

PP2CA **MAG**ICCGVVGETEPAAPVDSTSRASLRRLDLLPSIKIVADSAVAPPLENCRKRQKRETVVLSTLPGNLDDSNVRSNKKARSAVTNSNSVTEAE**ESFFSDV**----- 102
 HA11 MAEICYENETMMIETTATVVKKATTTTTRRRERSSSSQAARRRMEIRRFPVSGEQEPVFDGDLQRRRRRESTVAAST---STVPYETAKEVVVLC**ESLSSTVVALP**-----D 105
 HA12 MADI**CY**EDETSAC**ES**RPLWSSRKRWRIGVQFRMSPS**EM**NP**TA**STTE**EE**DK**SE**GIYKRNKQ**EE**YDFMNCASSSPSQSSPE**EE**SV**SL**EDSDV**S**ISD**GN**SSVNDVA**IP**SKKT**VKE** 114
 HA13 MAEICYEVVTDAC**PS**SV**VE**STPAHSRRRPRFQ**TV**MHEDWEKNCRRSKQ**EAL**ATRYSS**IP**RS**RE**DFSD**Q**NV**DVSS**----- 75

PP2CA ---PKIGTTSVCGRRRDMEDAVS**I**HPS**F**LQRNSE---NH**HF**YGVFDGHGCSHVAEK**CR**ERLHDIVKKEVEVMASDE---WTET**M**VKS**FQ**MD**KE**VSQRECNLVVNGATRS**MKN** 206
 HA11 PEAY**PKY**GVASVCGRRRDMEDAV**V**HP**FS**RHQ**TE**YSSTGFHYCGVYDGHGCSHVA**MK**CRERLHEL**V**REEFEADA---D---WEKS**M**ARS**FTR**MD**MEV**-----VALNADG-AA 206
 HA12 TDLR**PRY**GVASVCGRRRDMEDAV**L**HP**SF**VRKQ**TE**FSRTRWHYFGVYDGHGCSHVA**AR**CKERLHEL**V**Q**EAL**SD**KKE**---W**K**K**M**ERS**FTR**MD**KEV**-----VR**W**GET**VMSA** 218
 HA13 ---**PRY**GVSSVCGRRRDMEDAV**I**HP**S**SPKNS---EFP**Q**HYFGVYDGHGCSHVA**AR**CKERLHKL**V**Q**EAL**SSD**ME**EE**W**KT**M**ERS**FTR**MD**KEV**-----V**S**W**G**DS**VVTA** 175

PP2CA **SCR**CELQ**SP**CD**A**VGSTAVSVV**T**PEKIIVS**NC**GDSRAVLCR**NG**V**AI**PLSV**D**HK**PD**R**PE**LD**R**I**Q**Q**AG**GRV**IY**W**D**G**AR**VL**G**VL**A**MSRA**IG**D**N**Y**L**K**P**Y**V**I**P**D**PE**VT**V**T**D**R**T**D**E**D**E** 317
 HA11 **KCR**CELQ**RP**CD**A**VGSTAVSV**L**TPEKIIV**AN**CDSRAVLCR**NG**K**AI**LS**D**HK**PD**R**PE**LD**R**I**Q**Q**AG**GRV**IY**W**D**G**PR**VL**G**VL**A**MSRA**IG**D**N**Y**L**K**P**Y**V**I**S**R**PE**VT**V**T**D**R**AN**G**DD** 320
 HA12 **NCR**CELQ**TP**CD**A**VGSTAVSV**I**TPEKIIV**AN**CDSRAVLCR**NG**K**V**PL**SD**HK**PD**R**PE**LD**R**I**Q**Q**AG**GRV**IY**W**D**G**AR**VL**G**VL**A**MSRA**IG**D**N**Y**L**K**P**Y**T**S**EP**VT**V**T**D**R**T**E**D**E 331
 HA13 **NCK**CDLQ**TP**AC**D**VGSTAVSV**I**TPDKIV**AN**CDSRAVLCR**NG**K**V**PL**SD**HK**PD**R**PE**LD**R**I**EG**AGGRV**IY**W**DC**PRVL**G**VL**A**MSRA**IG**D**N**Y**L**K**P**Y**V**S**CE**PE**V**T**I**T**D**R**R**D**DD** 288

PP2CA **CL**ILASDGLWDVV**NET**AC**S**Y**ARM**CL---**RG**AGAG**DDS**-----DA**HN**AC**S**DA**AL**L**L**T**K**L**AL**AR**Q**SSD**N**SV**V**V**VD**L**R**K**RR**NN**Q**ASS 396
 HA11 **FL**ILASDGLWDVV**NET**AC**S**V**VR**MC**L**---**RG**K**V**NG**Q**V**SS**PER-EM**T**GV**G**AG**N**V**V**V**G**---G**D**L**PD**K**ACE**EA**S**L**L**L**T**R**L**AL**AR**Q**SS**D**N**SV**V**V**VD**L**R**R**DT** 411
 HA12 **FL**ILATDGLWDVV**NE**ACT**M**VR**MC**L**NR**K**SG**R**GR**R**RG**ET**QT**PG**RR**SE**EE**G**KE**EE**EV**GS**R**K**NG**K**R**GE**IT**D**K**ACT**EAS**V**L**L**T**K**L**AL**AK**H**SS**D**N**SV**V**V**VD**L**R**R**RR**R**H**VA 441
 HA13 **CL**ILASDGLWDVV**NET**AC**S**Y**ARM**CL---**RG**G**RR**Q**D**NE**DP**-----A**I**S**D**ACT**EAS**V**L**L**T**K**L**AL**AR**N**SS**D**N**SV**V**V**VD**L**R** 382

Supplementary information Figure S2 Sequence comparison of PP2CA with HAI1/2/3. The PP2CA-unique motif, shaded in orange, is conserved in HAI1/2/3.