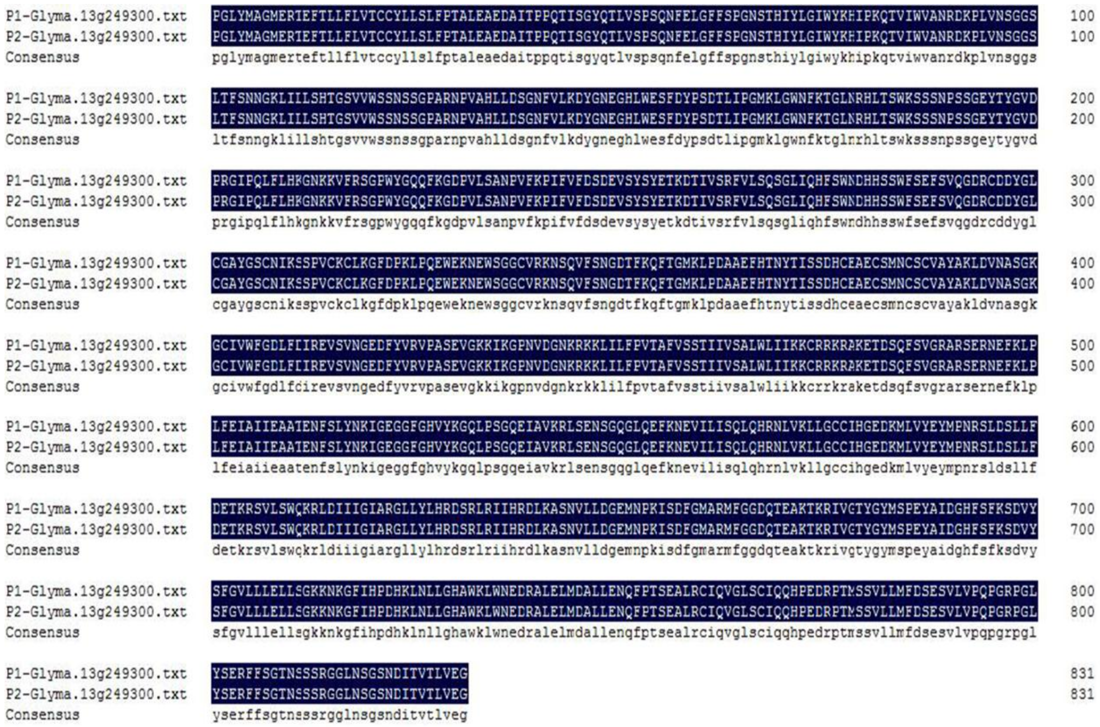

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P1-Glyma.13g249300.txt    PGLYMAGMERTEFTLLFLVTCCYLLSLFPTALEAEDAITPPQTISGYQTLVSPSQNFELGFFSPGNSTHIYLGIWYKHIPKQTVIWVANRDKPLVNSGGS    100
P2-Glyma.13g249300.txt    PGLYMAGMERTEFTLLFLVTCCYLLSLFPTALEAEDAITPPQTISGYQTLVSPSQNFELGFFSPGNSTHIYLGIWYKHIPKQTVIWVANRDKPLVNSGGS    100
Consensus                 pglymagmerteftllflvtccyllslfptaleaedaitppqtisgyqtlvspsqnfelgffspgnsthiylgiwykhipkqtviwvanrdkplvnsggs

P1-Glyma.13g249300.txt    LTFSNNGKLIILSHTGSVVWSSNSSGPARNPVAHLLDSGNFVLKDYGNEGHLWESFDYPSDTLIPGMKLGWNFKTGLNRHLTSWKSSSNPSSGEYTYGVD    200
P2-Glyma.13g249300.txt    LTFSNNGKLIILSHTGSVVWSSNSSGPARNPVAHLLDSGNFVLKDYGNEGHLWESFDYPSDTLIPGMKLGWNFKTGLNRHLTSWKSSSNPSSGEYTYGVD    200
Consensus                 ltfsnngklillshtgsvvwssnssgparnpvahlldsgnfvlkdygneghlwesfdypsdtlipgmklgwnfktglnrhltswksssnpssgeytygvd

P1-Glyma.13g249300.txt    PRGIPQLFLHKGNKKVFRSGPWYGQQFKGDPVLSANPVFKPIFVFDSDEVSYSYETKDTIVSRFVLSQSGLIQHFSWNDHHSSWFSEFSVQGDRCDDYGL    300
P2-Glyma.13g249300.txt    PRGIPQLFLHKGNKKVFRSGPWYGQQFKGDPVLSANPVFKPIFVFDSDEVSYSYETKDTIVSRFVLSQSGLIQHFSWNDHHSSWFSEFSVQGDRCDDYGL    300
Consensus                 prgipqlflhkgnkkvfrsgpwygqqfkgdpvlsanpvfkpifvfdsdevsysyetkdtivsrfvlsqsgliqhfswndhhsswfsefsvqgdrcddygl

P1-Glyma.13g249300.txt    CGAYGSCNIKSSPVCKCLKGFDPKLPQEWEKNEWSGGCVRKNSQVFSNGDTFKQFTGMKLPDAAEFHTNYTISSDHCEAECSMNCSCVAYAKLDVNASGK    400
P2-Glyma.13g249300.txt    CGAYGSCNIKSSPVCKCLKGFDPKLPQEWEKNEWSGGCVRKNSQVFSNGDTFKQFTGMKLPDAAEFHTNYTISSDHCEAECSMNCSCVAYAKLDVNASGK    400
Consensus                 cgaygscniksspvckclkgfdpklpqeweknewsggcvrknsqvfsngdtfkqftgmklpdaaefhtnytissdhceaecsmncscvayakldvnasgk

P1-Glyma.13g249300.txt    GCIVWFGDLFCIREVSVNGEDFYVRVPASEVGKKIKGPNVDGNKRKKLILFPVTAFVSSTIIVSALWLIIKKCRRKRAKETDSQFSVGRARSERNEFKLP    500
P2-Glyma.13g249300.txt    GCIVWFGDLFCIREVSVNGEDFYVRVPASEVGKKIKGPNVDGNKRKKLILFPVTAFVSSTIIVSALWLIIKKCRRKRAKETDSQFSVGRARSERNEFKLP    500
Consensus                 gcivwfgdlfcirevsvngedfyvrvpasevgkkikgpnvdgnkrkklilfpvtafvsstiivsalwliikkcrrkraketdsqfsvgrarsernefklp

P1-Glyma.13g249300.txt    LFEIAIIEAATENFSLYNKIGEGGFGHVYKGQLPSGQEIAVKRLSENSGQGLQEFKNEVILISQLQHRNLVKLLGCCIHGEDKMLVYEYMPNRSLDSLLF    600
P2-Glyma.13g249300.txt    LFEIAIIEAATENFSLYNKIGEGGFGHVYKGQLPSGQEIAVKRLSENSGQGLQEFKNEVILISQLQHRNLVKLLGCCIHGEDKMLVYEYMPNRSLDSLLF    600
Consensus                 lfeiaiieaatenfslynkigeggfghvykgqlpsgqeiavkrlsensgqglqefknevilisqlqhrnlvkllgccihgedkmlvyeympnrsldsllf

P1-Glyma.13g249300.txt    DETKRSVLSWQKRLDIIIGIARGLLYLHRDSRLRIIHRDLKASNVLLDGEMNPKISDFGMARMFGGDQTEAKTKRIVGTYGYMSPEYAIDGHFSFKSDVY    700
P2-Glyma.13g249300.txt    DETKRSVLSWQKRLDIIIGIARGLLYLHRDSRLRIIHRDLKASNVLLDGEMNPKISDFGMARMFGGDQTEAKTKRIVGTYGYMSPEYAIDGHFSFKSDVY    700
Consensus                 detkrsvlswqkrldiiigiargllylhrdsrlriihrdlkasnvlldgemnpkisdfgmarmfggdqteaktkrivgtygymspeyaidghfsfksdvy

P1-Glyma.13g249300.txt    SFGVLLLELLSGKKNKGFIHPDHKLNLLGHAWKLWNEDRALELMDALLENQFPTSEALRCIQVGLSCIQQHPEDRPTMSSVLLMFDSESVLVPQPGRPGL    800
P2-Glyma.13g249300.txt    SFGVLLLELLSGKKNKGFIHPDHKLNLLGHAWKLWNEDRALELMDALLENQFPTSEALRCIQVGLSCIQQHPEDRPTMSSVLLMFDSESVLVPQPGRPGL    800
Consensus                 sfgvlllellsgkknkgfihpdhklnllghawklwnedralelmdallenqfptsealrciqvglsciqqhpedrptmssvllmfdsesvlvpqpgrpgl

P1-Glyma.13g249300.txt    YSERFFSGTNSSSRGGLNSGSNDITVTLVEG                                                                          831
P2-Glyma.13g249300.txt    YSERFFSGTNSSSRGGLNSGSNDITVTLVEG                                                                          831
Consensus                 yserffsgtnsssrgglnsgsnditvtlveg
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Fig. S3 Multiple sequence alignment depicting the amino acid sequence conservation of P1 (CSSL3228) *Glyma.13g249300* gene with P2 (NN1138-2) gene (*Glyma.13g249300*) in soybean.