

Supplementary data 1. Amino acids sequences related to GH3 proteins in *C. canephora* available at Coffee Genome Hub website. Three (Cc00_g28970, Cc02_g39040 and Cc00_g04550) out of the twenty amino acid sequences lacked the domains commonly shared by GH3 proteins (PLN02247 and pfam03321); therefore these sequences were not selected for analysis.

>CcGH3.1

METDWNTKALEFIEEMTKNAGEVQKMVLADILKQNGETEYLQRFNLDGATDTKTFTSKVPCITY
EDIRPEIQRMENGDRSAILTALPVSDFLSSGTTSGKRKLIPMPEEEWNRQVLSSLEIPVMNVYV
PDLNRGKGLYFYFSWPEIRTPGGQMILTALNKYYRSEHFKNQRRDPYTQYTSPIESVLCTDYVQ
SMYVQLLCGLYQHKQINRVGASSASALLRVIKFFELNWQDLVLDIRVGSNPKITYEPLRECMAR
IMKSDPELADFLTIECSGENWEGIIQRIWPNAKYLGTIITGSMIQYAPSLDYSSGGLPIATSKYASS
ECCFGINLNPISKPEDVSFTFMPNLAYFEFIPQEHSSNMDIGNSTVTTPDLINLVDVEVGKDYEV
VITTHAGLYRYQMGDILRVTFGHNSAPKFKFLRRKGVLLSIAGDKTDEVELQMAMDNASQILQE
YSVSLVDYTSHASKKIAPGHYVIYWELSVGVLGDSDKNAQSDEVISRCCPIIENSFSLIYKQHRVH
GAIAALEIRVLKNGTFQDLVEFAVSRGASIGQYKVPRCVETGPVLEFLDSRVVSSHFSPLCLSLAS
EESI*

>CcGH3.2

MLPTFDPRDTEAGSRILEDITSNAGHIQEQVLEEILTKNASTDYLSFLNGHSDKGLFKNKVPVVD
YEDIKIYIDRIALDGEPSRILTNEISITELMISSGTSKKQKQWIPKTAEEGEPGPSFFVSLLLFELRCLH
GLNDGKALFFVLINPDIHTPGGLVLRTTTASEIKNRKDRYPEVILCEDTNQSLYSQLLCGLVQRDA
IVSIGTFFASGLQRIIKFFEEHWQEMSSNIRTGQMSDWITDPCKKRTVSLILSKQMPDLADSIDLC
QEKSWEGIIKKIWPRTKYVQAIITGSMAQYIPALEFYTGRLPVVSPAYVSSEACFGVNFKPLCNPY
DVSYTFIPNMAYYEFIPIGNHQDPNCTNSKDAHLKDHIVDLANVKIGQHYELLVTTCTGLYR
MGDILLVTGFHNITPQFKFVQRRNVVLSIDTDKTTEQDLQNAVTIAMHILEPLGFFLLDYSSYADT
SSIPGHYVLFWELQLRSNNDIPELDQVKMEKCCSLVEQSLDQKYKLLRNQSISTIGPLEIRVVKQG
TFNVLMDFYVSRGTSLNQYKTPKNIKSEKAIEILDSRVVGKFYSREVPNQDS*

>CcGH3.3

MTYGGFQGASYDIWVIKFFKENWQEMSSNIRTGQMSDWITDPNCKRAVSLILSKQMPDLADSID
RVCQEKSWEGIIKKIWPRTKYVMAITGSMAQYIPALEVYTGGPLPVVSPVYGSSEAVFGINMKPL
CRPYDVSYTFIPNMAYYEFIPIDNHQDPNCTIRKDAHLKDHIVDLANVKIGQHYELLVTTTRVLSG
LYRYRMGDILLVTGFHNITPQFKFVQRRNVVLSIDTDKTTEQDLQNAVTIAMHILEPLGLFLLDYS
SYADTSSIPGHYVLFWELQLRSNDDFPVLDQVNMEKCCSLVEQSLDQKYKLLRNQSIRTFNVLM
DFYVSQGTSLNQYKTPKNIKSEKAIEILDSRVVGKFYSREVPNQDS*

>CcGH3.4

MLPTFDPTDTEAGSRILEDITSNAGHIQEQVLEEILTKNASTDYLSKFLNGHSDKGLFKNKVPVVD
DYEDIKIYIDRIALDGEPSRILTNEISITELLKSSGTSKKQKQWIPKTAEEGERRAFICCLRDVTNLRY
LQGLSDGKALLFVLINPDIHTPGGLVLRTTASEIKNRKDRYPQFILCEDTNQSLYGLLCGLVQR
DAIVSVGTFFASGLLRIIKFFEEHWQEMSSNIRTGQISAWITDPNCKRAVSLILSKQMPDLADSIDL
VCQEKSWEGIIKKIWPRTKYVLAITITGSMAQYIPALEFYTGGLPVVSSLYGSSEAFFGINMKPLCS
PYDVSYTFIPNMAYYEFIPIDNHQDPNCTNRKDAHLKDHIVDLANVKIGQHYELLVTTFTGLYR
YRMEDILLVTGFHNITPQFKFVQRTNVVLSIHTDKTTEQDLQKAVAIAMQILQPLGFFLLDYSSY
ADTSSIPGHYVLFWELQLRPNDTPELDQVKMEKCCSLVEQSLDQKYKWLNRNQSISTIGPLEIRV
VKQGTFTNVLMDFYVSQGTSLNQYKTPKNIKSEKAIVILDSRVVGKFYSREVPNQDS*

>CcGH3.5

MLPTFDPRDTEAGSRILEDISSNAGHIQEQVLEEILTKNASTDYLSFLNGHSDKGLFKNKVPVVD
YEDIKIYIDRIALDGEPSRILTNEISITELLISSGTSKKQKQWIPKTAEEGERRAFFFCLLATVQNRYL
HGLNDGKALFFVLINPDIHTPGGLVLRTTASEIKNRKDRYPEVIFCEDTNQSLYSQLLCGLVQRD
AIVSIGTFFASGLQRIIKFFEEHWQEMSSNIRTGQMSDWITDPCKKRTVSLILSKQMPDLADSIDLV
CQEKSWEGIIKKIWPRTKYVQAIITGSMAQYIPALEFYTGRLPVVSPAYVSSEACFGINLKPLCSPY
DVSYTIIPNMAYYEFIPIGNHQDPDCTNSKDAHLKDHIVDLANVKIGQHYELVTTCTGLYRYRM
GDVLLVTGFHNITPQFKFVQRRNVVLSIDTDKTTEQDLQNAVTIAMHILEPLGFFLLDYSSYADTS
SIPGHYVLFWELQLRSNDDFPVLDQVKMEKCCSLVEQSLDLQYKMLNRNSISTIGPLEIRVVKQG
TFNVLMDFYVSRGTSLNQYKTPKNIKSEKAIEILDSRVVGKFYSTEVNPQDS*

>CcGH3.6

MSSNIRTGQMSDWITDPNCKRAVSLILSKQMPDLADSIDLVVCQEKSWEGIIKKIWPRTKYVMAIT
GSMAQYIPALEFYMGGLPVVSPLYGSSEALFGINMKPLCSPYDVSYTFIPNMAYYEFIPIDNHQD
PNCTNRKDAHLKDHIVDLANVKVVGQHYELLVTTFTGLYRYRMGDIVLVTGFHNITPQFKFGQR
TNVLSIHTDKTTEQDLQKAIATAIQILEPLGFFLLDYSSYADTSSIPGHYVLFWELQLRSNDDIPE
LDQVKMEKCCSLVEQSLDQYKMLKNQSISTIGPLEIRVVKQGTFTNVLMDFYLSQGTSLNQYKTP
KNIKSEKAIEILDSRVVGKFYSREVPNQDS*

>CcGH3.7

METDWNTKALEFIEEMTKNAGEVQKMVLADILKQNGETEYLQRFNLDGATDTKTFTSKVPCITY
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VPDLNKGKGLYFYFPWPPEIRTPGGQMILTALTKFYRSEHFKSQRLDPYTQYTSPYESVMCTDYV
QSMYVQLLCGLYQHKQINRVGASSASALLRVIKFFELNWQDLVHDIRVGS LNPKITYEPLRECM
AQVMKSDPELADFLTIECSRGNWEGIIQRIWPNAKYLQTIITGSMIQAPLL VYYSGLPIATAKY
ASSECCFGINLNPISKPEDVSFTFMPNLAYFEFIPQEHLSSKMDIVNIVITTHAGLYRYQMGDILRV
TGFHNSAPNFKFLRRKGVLLSIELDKTDEVELQMAMDNASQILQEYNVCLVDYTSHASKKMAP
GHYVIYWELSVRDSKNAQSDEVISRCCPIIENSFSLIYKQHRVHGAIAALEIRVLKNGTFQDLVE
FAVSRGASIGQYKVPRCVETGAVLEFLDSRVVSSHFSPLSLASEESI*

>CcGH3.8

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LEFYTGGLPVVSPLYGSSEAFFGINMNPCLSPYDVSYTFIPNMAYYEFLPIDNHQDPNCTYRKDA
HLKDHLDLNNVKIGQHYELLVTTFTGLYRYRMGDILLVTGFHNSTPHFKFVQRTNVVLSIHTDK
TTEQDLQKAVAIAMQILEPLGFFLLDYSSYADTSSIPGHYVLFWELQLRSNDDIPELDQVKMEKC
CSLVEQSLDQKYKLLRNQSIISTIGPLEIRVVKQGTFFNVLMDFYVSQGTSLNQYKTPKNIKSEKVE
ILDSRVVGKFSREVPNQDS*

>CcGH3.9

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MPIINQYVGGLDEGKAMFLYFVKAEMSTPCGLPARTVLT SFYKSQHFKNRSHDPYNDFTSPDQTI
LCYDSNQSMYCQLLAGLVFRHQVLRGAVFASAFRLAISFLERNWRKLCQDIRTGKLDHAMITD
AQCSAMYSRVLLRPQPLVADEIESICSSKSWKGIVRRLWPKAKYIEAVITGSMISQYIPSLEYYS
GKLPLVCTMYASSECYFGVNLKPFCKPADVSFTLLPNMGHFEFIPLGESATWSIDLDEEEEEEEV
PPNKLVDLVHVRVGCY YELVVTTFAGLYRYRIGDVLQVTGFHNQAPQFRFICRRNVVLSVDND
KTNEEDLHKSITA AKKLEPYNALLVEYTSCADASTVP GHYVIYWEIAYNNGLVDEAFAIDPTVL
QECCAAVEERLDYTYRRCRTLDKSVGPLEIRIVEAGTFESLMDFFINQGASINQYKTPRCIKSKAA
LKLLNSNVKASYFSSRDPCWNP*

>CcGH3.10

MAVDSVLSSPLGPPACEKDAKALRFIEEMTRNADV VQEKVLAELTRNGQTEYLQRFKLGFTD
RLTFKSEIPVITYEDLQPEIQRIANGDRSHILSAHPISEFLTSSGTSAGERKLMPTIKEELDRRQLLYS
LLMPVMNL YVPGLDKGKGLYFLFVKSETKTPGGLLARPVLTSY YKSDHFKTRPYDPYNVYTSPN
EAILCPDSFQSMYAQMLCGLYEREQVLRVGAVFASGLLRAIRFLNLNWKQLTHDIRTGS LNPRV
TDPLVRECT*

>CcGH3.11

MAYFEFLPHDPNSPGFTRDSPPKLVDLADVEIGKEYELVITTYAGLYRYRVGDILRV TGFHNSAP
QFRFVRRKNVLLSIDS DKTDEAELQKAVENASQLLREYNTSVVEYTSFADAKTIPGHYVIYWELL
VKDAAHSPSDEALNGCCLAMEESLNSVYRQGRVADNSIGPLEIRVVKSGT FEELMDY AISRGASI
NQYKVPRCVSFTPIVELLDSRVVSVHFSPSLPRWTPERRR*

>CcGH3.12

MKAMHSPCCSPEEVIFGPDFHQSLYCHLLCGLIQREEVQVISSTFAHSIVFAFRTFEQDWEELCTDI
REGVLSSRISVPSVRTAMSKLLKPNPELADLIHNKCQGLSNWYGLIPELFPNTRYIYGIMTGSMEP
YLKCLRHYAGELPLLSADYGSSEGWIGVNVNPKLPPEMATFAVL PNIGYFEFIPLRQSLDGLEAK
PVGLAEVKAGEEYEVIVTSFAGLYRYRLGDVVKVKG FHNSTPELQFICRRNLLL TINIDKNTEKD
LQLAVEAAAKVLAENRLEVVDFTSRIDSSTEPGHYVIFWEISGEASDEVLEECCNCLDKSFLDAG
YLSSRKVKAIGALELRIVKRGTFFHKILDHYVGLGAAVSQFKTPRCVGP TNNKVLQILCNNVVKSY
SSTAF*

>CcGH3.13

MPEAPKVSSTNHQESCLDDKNQQVLQFIEDVTSNAKEVQRRVLNEILSRNAGVEYLQRHGFNGQ
IDYETFKSTFPVVTYDDLKPDVDRIANGDTSPILCSQPISECLTSSGTS GGERKLMPTIEEELGRRSF
LYSLLMPVMNQFVLDDLKGKGM YFLFVKSEAKTPGGLLARPVLTSY YKSSHFRDRPYDPYASY
TSPNEAILCSDSYQSMYSQMLCGLCQKDEVLRVGAVFASGFIRAIRFLQNHWP LNCNDIRTGTLN
PEIIDPSVREAVVKILKPNPQLAEVLEAE CRKESWKGII PRIWPNTKYIDVIVTGTMSQYIDTLNFY
GNNLPLVCTMYASSECYFGVNLNPLCMPSEVVYTLIPTMAYFEFLPVTSENEPVPLNPNKHHKL
DLVDVQLGQDYELVITTYAGLYRYHVG DILRVAGFKNKAPQFTFICRKNVALSIDSKTDEVEL
HNAVTKAANSHLLQFDASLIEYTSYADTSTIPGHYVLYWEIGFNSAKSIPESVFEDCCLTVEESLN
SVYRQGRVSDNSIGPLEIKVVKNGTFDKVMDFAISNGASINQYKAPRCVKYAPIVEILNSGVVFN
YFSPKCPKWSPGHKQWCTN*

>CcGH3.14

MERNGEYDIIGWFDEVAETADSVQTQTLSQLRLNNGVEYLLKKWFRDINIQEMEENALESLFTSL
VPLASHADLEHYIQRIADGDDAPLLTQEAITNLSLSSGTTEGRQKFVPFTRHSSKTTLQIFKLA
YRSRIYPIREGGRILELIYSSKQFKTKGGLTVGTATTHYYASEEFKIKQEQTCSFTCSPEAVISSGD
YNQSTYCHLLLGLHFRDEVEFITSTFAYSIVQAFRSFEELWREICDDIREGSLSSRITITKVRNAV
DIISPNPCLASRIASTCEELEEKDWFCMIPKLWPNKAYVYSIMTGSMQPYLRKLRYAGNLPLVS
ADYGSTESWIGVNVDPSSPPEKVTFAVMPNFSYFEFIPLHRQSQQNANSNTDDFIEEDPVPLSQVK
LGQEYEVLTFTTGLYRRLGDVVEVAGFHKKIPKLNFCRRKLILTVNIDKNTEKDLQLVVERGS
QALSKSKAELVDFTSHADAAKQPGHYVIYWEINGEVEERVLRRECCREMDASFVDHGYVVSRR
NSIGPLELCIVEKGTFFKILEHFIRNGAALSQFKIPRCTSNQVLLKILDASTIKRFRSTAYGQEL*

>CcGH3.15

MPEAPKDEGAYAHADTNTIYSVAEEKNKKFLQFIEEVTANADEVQKRVLAEILSRNAHVECLK
RHGLNGQTDRETFKKIMPVTYEDIQPDVNRIANGDKSQIICSQPISEFLTSSGTSGGERKLMPTTE
EELERRSLLYNLLMPVMSQFVPGLERGKGMFLFIKSEAKTPGGLVARPVLTSYKSSHFKNRSF
DPYMNYSPTNCPDSYQSMFSQMLCGLCLNKEVLRVGAVFASGFIRAIRFLEKHSLLCNDI
RTGTNLPRITDPSVREAVMKILKPDQLAEFIEGECGMESWQGIITRLWPNTKYIDVIVTGTMSQY
IPTLDYYSNGLPLVCTMYASSECFGVNLNPLCKPSEVSYTLIPTLGYFEFLPVDRNNGVTNCISM
PKSLNGKEKQELVDLADVKGQYELVVTYAGLYRVRGDLRVAGFKNKAPQFNFCRKNV
VLSIDADKTDEVELQNAVKAESHLVPFDAQVTDYTSYADTTTIPGHYVLFWELSLNGSTPIPPS
VFEDCCLAVEESLNSVYRQGRVSDKSIGPLEIKIVEAGTFDKLMDYALILGASINQYKTPRCVKFA
PIVELLNSRVKASYCSPKCPKIAGHKQWNINVK*

>CcGH3.16

MAVDSTPLAPPACENDAKALQFIEDMTRNCDSVQEKVLAEILSRNAQTEYLRDFKLGGATDRDS
FKSKIPVVTYEDLHPYIQRIANGDRSPILSSHPISEFLTSSGTSAGERKLMPTIHEEWDRRQKLYSL
MPVMNLVYVPLDKGKGLYFLVKAETPSGLVARPVLTGYKSDKFKNRPYDPYLVTSPDE
AILCADSFQSMYTQMLCGLLMREEVLRMGAVFASGLLRAIRFLQLNWKQLSEDIKTGVLNPKVT
DPSVRKRMAEILKPNSDLADFIVKECEGQNWDRITRIWPNTKYLDVIVTGAMAQYIPTLDYYSV
GREYELVITTYAGLCRYRVGDILRVTFHNSAPQFKFIRRNVLVLSIDADKTDEAELQKGIENASA
LLREFDTRVVEYTSYADTKIIPGHYVIYWELLVKDPANPPTHEVLNQCCLAIEEALNSVYRQGRV
ADNSIGPLEIRVVKNGTFFELMDYAISRGASINQYKVPKRCVSFAPIMELLDSRVVSVHYSPAAPH
WAPERRR*

>CcGH3.17

MPLPALDSTDSEALLELLEKVTADASQIQDELLQEVLTNTANTQYLKGFLNGYSDKQLFKKAVP
VVEYQDIEPFVDRIANGESSHLISAHPITELLSSGTSGGKRKAIPTTAEPRRRAFYASLTATILNK
HIEFWNQGKQMNFRFIMPEMTTLGGLAVTNVSSNFRSRMQNRSNCWNNDTSPDEVILCQDIK
QSMYQQLCGLVQRDAVVRIGTTYASGFLRVIKFLEEHWQELCSNIKTGHISDWIDPGCQKAVS
SILSQMPLGLADSIECRSGSWGIVKRLWPRTKCIEVVSTGTMTQYIPNLEFYCGGVPLVSMYY
AASEGFFGLNLKPLSDPNVSYTLVPWMAYYDTLGDHDLKGELVDLVNVQIGQYELVVTFT
GLYRVRVGDLVMTDFRNNTPQFKVVQRRNVVLSIDLKTTEGGLKAVSKAMQILEPLGCLLT
DYSSYADMSCFPGHYVLFWELQMRENAGIAAVLERVQMEGCCNVVEESLDGMYKTLRRRSNVI
DPLEIRVVKRGTFDGLMDLFLSEGASLNQYKTPKSIKSEKAIQFLNSMVVETFFSRVLPAPPTG*

>Cc00_g28970_not selected for analysis

MARGWLTWPIGLKGLNHGVNLFKLTIMLPTFDPRDTEAGSRILEDITSNAGHIQEQVLEKILTKNAS
SDYLGFLNGHSDKGLFKNKVPVVDYEDIKIYIDRIALDGEPSRILTNEISITELLKSSGTSGGTQK
WIPKTAEGERRAFFSCLCDTVLNRYLQGLSDGKALLFVLINPDIIHTPGGLVLRRTSESEIKNRKD
RYPQFILCEDTNQSLYSQLLCGLVQRDAIASVGTYSRVC*

>Cc02_g39040_not selected for analysis

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RWGLDGRDTPESYKSCVPLVTHEDELPYINRIVDGDSSILTGNPITTISLSSGTTGRMPKFVPFND
ELMESTMQIYKTSYSFRNRQVLHFLASRKFDWFSGFPYMAFRSHIDLSCGSPCLNYV*

>Cc00_g04550_not selected for analysis

MRMKGWITWAMGLKELNHGVNLFKLTIMLPTFDPRDTEAGSRILEDITSNAGHIQEQVLEEILTK
NASTDYLGFLNGQSDKGLFKNKVPVVDYEDIKIYIDRIALDGEPSRILTNEISITELLKSSGTSGGK
QKWIPKTSEGERRAFFSCLCDTVLNRYFQGLNDGKALLFVLINPDIIHTPGGLLRRTASESEIKNR
KDRFPQFILCEDTNQSLYSQLLCGLVQ*