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|------------------------|---|-----|
| P1-Glyma.13g249300.txt | EGLYMAGMERIEFTLLFLVTCVLLSLFPTALEAEDAITPPQTISGYQTLVSPSQNFELGFFSPGNSTHIVLGIWYKRIKQTVIIVWANRDKPLVNSGGS | 100 |
| P2-Glyma.13g249300.txt | EGLYMAGMERIEFTLLFLVTCVLLSLFPTALEAEDAITPPQTISGYQTLVSPSQNFELGFFSPGNSTHIVLGIWYKRIKQTVIIVWANRDKPLVNSGGS | 100 |
| Consensus | pglymagmertefllflvtccyllslfptaleaedaippqtisgyqtlvpsqnfelgffspgnsthiylgiwykhipkqtviiwanrdkplvnsqgs | |
| P1-Glyma.13g249300.txt | LTFSNNGKLIILSHTGVSVMSSNSGGPARNFVAHLIDSGNFVLDYGNEGHLWESFDYPSDTLIPGMKLGWNFKTGLNRHLTSWKSSSNPSSGEYTYGVD | 200 |
| P2-Glyma.13g249300.txt | LTFSNNGKLIILSHTGVSVMSSNSGGPARNFVAHLIDSGNFVLDYGNEGHLWESFDYPSDTLIPGMKLGWNFKTGLNRHLTSWKSSSNPSSGEYTYGVD | 200 |
| Consensus | ltfsmngkllilshgtgsvvmssnsggparnpvahllidsgnfvldygneghlwesfdypsdtlipgmklgwnfktglnrhltswksssnpsgeytygvd | |
| P1-Glyma.13g249300.txt | PRGIPQLFLHKGKRVFRSGPWYQQFKGDFVLSANFVFRPIFVFDSEVSYSETKDTIIVSRFVLSQSGLIQHFSWNDHSSWFSEFSVQGDRCDDYGL | 300 |
| P2-Glyma.13g249300.txt | PRGIPQLFLHKGKRVFRSGPWYQQFKGDFVLSANFVFRPIFVFDSEVSYSETKDTIIVSRFVLSQSGLIQHFSWNDHSSWFSEFSVQGDRCDDYGL | 300 |
| Consensus | prgipqlflhkgkrrvfrsgpwyqqfkgdvpvlsanpvfrpifvfdsevsysetkdtivsrfvlsqsgliqhfswndhsswfsefsvqgdrcddygl | |
| P1-Glyma.13g249300.txt | CGAYGSCNIKSSVCKCLKGFDPKLPQEWKNEWSSGGCVRKNSQVFSNGDTFKQFTGMKLPDAAEFHTNYTISSDHCEAECMNCSCVAYAKLDVNASGK | 400 |
| P2-Glyma.13g249300.txt | CGAYGSCNIKSSVCKCLKGFDPKLPQEWKNEWSSGGCVRKNSQVFSNGDTFKQFTGMKLPDAAEFHTNYTISSDHCEAECMNCSCVAYAKLDVNASGK | 400 |
| Consensus | cgaygscniksspvckclkgfdpklpqeweknewsggcvrknsqvfsngdtfkqftgmklpdaaefhtnytiessdhceaecsmncscvayakldvnaqsk | |
| P1-Glyma.13g249300.txt | GCIVWFGDLFIIREVSVNGEDFYVRVPASEVKGKIKGENVDGNKRKLLIFPVTA FVSSTIIIVSALWLIKKCRKRKREKETSQFSVGRARSERNEFKLP | 500 |
| P2-Glyma.13g249300.txt | GCIVWFGDLFIIREVSVNGEDFYVRVPASEVKGKIKGENVDGNKRKLLIFPVTA FVSSTIIIVSALWLIKKCRKRKREKETSQFSVGRARSERNEFKLP | 500 |
| Consensus | gcivwfgdlfiirevsvngedfyvrvpasevkgkikgenv dgnkrkllifpvtafvssstiiivsawl iikkcrkrkretsqfsvgrarsernefklp | |
| P1-Glyma.13g249300.txt | LFEAIIIEAATENFSLYKIGEGGFHVKYKQLPSSGQEIIVKRLSENSGGLQEFKNEVILISQLQHRNLVKLLGCCIHGEDKMLVVEYMPNRSLSLDF | 600 |
| P2-Glyma.13g249300.txt | LFEAIIIEAATENFSLYKIGEGGFHVKYKQLPSSGQEIIVKRLSENSGGLQEFKNEVILISQLQHRNLVKLLGCCIHGEDKMLVVEYMPNRSLSLDF | 600 |
| Consensus | lfeaiaieaatenfslynkigeggfghvykqqlpsgqeiavkr lsen sgglqefknevilisqlqhrnlvklgccihgedkmlvveympnrslsdlf | |
| P1-Glyma.13g249300.txt | DETRKRSVLSWCKRLDIIIGIARGLLYLHRDSRLRIIHRDLKASNVLLDGMNPKISDFGMARFGGDQTEAKTRIVCTYGYMSPEYAIIDGHFSEKSDVY | 700 |
| P2-Glyma.13g249300.txt | DETRKRSVLSWCKRLDIIIGIARGLLYLHRDSRLRIIHRDLKASNVLLDGMNPKISDFGMARFGGDQTEAKTRIVCTYGYMSPEYAIIDGHFSEKSDVY | 700 |
| Consensus | detkrsvlswckrldiigiargllylhrdsrlriihrdlkasnvlldgemnpkisdfgmarfggdqteaktkrivctygymspeyaidghfseksdvy | |
| P1-Glyma.13g249300.txt | SFGVLLLELLSGKKNKGFIIHPDHKLNLLGHAWKLWNEDRALELMDALLENQFPTSEALRCIQVGLSCIQQHPEDRPTNSSVLLMFDSESVLPQGRGRL | 800 |
| P2-Glyma.13g249300.txt | SFGVLLLELLSGKKNKGFIIHPDHKLNLLGHAWKLWNEDRALELMDALLENQFPTSEALRCIQVGLSCIQQHPEDRPTNSSVLLMFDSESVLPQGRGRL | 800 |
| Consensus | sfqvllellsgkknkgfihpdhkl nllghawklwnedralelmdallenqfptsealrciqvglsciqqhpedrptnssvllmfdsesvlpqgrgrl | |
| P1-Glyma.13g249300.txt | YSERFFSGTNSSSRGGLSGNSNDITVTLVEG | 831 |
| P2-Glyma.13g249300.txt | YSERFFSGTNSSSRGGLSGNSNDITVTLVEG | 831 |
| Consensus | yserffsgtnsssrqglnsgnditvtlveg | |

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.