

(A)

Gh_D13G0089	MEKLCVVPERLKRVEESHIDDLPSLSSLLQLFLSLPQIHQLISELAAEPSTQAGLCG	60
Gh_D13G0089_N5	MEKLCVVPERLKRVEESHIDDLPSLSSLLQLFLSLPQIHQLISELAAEPSTQAGLCG *****	60
Gh_D13G0089	KNEGAALDLKQGNQCYSSGDHSQALRCYSQALRLAPIDAHTTGKNLVATLYLNRASLFH	120
Gh_D13G0089_N5	KNEGAALDLKQGNQCYSSGDHSQALRCYSQALRLAPIDAHTTGKNLVATLYLNRASLFH *****	120
Gh_D13G0089	KMGLPMESLRDCSRALEISPCYPKVWYRRGKVNATLGNVEDSVHDLVSAKDMEPSIGGKK	180
Gh_D13G0089_N5	KMGLPMESLRDCSRALEISPCYPKVWYRRGKVNATLGNVEDSVHDLVSAKDMEPSIGGKK *****	180
Gh_D13G0089	QIERELDMLARHHEKTTAKPASQKSVEIPDVPSEIKLQCVKTPDKGRGMVQFDIPQASL	240
Gh_D13G0089_N5	QIERELDMLARHHEKTTAKPASQKSVEIPDVPSEIKLQCVKTPDKGRGMVQFDIPQASL *****	240
Gh_D13G0089	IHAEPYAVVILKHCRETHCHYCLNELPADTIPCSLPLYCSQHCQVQAGGPIHIPDT	300
Gh_D13G0089_N5	IHAEPYAVVILKHCRETHCHYCLNELPADTIPCSLPLYCSQHCQVQAGGPIHIPDT *****	300
Gh_D13G0089	MVGSNFKPTLECIPEHKHECQGVHWPAILPSDVLVLAGRVVVKTMQKQGFQDVPNLSETL	360
Gh_D13G0089_N5	MVGSNFKPTLECIPEHKHECQGVHWPAILPSDVLVLAGRVVVKTMQKQGFQDVPNLSETL *****	360
Gh_D13G0089	GLCESYSKMPESKLELHIYSIVLLFCLHHSFSSELSINGDSASQIVILLSQIRVNSIAV	420
Gh_D13G0089_N5	GLCESYSKMPESKLELHIYSIVLLFCLHHSFSSELSINGDSASQIVILLSQIRVNSIAV *****	420
Gh_D13G0089	VRMRSNTNDSYDQDWFQNFQSFGEAEAASSVEQVRVQALYKAASLFNHSCLPNIHAYFM	480
Gh_D13G0089_N5	VRMRSNTNDSYDQDWFQNFQSFGEAEAASSVEQVRVQALYKAASLFNHSCLPNIHAYFM *****	480
Gh_D13G0089	SRTLLLRTEFVSGGCALELSYGPQVQWQDCKDRLRFLEEEYFFRCWCCGCSEVNESDLV	540
Gh_D13G0089_N5	SRTLLLRTEFVSGGCALELSYGPQVQWQDCKDRLRFLEEEYFFRCWCCGCSEVNESDLV *****	540
Gh_D13G0089	ISGFCCVNPNC SGVVL DNLVANCEKQKPNVPETISNKSHLQVHELKIDIDIKKVAQISLDQ	600
Gh_D13G0089_N5	ISGFCCVNPNC SGVVL DNLVANCEKQKPNVPETISNKSHLQVHELKIDIDIKKVAQISLDQ *****	600
Gh_D13G0089	TQSSFHVDSGYCLKCGSYCNFASRSKEVKKAWTDFRRLQDSIASKDTC G TNL T DALRSLG	660
Gh_D13G0089_N5	TQSSFHVDSGYCLKCGSYCNFASRSKEVKKAWTDFRRLQDSIASKDTC S TNL P DALRSLG *****	660
Gh_D13G0089	LLRSILHAYNKGIAEAEDILAKAFCFIGDFEPARDHCKASIEILEKLYGPNHIAIGYELA	720
Gh_D13G0089_N5	LLRSILHAYNKGIAEAEDILAKAFCFIGDFEPARDHCKASIEILEKLYGPNHIAIGYELA *****	720
Gh_D13G0089	KLASIQLALGDCTAVYKINRLSAIFSTYYGPHAGIIFPYLLVLERERSRIIQ	772
Gh_D13G0089_N5	KLASIQLALGDCTAVYKINRLSAIFSTYYGPHAGIIFPYLLVLERERSRIIQ *****	772

(B)

Gh_D13G0090	MAEFMELEAQDGVMTWNVVPGTKEEAGNCVVPVSAIYTPIKPFPNMLVL T YAPLRCRNC	60
Gh_D13G0090_N5	MAEFMELEAQDGVMTWNVVPGTKEEAGNCVVPVSAIYTPIKPFPNMLVL P YAPLRCRNC	60

Gh_D13G0090	SSVLNPFVMDFAAKIWIWPCFCHRSHPAHYASVSEENLPAELFPQYTTIEYKSPREAA	120
Gh_D13G0090_N5	SSVLNPFVMDFAAKIWIWPCFCHRSHPAHYASVSEENLPAELFPQYTTIEYKSPREAA	120

Gh_D13G0090	CLQSVFMFVIDTSIIEEEMAFKLSALSQVIGLFPDNLVGLITFGTLVHLHEIGFSTAPK	180
Gh_D13G0090_N5	CLQSVFMFVIDTSIIEEEMAFKLSALSQVIGLFPDNLVGLITFGTLVHLHEIGFSTAPK	180

Gh_D13G0090	TYVFKGSKDVSQKQLEQMGCFLNKPKPLTGVRDGLSSES IARFLLPASECEFAINSVLE	240
Gh_D13G0090_N5	TYVFKGSKDVSQKQLEQMGCFLNKPKPLTGVRDGLSSES IARFLLPASECEFAINSVLE	240

Gh_D13G0090	ELQKDPWPIPADQRASRSTGTALSVAASLLGACFPGSGARIMAFLLGGPSTEGPGAIVSKN	300
Gh_D13G0090_N5	ELQKDPWPIPADQRASRSTGTALSVAASLLGACFPGSGARIMAFLLGGPSTEGPGAIVSKN	300

Gh_D13G0090	LSEPIRSHKDLDKDSAPHYHKAIKFYETLAKQLVHGQHVLDLFAVAVDQVGAELKVVVE	360
Gh_D13G0090_N5	LSEPIRSHKDLDKDSAPHYHKAIKFYETLAKQLVHGQHVLDLFAVAVDQVGAELKVVVE	360

Gh_D13G0090	RTGGFVVLAESEFGHSVFKDTRLRRVFSQSGDKGLGLSSNGIFEVNCSDLKVKQVGLGPCASL	420
Gh_D13G0090_N5	RTGGFVVLAESEFGHSVFKDTRLRRVFSQSGDKGLGLSSNGIFEVNCSDLKVKQVGLGPCASL	420

Gh_D13G0090	EKRSPKCSDTIIGQGNTSAWKMCGLDQATSLCLVFDIVRKDIPDATVQSSSSQFYFQFLT	480
Gh_D13G0090_N5	EKRSPKCSDTIIGQGNTSAWKMCGLDQATSLCLVFDIVRKDIPDATVQSSSSQFYFQFLT	480

Gh_D13G0090	FYQHSSGEMRLRVTTLSRRWVAGPGSIQDLISGFDQAAAAAMARLVSFKMEIEAEFDPI	540
Gh_D13G0090_N5	FYQHSSGEMRLRVTTLSRRWVAGPGSIQDLISGFDQAAAAAMARLVSFKMEIEAEFDPI	540

Gh_D13G0090	RWLDKALIHICSRFGDYQKDTSSFSLSPRFSIFPQFMFHLRRSQFVQVFNNSPDETAYF	600
Gh_D13G0090_N5	RWLDKALIHICSRFGDYQKDTSSFSLSPRFSIFPQFMFHLRRSQFVQVFNNSPDETAYF	600

Gh_D13G0090	RMILNRENVANSVVMIQPSLVSYSFQSVPEPALLDVTAIAADRILLDSYFTVVI FHGST	660
Gh_D13G0090_N5	RMILNRENVANSVVMIQPSLVSYSFQSVPEPALLDVTAIAADRILLDSYFTVVI FHGST	660

Gh_D13G0090	IAQWRKAGYHDLPEHQAFQALLQAPRDDADAI INERFPVPRLVICDQHGSQARFLLAKLN	720
Gh_D13G0090_N5	IAQWRKAGYHDLPEHQAFQALLQAPRDDADAI INERFPVPRLVICDQHGSQARFLLAKLN	720

Gh_D13G0090	PSASCNSDGHRRPGDII FTDDVSFEVFLDHLQRLAVQ 757	
Gh_D13G0090_N5	PSASCNSDGHRRPGDII FTDDVSFEVFLDHLQRLAVQ 757	

Figure S7. Alignment of protein sequences of (A) Gh_D13G0089 and (B) Gh_D13G0090 that have amino acid change(s) (highlighted in red) in the N5 mutant.