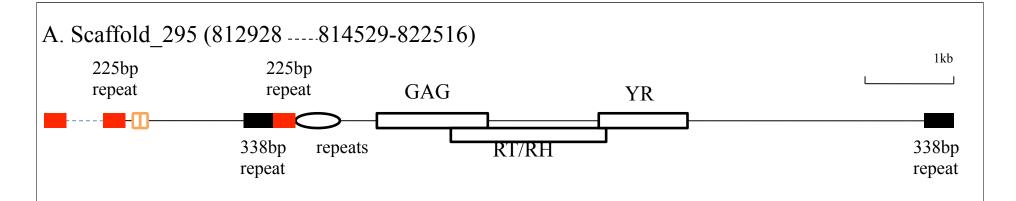
Additional file 9. Genomic organization of the tyrosine recombinase domain-encoding retroelement found adjacent to the VCBP2/5 gene cluster. A. The gene consists of three main open reading frames, GAG-like, RT/RH –like, and tyrosine recombinase –like, on alternate reading frames. The gene is flanked by direct repeats (rectangles); duplication of direct repeats (red) are found upstream. B. Amino acid sequence homology with a Ngaro retrotransposon from *Lytechinus variegates* (green sea urchin); separated by domain.



B. Comparison of amino acid sequence with green sea urchin (Lytechinus variegates) Ngaro1

	GAG		RT/RH		YR
295_GAG Lv_GAG_DAA01766. 1	MPPTRRSKRNRKPKNANPDDPTEKEPPYDPNKDPKDPPPNVSE		LAFPLOIR———PRPPRPAPRPAGLTHTRPGPR——POPKMSPTGTVFASTGPMTSV CWWPLMVRGSATIYPMPLAISSTEGSTARENLFPSEERDPEFMAHPAEACALPLIEASAC :** :* * * : : : : : : : : : : : : : :	295_YR Lv_YR_DAA01768. 3	PWOTKHNGHSLPPTDOPIPSGLPTYGPSSDNYTATPATEHLNRTINDLLSSSLAPSTLRA —CTISISDAEVP—CVSTGGRPGGRGGSSPSLEELAIERSRLLMASRAARTHTT ::: :* :* :* :.* * ::*: *. ** :* ** :* ** :*
295_GAG Lv_GAG_DAA01766. 1	QVSALTSVTERLAKH IESSGSHSEOPDPSLPPAVLDPRHSKDTLVDR I I GEENDLFVVKT SOSOVVDVDEKSGRPRSKVSDKMAELDLDLVGREGOAPVGRS I AWHE I VAGESDTGSSGO * : . * * : : . * : : * . * . *	295_RT/RH Lv_YR_DAA01767. 2	SKPSAPTITHAISATVESTKLTNAPKKPPRTLPTPVDVRPLQYY EAKLASMSTSVPAARROVMGLSSVAKGGPVPVPLAVNRSTASAVSSIAPTPIKLARLVPM * . : * . : * : * * * * * * * * * *	295_YR Lv_YR_DAA01768. 3	YROAWQLFRKFSLOVHGKDLAIPPISTDLLTGFVGYLYNEGLAAATISSKLSAIGFVHKM YSIALGAYVKF-CKVYGYDPQLPPN-VEWVAQFISYLSFMGYAGSTIGTYISGLAFYMSS * * : ** : *: * * :** : :** : : : : : :
295_GAG Lv_GAG_DAA01766. 1	TDNINRSKDKDK ITSETTNKT IPPAP TTTTSHLOTG (HVPLDSGVPT AQPAVSVPARSAGVAEDLGLDLVEVGVERSEPQAPRLSAVLGAPEPFSSACDPLGVEVAI :: *** ** **. *.	295_RT/RH Lv_YR_DAA01767. 2	LRGYP-ORDKOYLLDGFVFGFPLEYFGPRSRPL IFPPOPNDSHFPI IHDKLOGE IEAGRV LATYPNOEHAOCLYNGFKFGFSLHFEGDRVPLVVKNLKSAFEHMDALKKKLRDE IDLGRI * ** * . * * :** **** ** : :	295_YR Lv_YR_DAA01768. 3	LGIPDPSQAFVIOKLLHAARKS-ORPDGRRPITPSILKTLIDALTSALPSFYDHOLYKTL SGLKDVTKSFVITRLIEGCRRSTLRRDARHPITLSVLNRMLAYLRHVCGSHYDVLMYSAA *: *:::*** :*:*: * * *.*:*** *:*::: * . *.** :*::: * * * ** :*::*** :*:*:
295_GAG Lv_GAG_DAA01766. 1	HIKDKIWSNKYVDFKOLLPN-LCTDPLYTVSLTDSLTPTLTIANRPSPQESRRL SLKEKIWASEYIDLGVLLKHNNARDEFGALSVGDTTLSLCQSGSGLGLQLQPQSKAKKIM :*:***::*: **: **: :::::::::::::::::::	295_RT/RH Lv_YR_DAA01767. 2	AGPFSSPPYNNLFLSPLYAVPKKVPGKFRLIHDLSHPKGLSVNDGIPPELSSVTYSSIDT VGPFVVPPFENNRGSPVGLVPKKAPGEFRNIGHLSAPRGNSVNDGIPEGGCTVTYSSFDS .*** **:*: **: ****.**:*:* *: ********	295_YR Lv_YR_DAA01768. 3	FLFTFYSLARISEVTATSSSNHTLHLSDVTVOTT—POPSLSVTFRSYKHSSPGLPPTI FSVAFYGLLRVSELTVESRHRCESILOHTDVRVTGDAPHRRVELFLRKSKTDORGNGCTI * .:** * *:**:* * * *
295_GAG Lv_GAG_DAA01766. 1	TIDOWTSAFLVFOFIYMOOHPOHOPHLVSYLHLIRDLASRRA—OWGKYDEOFRHRETS SVEOWTSVFLVFASIYAEKHIERSRELMKYMDLIRHAARAFAGYGWRDYDTOFRSKOARL :::****, **** *** ::* ::, .*:, ***, ** * * .** ****::*	295_RT/RH Lv_YR_DAA01767. 2	AIGYIKSLGPGCYLAKTDIESAFRLIPIHPHDYHLLGFYWNGNFYFDKCLPMGSSMSCAI AVDIVTOLGRGALMGKTDIKSAFRLLPVHPKDFELLGMYIDGRYYFDRCLPMGCAVSCST *: ** * ***********************	295_YR Lv_YR_DAA01768. 3	SIASOPGSSYCPVDNFTKYLSLRGKCAGCLFLYRSGRPVSSDYFSHVLRTCAOHANLDPR SIP-ELGTVSCPVMAVIRYLEIRPKNGGAFFCSYGALPLTRREFGNMIKRCLTYGDMPAA **. : *: *** .:**.:* .: *: *: *: *: ::: * .::: *
295_GAG Lv_GAG_DAA01766. 1	PDTPWNTPHLOLYVDALTGIPPPDOAAAPOTS — APTRRADTHOTRPOTRPKDV PGRSWASVDAEL WLMLVASNGPRORHNLPHAPRHOFYRGEYGARKSFPFGGKGPGANGTP *. * : : *:: * :: *:: : *:: :: :: :: :: ::	295_RT/RH Lv_YR_DAA01767. 2	FESFSSALEWIARTKLHIRFPTHILDDFLFAA-KTYRQCYHDLNTFSNMCKDVGVPLAEG FECFSTFLEFCARKVAKSONIVHYLDDFFFAGGPASEDCRRAMHCFEAICERFGVPIARE **. **: **: **: * *******	295_YR Lv_YR_DAA01768. 3	AYTAHSFRIGAATYAAOTGASDSOLRALGRWISSGAFKKYIRS
295_GAG Lv_GAG_DAA01766. 1	PHGYCFRFHRPDDOCFK-ALCPYNHTCYICNSGKHKAYOCTOKTAANATNSRRR SRGVCFAFNR-GKOMRGKACIYEHKCSRCQATGHGAKOCSOGRAGSSPAGSK- .:* ** *: * :*: * *:*. * :: * * **: * :	295_RT/RH Lv_YR_DAA01767. 2	KTYTPDTTMSFLGIELDTVVMEARLPLDKLTKCODOLSSFLGLSSATLKOIOSLVGLLNH KTEGPTTOLSYLGLVIDSVSOOVRVPEDKIEKLVGKLNWAVOKOKISLRDIOSIVGSLNF ** * * ::***: ** : , *: * : * : * : * :		
		295_RT/RH Lv_YR_DAA01767. 2	VCOVVPPGRAFLRRLIDLTKSQSPPNCNIPIPOHVRRDLHMWYTFLKDFNGRSFFLDERF VCKAIAPGRAFMRRLIDLTKSVKRPFHMVRLTRGAKADLRVWLEFLAHFNGQVFFRAPGW **: ****** ********* * : : : : **:* ** *** *** : *** :		
		295_RT/RH Lv_YR_DAA01767. 2	ISNSTLHLYTDAAASLQYGAVCGTAWFYGSWPTSLCS—RNITILEFYPIVVALHVWGOP FGSEEIOFFTDAAAGIGFGIFFGGRWAQSRWPADFQADRRSIAFLELFPIWYGLEIWGME ::::*******::** * * **::: *,*::**::**::**		
		295_RT/RH Lv_YR_DAA01767. 2	WANHSILLHTDNESLVHIINROTSKNPLIMPLVRRFVLICLRRNILYRATHVPGKONIMA LKDKNILFNCONGAVVAVLNKGSALCPDIMVLVRKVVIICLSNNIVLRARHVHGCONGIA ::.**:: **::*::*::*:: *****************		
		295_RT/RH Lv_YR_DAA01767. 2	DTLSRLQINRFOADFOHMDPHPTTIPPHLOPNTLIGP—— DALSRFOMPRFHALAPGAAREGVEVPVRLWKSWLSREVDC *:***:*: **: *		