

JVMP17-1	-----WNKQK I TWR-----VEN-----FGNDGLSPERVKMFENALGKWSG	36
JVMP17-2	-----WNKRNL TWA-----IAN-----SNNDN I KDEDVKET I LNALKKWSA	36
A8QL59	SN I TVVRMR I FE I LNYVNL YYK I LNIHVVL I GLEVWSEDEK I L I NGSSSEL TVRSFAAWRH	60
ABN72537	RNKP I I KRRVYELVN I LNT I LRRLNFH I AL I GLE I WSKRDK I NVQSDVKATLKSFGKWRE	60
Q90Z13	RNL TLRTRMFDVN I VNQ I LQR I NI HVAL I G I E I WSKEDK I I VQSVPDVTLKLFATWRE	60
Q8AW15	RNL TTVRTRMYD I VNV I NV I YQRMN I HVALVGLE I WSNKDKF I LRSAADVTLKLFATWRE	60
Q9DGB9	RNL TAVRTRMYD I VNV I TP I YHRMN I HVALVGLE I WSNTDK I I VQSSADVTLDLFAKWRA	60
042138	DNLDK I KTR I FE I VNTMNEF I PLN I RVAL I CLE I WSDKDKFNMTSAANVTS I SFRNWRA	60
ABG26979	RKL TEVKTWVYE I VNTLNE I YRYLY I RVALVGLE I WSNGLSNVTL SADDTLDSFGEWRK	60
Q9w6M5	GDLDK I KTKMYE AANNMNEYRYMFFRVVMVGL I I WTEEDK I TVKPDVDYTLNFAFEWRK	60
C9E1S0	GDLDK I KTRMYE I VNTVNE I YRYMY I HVALVGLE I WSNEDK I TVKPEAGYTLNFAFEWRK	60
C9E1R8	GDLDK I KTRMYE I VNTVNE I YRYMY I HVALVGLE I WSNEDK I TVKPEAGYTLNFAFEWRK	60
093523.2	GDLDK I KARMYELAN I VNE I LRYLYMHAALVGLE I WSN GDK I TVKPDVDYTLNSFAFEWRK	60
Q8QG88	GDLDK I KARMYELAN I VNE I LRYLYMHAALVGLE I WSN GDK I TVKPDVDYTLNSFAFEWRK	60

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JVMP17-1	VTN I EFEE I KTGEPI WFRFVRGAHGDPP-----FRTPGSTVLAHAFYPFDSRTPLSGD	91
JVMP17-2	I TE I DFTEDK-NNPD I WIRFTRKYHNDASP-----FDGRGE-LAHAFYPAN--DELSGD	87
A8QL59	SDL-----LKHKRNDAQLL TG I HFDKRV---LG I AF I GGMCNNFTSVG	101
ABN72537	KKL-----LPRKRNDAQLL TR I DFNGNT---VGLAALGSLCSVKYSVA	101
Q90Z13	SVL-----LKRKNHDNAHL TG I NFNGPT---AGLAYLGG I CKPMYSAG	101
Q8AW15	TDL-----LKRKSHDNAQLL TG I NFNGPT---AGLGYLGG I CNPMYSAG	101
Q9DGB9	TDL-----LSRKSHDNAQLL TG I NFNGPT---AGLGYLGG I CNTMYSAG	101
042138	TDL-----LKRKSHDNAQLL TV I DFDGPT---IGKAYMASMCDPKRSVG	101
ABG26979	RDL-----LRRKSHGNAQLL TA I DFNGTT---IGLAHVASMCELRKSTG	101
Q9w6M5	TYL-----LAEEKHDNAQL I TG I DFRGSI ---IGYAY I GSMCHPKRSVG	101
C9E1S0	TDL-----LTRKKHDNAQLL TA I DLD-RV---IGLAYVGSMPCHPKRSTG	100
C9E1R8	TDL-----LTRKKHDNAQLL TA I DLD-RV---IGLAYVGSMPCHPKRSTG	100
093523.2	TDL-----LTRKKHDNAQLL TA I DFNGPT---IGYAY I GSMCHPKRSVA	101
Q8QG88	TDL-----LTRKKHDNAQLL TA I DFNGPT---IGYAY I GSMCHPKRSVA	101

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JVMP17-1	VHFNDDKVFT I ESPSGKDLLW I SVHELGHS I GLDHS DVKS-----S I MYPYRYGYPGL	144
JVMP17-2	VHYDDDEVFS I KSSQGRDLLW I TVHEVGHS LGLDHS GTQG-----SVMNAFYRETKGL	140
A8QL59	-----A I QDNS I HAVL I AATMTHELGHNLGMNHD TDSCT-CNTGPC I MKAALNFKPPY	153
ABN72537	-----V I QDYSKRTSMVASTMAHEMGHNLG I NHDRASCTSCGSNKC I MATKRT-KPAS	153
Q90Z13	-----I VQDHNK I HHLVA I AMAHEMGHNLGMDHDKDTCT-CRAKACVMAGT LSCDASY	153
Q8AW15	-----I VQDHNK I HHLVA I AMAHEMGHNLG I DHDKDTCT-CGAKSCVMAGT LSC EASY	153
Q9DGB9	-----I VQDHSK I HHLVA I AMAHEMGHNLGMDHDKDTCT-CGTRPCVMAGAL SCEASF	153
042138	-----I I QDHST I NLMMAVTMAHEMGHNLGMDHDEKYCT-CGAKSCVMAKALSRQPSK	153
ABG26979	-----I VQDHSP I NLLVAVTMAHEMGHNLG I RHDKKYCT-CGGYSC I MSAVLSHQASK	153
Q9w6M5	-----I I QDYSP I NLVAV I MAHEMGHNLG I HHDDGYCY-CGGYPC I MGPS I SPEPSK	153
C9E1S0	-----I I QDYSE I NLVVAV I MAHEMGHNLG I NHDSGYCS-CGDYAC I MRPE I SPEPST	152
C9E1R8	-----I I QDYSE I NLVVAV I MAHEMGHNLG I NHDSGYCS-CGDYAC I MRPE I SPEPST	152
093523.2	-----I VEDYSP I NLVVAV I MAHEMGHNLG I HHDTDFCS-CGDYPC I MGPT I SNEPSK	153
Q8QG88	-----I VEDYSP I NLVVAV I MAHEMGHNLG I HHDTDFCS-CGDYPC I MGPT I SNEPSK	153

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JVMP17-1	DFELTPDDV-----RGAQAL-----YG-	161
JVMP17-2	DFNLHADD I -----KGAQSL-----YG-	157
A8QL59	EFSSCSYWFQNY I MTKSAQC I LNDPLTTD I VPTA I CGN	192
ABN72537	RFSSCSVREHQRYLLRDRPQC I LNKPL I TD I VAPA I CGN	192
Q90Z13	LFSDCSRQEHRFL I KNMPQC I LKKPLKTDVVSPPVCGN	192
Q8AW15	LFSDCSRKEHQAF I LKMPQC I LKKPLKTDVVSPPVCGN	192
Q9DGB9	LFSDCSQKDHREF I LKNMPQC I LKKPLKTDVVSPAVCGN	192
042138	LFSNCSQEDYRKYL I KRRPKC I LNEPNGTD I VSPPVCGN	192
ABG26979	YFSNCSYNQYWN I NFYKQC I LNEPLRTD I VSPPVCGN	192
Q9w6M5	FFSNCSY I QCWDF I MNHNPEC I DNEPLGTD I I SPPLCGN	192

C9E1S0	FFSNCSYFECWDFIMNHNPECILNEPLGTDIISPPVCGN	191
C9E1R8	FFSNCSYFECWDFIMNHNPECILNEPLGTDIISPPVCGN	191
O93523.2	FFSNCSYIQCWDFIMKENPQCILNEPLGTDIVSPPVCGN	192
Q8QG88	FFSNCSYIQCWDFIMKENPQCILNEPLGTDIVSPPVCGN	192
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Supplementary Figure S1. Alignment analysis of JVMP17-1 and 17-2 M domains compared to that of other SVMs M domain. A8QL59 : *Naja atra*, ABN72537 : *Bungarus multicinctus*, Q90ZI3 : *Protobothrops flavoviridis*, Q8AWI5 : *Gloydius halys*, Q9DGB9 : *Crotalus atrox*, O42138 : *Agkistrodon contortrix laticinctus*, ABG26979 : *Sistrurus catenatus edwardsi*, Q9w6M5 : *Deinagkistrodon acutus*, C9E1S0 : *Agkistrodon piscivorus leucostoma*, C9E1R8 : *Crotalus viridis*, O93523.2 : *Bothrops jararaca*, Q8QG88 : *Bothrops insularis*. Identical, similar, and weakly similar amino acids are indicated by asterisks, colons and dots, respectively.

Supplementary Table S1. Comparison of *N. nomurai* JVMP 17-1 and JVMP 17-2 deduced amino acid sequence with a BLAST analysis

	Scientific name	Description	identity (%)	Genbank No.
JVMP17-1	<i>Hydra vulgaris</i>	MMP-24	42.18	XP_012564333.2
	<i>Acropora digitifera</i>	MMP-24-like	40.16	XP_015771447.1
	<i>Orbicella faveolata</i>	MMP-24-like	39.84	XP_020618480.1
	<i>Nematostella vectensis</i>	MMP-17	37.38	EDO48606.1
	<i>Apis cerana</i>	MMP-14 isoform	37.27	XP_016905171.1
	<i>Exaiptasia diaphana</i>	MMP-17-like	36.33	XP_020891959.1
	<i>Bufo gargarizans</i>	MMP-17-like	35.49	XP_044130425.1
JVMP17-2	<i>Hydra vulgaris</i>	MMP-24	37.72	XP_012564333.2
	<i>Acropora millepora</i>	MMP-24-like	37.25	XP_029201938.2
	<i>Orbicella faveolata</i>	MMP-24-like	39.58	XP_020618480.1
	<i>Xenopus laevis</i>	MMP-17	35.98	XP_041433135.1