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ZmGH3      MAVMAEVVSTTGAALRSPATQOPAAGAAGKGLAEKLOFIEDMTSNVDAVQERVVLEGEILARNADTEY
At5g54510 (GH3.6) MPEAPKIAAL-----EVSDESIAEKNNKLOFIEDVTINADDVQRRVLEEILSRNADVEYLK-RHGLEGRTRDRE 68
At4g27260 (GH3.5) MPEAPKKESSL-----EVFDLTLDCNNKOKLQIEELTSSNADCVORQVLEEILTRNADVEYLK-RFDLNGRTDRE 68
At1g59500 (GH3.4) MAVDSLLOS-----GMASPITISETEVKALKFIEEITRNPFDSVQEKVLGEILSRNSNTEYLK-RFDLNGAVDRK 67
At2g23170 (GH3.3) MIVDSALRS-----PVM-HSPSTIKDVKALRFIEEMTRNDFVQKKVIREILSRNSDTEYLK-RFGLKGFDRK 66
At4g37390 (GH3.2) MAVDSPLOS-----RMVSAITISEKDVKALKFIEEMTRNPFDSVQEKVLGEILTRNSNTEYLK-RFDLDGVVDRK 67

ZmGH3      TFRAKVPMATYEDLOPYIRRIADGDRSPILSCHPVSEFLTSSGTSGGERKLMPTIEDELNRRQLLYSLQMPVMNLVYVPGMD 162
At5g54510 (GH3.6) TFKHIMPVVYEDIQPEINRIANGDKSOVLCSNPISSEFLTSSGTSGGERKLMPTIEEELDRRSLLYSLMPVMDQFVPGLD 149
At4g27260 (GH3.5) TFKNIMPVITYEDIEPEINRIANGDKSPILSSKPISEFLTSSGTSGGERKLMPTIEEELDRRSLLYSLMPVMQSFVPGLE 149
At1g59500 (GH3.4) SFKSKVPVVIYEDLKITIQRISNGDRSPILSSHPITIEFLTSSGTSAGERKLMPTIEEDINRRQLLGNLLMPVMNLVYVGLD 148
At2g23170 (GH3.3) TFKTKVPVVIYDLDKPEIQRIANGDRSMILSSYPITIEFLTSSGTSAGERKLMPTIEEDINRRQLLYSLMPVMNLVYVGLD 147
At4g37390 (GH3.2) TFKSKVPVVIYEDLKPEIQRTISNGDCSPILSSHPITIEFLTSSGTSAGERKLMPTIEEDLDRRQLLYSLMPVMNLVYVGLD 148

ZmGH3      KGKALHFLFVKSEITKTPGGLAARPVLTSSYKSNHFRNRPFDAVNNYTSPTAAILCADAFQSMYAQMVCGLCQXQDVLRXGX 243
At5g54510 (GH3.6) KGKGYFLFIKSESKTPGGLPARPVLTSYKSSHFKNRPYDPYTNYSPTNQTILCSDSYQSMYSQMLCGLCCHKVLRVGA 230
At4g27260 (GH3.5) NGKGYFLFIKSESKTPGGLPARPVLTSYKSSHFKNRPYDPYTNYSPTNQTILCSDSYQSMYSQMLCGLCCHKVLRVGA 230
At1g59500 (GH3.4) KGKGLYFLFVKSEITSGGLPARPALTSYKSDYF--RTSDSDSVYTSPEAILCSDSSQSMYTMQLCGLLVRHEVRLGA 227
At2g23170 (GH3.3) KGKALYFLFVKIESTKTPGGLPARPVLTSYKSECFKRRPNPYNVYTSPTNQTILCSDSSQSMYTMQLCGLLVRHEVRLGA 228
At4g37390 (GH3.2) KGKGLYFLFVKSESKTSGGLPARPVLTSYKSDHFKNRPYDPYTNYSPTNQTILCSDSSQSMYAQMVCGLLVRHEVRLGA 229

ZmGH3      VFASGLLRAXRFLQLNWEQAEDIXAGSXTPRXTDPSVREAVAGIL-RXDPXXXLVRSECSKGD-WAGIITRIWPSTKYL 322
At5g54510 (GH3.6) VFASGFIRAIKFLKFWPELARDIRGTLSSEITDSSVREAVGETIL-KDPKPLADFVESECRK-TSWQGIITRIWPNTKYV 309
At4g27260 (GH3.5) VFASGFIRAIKFLKFWIELVRDIRGTLSSEITDPSVREAVAKIL-KPSPKPLADFVEFECKK-SSWQGIITRIWPNTKYV 309
At1g59500 (GH3.4) VFASGLLRRAISFLQNNWKELECDISTGTLSSEITDPSVREAVAGIL-KPSPKPLADFVEFECKK-SSWQGIITRIWPNTKYV 307
At2g23170 (GH3.3) VFASGLLRRAISFLQNNWKELECDISTGTLSSEITDPSVREAVAGIL-KPSPKPLADFVEFECKK-SSWQGIITRIWPNTKYV 309
At4g37390 (GH3.2) VFASGLLRRAISFLQNNWKELECDISTGTLSSEITDPSVREAVAGIL-KPSPKPLADFVEFECKK-SSWQGIITRIWPNTKYV 309

ZmGH3      DVIVTGAMAQYIPTLKYSSGGLPMACTMYASSEYFG-NLRPMCDPSEVSYTLMPNMCFEFLPMDSAAASGGGAS----- 397
At5g54510 (GH3.6) DVIVTGIMSOYIPTLDYSSNGLPLVCTMYASSEYFGVNLRFPLCKPSEVSYTLIPNMAYFEFLPVRNNSGVTSSISLPKAL 390
At4g27260 (GH3.5) DVIVTGIMSOYIPTLDYSSNGLPLVCTMYASSEYFGVNLRFPLCKPSEVSYTLIPSMAYFEFLPVRNNSGVTNSINLPKAL 390
At1g59500 (GH3.4) DVIVTGAMAEYIPVLEYSSGGLPMACTMYASSEYFGINLPMCKPSEVSYTLIPNMAYFEFLPHHHDGCGVEA----- 382
At2g23170 (GH3.3) DVIVTGAMAQYIPVLEYSSGGLPMACTMYASSEYFGINLPMCKPSEVSYTLIPNMAYFEFLPHH-----EYPT---- 379
At4g37390 (GH3.2) DVIVTGAMAQYIPTLEYSSGGLPMACTMYASSEYFGINLPMCKPSEVSYTLIPNMAYFEFLPHHHDGCGAAEASL---- 386

ZmGH3      -----Q-----LVDLARVEVGREYELVITTYAGLNRYRVGDLQVTFGHNSAPQKFFVRRKNVLLSIESDKTDEAELQNAV 468
At5g54510 (GH3.6) TEKEQQE-----LVDLVDVKLQGEYELVITTYAGLYRYRVGDLVLSVAGFKNNAPOQFSFTGRKNVLLSIESDKTDEVELQNAV 467
At4g27260 (GH3.5) TEKEQQE-----LVDLVDVKLQGEYELVITTYAGLYRYRVGDLRVTFGHNSAPQKFFVRRKNVLLSIESDKTDEVELQNAV 467
At1g59500 (GH3.4) -----TIS-----LVDELADVEVGKEYELVITTYAGLYRYRVGDLRVTFGHNSAPQKFFVRRKNVLLSIESDKTDEAELQNAV 454
At2g23170 (GH3.3) ---EKSE-----LVDELADVEVGKEYELVITTYAGLNRYRVGDLQVTFGHNSAPQKFFVRRKNVLLSIESDKTDEAELQNAV 453
At4g37390 (GH3.2) ---DETIS-----LVELANVEVGKEYELVITTYAGLYRYRVGDLRVTFGHNSAPQKFFVRRKNVLLSIESDKTDEAELQNAV 460

ZmGH3      ERAS--ALLRPHGAAMVEYTSQAMTKSIPGHYVIYWELLAKCPAGCAAVGEGTLERCCLEMEELNLYVYRQSRVADKSIAP 547
At5g54510 (GH3.6) KNAV--TFLVFPDASLSEYTSYADTSSIPGHYVLFWELCLGNTP-IPPS--VFEDCCLTIEESLNSVYRQGRVSDKSIAP 543
At4g27260 (GH3.5) KNAV--TFLVFPDASLSEYTSYADTSSIPGHYVLFWELCLGNTP-IPPS--VFEDCCLAVEESFNIVYRQGRVSDKSIAP 543
At1g59500 (GH3.4) ENAS--RLLAEQGTRVIEYTSYADTKTIPGHYVIYWELLSRDQSN-ALPSEVMAKCCLEMEESLNVYRQSRVSDKSIAP 532
At2g23170 (GH3.3) ENAS--LLLGEQGTRVIEYTSYAEKTKIPGHYVIYWELLVKGDTN-P-PNDEVMAKCCLEMEESLNSVYRQSRVADKSIAP 530
At4g37390 (GH3.2) ENAS--RLFAEQGTRVIEYTSYAEKTKIPGHYVIYWELLGRDQSN-ALMSEVMAKCCLEMEESLNSVYRQSRVADKSIAP 538

ZmGH3      AGDPGVPAAGHLRGAHGRHLPRRVDPVOGAPVRDVPAAHRAAPGLPRRVQPLEFR-----AAALDRRPAALRSGSGSD 619
At5g54510 (GH3.6) LEIKMVESGTF---DKLMDYAISLGASINQYKT-----PRCVKFAPIEELNLSRVVDSYFSPKCPKWPVGHKQWGSN 612
At4g27260 (GH3.5) LEIKIVEPETF---DKLMDYAISLGASINQYKT-----PRCVKFAPIEELNLSRVVDSYFSPKCPKWPVGHKQWGSN 612
At1g59500 (GH3.4) LEIRVVOVNGTF---EELMDFSISRGSINQYKV-----PRCVSLTPIMKLLDSRVVSAHFSPLPFWSPERRH 597
At2g23170 (GH3.3) LEIRVVKNGTF---EELMDYAISRGASINQYKV-----PRCVSFTPIVELLDSRVVSTHFSPALPFWSPERRR 595
At4g37390 (GH3.2) LG-----DTG-----GTERYV 549

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Supplemental Figure 1. Protein alignment of the GH3-like protein from maize (ZmGH3; Genbank accession CV985267) with homologs from *A. thaliana*.