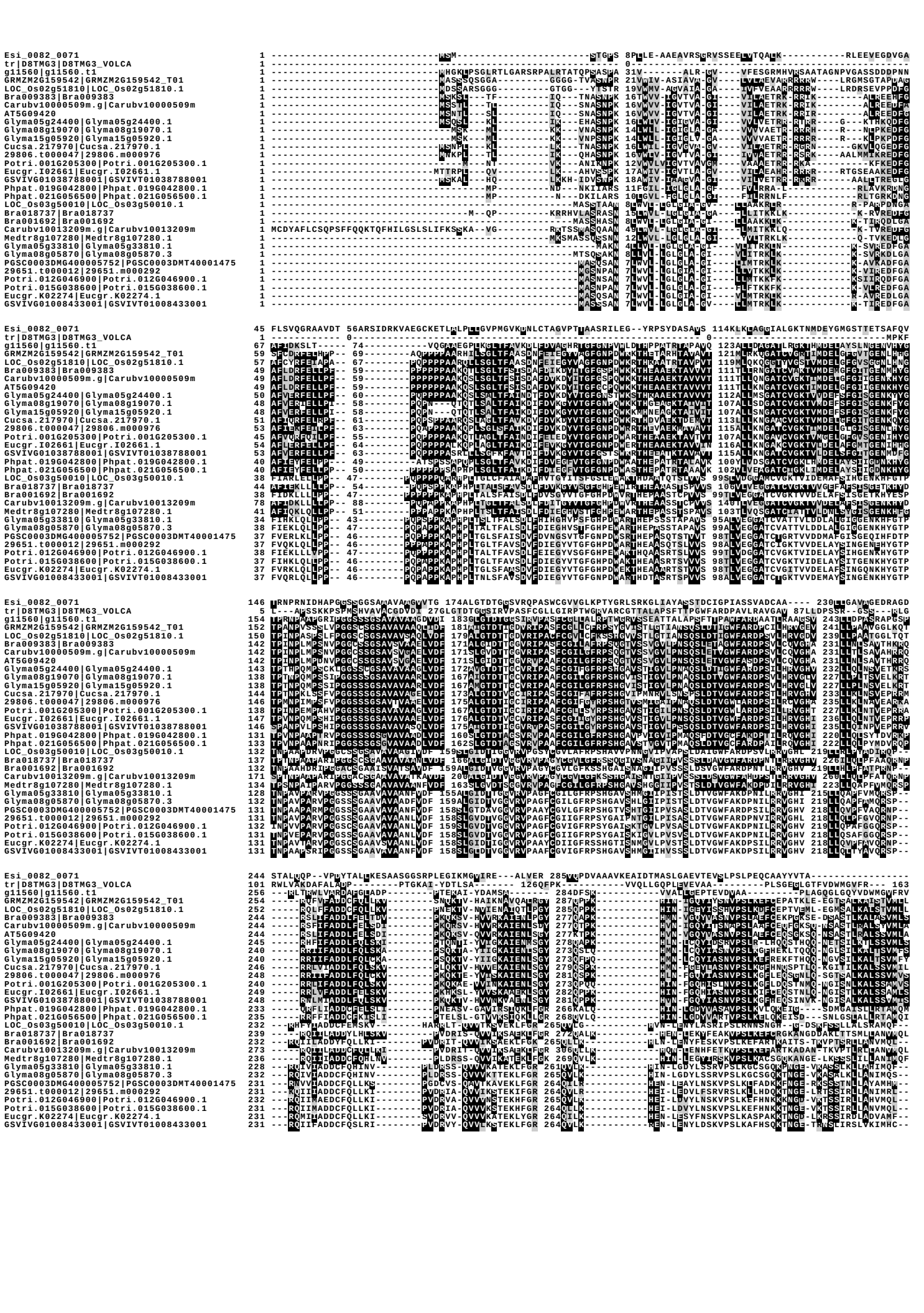

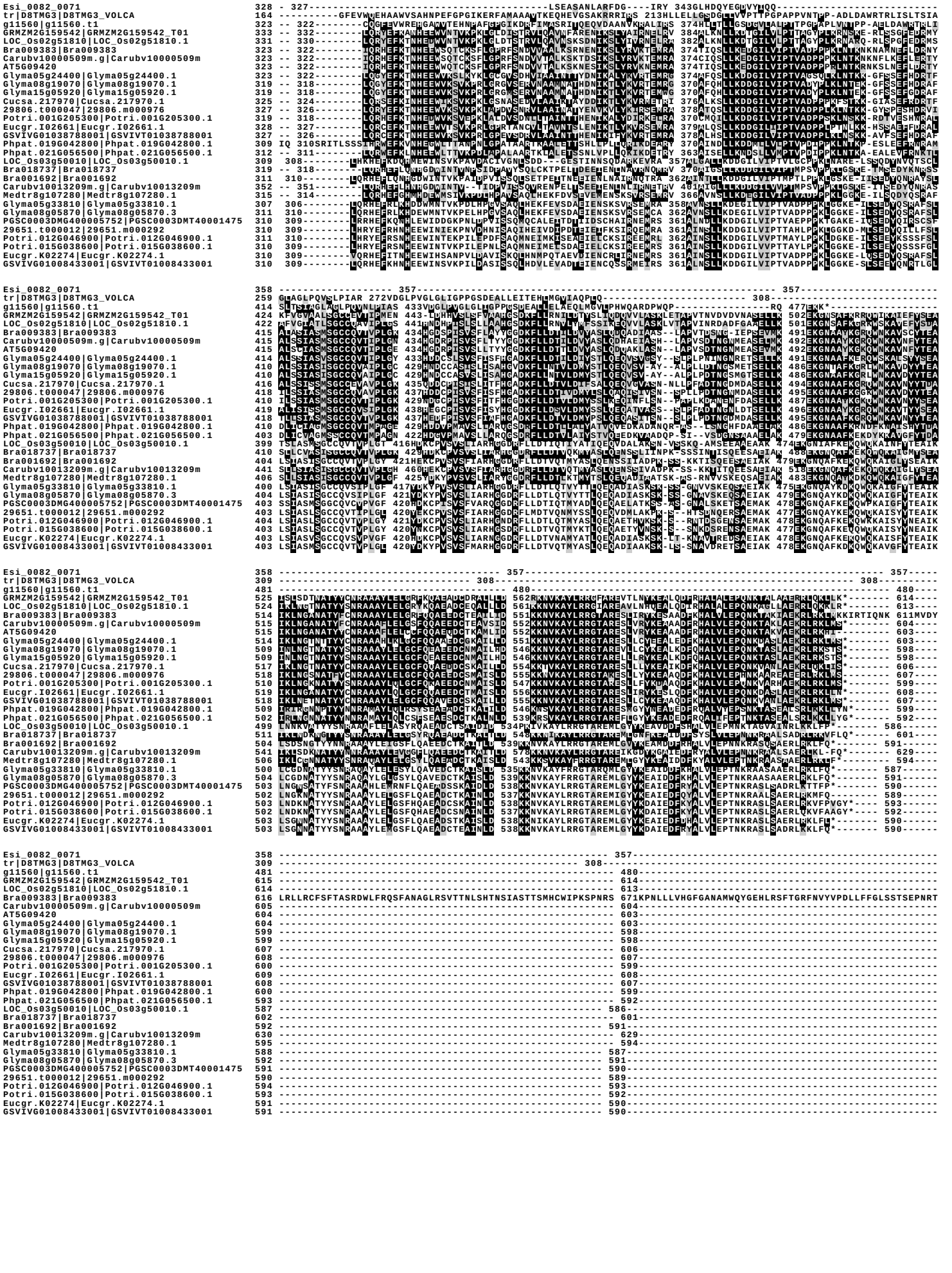

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Esi_0082_0071                                   358 --------- 357------------------------------------------------------------ 357--------------------------------
tr|D8TMG3|D8TMG3_VOLCA                           309 ---- 308------------------------------------------------------------ 308--------------------------------
g11560|g11560.t1                                481 ---------- 480------------------------------------------------------------ 480--------------------------------
GRMZM2G159542|GRMZM2G159542_T01                  615 ---------- 614------------------------------------------------------------ 614--------------------------------
LOC_Os02g51810|LOC_Os02g51810.1                 614 ---------- 613------------------------------------------------------------ 613--------------------------------
Bra009383|Bra009383                             722 ESFQARCLMR 731LMEAHGVHTMNIVGISYGGFVGYSLAAQFPEKVEKLVLCCAGVCLEEKDMEDGLFKVPNL 791EEATEILIPQTPEKLKELIRFSFVKPIRGVPS
Carubv10000509m.g|Carubv10000509m               605 ---------- 604------------------------------------------------------------ 604--------------------------------
AT5G09420                                       604 ---------- 603------------------------------------------------------------ 603--------------------------------
Glyma05g24400|Glyma05g24400.1                   604 ---------- 603------------------------------------------------------------ 603--------------------------------
Glyma08g19070|Glyma08g19070.1                   599 ---------- 598------------------------------------------------------------ 598--------------------------------
Glyma15g05920|Glyma15g05920.1                   599 ---------- 598------------------------------------------------------------ 598--------------------------------
Cucsa.217970|Cucsa.217970.1                     607 ---------- 606------------------------------------------------------------ 606--------------------------------
29806.t000047|29806.m000976                     608 ---------- 607------------------------------------------------------------ 607--------------------------------
Potri.001G205300|Potri.001G205300.1             600 ---------- 599------------------------------------------------------------ 599--------------------------------
Eucgr.I02661|Eucgr.I02661.1                     609 ---------- 608------------------------------------------------------------ 608--------------------------------
GSVIVG01038788001|GSVIVT01038788001             608 ---------- 607------------------------------------------------------------ 607--------------------------------
Phpat.019G042800|Phpat.019G042800.1             600 ---------- 599------------------------------------------------------------ 599--------------------------------
Phpat.021G056500|Phpat.021G056500.1             593 ---------- 592------------------------------------------------------------ 592--------------------------------
LOC_Os03g50010|LOC_Os03g50010.1                 587 -------- 586------------------------------------------------------------ 586--------------------------------
Bra018737|Bra018737                             602 ---------- 601------------------------------------------------------------ 601--------------------------------
Bra001692|Bra001692                             592 -------- 591------------------------------------------------------------ 591--------------------------------
Carubv10013209m.g|Carubv10013209m               630 ---------- 629------------------------------------------------------------ 629--------------------------------
Medtr8g107280|Medtr8g107280.1                   595 ---------- 594------------------------------------------------------------ 594--------------------------------
Glyma05g33810|Glyma05g33810.1                   588 -------- 587------------------------------------------------------------ 587--------------------------------
Glyma08g05870|Glyma08g05870.3                   592 -------- 591------------------------------------------------------------ 591--------------------------------
PGSC0003DMG400005752|PGSC0003DMT40001475        591 -------- 590------------------------------------------------------------ 590--------------------------------
29651.t000012|29651.m000292                     590 -------- 589------------------------------------------------------------ 589--------------------------------
Potri.012G046900|Potri.012G046900.1             594 -------- 593------------------------------------------------------------ 593--------------------------------
Potri.015G038600|Potri.015G038600.1             593 -------- 592------------------------------------------------------------ 592--------------------------------
Eucgr.K02274|Eucgr.K02274.1                     591 -------- 590------------------------------------------------------------ 590--------------------------------
GSVIVG01008433001|GSVIVT01008433001             591 -------- 590------------------------------------------------------------ 590--------------------------------

Esi_0082_0071                                   358 -------------------------- 357------------------------------------------------------------ 357------------- 3
tr|D8TMG3|D8TMG3_VOLCA                           309 ----------------------- 308------------------------------------------------------------ 308-------------- 308
g11560|g11560.t1                                481 ---------------------------- 480------------------------------------------------------------ 480-------------
GRMZM2G159542|GRMZM2G159542_T01                  615 ---------------------------- 614------------------------------------------------------------ 614-------------
LOC_Os02g51810|LOC_Os02g51810.1                 614 ---------------------------- 613------------------------------------------------------------ 613-------------
Bra009383|Bra009383                             824 FFLWDFIDVMCTEFVEEKRDLIKSILKD 851RRLSDLPRIRQKTLIIWGEEDQIFPLELGYRLKRYIGENAEMVVIKKAGHAVNLEKSKEF 911LKHLKSFLIDSL*
Carubv10000509m.g|Carubv10000509m               605 ---------------------------- 604------------------------------------------------------------ 604-------------
AT5G09420                                       604 ---------------------------- 603------------------------------------------------------------ 603-------------
Glyma05g24400|Glyma05g24400.1                   604 ---------------------------- 603------------------------------------------------------------ 603-------------
Glyma08g19070|Glyma08g19070.1                   599 ---------------------------- 598------------------------------------------------------------ 598-------------
Glyma15g05920|Glyma15g05920.1                   599 ---------------------------- 598------------------------------------------------------------ 598-------------
Cucsa.217970|Cucsa.217970.1                     607 ---------------------------- 606------------------------------------------------------------ 606-------------
29806.t000047|29806.m000976                     608 ---------------------------- 607------------------------------------------------------------ 607-------------
Potri.001G205300|Potri.001G205300.1             600 ---------------------------- 599------------------------------------------------------------ 599-------------
Eucgr.I02661|Eucgr.I02661.1                     609 ---------------------------- 608------------------------------------------------------------ 608-------------
GSVIVG01038788001|GSVIVT01038788001             608 ---------------------------- 607------------------------------------------------------------ 607-------------
Phpat.019G042800|Phpat.019G042800.1             600 ---------------------------- 599------------------------------------------------------------ 599-------------
Phpat.021G056500|Phpat.021G056500.1             593 ---------------------------- 592------------------------------------------------------------ 592-------------
LOC_Os03g50010|LOC_Os03g50010.1                 587 ------------------------- 586------------------------------------------------------------ 586------------- 58
Bra018737|Bra018737                             602 ---------------------------- 601------------------------------------------------------------ 601-------------
Bra001692|Bra001692                             592 ---------------------------- 591------------------------------------------------------------ 591------------- 59
Carubv10013209m.g|Carubv10013209m               630 ---------------------------- 629------------------------------------------------------------ 629-------------
Medtr8g107280|Medtr8g107280.1                   595 ---------------------------- 594------------------------------------------------------------ 594-------------
Glyma05g33810|Glyma05g33810.1                   588 ------------------------- 587------------------------------------------------------------ 587------------- 58
Glyma08g05870|Glyma08g05870.3                   592 ------------------------- 591------------------------------------------------------------ 591------------- 59
PGSC0003DMG400005752|PGSC0003DMT40001475        591 ------------------------- 590------------------------------------------------------------ 590------------- 59
29651.t000012|29651.m000292                     590 ------------------------- 589------------------------------------------------------------ 589------------- 58
Potri.012G046900|Potri.012G046900.1             594 ------------------------- 593------------------------------------------------------------ 593------------- 59
Potri.015G038600|Potri.015G038600.1             593 ------------------------- 592------------------------------------------------------------ 592------------- 59
Eucgr.K02274|Eucgr.K02274.1                     591 ------------------------- 590------------------------------------------------------------ 590------------- 59
GSVIVG01008433001|GSVIVT01008433001             591 ------------------------- 590------------------------------------------------------------ 590------------- 59

Esi_0082_0071                                   358 57
tr|D8TMG3|D8TMG3_VOLCA
g11560|g11560.t1                                481 480
GRMZM2G159542|GRMZM2G159542_T01                  615 614
LOC_Os02g51810|LOC_Os02g51810.1                 614 613
Bra009383|Bra009383                             924 923
Carubv10000509m.g|Carubv10000509m               605 604
AT5G09420                                       604 603
Glyma05g24400|Glyma05g24400.1                   604 603
Glyma08g19070|Glyma08g19070.1                   599 598
Glyma15g05920|Glyma15g05920.1                   599 598
Cucsa.217970|Cucsa.217970.1                     607 606
29806.t000047|29806.m000976                     608 607
Potri.001G205300|Potri.001G205300.1             600 599
Eucgr.I02661|Eucgr.I02661.1                     609 608
GSVIVG01038788001|GSVIVT01038788001             608 607
Phpat.019G042800|Phpat.019G042800.1             600 599
Phpat.021G056500|Phpat.021G056500.1             593 592
LOC_Os03g50010|LOC_Os03g50010.1                 587 6
Bra018737|Bra018737                             602 601
Bra001692|Bra001692                             592 1
Carubv10013209m.g|Carubv10013209m               630 629
Medtr8g107280|Medtr8g107280.1                   595 594
Glyma05g33810|Glyma05g33810.1                   588 7
Glyma08g05870|Glyma08g05870.3                   592 1
PGSC0003DMG400005752|PGSC0003DMT40001475        591 0
29651.t000012|29651.m000292                     590 9
Potri.012G046900|Potri.012G046900.1             594 3
Potri.015G038600|Potri.015G038600.1             593 2
Eucgr.K02274|Eucgr.K02274.1                     591 0
GSVIVG01008433001|GSVIVT01008433001             591 0
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