PHRA GENE06425 WC-1	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	10 20 30 40 50 60 70 80 90 100 110 120 130 140 150
	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	160 170 180 190 200 210 220 230 240 250 260 270 280 290 300 AEVLPACESDTIMANSAWEVNTGITSNLSYSDSAAKSYVYPIDOOOCHDAPSSSSSFSDSSHSSSFSDSFEDEIENSCSFETHESEPNAQS
	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	310 320 330 340 350 360 370 380 390 400 410 420 430 440 450 ALSVHINSCLINF_UNRLTPHOLM2 CALMACSSSLNAPSPLGLP VYSRSGFDLLSVLAFV2ARPDPKIALGFVDFSSSEVVILVRRYDNPIIVCSRSFCRLTGYEEHEVICKNCRFLCSPNCVOPKGEYRRFTSNE MCSSSLNAPSPLGLP VYSRSGFDLLSVLAFV2ARPDPKIALGFVDFSSSEVVILVRRYDNPIIVCSRSFCRLTGYEEHEVICKNCRFLCSPNCVOPKGEYRRFTSNE VSQDAASTPATTF SPSLSATTOT TRIG PPPPFS/TINAFTPAPFTSTPSGCCASQTKS TYSKSGFDL LSVLAFV2ARR TYSK TVTLND PIIV SDKTNLTGY TCGNCK0CKRFLCSPNCVOPKGEYRRFTSNE VSQDAASTPATTF SPSLSATTOT TRIG PPPPPFS/TINAFTPAPFTSTPSGCCASQTKS TYSKSGFDL LSVLAFV2ASR TVTLND PIIV SDKTNLTGY TCGNCK0CL TCGNCK0CL TYRE TVTLND PIIV SDKTNLTGY TCGNCK0CL TCGNCK0CL <td< th=""></td<>
	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	460 470 480 490 500 510 520 530 540 550 560 570 580 590 600 AVSYLKKHLVADKECCTSIINYRKSGLAFINLVTVIPIKGGDISSPHEDDKVIYHVGFCVDLTEQPNAILEKLKDGSYIANFAANNPLTINPPSISFCGGGSLGSCAMESIMSRDREMCSISAFEMTSEFFAMIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFINLVTVIPIKGGDISSPHEDDKVIYHVGFCVDLTEQPNAILEKLKDGSYIANFAANNPLTINPPSISFCGGGSLGSCAMESIMSRDREMCSISAFEMTSEFFAMIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFINLVTVIPIKGGDISSPHEDDKVIYHVGFCVDLTEQPNAILEKLKDGSYIANFAANNPLTINPPSISFCGGGSLGSCAMESIMSRDREMCSISAFEMTSEFFAMIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFINLVTVIPIKGGDISSPHEDDKVIYHVGFCVDLTEQPNAILEKLKDGSYIANFAANNPLTINPPSISFCGGGSLGSCAMESIMSRDREMCSISAFEMTSEFFAMIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFINLVTVIPIKGGDISSPHEDDKVIYHVGFCVDLTEQPNAILEKLKDGSYIANFAANNPLTINPPSISFCGGGSLGSCAMESIMSRDREMCSISAFEMTSEFFAMIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFINLVTVIPIKGGDISSPHEDDKVIYHVGFCVDLTEQPNAILEKLKDGSYIANFAANNPLTINPPSISFCGGGSLGSCAMESIMSRDREMCSISAFEMTSEFFAMIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFINLTYPT SLINYRK-GGRSLAFFANIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFFANIEDPLEMSNHPISMCAN SLINYRK-GGRSLAFFANIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFFANIEDPLEMSNHPISMCAN SLINYRK-GGRSLAFFANIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFFANIEDPLEMSNHPISMCAN SLINYRK-GGRSLAFFANIEDPLEMSNHPISMCAN AVSYLKKHLVADKECCTSIINYRKSGLAFFANIEDPLEMSHFANIEDPLEMSNHPISMCAN <
	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	610 620 630 640 650 660 670 680 690 700 710 720 730 740 750 ADSLESSVISSNIGSINGUNSULVNCSFCNHPLSLLLEVAPDEIEVVSLKGTELVCGSVRFVLGYEPEELVGKALSDICHFALVCPLTRELKESSATGSTAPGSGTSPDGELALTSRCSHEVKFFAVNLLFFARTKSDCVVVVECR ADSLESSVISSNIGSINGUNSULVNCSFCNHPLSLLLLEVAPDEIEVVSLKGTELVCGSVRFVLGYEPEELVGKALSDICHFALVCPLTRELKESSATGSTAPGSGTSPDGELALTSRCSHEVKFPAVNLLFFARTKSDCVVVVECR ADSLESSVISSNIGSINGUNSULVNCSFCNHPLSLLLLEVAPDEIEVVSLKGTELVGPSVRFVLGYEPEELVGKALSDICHFALVCPLTRELKESSATGSTAPGSGTSPDGELALTSRCSHEVKPFAVNLLFFARTKSDCVVVVECR ADSLESSVISSNIGSINGUNSULVNCSFCNHPLSLLLLEVAPDEIEVVSLKGTELVGPSVRFVLGYEPEELVGKALSDICHFALVCPLTRELKESSATGSTAPGSGTSPDGELALTSRCSHEVKPFAVNLLFFARTKSDCVVVVECR
	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	760 770 780 790 800 810 820 830 840 850 860 870 880 890 900 GRLEVEPGKGR&AIMLSGFAKEMSMLLWSAIASAGGISHPQ1VAKSLSGEDGKTRLVTVEVSTEHWGTITRTGSLLIVSKCVKDILCWDETELMGKCVWSYLLDEFARRVGKELANIGCAMGTMEAPGSLP RKIFCFMTRCDG GRLEVEPGKGR&AIMLSGFAKEMSMLLWSAIASAGGISHPQ1VAKSLSGEDGKTRLVTVEVSTEHWGTITRTGSLLIVSKCVKDILCWDETELMGKCVWSYLLDEFARRVGKELANIGCAMGTMEAPGSLP RKIFCFMTRCDG GLEVEPGKGR&AIMLSGFAKEMSMLLWSAIASAGGISHPQ1VAKSLSGEDGKTRLVTVEVSTEHWGTITRTGSLLIVSKCVKDILCWDETELMGKCVWSYLLDEFARRVGKELANIGCAMGTMEAPGSLP
	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	910 920 930 940 950 960 970 980 990 1000 1010 1020 1030 1040 1050 \$2AEVELULYPSAIDSSILHSSCAISEAPTIYOIRLYDEATSSTGIRSSEAATMHPLR ENVEKILEISRESSWOYELOCMRYMNERLREEIMSLEGDE
	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	1060 1070 1080 1099 1100 1120 1130 1140 1150 1160 1170 1180 1190 1200
	PHRA-BAF56991 GENE06425 WC1-ESA41977 Clustal Consensus	1210 1220 1230 1240 1250 PPPTSNVSST1AISMEMPEMENPEMENPEMENPEMENENGENGT PPPTSNVSST1AISMEMPEMENPEMENENGENGENGENGENGENGENGENGENGENGENGENGEN

Supplementary Fig. S2. Multiple sequence alignment among *WC-1* (GenBank no. ESA41977), *PHRA* (GenBank no. BAF56991), and GENE06425. Multiple sequence alignment was performed by CLUSTALW.