

[illegible]

BraA01g003170.3C
 BraA01g034300.1

10 20 30 40 50 60 70 80 90 100 110 120 130 129
 1 MGCQCSCDSEHQFLGKDGAGPFPQVTQNHRRGATTADNGGIGGGVADGGGGGGG--PSPSEFSPDLKAATNPFSSDNIVSESGEKAPFLVYKGRLNRRHRAVKKFTKMAWPDFHQFAYGFYV----VLKV
 1 MGCQCSCDSEHQFLGKDGAGPFPQVTQNHRRGATTADNGGIGGGVADGGGGGGG--PSPSEFSPDLKAATNPFSSDNIVSESGEKAPFLVYKGRLNRRHRAVKKFTKMAWPDFHQFEEAWGVGKFRHNRLL
 132 131

140 150 160 170 180 190 200 210 220 230 240 250 260
 130 ETFLSVSG--VIVIKWETFLNAYFYFLFTGTENGQITLWAMRLRVGYTIAEALDYCSTEGRPLVHDLNAYRVLFDGDDGPRLCFGLMKNKSRDGGKSYSTNLAYTFPEYLRNGRVTFESVYTSFGTVLLDLLSG
 132 ANLIGYCGDGERLLAEFMPNDTLAKHLFWENQITLWAMRLRVGYTIAEALDYCSTEGRPLVHDLNAYRVLFDGDDGPRLCFGLMKNKSRDGGKSYSTNLAYTFPEYLRNGRVTFESVYTSFGTVLLDLLSG
 264 263

260 270 280 290 300 310 320 330 340 350 360 370 380 390
 261 KNIIPFSHALDMLRGKKNILLMDSHLEGKFSTEATVYVVELASQCLOYPEPRRPNTKDLVATLAPLOTKSDVPYSVMGLIKHNEAPSTFQRPRLSPGLFEACSRMDLTAHQILVMTHYRDDEGTNLSQFEWTE
 265 KNIIPFSHALDMLRGKKNILLMDSHLEGKFSTEATVYVVELASQCLOYPEPRRPNTKDLVATLAPLOTKSDVPYSVMGLIKHNEAPSTFQRPRLSPGLFEACSRMDLTAHQILVMTHYRDDEGTNLSQFEWTE
 393 392

400 410 420 430 440 450 460 470 480 490 500 510
 394 QMKMDLDAKRRGDDAFREKDFKTAIDCYSGFDVGTMTSPSTVFGRRSLCYLLCDGPDAAALRMDAGACVYDPWFATFYMQSVLAKLNNNTAADMLNEASGLEEKRRGGGK
 398 QMKMDLDAKRRGDDAFREKDFKTAIDCYSGFDVGTMTSPSTVFGRRSLCYLLCDGPDAAALRMDAGACVYDPWFATFYMQSVLAKLNNNTAADMLNEASGLEEKRRGGGK
 511 507

[illegible]

BrsA02g23730.3C1-081
 BrsA02g23600.1-081
 1 M T K F F V F A F G Y K T I E T F D E E D A P G K C A N T L T A V A A T K T G F L I L F G G A T A I E G G S V S F P G I L A G V T N S V H S Y G V L T R K W T A L P A G E F S P A A H A A A A V M V F G G D I Q A G H S T D E L Y L T N D K Y K W H V V G Q E G P G F R Y G H M L V S G R Y L V T Y G N D K R A I
 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
 BrsA02g23730.3C1-081
 BrsA02g23600.1-081
 119 S S A W A L T A G T K Y A M R L N F Q D G F S A R M Y A S G A R S D S M F L C G O R D T L G V P G D A Y G L L M H R N G W E N T L A P G V A P S P R Y Q H A A V F G A R L V S G G V L R G S R V I D A E A C V A L D T A G V H D I N Q G V T S A R G S K V G M D Q F S F E L M R C H R A A S V G I R I Y V H G D R G D L D F I
 190 200 210 220 230 240 250 260 270 280 290 300 310 320 330 340 350 360 370 380 390 400
 BrsA02g23730.3C1-081
 BrsA02g23600.1-081
 351 V A E N T F Q S D I S S L S A S D R T Q S S D T P R F S Y A A R F P G S E F A S E M S L E N S L E K L T E A S A A Q V A S S V M A A Q L S G S A S I G E F S A S D S S T V T I T O F T E G D V N L F R A V V A K E T Y G S G M V R L S D G F O N E S R M V F M N S D V F Q T K F T R S G P Q L N K V I S A L I
 351 360 370 380 390 400 410 420 430 440 450 460 470 480 490 500 510 520 530 540 550 560 570
 BrsA02g23730.3C1-081
 BrsA02g23600.1-081
 535 R P N N K F P N R K F L L O G Y E V G E L C A Y A G I F M H E T V I Q L K A F I K V G D L H G G D L M R F E Y G F F S T A G D V T I D L F O G Y V D R S H E T I T L L A I E Y F E N L I R G H A E A I N A L F G L E R G E N D G I N A W T F N O L F Y L P A L L E N K I C H M G I G R S I S S V
 535 540 550 560 570 580 590 600 610 620 630 640 650 660 670 680 690 700 710 720 730 740 750
 BrsA02g23730.3C1-081
 BrsA02g23600.1-081
 707 S E I K E F P T A S G S L L I N D L W S D T F E N D S I G I R P A G F O L V T F P O R T E F T K K N K L L I R A H C W M D F E R F A G O L I T F A T N Y G C O T A N N A G A L V V R G L V K F I L H F P F I L S F S N S F E S G D A W M L K E L Y K I C A G A K Y E T A Y S T R E T T G L I
 707 710 720 730 740 750 760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 910 920

BraA03g10270.3C
 BraA03g15800.1

1 MSCTPSPRSFNAIRILLARILLRSVQVGLNSVCTCTDTRILLSSQSPGPMHMDTYGILHSRLPIYSYSTPIGRILLASVAKVVFVLEFLRNLLPSPSSSTVAFVELALLRLSGPPLPSVGSFEGNTAFGISL 136
 1 -----MAAGGGGGGGSSGRTP-----TWKRENN-----KRR-----ERNRR-----AITAKIYSQ-----42

BraA03g10270.3C
 BraA03g15800.1

130 PIRGGGNYKLLKHCDNNEVLKALCLEAGWIVEDDGTTRYKDGSKPIASDMLGTPPTFTSTNSSIQASPOSSAFSPAPSYHGVSFSSSPSPSRDGNPSYLLPLHNIASSIPANLPLRTSNAPVTPPLSPSTSR 276
 43 -LRGGGNYKLLKHCDNNEVLKALCLEAGWIVEDDGTTRYKDGSKPIASDMLGTPPTFTSTNSSIQASPOSSAFSPAPSYHGVSFSSSPSPSRDGNPSYLLPLHNIASSIPANLPLRTSNAPVTPPLSPSTSR 179

BraA03g10270.3C
 BraA03g15800.1

277 GSKKLLMTQQLPRHLLFASPSPTTAAAGHOTPTTPECDREEESSFEDESGRWINFGSTAPSSPTNLVQGTSMVIDMKRSDGMSGWNNNGSEFFENGTKPWGEWIEHIEVAVEDLELTIGOTNRC- 408
 281 GSKKLLMTQQLPRHLLFASPSPTTAAAGHOTPTTPECDREEESSFEDESGRWINFGSTAPSSPTNLVQGTSMVIDMKRSDGMSGWNNNGSEFFENGTKPWGEWIEHIEVAVEDLELTIGOTNRC- 310

Bra009g13180.3C1-153
 Bra009g170200.1A-277

1 M T S G T R T P T W K E R E N N K R R E R R R A I A K I F A G R I H N G K L K H C N D N E V L K A L C N E S G M T V E D D G T T R Q C G P F D R M E L N R G S T A S F C S S Y P S P P R G S Y N P S P S S S F P S P T I F G D A N S L I P W L K N L S S S P S K L F 31
 150 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 312

Bra009g13180.3C1-153
 Bra009g170200.1A-277

32 P R G D V T P S G W L S G M T F S G P S S F T L S V S R N K F P Q E A F K M G D C N S P A I A A G V D N S O V F M A G M V A E A F A G S N A I G M K P K W E E I N G E C V S D E L T L G N S R T N 153
 160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 310 312

Fig. S7 Alignment of BR signaling pathway proteins between MM and Chiifu.