLMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ASYDDVKAAIKA-----ASEGALKGILGYTDEDLVSNDFVGDTRSSIFDAN
TaGAPDH6  AFLAKVINDRFVIGELMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ATYDQIKAAIKE-----ESEGNLKGILGYVDEDLVSTDFQGDNRSSIFDAK
TaGAPDH7  AFLAKVVHEEFGILEGLMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ASYDDVKAAIKA-----ASEGALKGILGYTDEDLVSNDFVGDTRSSIFDAN
TaGAPDH8  AFLAKVINDRFVIGELMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ATYDQIKAAIKE-----ESEGNLKGILGYVDEDLVSTDFQGDNRSSIFDAK
TaGAPDH9  AFVAVVHEEFGILEGLMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ASYDDVKAAIKA-----ASEGALKGILGYTDEDLVSNDFVGDTRSSIFDAN
TaGAPDH10  AFLAKIINDNFVIGELMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ASYDDIKKLPFAHVTRMSLMSIQIIFRAASEGKLGIMGYVEDDLVSTDFVGDTRSSIFDAK
TaGAPDH11  AFVAVVHEEFGILEGLMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ASYDDVKAAIKE-----ASEGALKGILGYTDEDLVSNDFVGDTRSSIFDAN
TaGAPDH12  AFLAKIINDNFVIGELMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ASYDDIKKAI-----KAASEGKLGIMGYVEDDLVSTDFVGDTRSSIFDAK
TaGAPDH13  AFVAVVHEEFGILEGLMTTVHMTATQKTVGFGPSKDWGGRAASFNLIESTGAAKAVGKVLPELNGKITGMAFRVPTVLSVVDLTVRLAKP-----ASYDDVKAAIKE-----ASEGALKGILGYTDEDLVSNDFVGDTRSSIFDAN
Consensus  ap k fgi g mtt h t q d s d r r a n i p stgaakav vlp l gkl g rvpt vsvvdl k a l gi e vs df ss da

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TaGAPDH1  LSMVMGDDMVVIAWYDNEWGYSQRVVDLADIVADQ
TaGAPDH2  LSMVMGDDMVVIAWYDNEWGYSQRVVDLADIVANQ
TaGAPDH3  AGIALNDNFVVLVSWYDNEWGYSQTRVVDLIRHMHSS
TaGAPDH4  AGIALNDNFVVLVSWYDNEWGYSQTRVVDLIRHMHSS
TaGAPDH5  AGMGLSSFFMLVSWYDNEWGYSNRVLDLIAHMAIV
TaGAPDH6  AGIALNDNFVVLVSWYDNEWGYSQTRVVDLIRHMHST
TaGAPDH7  AGMGLSSFFMLVSWYDNEWGYSNRVLDLIAHMAIV
TaGAPDH8  AGIALNDNFVVLVSWYDNEWGYSQTRVVDLIRHMHST
TaGAPDH9  AGMGLSSFFMLVSWYDNEWGYSNRVLDLIGHMSIV
TaGAPDH10  AGIALNDHFVVLVSWYDNEWGYSNRVVDLIRHMART
TaGAPDH11  AGMGLSSFFMLVSWYDNEWGYSNRVLDLIGHMALV
TaGAPDH12  AGIALNDHFVVLVSWYDNEWGYSNRVVDLIRHMART
TaGAPDH13  AGMGLSSFFMLVSWYDNEWGYSNRVLDLIGHMVLV
Consensus  k wydnewgys rv dl

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Figure S1 Multiple alignment of wheat GAPDH amino acid sequences. The alignment was trimmed manually and the results were generated by DNAMAN.

The identical sequences are displayed in gray.