Alignment Report of Untitled ClustalV (PAM250)

Saturday, March 11, 2017 04:29 PM

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Majority          XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXX

                          10        20        30        40        50        60        70        80

Gnp4                                                                                               81
Sb06g014520                                                                                        81
XP_003579650.1                                                                                     81
XP_008663842.1                                                                                     81
Os12g0600200                                                                                       81
Os03g0632800      MQPAPASPPKADGGEDEEEECSRAVVKEEPHHQQEEDDDDAAAAADGGEDEKEKVEEEEVEERGRRRRGRPGRKRGRRSGG 81
Os03g0798200                                                                                  MQGAT 81
Os03g0741700                                                                                       81
Os12g0479100                                                                                       81
Os01g0928400                                                                                       81
At1g06770                                                                                          81
At3g23060                                                                                          81
At2g30580                                                                                          81
At1g28080                                                                                          81
At5g13250                                                                                          81

Majority          XXXXXXXXXXXXXXXXXXXXXXXXX-----XCXXLLRDATTISECLH-TFCRXCIXEKITDEEVESCPVCNIDLGHRPLEK

                         90       100       110       120       130       140       150       160

Gnp4                            MVPARSLAHPH-----PHLVRRRRDHAAAAHGATARCDDDDDGVVTPRGPTRYMAQEPINHHQHQH- 156
Sb06g014520                     MVPARN     -----LQPPLLRDAHATPCAAAAAAG     LGVTPTAASSHMAQEPIDKHHSEPS 157
XP_003579650.1                  MVPAR      ----- NLQLLRDEHGTPPFVAR        GVDAVTAQPHHMAQEPINQESPKP- 156
XP_008663842.1                           -----                                     MAQDPSRPHRHSSK 157
Os12g0600200                             MKYAPIY      LLTLS-CLHYAVCRKCIYKKINDEELEHCPVCKIDLGCAPLEK 161
Os03g0632800      GGGSAAAAAAARGGVVMVKRELLARCMTCPLCGRLLRDATTVSECLH-TFCRKCIYEKLNDEEVESCPVCKIDLGCTPVEK 161
Os03g0798200      PGDAAGEEVGGGGDVVMVRRASVAACLTCPLCGRLLRDATTISECLH-TFCRKCIHEEFVDKESCCCPTCNIDLGCAPLEK 161
Os03g0741700             MGAARGGVRRVRREALVACMTCPLCKGLLREATAITECLH-TFCKECIMEKIDDEEVDHCPVCNIDLGCDPEEK 161
Os12g0479100                             -----                                     MAQDPSHPHRQS K 157
Os01g0928400                             -----                            MVPARSRLFHHDSSSSSKRGGGN 157
At1g06770                      MMIKVKKETMRACLSCSICDNILRDATTISECLH-TFCRKCIYEKITEDEIETCPVCNIDLGSTPLEK 161
At3g23060                      MLTKVLSKEVKPCLACPICTNPFKDATTISECLH-TFCRSCIRNKFINERVNACPVCNVNLGVFPLEK 161
At2g30580                  MEGDMVAKVKRETVVACMTCPLCDKLLRDATTISECLH-TFCRKCIYEKITEDEIESCPVCDIDLGGTPLEK 161
At1g28080                                -----             MTNMVPLESSTLFGVYGGFTDSMMMRETTTNNQDPSGD 157
At5g13250                                -----    MVSAAESSSS---------------TSTLLLPCAFANSFAFMRLLQK 142
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Majority        LRPDHNPQDVRAKIFXXPLKRKKVQAPEVAAHVVLPAKRKERSXSSLVVXTPXVSAQAGTTGRRTKAXTRKXAGALXXXXX
                      170       180       190       200       210       220       230       240
Gnp4            -DPPKQPPPR---------EADD---DH---HRIQE  -----REPLPPPTTTTRNQRLQLQLGGDGHHN----------- 205
Sb06g014520     TKPPPPPPPQERQQQQQQA  DDQHTRHAHAHREQQQQLTLR   PLQPAGSSHQEAAGTSGSSSGG SSGNGGAG      238
XP_003579650.1  -QQ HQVPPQ---------EEEDEQP  ---     AVLP-PP                           QPAGTSGSSSG 223
XP_008663842.1  DTAAQQPEPEHQHEHEQQP  PAEILHQLAPQAQPQPPHDVH             EPAAAASSSSS SDAGS          238
Os12g0600200    LRADHNIQDVRSKIF  PLKRKKVNAEEVESPIAPPAKRKERSISSLVVNTPEITP KSLTGRRTRASTRKSAAALRDLGP 242
Os03g0632800    LRADHNLQDVRSKIF  PFKRKKISADEVAAPVLLPSKRKERSISSLVVDTPTVTP TGLTGRRTRAVTRK AAALR---- 238
Os03g0798200    LRVDHSMQFVRSRIF  PFKRRKVENPEIICPVASPVKRKERSLSSLTIPAPQVSIQKCLTKRRTKASC------LR     236
Os03g0741700    LRPDHNVQDIRNKVF  PLKVKKVGAP KAPTVTLPVKRKQRSLSSLVVDTPRVAVQTGLTGRRTKTARRTAVSHVNSPGN 242
Os12g0479100    DTA----------------AAP--------------------PPPPPQEQPQQQQ---------  P     ELITAPPPR 193
Os01g0928400    SSSSCTPQYCIATQLDAAAAAAPARRRHHHHHQLAMAPPEDD             AAAGTSSRGGGAGDDDDGDK       238
At1g06770       LRPDHNLQDLRAKIF  ALKRRKVKAPGIVS   LPGKRKERSISSLVVSTPMVSAQAGTTRRRTKAPTRK   ELR NGS 242
At3g23060       LRSDCTWQDLKLKIYRAMMESLKKAGPKTVAASVKSSKKKRKSRTSLRVSSSRVSSSPDTPLEPANVVVEPPNVVVEEKHR 242
At2g30580       LRPDHILQDLRAKLF  PLKRKKERAPEVVSSISLPAKRKERSISSLVVSTPRVSAQAGTTGKRTKAA---TRK   D--- 236
At1g28080       TCSVSDPAPGSTDYYNISSSPVKDDGTAPKNDVVCSINVDDNKDKSWLRLGIGPEENTDGSYKLQRCCSKNGSGRE      238
At5g13250       THHFSAVSEDDDNNKDIHLGSDHHQAKDNNHHQV------FRRECSFMADQEEPRSTTSRLSSKEDDHDNNS-----NNNN 212

Majority        XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXLXXXXXKXPQXXRXXXXXXXXXSXSXXEXXXXXXXX
                     250       260       270       280       290       300       310       320
Gnp4            -----------HHHHHHQEVAGTSGSSSGGSSSNNGGGG                                           275
Sb06g014520                                            DWLRLGLAPAYPSAA--------------------------- 292
XP_003579650.1  GNSSSNGGGGG                                        GGGDWLRLGLGPSAAASASGTEADLFAAAD 304
XP_008663842.1                                         SWLQLGIGGPSPSSPP  RRKRPRRDDD               319
Os12g0600200     IIPPVKKD            SDNTNKNADNSS------------LLDSLSKVPQTRRQVLSNAETSSHPSSKDKGGDDKD 311
Os03g0632800    G--------LGPGIDDPVKKE            IDNGEKHAQNSSLPTNLGKVPQTRRQMSSNAEASNHSSNKDTEGDRKD 311
Os03g0798200                                              NFPLHST------SR         GSKDTSKKLGG     311
Os03g0741700    NGTIKLANK            SEGRDHKTQKIS----------AAQSAKMTKTGNKKKNNTDVDVTIQSSSEDRKD  DHT 313
Os12g0479100    DDVAHQ             EPSTSSSSGGGGTDAAG                                              274
Os01g0928400                                           DWLQLGLAAAAPTATA----PAAAAAPSSSTPTAP        315
At1g06770       LAERTVKKE            ESSGDELLESTS------------SPDTLNKFTQNKRQSKKS CKESISNKENKDGD  E 311
At3g23060       ETVLAL---------QSTRKPIITFQKRGRKASLP---KKIDSKPEPELPPKEPKIKNLFDLNNEPEDNGLDEAEGSTFQE 311
At2g30580       ------VRGSGSFTKRTVKKE            EEFGDDHVESASSPETLKKFTQNKRQSSYANPNQSLSNRRNKDVD  E 311
At1g28080                                              NSLELSLFSSSSTAVS---------SSIDHLPTQPLQLPYHH 310
At5g13250       INNNNNNEAEDHEMRQQGWLR                                              LSLGHEEDVKPDLD 293
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Majority         XXXXXXXL-WKPLNXLVXXXXXRKXXXSXXXXXXXXXXXXX---XXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXXEXXX
                     330       340       350       360       370       380       390       400
Gnp4             TRDW-LRLATGPASPGASAGSDHDLFPSTTTTAPAPQPPTP---TPTPTPTPTPRHHHHDVLVLPG  MP PPGSFLRPGP 352
Sb06g014520      ------------THPGVAFAADRAAGPPSPLLLSSSEPQRP---P  PPPPLLSSQRPPG  ----MG--FPPGPFLHQAA 352
XP_003579650.1       -                 RGPRQEMLVLPALDMPMPP---GAFPRPG               ------------    369
XP_008663842.1                            ---------       ---                                 DDDA 388
Os12g0600200     LDKS  EL-WRPLNCLVEAASKTKSYRSSS   AARGNQPT                     ESP SSANASRTKAREY   391
Os03g0632800     LADKTDEL-WRPLNCLVE------------AAN--------RTKSSRSSSQSPFVKREQLS                     371
Os03g0798200             -WRPLGCQLKLGKDKKSLKSSVKDTNRTKSKSG                     DTD DGAPASKAKAREP   391
Os03g0741700     I--DKEDL-KKPLNSLVDTANRTKFFRSGPKGQAAKEDKI----------------KNSIKLLA             EDDT 375
Os12g0479100        LSLQLGLGPSAPGSPSSSRRKR---------PRTDAHH---                                      343
Os01g0928400                                              ---                     ELDV-FAAKQY----- 387
At1g06770        PWDSKMD -WKPLN----------FLVEVANGTK-------PLKSSASQGSGSKSEHA                     NV 374
At3g23060        VVPKEKDL-CKPIFSLSVTLNINDTPPDIVEPEISSDDDTEESVEPIQNKCVVNRETKEVPVQVNQNSLLISSDRDREDNS 391
At2g30580        PWDSKLHL-WKPLNFLVDVANGTK          DPKSELG                     NASHNDVQGSKTKTKDH   391
At1g28080        DQLLTMR---GPS                            ---                        LVYNHQ------- 378
At5g13250        HRQ---QHQTDPT-------ARRDSFLELNLSSGGSNREEE---VGLPLSSLFHHQHQAGGMMINPL-------------- 347

Majority         XXXXXX-------XXXXXXXXXXXXXK---------GXXXX--XX-XXPXXLP-R--KRTGXXXRRP--------------
                    410       420       430       440       450       460       470       480
Gnp4             AMP                 GIPQAS  IPTHMLRAA    --  --PPW LPPWS-P VAAP   PPLLPFPHQ---HRA 425
Sb06g014520      HG                   IPQAS  IALPVPRAG    --  --PPW LPPWS-PSAVAPPPPPSLIPFGF---GHGA 425
XP_003579650.1       IPQASMQIPDGGPRAG      PP---------WQMP--PW--SP A-------Q--QHQQQPFLLPFAHQAQAQRA 428
XP_008663842.1   G      PSTATSSVQPAAAPPPQLPPQLLLSLQPAGRPS    --SSSSSAP---APAPARAV----------------- 447
Os12g0600200         L-------------LKSKVQDEK---------K--E    VPVATVPF-KRKGPGRGRKPAQP-------------- 433
Os03g0632800      DSP GSTSVNKTKSREY      MQK---------SKIEDDKKD    VPLLKRKNQRTG   RRR-------------- 429
Os03g0798200         FT--------------------R---------                YGRAAKRTG    RK-------------- 429
Os03g0741700     EDKLVVTGR----KVMPC      SNK---------LKVKEENNRS  PSQSASSKDKTTSDYELRK-------------- 429
Os12g0479100                                              EAAAG      PSTS        AADPQLPELRLSVLHPG 424
Os01g0928400     -----------------NGR     PPLFPLPILRSYHHHHHHQYG------------HGGGRCPPPSFFPFAR------- 432
At1g06770        SRNQFQGS---KTKTKNK      KRK---------CKREDDKSNNGDPTTSETVTPKRMRTTQRKR-------------- 429
At3g23060        GQKL---------KTNGAATSRSRKKK---------GKKPVEKSYSLRPRIG-------------RR-------------- 427
At2g30580          -------------  KRKCKLE----------------EEISNNGDPTTSETATLKRTRRTRRKR-------------- 429
At1g28080        ---LMKPQTLLNRG     FSFPSSKPWIPQYMAP-----------FRPSSLSDRDVTNNNSLSRSCCV------------ 433
At5g13250        ---MFHTR                      PQDMIGPWAAA--AFRTP   FVPQNLTQPSSSSSGSLMMPLMGQYFGRSS 423
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Majority        -----SAXT-GDSSGXDAP-RVVLAPPXXXXXX--AAGVWFSLQASPDQEREXPFLPQIPRSYLRIKDGNXMTVSLLQKYL

                  490       500       510       520       530       540       550       560
Gnp4            FYAAPPTTTPPASSGFDAI-RVVLPPS  AVAA--AAGVWFVLQAAPLQGRE PFLPQIPRSYLRIKDGR VTVRLLTKYL  503
Sb06g014520     FY      TPGAGSGLDAI-RVVLPP      S--AAGVWFALQAAPHQGRE PFLPQIPRSYLRIKDGR VTVRLLIKYL  503
XP_003579650.1  FYAPGSTAS---ASGFDTI-RVVLPP     PV--PAGVWFVLQAAPHQGRE PFLPQIPRSYLRIKDGR MPIRLLIKYL  503
XP_008663842.1  ------APPP  P AHE------------AG-T------WFLLRAAPNQRREEPPLPHIPRSYLRVRDGRMMTVRVVMRYL  503
Os12g0600200    -----PAAAV    SS--HS--ASKHE  KL  LT--PVWFSLIASFDQKGA PPLPQIPTHYLRIKDDN MPASSIQKYI  503
Os03g0632800    -----ELHAQSDSK  --  PEAAATQNE  KK  FSSIWFSLVASFEQEGD PPLPQIPSHYLRIKDGN IPASSIQKYL  503
Os03g0798200    -----KLLMLKNKK    KRFKAKQPS  KKRR--FRALWFYLLAAFDQRGV PTLPQLPAKYLRIKDVD LPASIIQKYL  503
Os03g0741700    -----GQHA--DSQQGQIGSTRTGALHDG  IT   RPVWFLLVPSPDQKQD PRLPQLPTYYVRIKDGS LQTSLIQRYI  503
Os12g0479100    --PGPS    SSAS   AVGAVVAAAPPP  P AHEAGTWFVLRAAQNQRRE PPLPQIPRSFLRVRDGR MTVRVVMRYL  503
Os01g0928400    ----------PLRSSGDLPGVMRVISPPRRAAAADAAGLWLTLQASPDQFRE PILPQIPKSYLRIKDSN MKVEVVMKYL  503
At1g06770       -----SATTLGDSRN--LPQPDESSAKQE  RR  NGPVWFSLVASNDQEGG TSLPQIPANFLRIRDGN TTVSFIQKYL  503
At3g23060       -----TVNPAAGTTTPEAPVSVEEEMKVE  EGRNNNPVWFSLKPSKTQNIE MLLPPITACCIRVKDSN MTVSYLKKYL  503
At2g30580       -----SS TFGDSRIPLLPGAASLKQE  RR  NGH--VWFSLVASSNQEGE ASLPQIPANYLRIRDGN IPVSFIQKYL  503
At1g28080       -----------DEGGAGPSSEFRVLDPPR    RPHSGLWFLLQASQFQERE PFLPQVNKSYLRIKDGR ITVRLLIKYL  503
At5g13250       FQPQLIGNDNPDGVAGPSS-SLRVIDPPR    RPHSGIWFLLQASQNQTVE PFLPQIPKSYLRIKDGK MTVRLLMKYL  503

Majority        MNKLGLESESEXVEITCRGXPVXPXLTLQNL-----LWLXXR--XXXXXPXRLPASVGSSAKDFVMVLXYGRX--XXXXXX

                 570       580       590       600       610       620       630       640
Gnp4            VNKLGLEDESE VEITCRGRQLLPILTLQHV--RDSIW-CRRD-A  VSPSAAPDIPTADHHQHIMVLQYGRR--P       578
Sb06g014520     AGKLGLEDESE VRFIR         ILHHNSN     -    - LL--P                       --        578
XP_003579650.1  VNKLGLEDESE VEITCRGRPLLPFMTLQHL--RDSIW-CQRD-A  VSPLVAPDMSTAN   HIMVLQYGRR--T       578
XP_008663842.1  VNKLGLDDDSQ LEITCRGQRLQPTMTLQQV--RDTIWRPAVP-  AEAAAVLPA-PGSRSTDHIMTLHYCRS--        578
Os12g0600200    MQKLSLPSETE VEISCCGQPVNPIQPLRNLIE---RWLR---FGP   ARTLQTVVGSSGGDYVMVISYGRPKAA       578
Os03g0632800    MQKLGLPNEAE VEINCCGQPVNPTQPLCNLVE---VWLRGRS   TQTT---QTMIGSPAKEFVMVLTYGRPKAITP     578
Os03g0798200    AQKLNLSSETE VEVLCGGKVVNQGMTLHDLAD---CWLEK---GP   KSRMRSSVGSPATGFMVTLFYRRPDVDVSSSP  578
Os03g0741700    MNKLDLASEDE VEITCHGEAISPSTTLQGLLE---LWLKSS---P   VEQVQASLGAQAKEFVMELGYRRPQRPPSS    578
Os12g0479100    VNKLSLEDDS                   QV--KG        -       VRPS-VTSWVTPHD        --        578
Os01g0928400    AGKLGLTQSH                 LQRAASSSLL---AGQ-K  CQRQHLVLITATKLQGRRRRRRRG  --        578
At1g06770       MRKLDLESENE IEIKCMGEAVIPTLTLYNLVD---LWLQKSS---N  HQRFAALVGSSAKDFTMVLVYARKLPECNM    578
At3g23060       MVKLGLESEDQ VEIWLRDEPVCSSLTLHNLVD---WWVQTT---PL  PERQSAMVGSSAAEFIMDLYYSFKSDASDSGS  578
At2g30580       MRKLDLKSEDE VEITCMGEPVIPTLQLHSLVD---LWLETTS---K  HQRVAASIGSSAKEFVMVLVYSRKLPECNN    578
At1g28080       MKKLELDSESE VNI                            -                             --        581
At5g13250       VNKLRLEHESQQVEIRCRGQELEPVLTLQHV--RDAIWRGSRD-TSSLSQNITL-LPNSSTSDHLMVLHYGRT--IS      578
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Majority              X X X X X X X X X X X X
                         650        660

Gnp4                                                            590
Sb06g014520                                                     590
XP_003579650.1                                                  590
XP_008663842.1                                                  590
Os12g0600200                                                    590
Os03g0632800                                                    590
Os03g0798200          A P P Q P D T E S C H S                   590
Os03g0741700                                                    590
Os12g0479100                                                    590
Os01g0928400                                                    590
At1g06770                                                       590
At3g23060             A S E                                     590
At2g30580                                                       590
At1g28080                                                       590
At5g13250                                                       590
```

Decoration 'Decoration #1': Shade (with solid black) residues that match the Consensus exactly.