

Supplementary file 1

A developmental shift in venom toxin expression underpins a major prey switch in Australian brown snakes

Jory van Thiel, Cara F. Smith, Taline D. Kazandjian, Rohit N. Patel, India C. Cullen, Stephanie French, Rachael Da Silva, Laura-Oana Albulescu, Nathan Dunstan, Jeroen Kool, Michael K. Richardson, Stephen P. Mackessy, Nicholas R. Casewell, R. Manjunatha Kini, Anthony J. Saviola, Timothy N.W. Jackson¹, and Cassandra M. Modahl

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- Fig. S25. Ancestral state estimation of adult body size in the monophyletic *Oxyuranus-Pseudonaja* clade reveals a significant reduction in the ringed brown snake (*Pseudonaja modesta*).

Table S1-S5

- Table S1. Presence and absence of venom gene families in our Australian brown snake species (*Pseudonaja* spp.).
- Table S2. Overview of differential venom gene expression analysis between hatchling and adults venom glands of Eastern brown snake (*Pseudonaja textilis*) identified by DESeq2 algorithm.
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- Table S5. Overview of *venom and tissue* samples included in this study.
- Table S6. Overview of snout–vent length data for ancestral state estimation analysis.

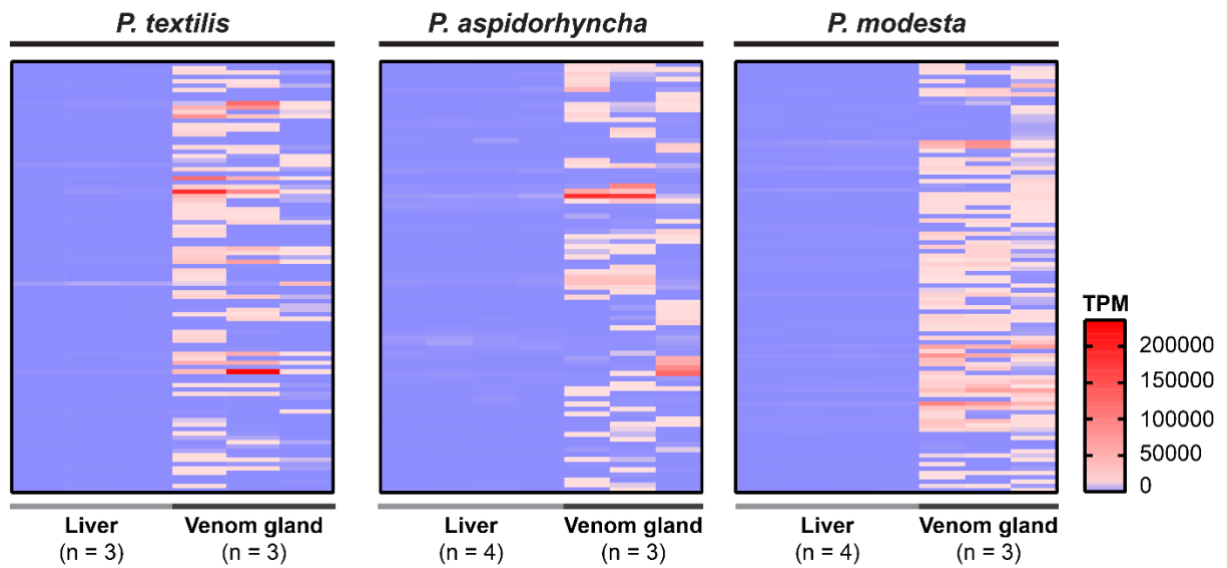


Fig. S1. Comparative expression levels of identified venom toxin transcripts in liver and venom gland tissues. Abbreviation: TPM, transcripts per million.

	10	20	30	40	50	60	70	80
REF.LFX1.Q1L659	SNVFLKSKVA	NRFLQRTKRA	NSLFEEFKSG	NIERECIEER	CSKEEAREAF	EDDEKTETFW	NVYVDGDQCS	SNPCHYGGTC
REF.LFX2.Q1L658			V					R.I.
REF.VFX.Q56VR3			V		V			R.I.
PTE.VFX.ID04			V		V			R..
PTE.VFX.ID05			V					R.I.
PTE.VFX.ID07			V		V			R..
PTE.VFX.ID06			V		V			R..
PAS.VFX.ID03			V					R.I.
PAS.VFX.ID02			V					R.I.
PAS.VFX.ID01			V					R.I.
PTE.VFX.ID03			V					R.I.
PTE.VFX.ID01			V					R.I.
PTE.VFX.ID02			V					R.I.
QMI.Q58L95			R		V			R..
OSC.Q58L96			Y.R		V			R..
CNI.B5G6G5		S	I.A	K	V	N		R..
PPO.Q58L93	E	S	RP	K	I	K.N.A		R..
NSC.Q58L94		S	IRP	K	V	N		R..
HST.P83370		S	IRP	K	V	N		H..
NSC.P82807		S	IRP	K	V	N		R..
TCA.P81428		S	IRP	K	V	N		R..
DVE.A6MFK7	N		G.IYPA	F.V		A	T	L
DVE.A6MFK8	N		I.IRP	V.K		V	Q.N.A	T.L

	90	100	110	120	130	140	150	160
REF.LFX1.Q1L659	KDGIGSYTCT	CLSGYEGKNC	EYVLYKSCR	DNGDCWHFCK	PVQNGIQCS	AESYLLGEDG	HSCVAGGDFS	CGRNIKTRNK
REF.LFX2.Q1L658			R	N	H.D	G	N	
REF.VFX.Q56VR3			R	N	S.D	G	N	
PTE.VFX.ID04			R	N	S.D	G	N	
PTE.VFX.ID05			R	N	S.D	G	N	
PTE.VFX.ID07			R	N	S.D	G	N	
PTE.VFX.ID06			R	N	S.D	G	N	
PAS.VFX.ID03			R	N	S.D	G	N	
PAS.VFX.ID02			R	N	S.D	G	N	
PAS.VFX.ID01			R	N	S.N	G	N	I
PTE.VFX.ID03			R	N	S.D	G	N	
PTE.VFX.ID01			R	N	S.D	G	N	
PTE.VFX.ID02			R	N	S.D	G	N	
QMI.Q58L95		F	R	N	D	G	N	
OSC.Q58L96			R	N	D	G	N	
CNI.B5G6G5		PN	K.FE	F.N	S.E	R.D	E	A
PPO.Q58L93		PN	HL.F	F.F	DT	R.D	E	A
NSC.Q58L94		PN	K.F	F.N	R.SET	V	E	A
HST.P83370		PN	K.F	F.N	R.SET	R.V	E	A
NSC.P82807		PN	K.Q	F.N	R.SET	R.V	E	A
TCA.P81428		PN	K.Q	F.N	R.SET	R.V	E	A
DVE.A6MFK7		A	HD.L	N	DT	G.R.DN	F.I.E	S
DVE.A6MFK8		P	H.VV	L.F	N	DT	G.R.V	F.I.E

	170	180	190	200	210	220	230	240
REF.LFX1.Q1L659	REANLPDFQT	DFSDDYDEID	ENNFEVETPTN	FSGLVLTQVS	QNATLLKKSD	NPSPDIRVVN	GTDCKLGECP	WQALLLNDEG
REF.LFX2.Q1L658						I	M	A.VDEKE
REF.VFX.Q56VR3	S				H	I	M	A.VD.KK
PTE.VFX.ID04	S					I	M	T.VDEKE
PTE.VFX.ID05	S					I	M	T.VDEKE
PTE.VFX.ID07	S					I	M	T.VDEKE
PTE.VFX.ID06	S					I	M	T.VDEKE
PAS.VFX.ID03	S.L				P.I	I	M	A.VD.KK
PAS.VFX.ID02	S				P.I	I	M	A.VD.KK
PAS.VFX.ID01	S				P.I	I	M	A.VD.KK
PTE.VFX.ID03	S				TP.I	I	M	A.VD.KK
PTE.VFX.ID01	S				P.I	I	M	A.VD.KK
PTE.VFX.ID02	S				P.I	I	M	A.VD.KK
QMI.Q58L95	S					I	M	V.VDEKE
OSC.Q58L96	S				I	I	M	V.VDEKE
CNI.B5G6G5	S				K.I	II	M	V.DEDD
PPO.Q58L93	S					II	M	V.DK
NSC.Q58L94	S				K.V	I	M	V.I.EK
HST.P83370	S				K	I	M.S	V.I.EK
NSC.P82807	S				K	I	M	V.I.EK
TCA.P81428	S				K	I	M	V.I.EK
DVE.A6MFK7	S	A	LI		S	N	I	V.IDEK
DVE.A6MFK8	S.H	A	L		S	I	S	V.IDEH

	250	260	270	280	290	300	310	320	
REF.LFX1.Q1L659	DGFCGGTILS	PIYVLTAHC	INQTKYITVV	VGEIDISSKK	TGRLHSVDKI	YVHQKFVPA-	-----	--TYDYDIAI	
REF.LFX2.Q1L658	GV.....		.E.ET.S..	K.RIE	..P.L....	...K....PQ	KAY----	KFD LAA.....	
REF.VFX.Q56VR3	GV.....		.E.ET.S..	R.RAE	..P.L....V	...K....PK	KSQEFYEKFD	LVS.....	
PTE.VFX.ID04	GV.....		F.E.ET.S..	K.RVE	..P.L....	...K....PK	KSQEFYEKFD	LVS.....	
PTE.VFX.ID05	GV.....		F.E.ET.S..	K.RVE	..P.L....	...K....PK	RGYKFYEKFD	LVS.....	
PTE.VFX.ID07	GV.....		F.E.ET.S..	K.RVE	..P.L....-	-----PK	RGYKFYEKFD	LVS.....	
PTE.VFX.ID06	GV.....		F.E.ET.S..	K.RVE	..P.L....	...K....PK	RGYKFYEKFD	LVS.....	
PAS.VFX.ID03	GV.....		.E.ET.S..	R.RAE	..P.L....V	...K....PK	KSQEFYEKFD	LVS.....	
PAS.VFX.ID02	GV.....		.E.ET.S..	R.RAE	..P.L....V	...K....XK	KSQEFYEKFD	LVS.....	
PAS.VFX.ID01	GV.....		.E.ET.S..	R.RAE	..P.L....V	...K....PK	KSQEFYEKFD	LVS.....	
PTE.VFX.ID03	GV.....		.E.ET.S..	R.RAE	..P.L....V	...K....PK	KSQEFYEKFD	LVS.....	
PTE.VFX.ID01	GV.....		.E.ET.S..	R.RAE	..P.L....V	...K....PK	KSQEFYEKFD	LVS.....	
PTE.VFX.ID02	GV.....		.E.ET.S..	R.RAE	..P.L....V	...K....PK	KSQEFYEKFD	LVS.....	
QMI.Q58L95	GV.....		..EK.S..	K.RVE	..H.L....	...K....PK	KGYKFYEKFD	LVS.....	
OSC.Q58L96	.A.....		M.S..	N.R.N	P..L....	...PK	KGYEFYEKFD	LVS.....	
CNI.B5G6G5	.V.....	S.H.....	N.S.I	R.E	..I..LP..V	...T...PS	YLY-GHQNV	RK.....	
PPO.Q58L93	.V.....		.T.S.H.S.	R.E	..RH.L...A	...T...L-	-----	--	
NSC.Q58L94	EV.....	.H.....	SVS.I	R.E	..R..L....	...K....P-	--NSYYQNID	RFA.....	
HST.P83370	EV.....	.H.....	SVS.I	R.E	..R..L....	...T...PN	YYY-GHQNV	RVA.....	
NSC.P82807	EV.....	.H.....	SVS.I	R.E	..R..L....	...T...PN	YYY-VHQNV	RVA.....	
TCA.P81428	EV.....	.H.....	SVS.I	R.E	..R..L....	...T...PN	YYY-VHQNV	RVA.....	
DVE.A6MFK7	TA.G.....	.YF.....	..K..S.A.	..QV...R.E	..R..L....V	..T.P.Y.HV-	-----	--.N.....	
DVE.A6MFK8	KA.G.....	.YF.....	L...S.A.	..QV...R.E	..RH.LH...A	..M.S.Y.R.-	-----	--.H.....	
	330	340	350	360	370	380	390	400	
REF.LFX1.Q1L659	IQLKT-PIQF	SENVVPACLP	TADFANQVLM	KQNFQIVSGF	GRTRERGKTS	NTLKVVTLPY	VDRHTCMLSS	NFPITQNMFC	
REF.LFX2.Q1L658	..M.-..			..D.....	..IF.K.PK.	K...LKV..	V..	ET...P...	
REF.VFX.Q56VR3	..M.S...			..D.....	..GIF...PN.	K...LKV..		PT...	
PTE.VFX.ID04	S...			..D.....	..HIF...PK.	K...LKV..			
PTE.VFX.ID05	S...			..D.....	..HIF...PK.	K...LKV..			
PTE.VFX.ID07	S...			..D.....	..HIF...PK.	K...LKV..			
PTE.VFX.ID06	S...			..D.....	..HIF...PK.	K...LKV..			
PAS.VFX.ID03	S...			..D.....	..GIF...PN.	K...LKV..	V..	ET...PT...	
PAS.VFX.ID02	S...			..D.....	..GIF...PN.	K...LKV..	V..	ET...PT...	
PAS.VFX.ID01	S...			..D.....	..GIF...PN.	K...LKV..	V..	ET...PT...	
PTE.VFX.ID03	..M.S...			..D.....	..GIF...PN.	K...LKV..		PT...	
PTE.VFX.ID01	..M.S...			..D.....	..GIF...PN.	K...LKV..		PT...	
PTE.VFX.ID02	..M.S...			..D.....	..GIF...PN.	K...LKV..		PT...	
QMI.Q58L95	..M.-..			..D...I...	..IF.K.PK.	K...LKV..	V..	ES...PT...	
OSC.Q58L96	L.M.-..			..D.....	..IF.K.PQ.	K...LKV..		ES...PT...	
CNI.B5G6G5	..RM.-..		..VK...	..D.....	QY..Q..	I.V..	..R.....	D...P...	
PPO.Q58L93	-..			..D...I...	..H..SG.Q.	I..		D.R...P...	
NSC.Q58L94	..RM.-..		..KE...	..DS...	QSI.Y..	..I...I.V.		..R.....	
HST.P83370	..RM.-..		E...	..DS...	I.FKEP.	I.V.		D.R.....	
NSC.P82807	..RM.-..		E...	..DS...	I.FKEP.	I.V.		D.R.....	
TCA.P81428	..RM.-..		E...	..DS...	IQFKQP.	I.V.		D.R.....	
DVE.A6MFK7	-..		H.....	..D.....	..IE.K.P.	..I...MV..	I..T	KI...R...	
DVE.A6MFK8	LR.R.-..		DE...	..D.....	..LH...S.	DI...IRV..	...Y...PS..		
	410	420	430	440	450	460	470		
REF.LFX1.Q1L659	AGYDTLPQDA	CQGDSSGGPHI	TAYRDTHFIT	GIVSWGEGCA	QTGKYGVYTK	VSKFILWIKR	IIRQKQPSTE	SSTGRL	Liver
REF.LFX2.Q1L658	R..	T..V	S....	RN...I...	L...P....	..M...L...			Liver
REF.VFX.Q56VR3				RK.R..I..	L...P....	..M...L...			Venom
PTE.VFX.ID04					P....	..M...L...		95.75%	
PTE.VFX.ID05					P....	..M...L...		94.85%	
PTE.VFX.ID07					P....	..M...L...		93.96%	
PTE.VFX.ID06					P....	..M...L...		94.85%	
PAS.VFX.ID03	R..			RK.R..I..	L...P....	..M...L...		97.76%	
PAS.VFX.ID02	R..			RK.R..I..	L...P....	..M...L...		97.76%	
PAS.VFX.ID01	R..			RK.R..I..	L...P....	..M...L...		97.54%	
PTE.VFX.ID03				RK.R..I..	L...P....	..M...L...		98.88%	
PTE.VFX.ID01	X...			RK.R..I..	L...P....	..M...L...		98.88%	
PTE.VFX.ID02				RK.R..I..	L...P....	..M...L...		99.11%	
QMI.Q58L95	R..			KK...I...		..M...L...		79.79%	
OSC.Q58L96	R..					..M...L...		81.05%	
CNI.B5G6G5		G....	..N.....	KK.....	..N..P...A	MSL-----	-----	74.68%	
PPO.Q58L93	R..		..I.....	KK.....	..N..P...A	VM.KH.....		79.87%	
NSC.Q58L94		G...V	..I.....	RK.....	..N..P...K	MSL-----	-----	74.58%	
HST.P83370		..E.....	..G.....	RK.....	..R..P...K	MSL-----	-----	74.58%	
NSC.P82807			..I.....	RK.....	..R..P...K	MSL-----	-----	75.11%	
TCA.P81428			..I.....	RK.....	..P...K	MSL-----	-----	75.11%	
DVE.A6MFK7	..GNQ.E..	..E.....	..K...L.	G	RD...I...	..N.LP...T	..M.R.....	77.71%	
DVE.A6MFK8	..GNQ...	G....	..I.....G	RK...I...	..N..P...T	..M.RN.....		75.54%	

Fig. S2. Venom factor X sequence alignment. Our de novo transcripts were aligned with reference sequences from *Pseudonaja textilis* and other Australian elapid snakes. In the sequence alignment, dots (.) indicate identical residues with the reference (UniProt ID: Q1L659), while dashes (-) represent gaps. The percentages reflect the similarity between our transcripts and the *P. textilis* venom isoform (UniProt ID: Q56VR3), which was used as the reference.

	10	20	30	40	50	60	70	80
REF.LFV.Q593B6	AQLREYHIAA	QLEDWDYNPQ	PEELSRLSES	DLTFKKIVYR	EYELDFKQEK	PRDELSGLLG	PTLRGEVGD	LIIFYKNFAT
REF.VFV.Q7SZN0					E	A	S	
PTE.VFV.ID01						A	S	
PTE.VFV.ID02						A	S	
PTE.VFV.ID03						A	S	
PTE.VFV.ID04						A	S	
PTE.VFV.ID05						A	S	
PAS.VFV.ID01			P	K		A	S	
PAS.VFV.ID02			P	K		A	S	
PAS.VFV.ID03			P	K		A	S	
PAS.VFV.ID04			P	K		A	S	
OMI.Q58L90	R			E				
OSC.Q58L91	RL						S	
OSC.AAY47065	R						S	

	90	100	110	120	130	140	150	160
REF.LFV.Q593B6	QPVSIHPQSA	VYNKWSEGSS	YSDGTSDEVER	LDDAVPEGQS	FKYVWNITAE	IGPKKADPPC	LTAYAYSHVN	MVRDFNSGLI
REF.VFV.Q7SZN0								
PTE.VFV.ID01								
PTE.VFV.ID02								
PTE.VFV.ID03								
PTE.VFV.ID04								
PTE.VFV.ID05								
PAS.VFV.ID01		M						
PAS.VFV.ID02		M						
PAS.VFV.ID03								
PAS.VFV.ID04								
OMI.Q58L90								
OSC.Q58L91								
OSC.AAY47065								

	170	180	190	200	210	220	230	240
REF.LFV.Q593B6	GALLICKEGS	LNANGSQKFF	NREYVIMFSV	FDESKNWKYR	PSLQYTINGF	ANGTLPDVQA	CAYDHISWHL	IGMSSSPEIF
REF.VFV.Q7SZN0								
PTE.VFV.ID01							T	
PTE.VFV.ID02							T	
PTE.VFV.ID03	K	A					T	
PTE.VFV.ID04	K	A					T	
PTE.VFV.ID05	K	A					T	
PAS.VFV.ID01	K	A						
PAS.VFV.ID02	K	A						
PAS.VFV.ID03	K	A						
PAS.VFV.ID04	K	A						
OMI.Q58L90		A						
OSC.Q58L91		D.A						
OSC.AAY47065		D.A						

	250	260	270	280	290	300	310	320
REF.LFV.Q593B6	SVHFNQGITLE	QNHVKVSTIN	LVGGASVTAN	MSVSRGKWL	ISSLVAKHLQ	AGMYGYLNK	DCGNPDTLTR	KLSFRELRRRI
REF.VFV.Q7SZN0			D					MK
PTE.VFV.ID01								MK
PTE.VFV.ID02								MK
PTE.VFV.ID03								LKQW.K
PTE.VFV.ID04								LKQW.K
PTE.VFV.ID05								LKQW.K
PAS.VFV.ID01								LKQW.K
PAS.VFV.ID02								LKQW.K
PAS.VFV.ID03								LKQW.K
PAS.VFV.ID04								LKQW.K
OMI.Q58L90							H.N	
OSC.Q58L91								R
OSC.AAY47065								W

	330	340	350	360	370	380	390	400
REF.LFV.Q593B6	MNWEYFIAAE	EITWDYAPEI	PSSVDRRYKA	QYLDNFSNFI	GKKYKKAVER	QYKDSNFTKP	TYAIWPKERG	ILGPFVIRAKV
REF.VFV.Q7SZN0	K					E.G		K
PTE.VFV.ID01	K					E.G	T	K
PTE.VFV.ID02	K					E.G	T	K
PTE.VFV.ID03	K		S			E.G	T	K
PTE.VFV.ID04	K		S			E.G	T	K
PTE.VFV.ID05	K		S			E.G	T	K
PAS.VFV.ID01	K		S			E.G		K
PAS.VFV.ID02	K		S			E.G		K
PAS.VFV.ID03	K		S			E.G		K
PAS.VFV.ID04	K		S			E.G		K
OMI.Q58L90						E.G		K
OSC.Q58L91	K					E		K
OSC.AAY47065	K			-		E		K

	810	820	830	840	850	860	870	880
REF.LFV.Q593B6	AAEEVLNDYS	PIG-----	-----	-----	-----KSQ	VRsRAAKITTF	KKaIFRSYLD	DTFQTPSTGG
REF.VFV.Q7SZN0		-----	-----	-----	-----			
PTE.VFV.ID01		-----	-----	-----	-----			
PTE.VFV.ID02		KSQKLFW	KIEESELESR	KRIEKDKYIY	SEENIKK...			
PTE.VFV.ID03		KSQKLFW	KIEESELESR	KRIEKDKYIY	SEENIKK...			
PTE.VFV.ID04		-----	-----	-----	-----			
PTE.VFV.ID05		-----	-----	-----	-----			
PAS.VFV.ID01		-----	-----	-----	-----			
PAS.VFV.ID02		KSQKLFW	KIEESELESR	KRIEKDKYIY	SEENIKK...			
PAS.VFV.ID03		-----	-----	-----	-----			
PAS.VFV.ID04		KSQKLFW	KIEESELESR	KRIEKDKYIY	SEENIKK...			
OMI.Q58L90		-----	-----	-----	-----	LP		
OSC.Q58L91		-----	-----	-----	-----	LP		
OSC.AAY47065		-----	-----	-----	-----	LP		

	890	900	910	920	930	940	950	960
REF.LFV.Q593B6	EYEKHLGILG	PIIRAEDVDV	IEVQFRNLAS	RPYSLHAHGL	LYEKSSEGRS	YDDKSPELFK	KDDAIMPNGT	YTYVWQVPPR
REF.VFV.Q7SZN0			I..K...					
PTE.VFV.ID01			I..K...					
PTE.VFV.ID02			I..K...					
PTE.VFV.ID03			I..K...					
PTE.VFV.ID04			I..K...					
PTE.VFV.ID05			I..K...					
PAS.VFV.ID01			I..K...					
PAS.VFV.ID02			I..K...					
PAS.VFV.ID03			I..K...					
PAS.VFV.ID04			I..K...					
OMI.Q58L90					N			
OSC.Q58L91					N			
OSC.AAY47065					N			

	970	980	990	1000	1110	1120	1130	1140
REF.LFV.Q593B6	SGPTDNTEKC	KSWAYYSGVN	PEKDIHSGLI	GPILICQKGM	IDKYNRTIDI	REFVLFTFMVF	DEEKSWYFPK	SDKSTRAEKL
REF.VFV.Q7SZN0								CE...
PTE.VFV.ID01								CE...
PTE.VFV.ID02								CE...
PTE.VFV.ID03								CE...
PTE.VFV.ID04								CE...
PTE.VFV.ID05								CE...
PAS.VFV.ID01								CE...
PAS.VFV.ID02								CE...
PAS.VFV.ID03								CE...
PAS.VFV.ID04								CE...
OMI.Q58L90								CE...
OSC.Q58L91								CE...
OSC.AAY47065								CE...

	1150	1160	1170	1180	1190	1200	1210	1220
REF.LFV.Q593B6	IGVQ-SRHTF	PAINGIPYQL	OGLTMYKDN	VHWHLLNMGG	PKDIHVVNPH	QOTFTEEGRE	DNQLGVLPLL	PGTFASIKMK
REF.VFV.Q7SZN0	..-L...							
PTE.VFV.ID01	..-L...							
PTE.VFV.ID02	..-L...							
PTE.VFV.ID03	..-L...					Y		
PTE.VFV.ID04	..-L...					Y		
PTE.VFV.ID05	..-L...					Y		
PAS.VFV.ID01	..R-L...					Y		
PAS.VFV.ID02	..R-L...					Y		
PAS.VFV.ID03	..R-L...					Y		
PAS.VFV.ID04	..R-L...					Y		
OMI.Q58L90	..S.H...	..M...						
OSC.Q58L91	..-M...	..M...		V				
OSC.AAY47065	..-M...	..M...		V				

	1230	1240	1250	1260	1270	1280	1290	1300
REF.LFV.Q593B6	PSKIGTWLLE	TEVGENQERG	MQALFTVIDK	DKLEFMGLAS	GIIQDSQISA	SGHVGWYWEK	LARLNNTGKY	NAWSIIKKEH
REF.VFV.Q7SZN0								
PTE.VFV.ID01							AIF	
PTE.VFV.ID02							AIF	
PTE.VFV.ID03							AIF	
PTE.VFV.ID04							AIF	
PTE.VFV.ID05							AIF	
PAS.VFV.ID01							AIF	
PAS.VFV.ID02							AIF	
PAS.VFV.ID03							S.AIF	
PAS.VFV.ID04							S.AIF	
OMI.Q58L90						E	MF	
OSC.Q58L91							MF	
OSC.AAY47065							MF	

	1310	1320	1330	1340	1350	1360	1370	1380
REF.LFV.Q593B6	EHPWIQIDLQ	RQVVITGIQT	QGAMQLLKHL	YTVEYFFTYT	KDQGNWITFK	GRHSETQMHF	EGNSDGTTVK	ENHIDPPIIA
REF.VFV.Q7SZN0			..TV..Q.S	V..	E.....			
PTE.VFV.ID01			..TV...S	V..	E.....			
PTE.VFV.ID02			..TV...S	V..	E.....			
PTE.VFV.ID03			..TV...S	V..	E.....			
PTE.VFV.ID04			..TV...S	V..	E.....			
PTE.VFV.ID05			..TV...S	V..	E.....			
PAS.VFV.ID01			..TV...S	V..	E.....			
PAS.VFV.ID02			..TV...S	V..	E.....			
PAS.VFV.ID03			..TV...S	V..	E.....			
PAS.VFV.ID04			..TV...S	V..	E.....			
OMI.Q58L90			..TV...S	V..				
OSC.Q58L91			..TV...S	V..		...K...		
OSC.AAY47065			..TVH...S	V..		...K...		

	1390	1400	1410	1420	1430	1440	1450	1460
REF.LFV.Q593B6	RYIRLHPTKF	HNRPTFRIEL	LGCEVEGCSV	PLGMESGAIK	NSEITASSYK	KTWSSWEPS	LARLNKGR	NAWQPKVNNK
REF.VFV.Q7SZN0		Y.....					...E.G...	...E...
PTE.VFV.ID01		Y.....				...F.....	...E.G...	...E...
PTE.VFV.ID02		Y.....				...F.....	...E.G...	...E...
PTE.VFV.ID03		Y.....				...F.....	...E.G...	...E...
PTE.VFV.ID04		Y.....				...F.....	...E.G...	...E...
PTE.VFV.ID05		Y.....				...F.....	...E.G...	...E...
PAS.VFV.ID01		Y.....				...F.....	...E.G...	...E...
PAS.VFV.ID02		Y.....				...F.....	...E.G...	...E...
PAS.VFV.ID03		Y.....				...F.....	...E.G...	...E...
PAS.VFV.ID04		Y.....				...F.....	...E.G...	...E...
OMI.Q58L90		Y.T.....				...F.....	...E.G...	...E...
OSC.Q58L91		Y.T.....			D.....	...F.....		
OSC.AAY47065		Y.T.....			D.....	...F.....		

	1470	1480	1490	1500	1510	1520	1530	1540
REF.LFV.Q593B6	DQWLQIDLQH	LTKITSIITQ	GATSMTSMY	VKTFSIHYPD	DNSTWKPYLD	VRTSMEKVFT	GNNSDGHVK	HHFKPPILSR
REF.VFV.Q7SZN0								
PTE.VFV.ID01								
PTE.VFV.ID02								
PTE.VFV.ID03								
PTE.VFV.ID04								
PTE.VFV.ID05								
PAS.VFV.ID01					H.....			
PAS.VFV.ID02					H.....			
PAS.VFV.ID03								
PAS.VFV.ID04								
OMI.Q58L90			A.....					
OSC.Q58L91								N.....
OSC.AAY47065								N.....

	1550	1560	
REF.LFV.Q593B6	FIRIIPKTWN	QYIALRIELF	GCEVF
REF.VFV.Q7SZN0			Liver
PTE.VFV.ID01			99.23%
PTE.VFV.ID02			96.93%
PTE.VFV.ID03			96.17%
PTE.VFV.ID04			98.46%
PTE.VFV.ID05			98.46%
PAS.VFV.ID01			98.18%
PAS.VFV.ID02			95.90%
PAS.VFV.ID03			98.11%
PAS.VFV.ID04			95.83%
OMI.Q58L90			97.00%
OSC.Q58L91			96.15%
OSC.AAY47065			96.08%

Fig. S3. Venom factor V sequence alignment. Our de novo transcripts were aligned with reference sequences from Australian brown snakes (*Pseudonaja* species) and taipans (*Oxyuranus* species). In the sequence alignment, dots (.) indicate identical residues with the reference (UniProt ID: Q593B6), while dashes (-) represent gaps.

The percentages reflect the similarity between our transcripts and the *P. textilis* venom isoform (UniProt ID: Q7SZN0), which was used as the reference.

	10	20	30	40	50	60
REF. PLA2.Q9W7J4	SLDDFSNLIT	CANRGRSRL	DYAHYGCFCG	SGSGTTPVDD	LDRCCQVHDN	CFGDAEKLPA
PAF.UNW14929	..N.....	N.W		E	A...	
PAF.UNW14930	..N.....	N.W		E	A...	
PNU.UNW14933	..N..S...	N.W		E	E...	
PAS.PLA2.ID05	..N.....	N.W		E		
PTE.PLA2.ID07	..N.....	N.W		E	A...	
PTE.PLA2.ID08						
PMO.PLA2.ID01	D.I.....				Y.....	
PTE.PLA2.ID09						
REF. PLA2.Q9W7J3	..VE.RI..K	..HN..NV.	..D...Y..	K.....E	A..Y	.YD.....
PAS.PLA2.ID03	..VE.RI..K	..HN..NV.	..D...Y..	K.....E	A..Y	.YD.....
PAS.PLA2.ID04	..VE.RI..K	..HN..NV.	..D...Y..	K..R....E	A..Y	.YD.....
PTE.PLA2.ID06	..VE.RI..K	..HN..NV.	..D...Y..	K.....E	A..Y	.YD.....
PTE.PLA2.ID05	..VE.RI..K	..HN..NV.	..D...Y..	K.....E	A..Y	.YD.....
PTE.PLA2.ID04	..VE.RI..K	..HN..NV.	..D...Y..	K.....E	A..Y	.YD.....
PTE.PLA2.ID03	..VE.RI..K	..HN..NV.	..D...Y..	K.....E	A..Y	.YD.....
PAS.PLA2.ID02	..VE.RI..K	..HN..NV.	..D...Y..	K..R....E	A..Y	.YD.....
PAS.PLA2.ID01	..LQ.RI..K	..HN..DV.	..N...Y..	K.....E	A..Y	.YD.....
PMO.PLA2.ID02	..VE.RS..K	..HN..NVF	..VD...Y..	K.....E	A..Y	.YD.....
OSC.Q4VRI5	..LN.A...E	..H.T..A.	A..D...Y..	K..R...L.	H...D	.Y.E.....
OSC.AAZ22633	..LN.A...E	..H.T..A.	A..D...Y..	K..R...L.	D	.Y.E.....
OMI.AAZ22639	..L.A...E	..H.T..A.	A.V...Y..	K..R....E	D	.Y.E.....

	70	80	90	100	110	120
REF. PLA2.Q9W7J4	CNYLFSGPYW	NPYSYKNEG	EITCTDDNDE	CAAFICNCDR	TAAICFAGAT	YNDENFMVTI
PAF.UNW14929	..R.....			K.....		I..
PAF.UNW14930	..R.....			K.....	P	I..
PNU.UNW14933	..R.....	E...	K..	K.....		
PAS.PLA2.ID05			K..	K.....		I.T
PTE.PLA2.ID07	..R.....		V.....	K.....	P	I.T
PTE.PLA2.ID08						
PMO.PLA2.ID01	..Q..S...		K..	K.....	R..	K.....IST
PTE.PLA2.ID09			V.....			
REF. PLA2.Q9W7J3	..R.....		V.....	K.....	P	I..
PAS.PLA2.ID03	..R.....		V...K..	K.....	P	I.T
PAS.PLA2.ID04	..R.....		V...K..	K.....	P	I.T
PTE.PLA2.ID06	..R.....		V.....	K.....	P	I.T
PTE.PLA2.ID05	..R.....		V.....	K.....	P	I.T
PTE.PLA2.ID04			V.....	K.....	P	I..
PTE.PLA2.ID03						
PAS.PLA2.ID02	..R...A.Y	S.....	K.....K..	K.....	P	I.T
PAS.PLA2.ID01	..R...A.Y	S.....	K..	K.....	P	I.T
PMO.PLA2.ID02	..W...A.Y	S.....		Q.....	R.P	.DKD.WNINT
OSC.Q4VRI5	..M.S...F	S.....	KV.....	K.....		ISK
OSC.AAZ22633	..M.S...F	S.....	KV.....	K.....		ISK
OMI.AAZ22639	..M.S...F	S.....	KV.....	K.....		ISK

	70	80	90	100	110	120
REF. PLA2.Q9W7J4	KKKNICQ	Phospholipase A₂ 1				
PAF.UNW14929		93.70%				
PAF.UNW14930		92.91%				
PNU.UNW14933		92.13%				
PAS.PLA2.ID05		93.70%				
PTE.PLA2.ID07		91.34%				
PTE.PLA2.ID08		100.00%				
PMO.PLA2.ID01	..N....	89.76%				
PTE.PLA2.ID09		99.21%				
REF. PLA2.Q9W7J3		Phospholipase A₂ 2				
PAS.PLA2.ID03		98.43%				
PAS.PLA2.ID04		97.64%				
PTE.PLA2.ID06		99.21%				
PTE.PLA2.ID05		99.21%				
PTE.PLA2.ID04		99.21%				
PTE.PLA2.ID03		96.06%				
PAS.PLA2.ID02		93.70%				
PAS.PLA2.ID01		92.13%				
PMO.PLA2.ID02	ETD--	81.89%				
OSC.Q4VRI5	.RND...	76.38%				
OSC.AAZ22633	.RND...	77.17%				
OMI.AAZ22639	.RND...	77.17%				

Fig. S4. Group I phospholipase A₂ sequence alignment. Our *de novo* transcripts, which phylogenetically clustered with known procoagulant phospholipase A₂ (PLA₂) isoforms, were aligned with reference sequences from Australian brown snakes (*Pseudonaja* species) and taipans (*Oxyuranus* species). In the sequence alignment, dots (.) indicate identical residues with the reference (UniProt IDs: Q9W7J4), while dashes (-) represent gaps. The percentages indicate the similarity to either of the *P. textilis* procoagulant PLA₂ isoforms (UniProt IDs: Q9W7J4 and Q9W7J3).

	10	20	30	40	50	60		
REF.VTK2.Q90WA0	KDRPELCELP	PDTGPCRVRF	PSFYNPDEQ	KCLEFIYGGC	EGNANNFITK	EECESTCAA-	Textilinin 2	
PTE.KTSPI.ID08	...DF...	A.....	K	G	...K.N.L		86.44%	
PTE.KTSPI.ID05			K			RK	95.00%	
PTE.KTSPI.ID06							100.00%	
PTE.KTSPI.ID07	...K.....						98.31	
REF.VTK1.Q90WA1	...DF...	A.....	K				Textilinin 1	
OSC.Q6ITB7	...DF...	A.....G	K		...S.....		96.61%	
PAU.Q6ITB9	...DF...	A.....G	K		Q.....		96.61%	
OMI.Q6ITB5	...D.....	A.....G	K				96.61%	
OMI.Q6ITB4	...DF...	A.....G	K				98.31%	
OSC.Q6ITB6	...DF...	A.....G	K				98.31%	
PNU.UNW14913	N...DF...	A.....K	K				96.61%	
PAS.KTSPI.ID03	...DF...	A.....				GK	96.67%	
PTE.KTSPI.ID11	...DF...	A.....	L.K				98.31%	
PTE.KTSPI.ID09	...DF...	A.....	K				100.00%	
PTE.KTSPI.ID10	...DF...	A.....	K				100.00%	
PAS.KTSPI.ID04	...DF...	A.....	K				100.00%	
PMO.KTSPI.ID07	...DF...	A.....	K				100.00%	
REF.VTK6.Q90W96	...KF...	A.I...DDFT	GA.H.S.R.H	E.I.....	K.....N.Q		Textilinin 6	
PTE.KTSPI.ID12	...KF...	A.I...DDFT	GA.H.S.R.H	E.I.....	K.....N.Q	A...	98.31%	
PTE.KTSPI.ID13	...NF...	A.M...DDFT	GA.H.S.R.H	E.I.....	G...K.N.L		91.53%	
PTE.KTSPI.ID14	...DF...	A.M...DDFT	GA.H.S.R.H	E.I.....	G...K.N.L		91.53%	
REF.VTK5.Q90W97	...KF...L	...S.EDFT	GA.H.STRDR	E.I.....	G.....		Textilinin 5	
REF.VTK7.Q90W96	...KF...L	...S.EDFT	GA.H.STRDR	E.I.....	G.....K.L		Textilinin 7	
PAS.KTSPI.ID01	...NF...	A.M...DDFT	GA.H.STRDR	E.I.....	G...K.N.L	A..P-	83.05%	
PMO.KTSPI.ID08	...NF...	A.M...DDFT	GA.H.STRDR	E.I.....	G...K.N.L	A..P-	83.05%	
PAS.KTSPI.ID02	...NF...	A.M...DDFT	GA.H.STRDR	E.I.....	G...K.N.Q	A..P-	81.36%	
PTE.KTSPI.ID15	...KF...L	...DDFT	GA.H.STRDR	E.I.....	K.....N.Q	A...	89.83%	
PTE.KTSPI.ID16	...KF...L	...DDFT	GA.H.STRDR	E.I.....	G...K.N.L	P-	91.53%	
PTE.KTSPI.ID17	...KF...L	...DDFT	GA.H.STRDR	E.I.....	G...K.N.L	RK	90.00%	
REF.VTK4.Q90W98	...H.KF...	A...S.KGNV	...R...A.HH	Q...K.....	G...K.I	...K.....	Textilinin 4	
PAS.KTSPI.ID06	...KF...	A...S.KGNV	...R...A.HH	Q...K.....	G...K.I	...K...GK	95.00%	
PAS.KTSPI.ID05	...F....	A...S.KGNV	...R...A.HH	Q...K.....	G...K.I	...K...GK	93.33%	
PTE.KTSPI.ID02	...F....	A...S.KGNV	...R...A.HH	Q...K.....	G...K.I	...K.....	96.61%	
PTE.KTSPI.ID01	...H.KF...	A...S.KGNV	...R...A.HH	Q...K.....	G...K.I	...K.....	100.00%	
PAS.KTSPI.ID07	...H.KF...	A...S.KGNV	...R...A.HH	Q...K.....	G...K.I	...K.....	100.00%	
PAS.KTSPI.ID08	...KF...	A...S.KGNV	...R...A.HH	Q...K.....	G...K.I	...K.....	98.31%	
REF.VTK3.Q90W99	...NF.K...	AE...R.NAKI	...R...RQH	Q.I...L...	G...K.I	K.....	Textilinin 3	
PTE.KTSPI.ID04	...NF.K...	AE...R.NAKI	...R...RQH	Q.I...L...	G...K.N.L		84.75%	
PMO.KTSPI.ID01	...NF...	AE...L.NGHI	TR...RQH	Q.IK.L...	G...K.I	G...K...I-	93.22%	
PTE.KTSPI.ID03	...NF.K...	AE...R.NAKI	...R...RQH	Q.I...L...	G...K.I	K.....	100.00%	
PAS.KTSPI.ID09	...NF.K...	AE...R.NAKI	...R...RQH	Q.I...L...	G...K.I	K...K...I-	96.61%	
PMO.KTSPI.ID02	...P.NF.K...	AE...R.NGHI	TR...RQH	Q.I...L...	G...K.I	K...K...I-	88.14%	
PAS.KTSPI.ID11	...P.NF.K...	AE...R.NGKI	TR...RQH	Q.I...L...	G...K.I	K...K...I-	91.53%	
PMO.KTSPI.ID04	...P.NF.K...	AE...R.NGKI	TR...RQH	Q.I...L...	G...K.I	K...K...I-	91.53%	
PMO.KTSPI.ID03	...P.NF.K...	AE...R.NGKI	TR...RQH	Q.I...L...	G...K.I	...K...I-	89.83%	
PMO.KTSPI.ID05	...P.NF.K...	AE...R.NGKI	TR...RQH	Q.I...L...	G...K.I	K...K...IGK	88.33%	
PAS.KTSPI.ID10	...P.NF.K...	AE...R.NGKI	TR...RQH	Q.I...L...	G...K.I	...K...GK	88.33%	
PMO.KTSPI.ID06	...P.NF.K...	AE...R.NGKI	TR...RQH	Q.I...L...	G...K.I	...K...IGK	86.67%	

Plasmin-inhibiting KTSPI

Non-plasmin-inhibiting KTSPI

Fig. S5. Kunitz type serine protease inhibitor sequence alignment. Our *de novo* transcripts were aligned with both plasmin-inhibiting Kunitz type serine protease inhibitor (KTSPI) isoforms and non-plasmin-inhibiting KTSPI isoforms. In the sequence alignment, dots (.) indicate identical residues with the reference (UniProt IDs: Q90WA0), while dashes (-) represent gaps. The plasmin-inhibiting isoforms (in the literature commonly referred to as “textilinin-1” or “textilinin-2”) are characterized by two key amino acids for plasmin inhibition and specificity, namely arginine, 17R; and valine, 18V (both highlighted in bold). The other *Pseudonaja textilis* KTSPI isoforms have shown to lack any plasmin-inhibition. The percentages indicate similarity to one

of the seven previously identified *Pseudonaja textilis* KTSP1 genes (UniProt IDs: Q90WA1, Q90WA0, Q90W99, Q90W98, Q90W97, Q90W96 & B5L5Q1).

Factor X

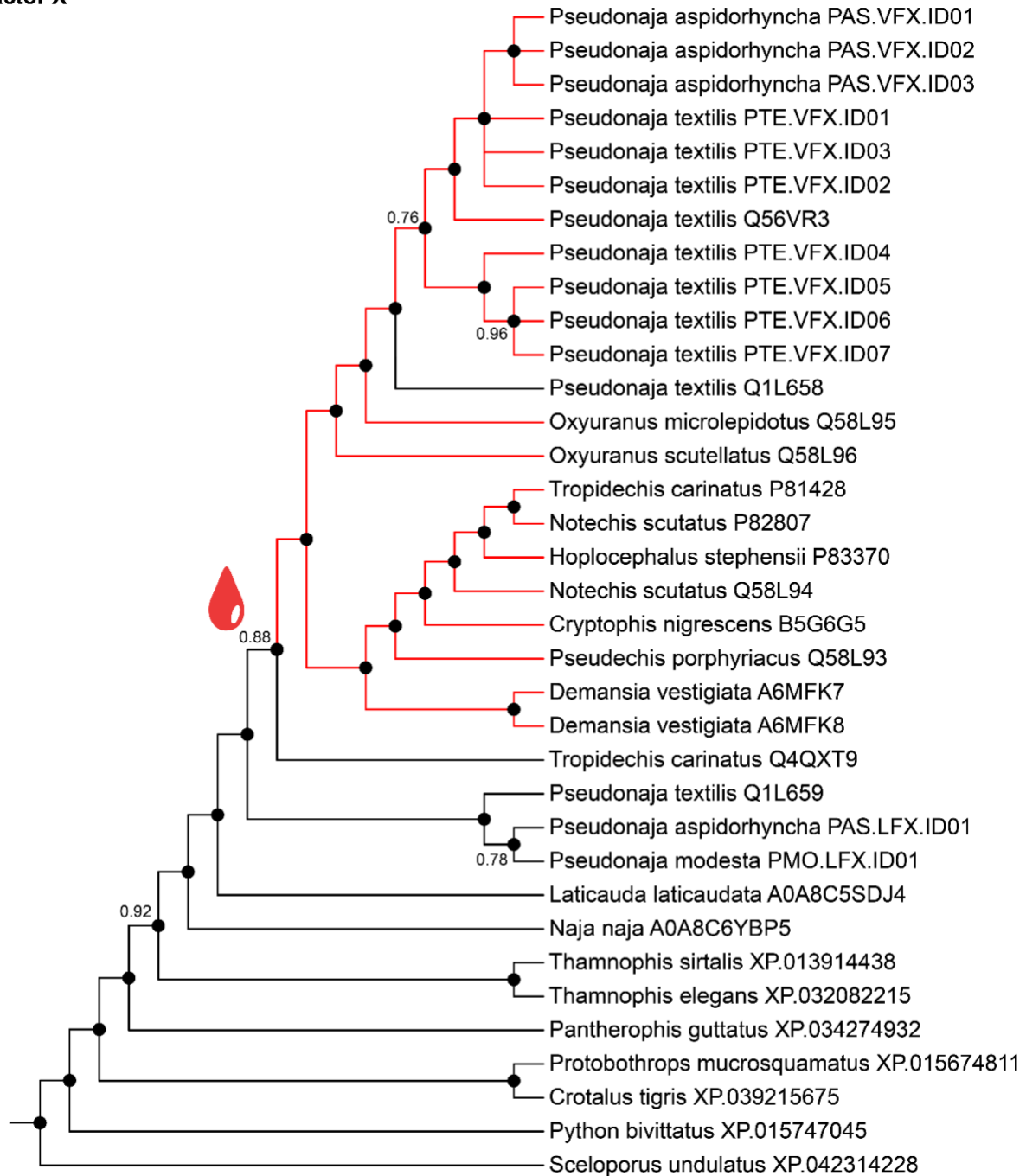


Fig. S6. Bayesian inference-derived amino acid phylogeny of factor X sequences. Only Bayesian posterior probabilities below 1.0 are displayed. Black branches indicate liver-specific genes and red branches indicate venom-specific genes. The tree was rooted using *Sceloporus undulatus* (eastern fence lizard) as a representative outgroup.

Factor X

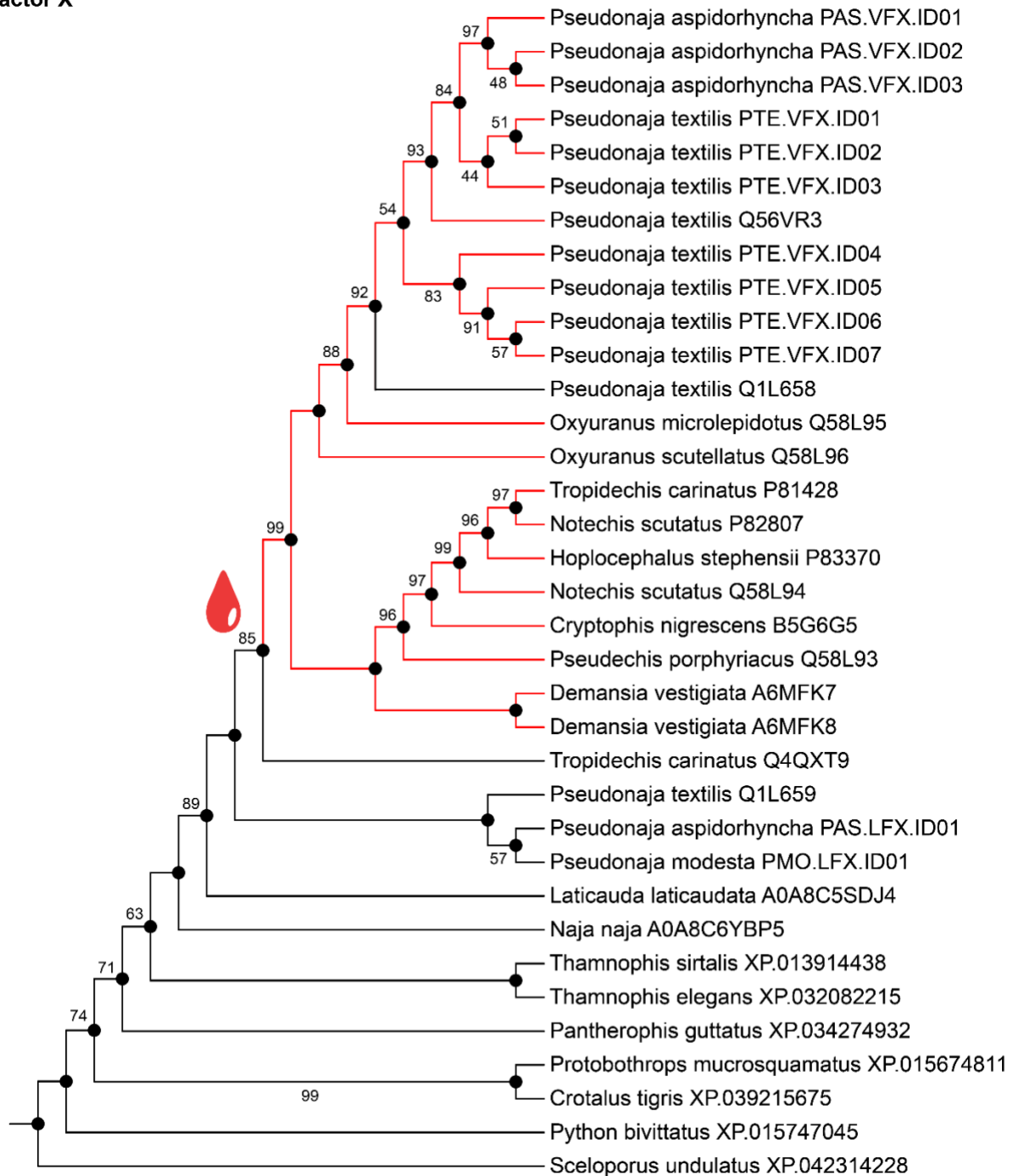


Fig. S7. Maximum-likelihood estimation-derived amino acid phylogeny of factor X sequences. Only bootstrap values below 100 are displayed. Black branches indicate liver-specific genes and red branches indicate venom-specific genes. The tree was rooted using *Sceloporus undulatus* (eastern fence lizard) as a representative outgroup.

Factor V

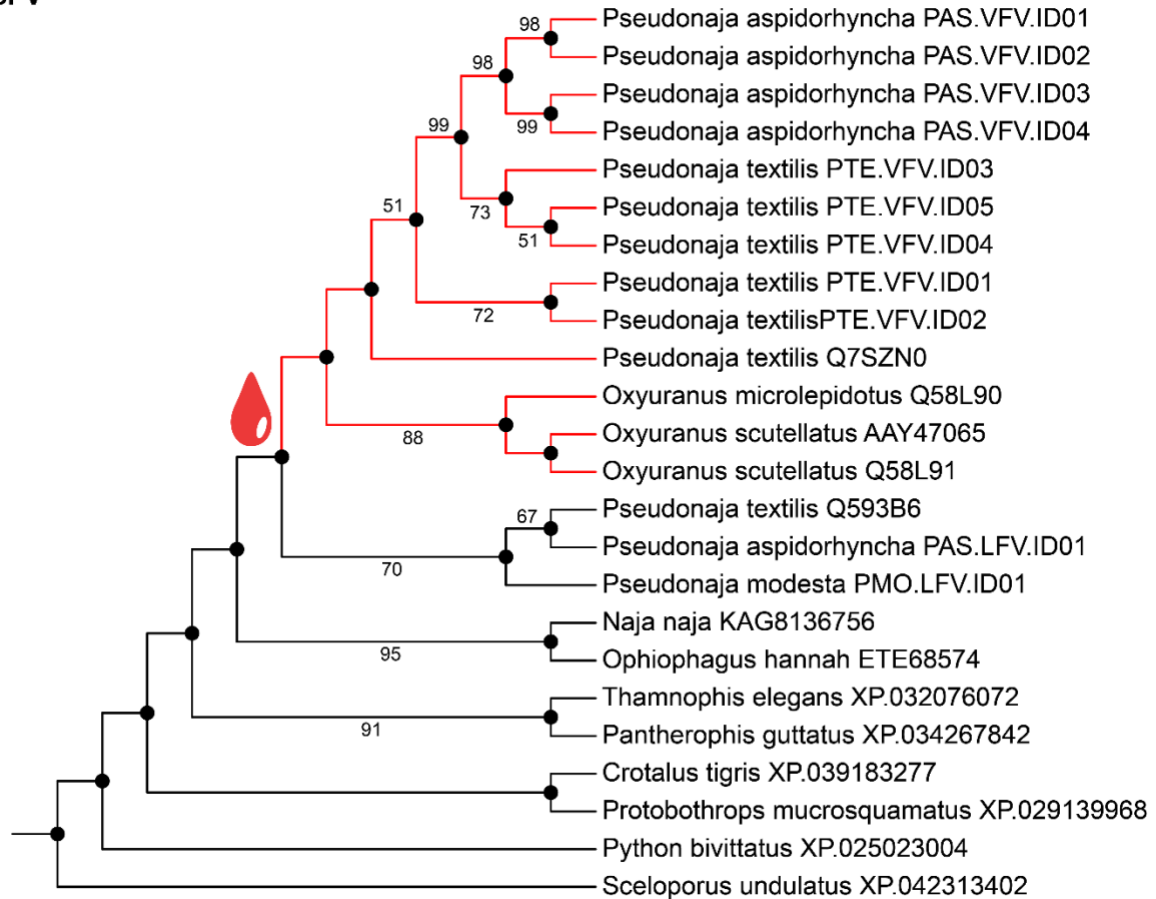


Fig. S8. Bayesian inference-derived amino acid phylogeny of factor V sequences. Only Bayesian posterior probabilities below 1.0 are displayed. Black branches indicate liver-specific genes and red branches indicate venom-specific genes. The tree was rooted using *Sceloporus undulatus* (eastern fence lizard) as a representative outgroup.

Factor V

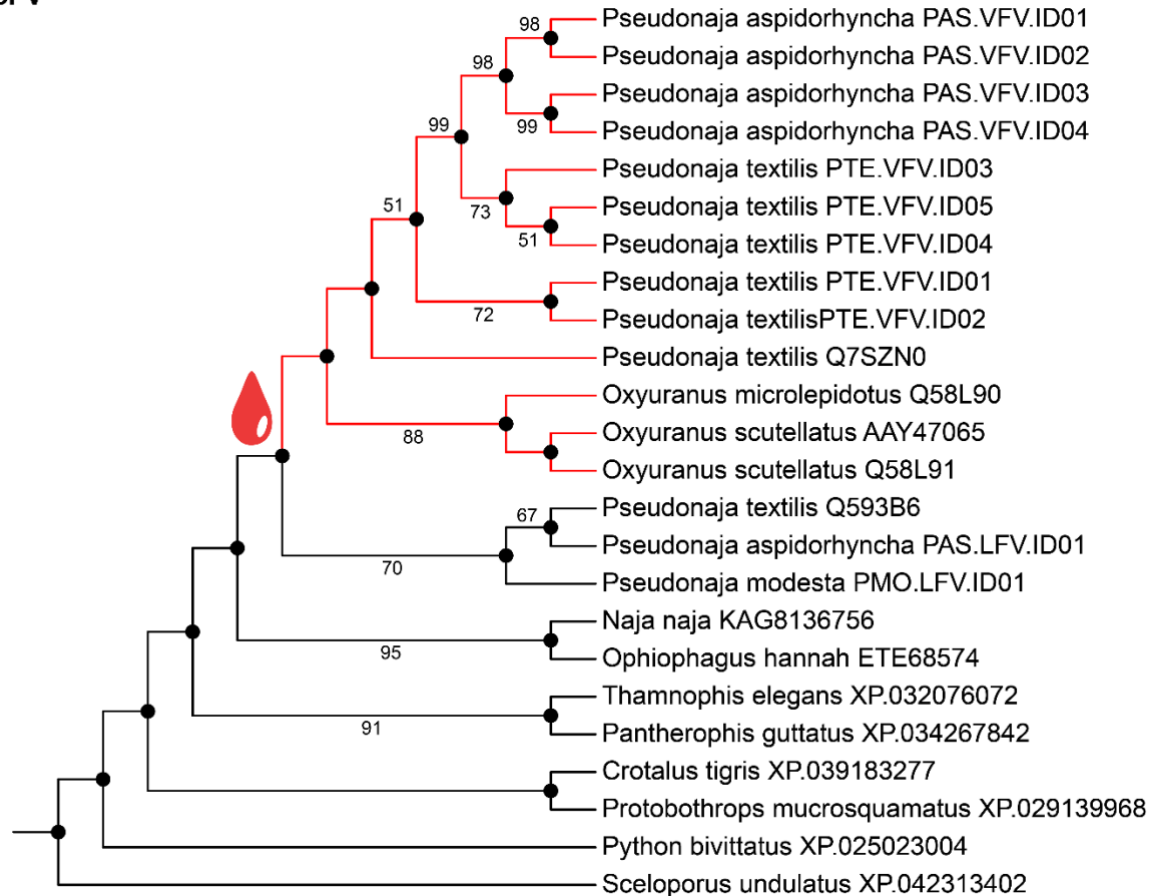


Fig. S9. Maximum-likelihood estimation-derived amino acid phylogeny of factor V sequences. Only Bootstrap values below 100 are displayed. Black branches indicate liver-specific genes and red branches indicate venom-specific genes. The tree was rooted using *Sceloporus undulatus* (eastern fence lizard) as a representative outgroup.

Group I Phospholipase A₂

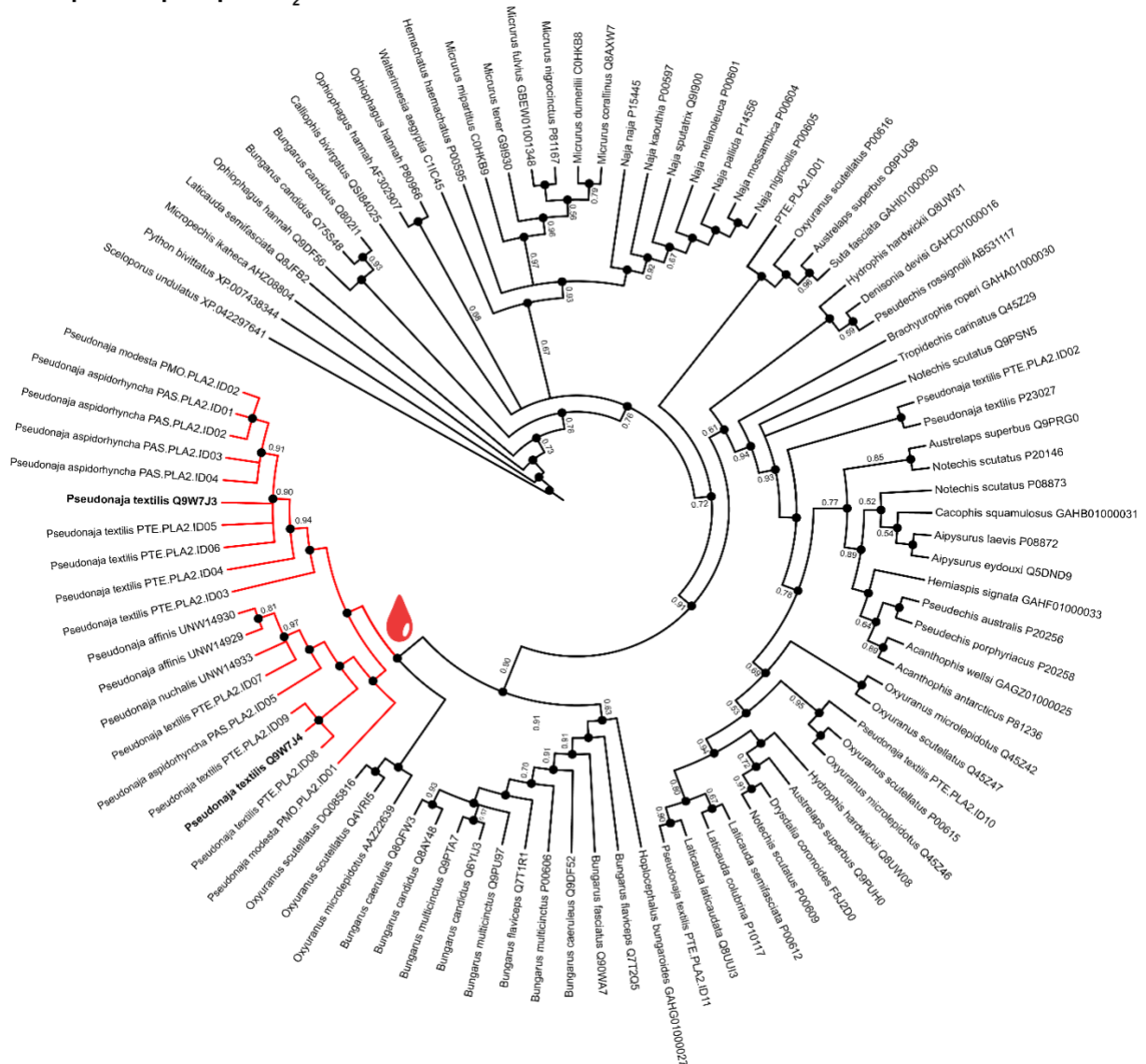


Fig. S10. Bayesian inference-derived phylogeny of group I phospholipase A₂ sequences from elapid venoms. The majority of our group I phospholipase A₂ (PLA₂) transcripts clusters with procoagulant isoforms (Q9W7J3 and Q9W7J4). Red branches indicate the inferred procoagulant PLA₂ cluster. Only Bayesian posterior probabilities below 1.0 are displayed. The tree was rooted using *Sceloporus undulatus* (eastern fence lizard) as a representative outgroup.

[illegible]

Fig. S11. Maximum-likelihood estimation-derived phylogeny of group I phospholipase A₂ sequences from elapid venoms. The majority of our group I phospholipase A₂ (PLA₂) transcripts clusters with procoagulant isoforms (Q9W7J3 and Q9W7J4). Red branches indicate the inferred procoagulant PLA₂ cluster. Only Bootstrap values below 100 are displayed. The tree was rooted using *Sceloporus undulatus* (eastern fence lizard) as a representative outgroup.

Kunitz-type serine protease inhibitors

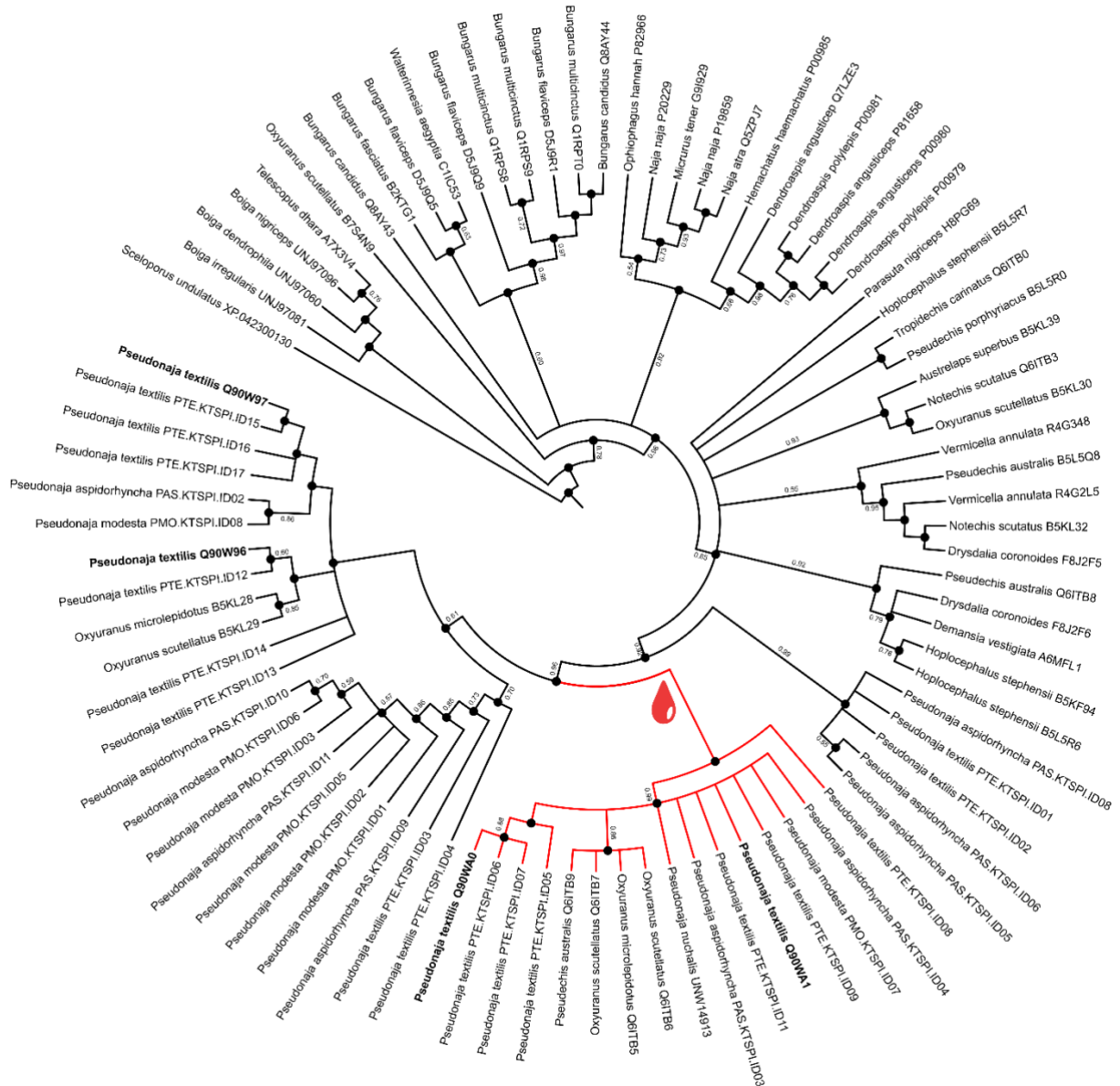


Fig. S12. Bayesian inference-derived phylogeny of Kunitz-type serine protease inhibitor sequences from elapid venoms. Several of our Kunitz-type serine protease inhibitor (KTSPi) transcripts cluster with plasmin-inhibiting isoforms (Q90WA1 and Q90WA0). Only this cluster contains the key amino acids for plasmin inhibition and specificity (i.e. arginine, 17R; and valine, 18V). Only Bayesian posterior probabilities below 1.0 are displayed. Red branches indicate plasmin inhibiting KTSPi sequences (with key amino acids) and black branches indicate non-plasmin inhibiting KTSPi

sequences (lack of key amino acids). The tree was rooted using *Sceloporus undulatus* (eastern fence lizard) as a representative outgroup.

Kunitz-type serine protease inhibitors

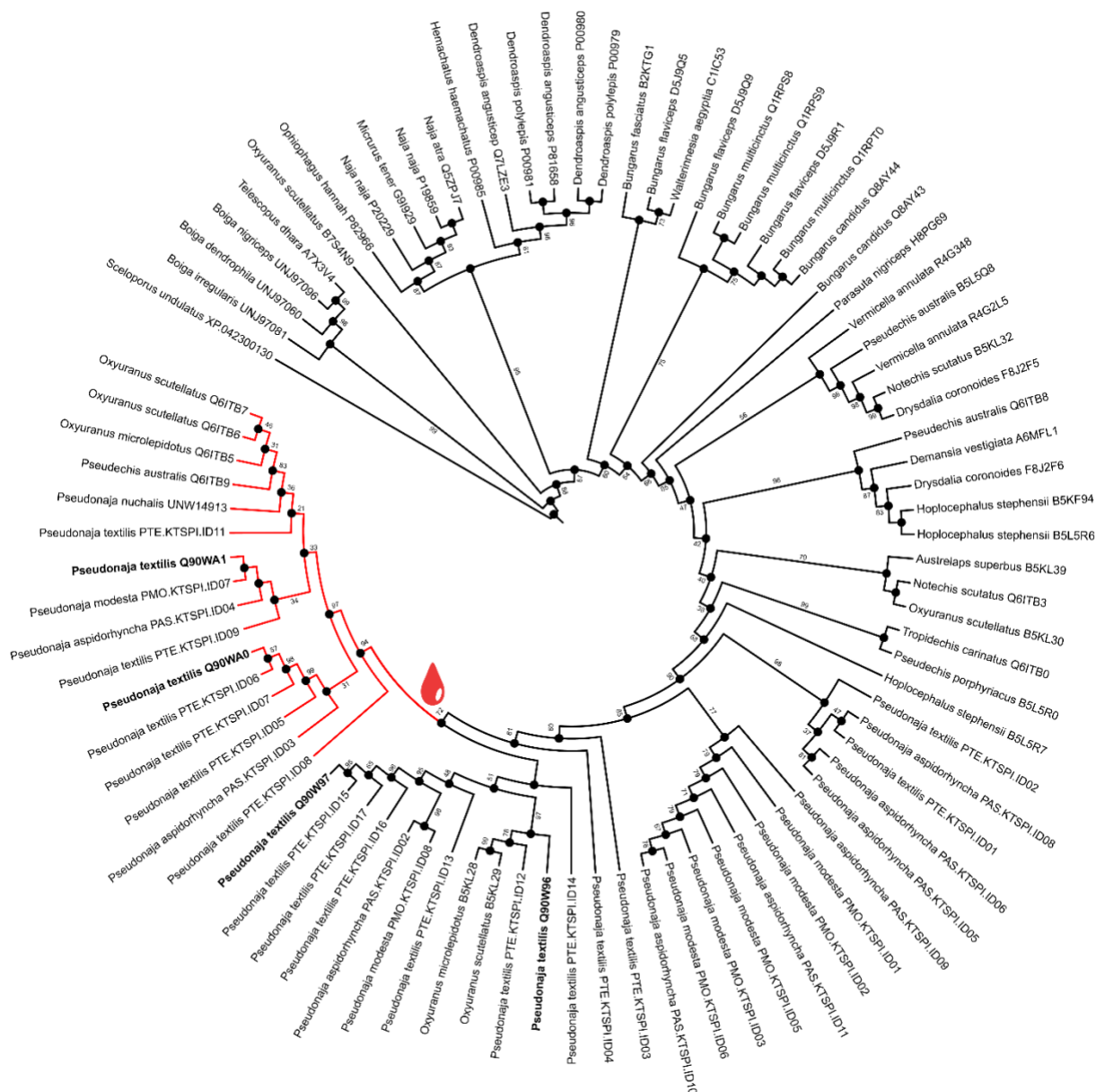


Fig. S13. Maximum-likelihood estimation-derived phylogeny of Kunitz-type serine protease inhibitor sequences from elapid venoms. Several of our Kunitz-type serine protease inhibitor (KTSP) transcripts cluster with plasmin-inhibiting isoforms (Q90WA1 and Q90WA0). Only this cluster contains the key amino acids for plasmin inhibition and specificity (i.e. arginine, 17R; and valine, 18V). Only Bayesian posterior probabilities below 1.0 are displayed. Red branches indicate plasmin inhibiting KTSP sequences (with key amino acids) and black branches indicate non-

plasmin inhibiting KTSPI sequences (lack of key amino acids). The tree was rooted using *Sceloporus undulatus* (eastern fence lizard) as a representative outgroup.

Short-chain 3FTx

AAD40967 PT-SNTX1 PMO.SC-3FTX.ID32 PTE.SC-3FTX.ID21	LTCYKGYHDT VVCKPHETIC YEYFIPATHG NAILARGCGT SCPGGIRPVC CRTDLCNK LTCYKGYHDT VVCKPHETIC YEYFIPATHG NAILARGCGT SCPGGIRPVC CRTDLCNK LTCYKGYHDT VVCKPHETIC YEYFIPATHG NAILARGCGT SCPGGIRPVC CRTDLCNK
AAD40968 PT-SNTX2 PTE.SC-3FTX.ID17	LTCYKGYHDT VVCKPHETIC YRYLIPATHG NAIPARGCGT SCPGGNHPVC CSTDLCNK LTCYKGYHDT VVCKPHETIC YRYLIPATHG NAIPARGCGT SCPGGNHPVC CSTDLCNK
AAD40969 PT-SNTX3 PAS.SC-3FTX.ID18 PTE.SC-3FTX.ID19	LTCYKGYHDT VVCKPHETIC YRYLVPATHG NAIPARGCGT SCPGGNHPVC CSTDLCNK LTCYKGYHDT VVCKPHETIC YRYLVPATHG NAIPARGCGT SCPGGNHPVC CSTDLCNK LTCYKGYHDT VVCKPHETIC YRYLVPATHG NAIPARGCGT SCPGGNHPVC CSTDLCNK
AAD40973 PT-SNTX7 PTE.SC-3FTX.ID09	LTCYKRYFDT VVCKPQETIC YRYIIPATHG NAITYRGCST SCPSGIRLVC CSTDLCNK LTCYKRYFDT VVCKPQETIC YRYIIPATHG NAITYRGCST SCPSGIRLVC CSTDLCNK

Long-chain-like 3FTx

A8HDK6 PT-LNTX-1 PAS.LCL-3FTX.ID01 PTE.LCL-3FTX.ID01	LICYLDFSVP HTCAPGEKLC YTRTWNDGRG TRIERGCAAT CPIPKKPEIH VTCCSTDRCN LICYLDFSVP HTCAPGEKLC YTRTWNDGRG TRIERGCAAT CPIPKKPEIH VTCCSTDRCN LICYLDFSVP HTCAPGEKLC YTRTWNDGRG TRIERGCAAT CPIPKKPEIH VTCCSTDRCN
A8HDK6 PT-LNTX-1 PAS.LCL-3FTX.ID01 PTE.LCL-3FTX.ID01	PHPKQKPH PHPKQKPH PHPKQKPH

Long-chain 3FTx

AAK15774 PT-PTb PMO.LC-3FTX.ID13 PAS.LC-3FTX.ID10 PTE.LC-3FTX.ID07	RTCFITPDVK SKPCPPGQEV CYTKTWCDGF CGIRGKRVDL GCAATCPTPK KTGIDIICCS RTCFITPDVK SKPCPPGQEV CYTKTWCDGF CGIRGKRVDL GCAATCPTPK KTGIDIICCS RTCFITPDVK SKPCPPGQEV CYTKTWCDGF CGIRGKRVDL GCAATCPTPK KTGIDIICCS RTCFITPDVK SKPCPPGQEV CYTKTWCDGF CGIRGKRVDL GCAATCPTPK KTGIDIICCS
AAK15774 PT-PTb PMO.LC-3FTX.ID13 PAS.LC-3FTX.ID10 PTE.LC-3FTX.ID07	TDDCNTFPLR PRGRLSSIKD TDDCNTFPLR PRGRLSSIKD TDDCNTFPLR PRGRLSSIKD TDDCNTFPLR PRGRLSSIKD

Fig. S14. Sequence alignment of three-finger toxins with identical, functionally confirmed neurotoxins. Our *de novo* three-finger toxin (3FTx) transcripts were aligned to identical, functionally confirmed neurotoxin sequences. The neurotoxin references are highlighted in bold. The following studies described the neurotoxins: short-chain 3FTx references: AAD40967, AAD40968, AAD40969, and AAD40973; long-chain-like 3FTx reference: A8HDK6; long-chain 3FTx reference: AAK15774. Note: only the *de novo* 3FTx transcripts that matched 100% identity are displayed above.

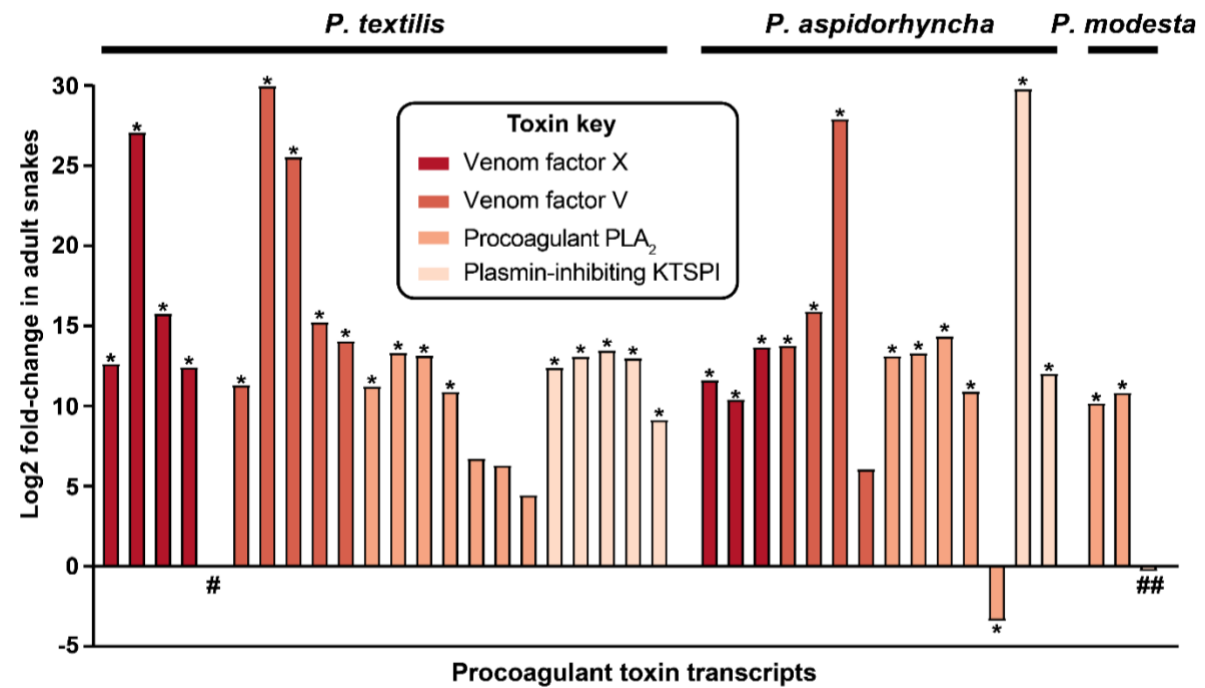


Fig. S15. Log2FoldChange of procoagulant toxin transcripts in adult venom gland tissue of Australian brown snakes (*Pseudonaja* spp.). DESeq2 differential gene expression analyses revealed that nearly all procoagulant toxin transcripts are upregulated in adult venom glands compared to hatchlings. Only one procoagulant PLA₂ transcript is significantly downregulated in *P. aspidorhyncha*. The asterisks (*) indicates statistically significant Log2FoldChange (adjusted p < 0.05). The single hashtag (#) indicates the presence of a venom factor Xa transcript that did not make a log2 fold change. The double hashtag (##) indicates the presence of a plasmin-inhibiting KTSPi transcript that did not make a log2 fold change. Abbreviation: KTSPi, Kunitz-type serine protease inhibitor; PLA₂, phospholipase A₂; TPM, transcripts per million.

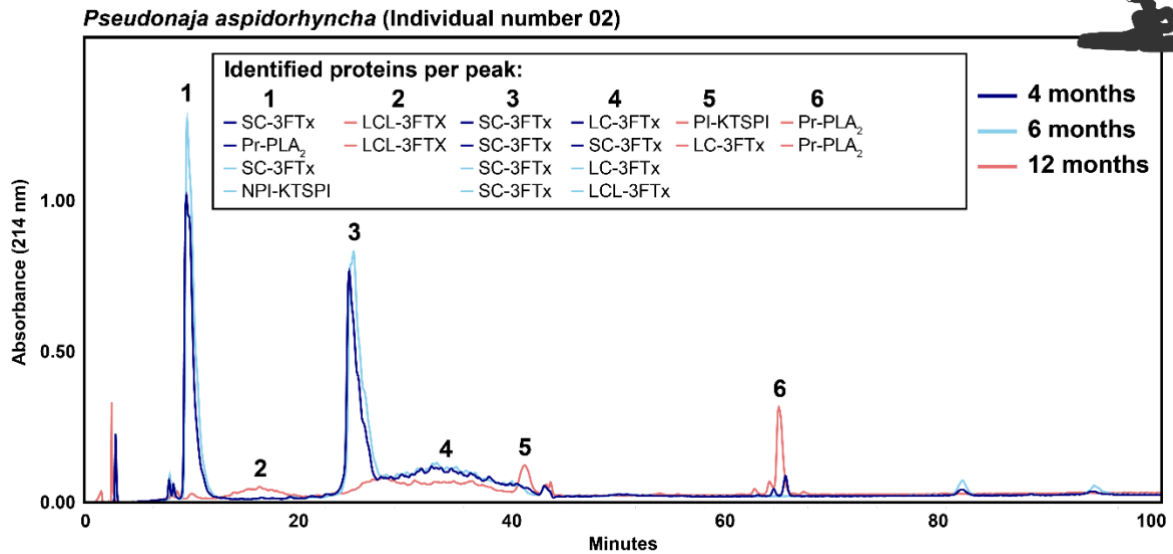


Fig. S16. Chromatographic venom profiles of Strap-snouted brown snake (*Pseudonaja aspidorhyncha*) individual number 02. Reverse-phase chromatographic separation of *P. aspidorhyncha* venom, followed by tandem mass spectrometry (liquid chromatography-mass spectrometry), revealed that, after the dietary shift, two out of four procoagulant toxin families were detectable. Specifically, only plasmin-inhibiting Kunitz-type serine protease inhibitors and procoagulant phospholipase A₂ were identified. The peak numbers corresponded to the two most abundant proteins observed in each respective peak. Notably, venom factor Va and venom factor Xa were absent from the detected peaks. Abbreviations: LC-3FTx, long-chain three-finger toxin; LCL-3FTx, long-chain-like three-finger toxin; NPI-KTSPI, non-plasmin-inhibiting Kunitz-type serine protease inhibitor; PI-KTSPI, plasmin-inhibiting Kunitz-type serine protease inhibitor; Pr-PLA₂, procoagulant phospholipase A₂; SC-3FTx, short-chain three-finger toxin.

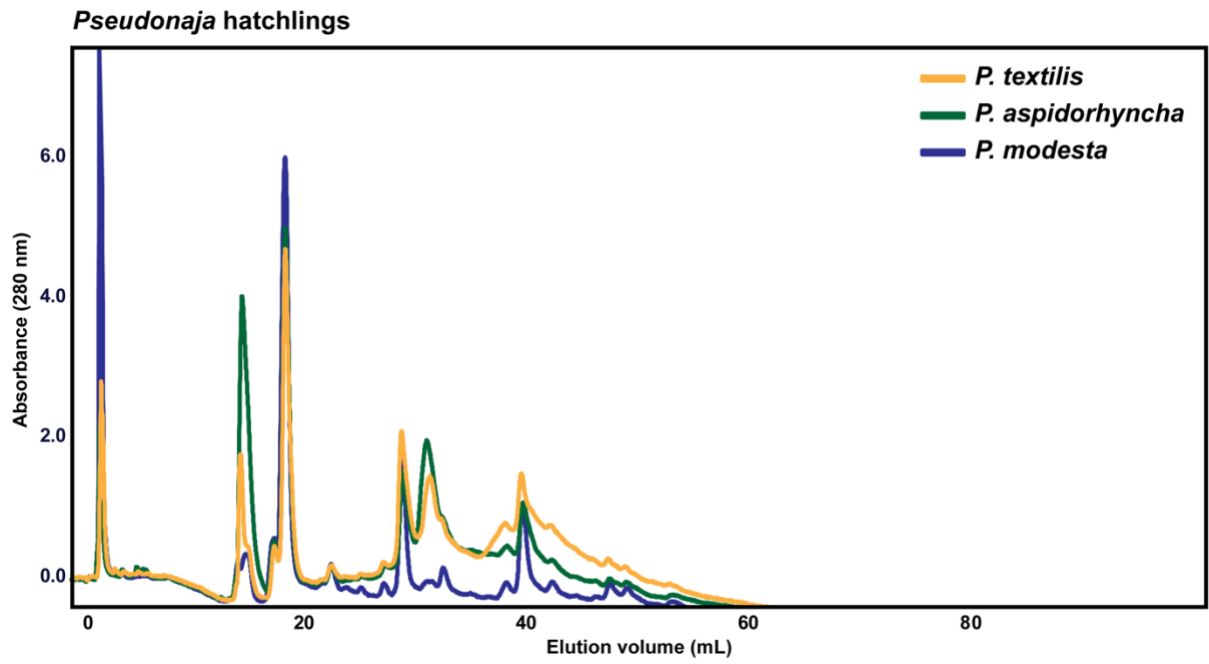


Fig. S17. Comparative chromatographic venom profiles of hatchling *Pseudonaja* species. Reverse-phase chromatographic separation of pooled hatchling venoms (n = 2 per species).

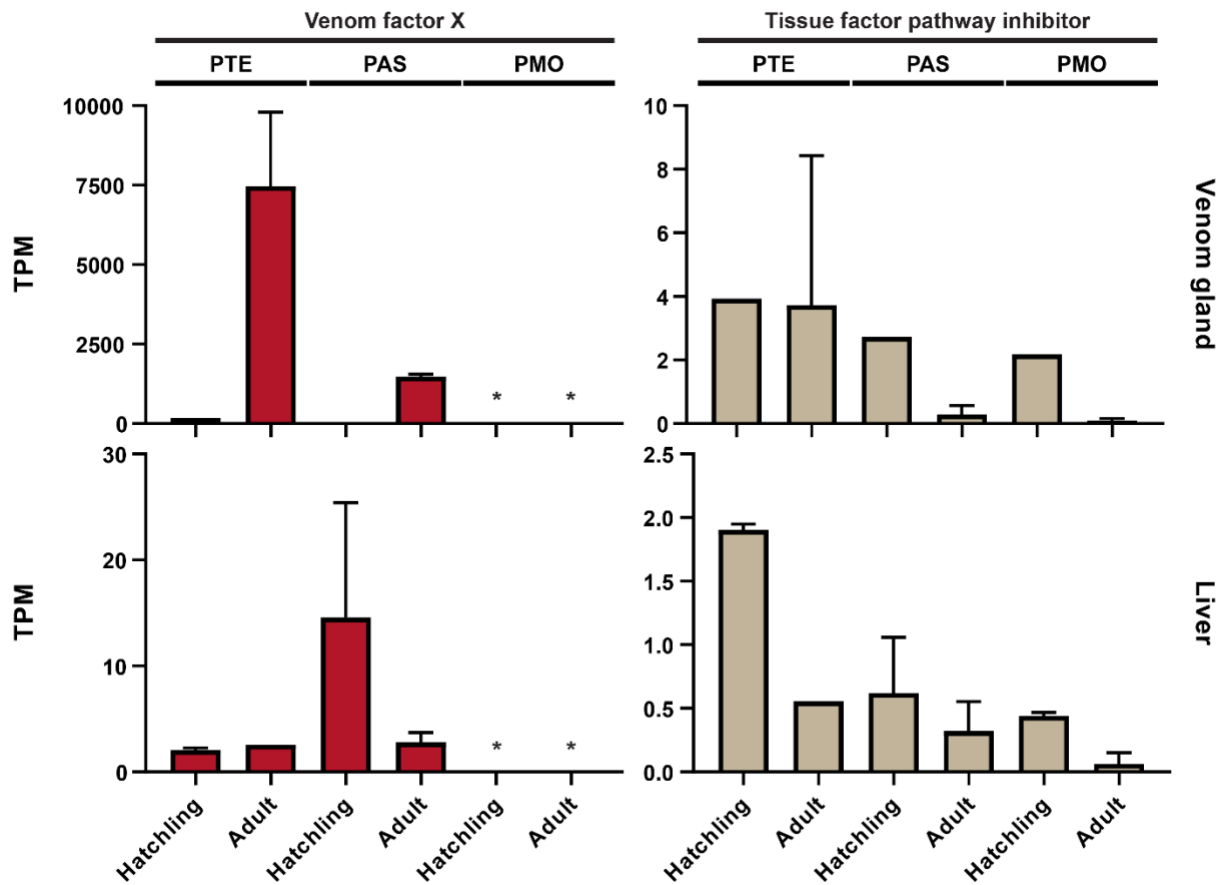


Fig. S18. Comparative expression levels of tissue factor pathway inhibitors in venom glands and livers. Total TPM value of tissue factor pathway inhibitors was calculated from each transcriptome, and the average was taken from each study group (i.e. hatchling or adult per species) and displayed together with the standard deviation. The expression levels of factor X only include the venom-specific isoforms. Each bar chart presents data from two biological replicates, except for the *Pseudonaja textilis* liver tissue, where only one measurement was taken. Asterisk indicates non-expression of genes (*). GenBank accession numbers: XM_026696930.1 and XM_026696931.1. Abbreviations: PAS, *Pseudonaja aspidorhyncha*; PTE, *Pseudonaja textilis*; PMO, *Pseudonaja modesta*; TPM, transcript per million.

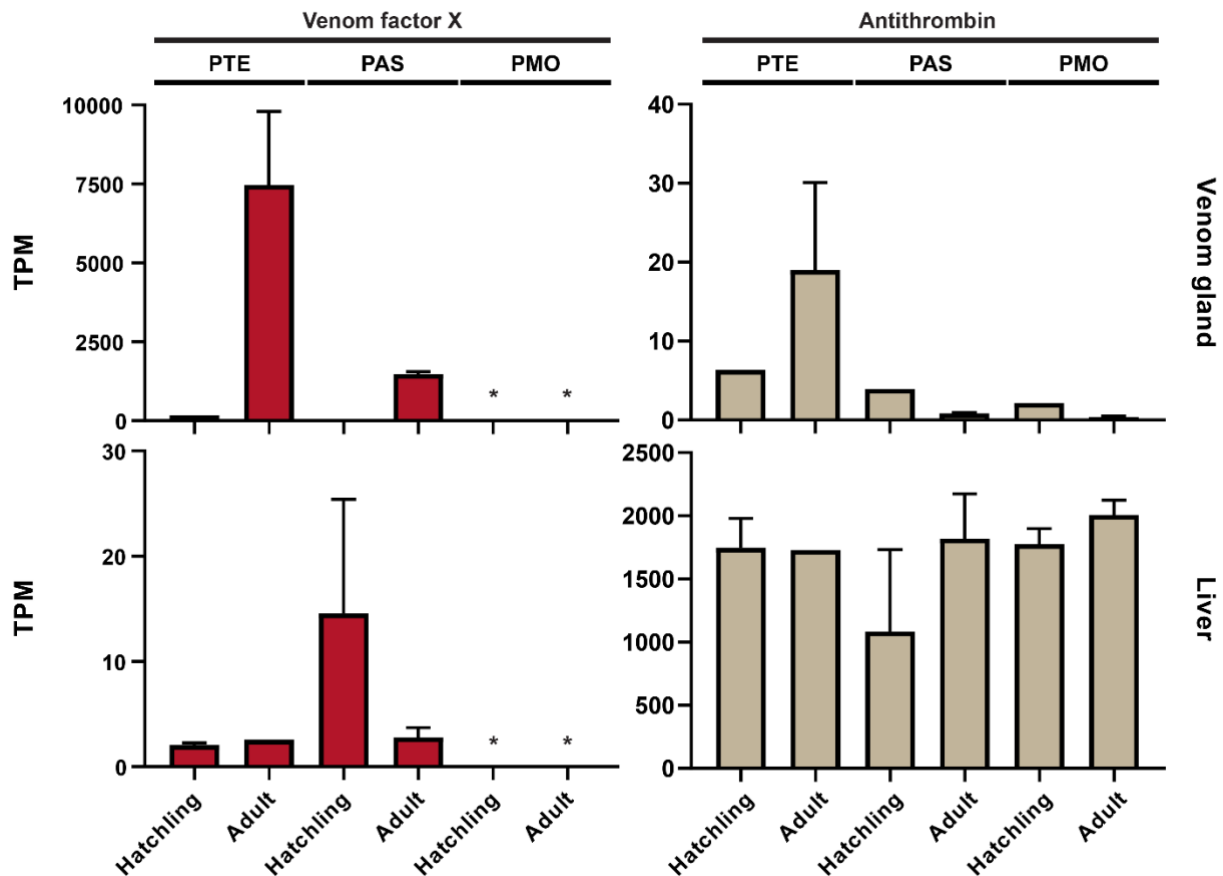


Fig. S19. Comparative expression levels of antithrombin in venom glands and livers. Total TPM value of antithrombin was calculated from each transcriptome, and the average was taken from each study group (i.e. hatchling or adult per species) and displayed together with the standard deviation. Each bar chart presents data from two biological replicates, except for the *Pseudonaja textilis* liver tissue, where only one measurement was taken. Asterisk indicates non-expression of genes (*). GenBank accession numbers: XM_026703355.1 and XM_026703356.1. Abbreviations: PAS, *Pseudonaja aspidorhyncha*; PTE, *Pseudonaja textilis*; PMO, *Pseudonaja modesta*; TPM, transcript per million.

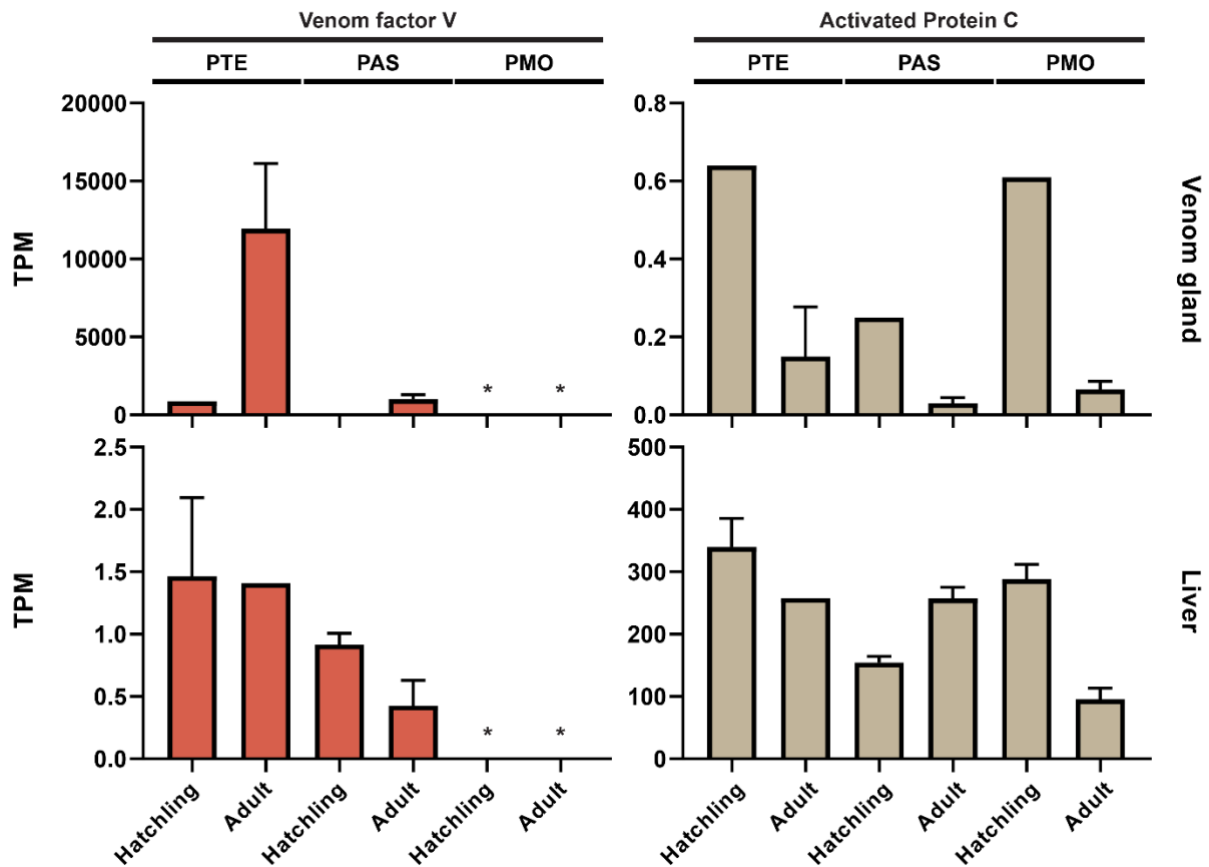


Fig. S20. Comparative expression levels of activated protein C in venom glands and livers. Total TPM value of activated protein C was calculated from each transcriptome, and the average was taken from each study group (i.e. hatchling or adult per species) and displayed together with the standard deviation. The expression levels of factor V only include the venom-specific isoforms. Each bar chart presents data from two biological replicates, except for the *Pseudonaja textilis* liver tissue, where only one measurement was taken. Asterisk indicates non-expression of genes (*). GenBank accession number: XM_026701308.1. Abbreviations: PAS, *Pseudonaja aspidorhyncha*; PTE, *Pseudonaja textilis*; PMO, *Pseudonaja modesta*; TPM, transcript per million.

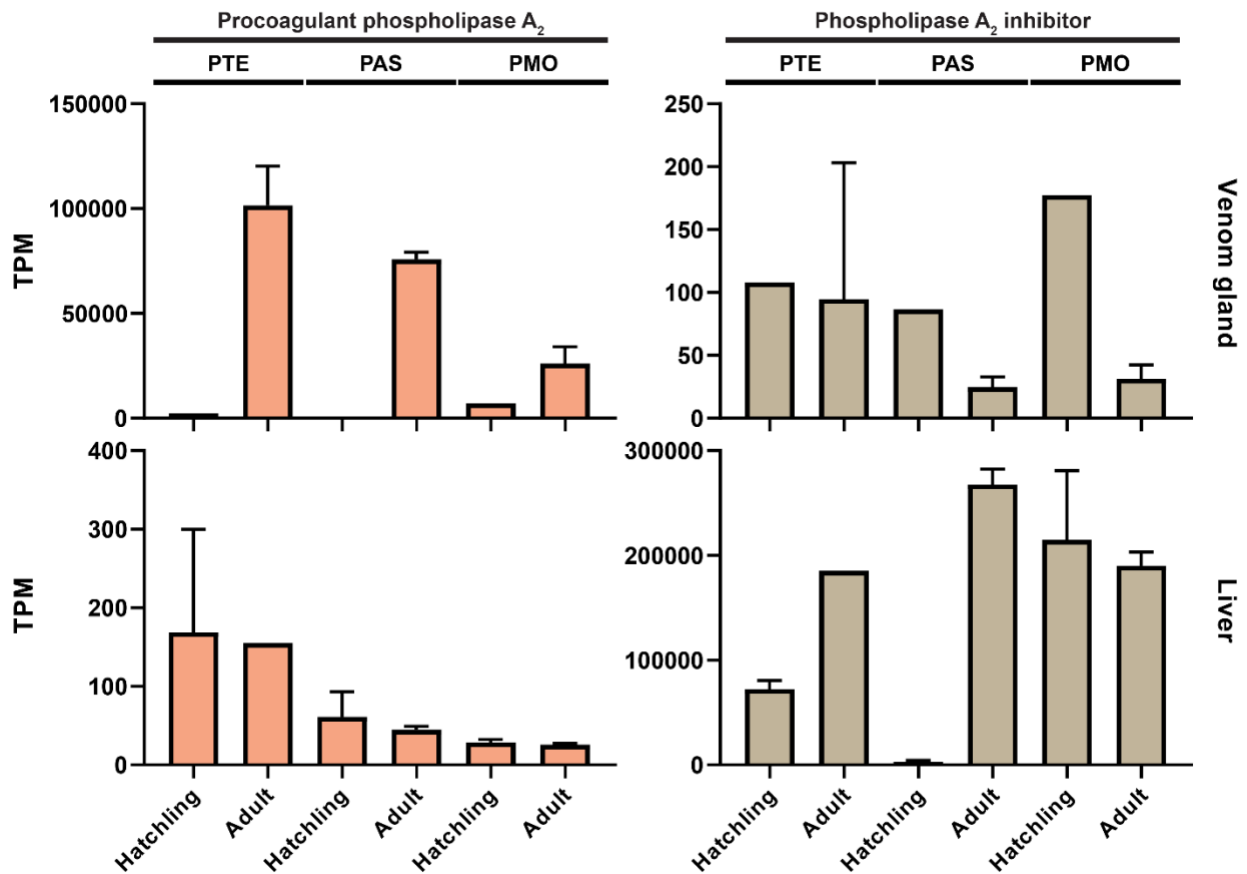


Fig. S21. Comparative expression levels of phospholipase A₂ inhibitors in venom glands and livers. Total TPM value of phospholipase A₂ inhibitors was calculated from each transcriptome, and the average was taken from each study group (i.e. hatchling or adult per species) and displayed together with the standard deviation. From the three structural classes of phospholipase A₂ inhibitors (PLA₂Is), only PLA₂I-β and PLA₂I-γ (both subunit A and B) were identified. PLA₂I-α was absent from both venom gland and liver transcriptomes. GenBank accession numbers: XM_026724407.1, XM_026726430.1 and XM_026724407.1 (PLA₂I-β, respectively) and XM_026725345.1, XM_026725750.1, XM_026725345.1, XM_026725634.1 and XM_026725634.1 (PLA₂I-γ, respectively).

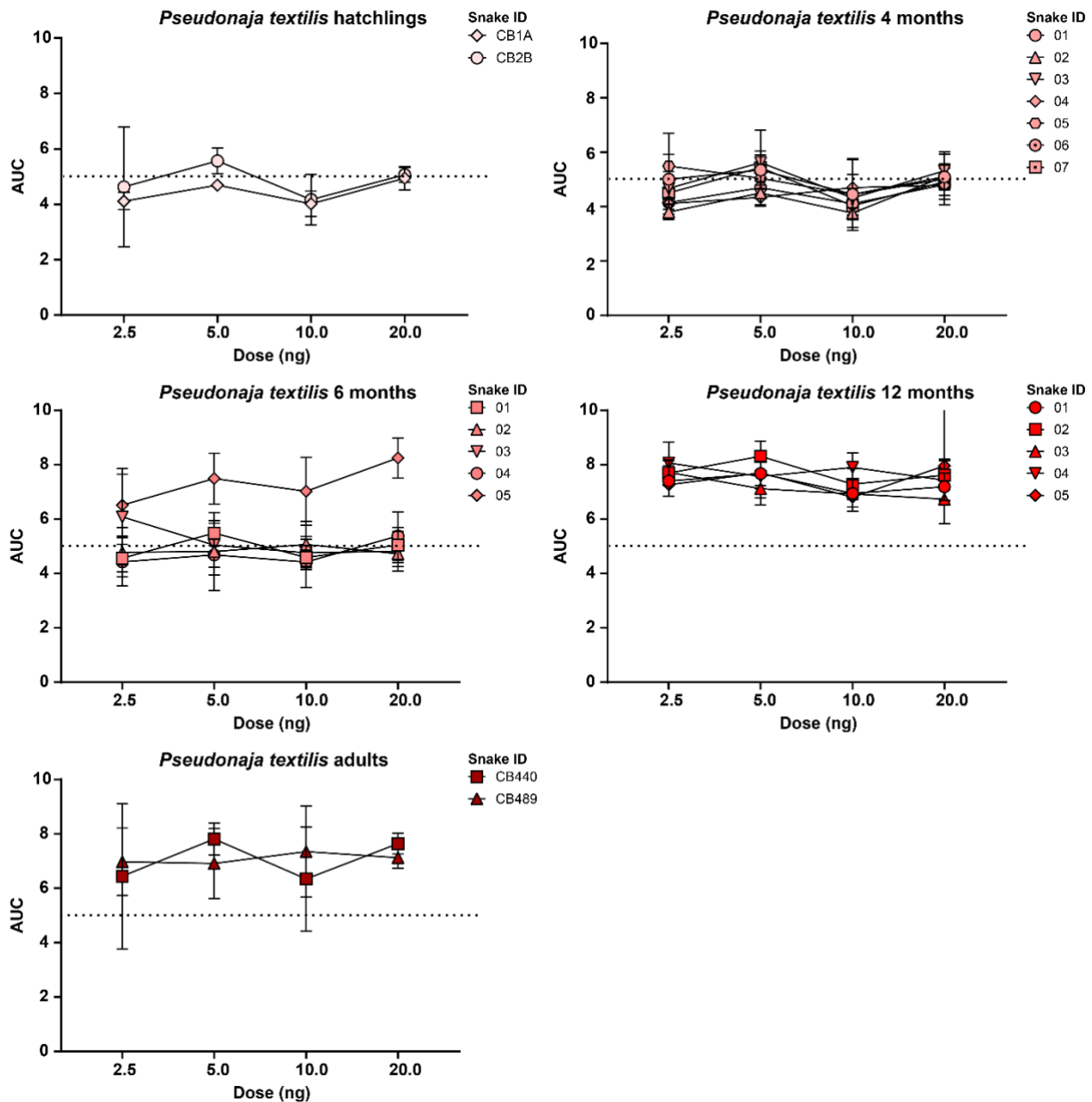


Fig. S22. Coagulation profiles for all Eastern brown snake (*Pseudonaja textilis*) venoms included in this study. Each data point represents the mean area under the curve (AUC) $\pm$ standard deviation. The black dashed line represents the negative control (no venom added) to account for spontaneous clotting (N=5).

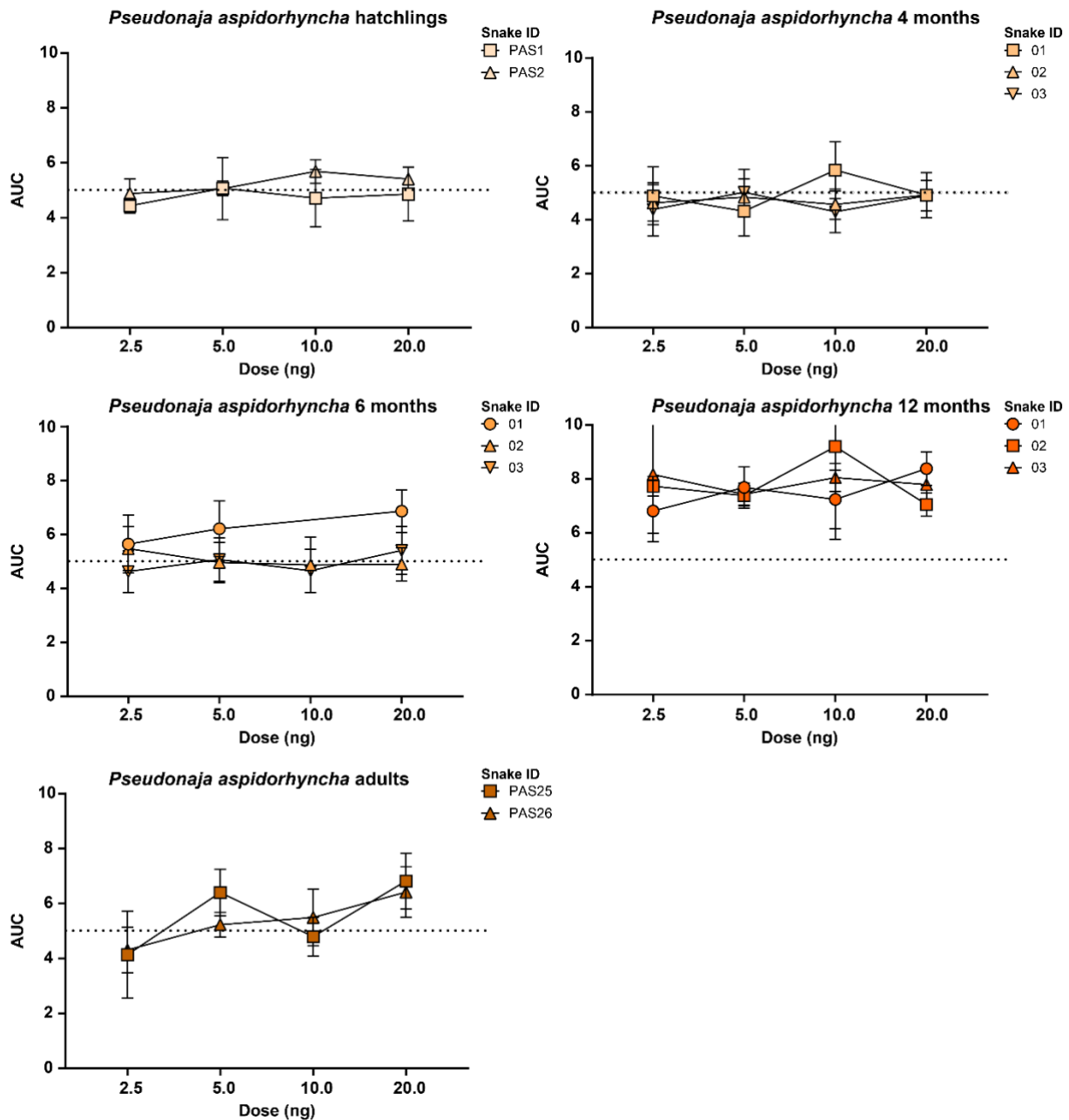


Fig. S23. Coagulation profiles for all strap-snouted brown snake (*Pseudonaja aspidorhyncha*) venoms included in this study. Each data point represents the mean of the area under the curve (AUC) $\pm$ standard deviation. The black dashed line represents the negative control (no venom added) to account for spontaneous clotting (N=5).

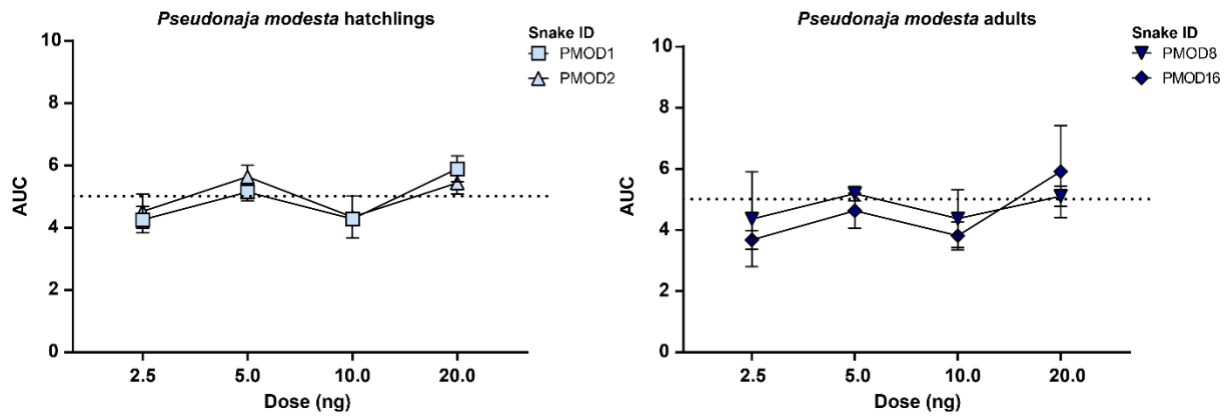


Fig. S24. Coagulation profiles for all ringed brown snake (*Pseudonaja modesta*) venoms included in this study. Each data point represents the mean of the area under the curve (AUC) $\pm$ standard deviation. The black dashed line represents the negative control (no venom added) to account for spontaneous clotting (N=5).

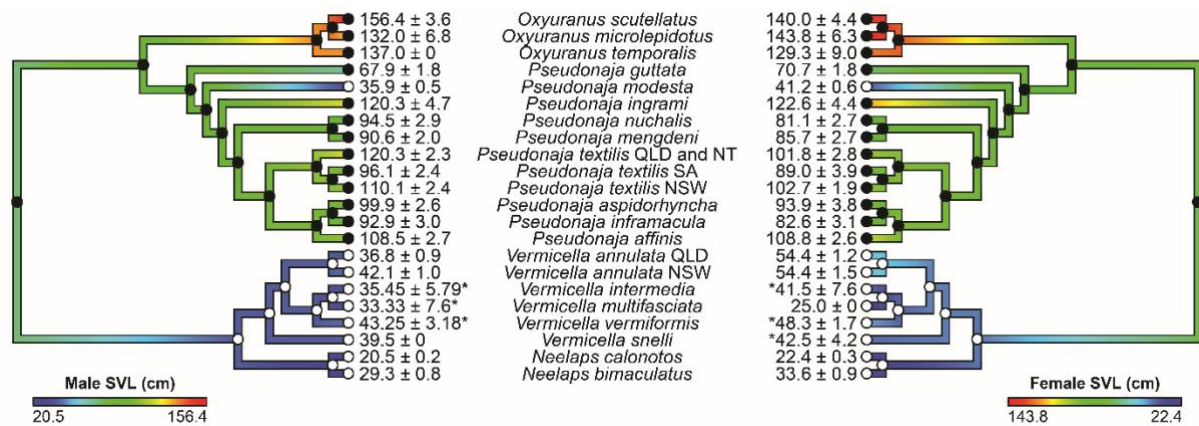


Fig. S25. Ancestral state estimation of adult body size in the monophyletic *Oxyuranus-Pseudonaja* clade reveals a significant reduction in the ringed brown snake (*Pseudonaja modesta*). Ancestral State Estimation (ASE) of the monophyletic *Oxyuranus-Pseudonaja* clade revealed that the reduction in adult body size in *P. modesta* corresponds with an evolutionary loss of mammalian prey. ASE was performed using snout-vent length (SVL) as a measure of adult body size, with the analysis rooted with the *Vermicella-Neelaps* sister clade. A color gradient, ranging from blue to red, represents SVL values, where blue indicates smaller SVL (reduced body size) and red indicates larger SVL (increased body size). The presence or absence of mammalian prey is denoted by a black circle (present) or a white circle (absent). An asterisk (*) denotes standard deviation rather than standard error. The analysis was performed separately on SVL data for males (left panel) and females (right panel) to account for sexual dimorphism. The asterisk (*) indicates standard deviation instead of standard error. Abbreviations: NSW, New South Wales; NT, Northern Territory, QLD, Queensland; SA, South Australia; SVL, snout-vent length.

Table S1. Presence and absence of venom gene families in our Australian brown snake species (*Pseudonaja* spp.). The presence of a toxin family, indicated by a black cross (X), is determined based on transcript expression level (i.e. transcriptomics) and protein abundance (i.e. proteomics) in any hatchling or adult brown snake. The transcriptomic threshold of being included was 10 transcripts per million (TPM) in any of the specimens. The proteomic threshold of being included was higher than 1% of the total intensity in any of the specimens. Abbreviations: 3FTx, three-finger toxin; 5'-NT, 5'-nucleotidase; ACHE, acetylcholinesterase; CRISP, cysteine-rich secretory protein; CVF, cobra venom factor; HYLA, hyaluronidase; KTSPi, Kunitz-type serine protease inhibitor; NGF, nerve growth factor; NP, natriuretic peptide; PDE, phosphodiesterase; PLA₂, phospholipase A₂; PLB, phospholipase B; CTL, C-type lectins; SVMP, snake venom metalloproteinase; VEGFA, Vascular Endothelial Growth Factor A; vFVa, venom factor Va; vFXa, venom factor Xa.

		<i>Pseudonaja textilis</i>		<i>Pseudonaja aspidorhyncha</i>		<i>Pseudonaja modesta</i>	
		Transcriptomics	Proteomics	Transcriptomics	Proteomics	Transcriptomics	Proteomics
1	3FTx	X	X	X	X	X	X
2	5'-NT					X	
3	ACHE	X		X		X	
4	CRISP	X	X	X	X	X	X
5	CVF	X		X			
6	HYLA	X		X		X	
7	KTSPi	X	X	X	X	X	X
8	NGF	X		X		X	
9	NP	X		X		X	
10	PDE	X		X		X	
11	PLA ₂	X	X	X	X	X	

12	PLB	X		X		X	
13	CTL	X	X	X	X	X	X
14	SVMP	X		X		X	
15	VEGFA	X		X		X	
16	vFVa	X	X	X	X		
17	vFXa	X	X	X	X		
18	WAPRIN	X		X		X	

Table S2. Overview of differential venom gene expression analysis between hatchling and adults venom glands of Eastern brown snake (*Pseudonaja textilis*) identified by DESeq2 algorithm. Only the venom gene families that include procoagulant toxins are shown. Abbreviations: KTSPI, Kunitz-type serine protease inhibitor; PLA₂, phospholipase A₂; vFXa, venom factor Xa; vFVa, venom factor Va; TPM, transcripts per million.

	Toxin-ID	Venom transcript	Hatchlings TPM	Adult 1 TPM	Adult 2 TPM	log2FoldChange in adults	Adjusted p-value	Toxin activity
1	PTE.KTSPI.ID09	KTSPI	1032.77	83295.19	31470.01	12.39	6.51641E-40	Coagulopathy
2	PTE.VFV.ID05	vFVa	275.61	3647.13	2277.29	11.30	4.25374E-33	Coagulopathy
3	PTE.PLA2.ID06	PLA2	591.74	16230.42	8337.99	11.23	4.41857E-25	Coagulopathy
4	PTE.KTSPI.ID07	KTSPI	1414.02	48966.53	82891.25	13.08	8.14508E-20	Coagulopathy
5	PTE.PLA2.ID05	PLA2	522.43	19926.95	37287.86	13.32	1.02455E-19	Coagulopathy
6	PTE.KTSPI.ID16	KTSPI	68.44	5684.9	6033.26	13.70	6.17938E-19	Unknown
7	PTE.PLA2.ID08	PLA2	1093.78	29289.38	69169.63	13.15	3.31167E-18	Coagulopathy
8	PTE.KTSPI.ID01	KTSPI	0	5117.48	911.05	14.93	1.59921E-17	Unknown
9	PTE.VFX.ID02	vFXa	91.14	2557.06	5774.23	12.63	1.04791E-16	Coagulopathy
10	PTE.KTSPI.ID11	KTSPI	0	4082.31	602.97	13.47	7.50297E-15	Coagulopathy
11	PTE.PLA2.ID12	PLA2	0	3623.55	0.08	26.39	1.38943E-14	Neurotoxicity
12	PTE.KTSPI.ID12	KTSPI	0	6936.19	6783.1	16.61	6.76919E-14	Unknown
13	PTE.VFV.ID04	vFVa	3.83	3648.92	22.33	29.97	1.09379E-11	Coagulopathy
14	PTE.VFX.ID03	vFXa	0	1537.22	0	27.07	8.49885E-11	Coagulopathy
15	PTE.PLA2.ID01	PLA2	0	11143.29	0	26.52	1.45213E-10	Neurotoxicity
16	PTE.PLA2.ID11	PLA2	0	5257.04	0	26.25	1.80978E-10	Neurotoxicity
17	PTE.VFV.ID03	vFVa	0	135.19	0.01	25.54	3.84709E-10	Coagulopathy
18	PTE.PLA2.ID02	PLA2	0	4899.45	0	25.24	6.17376E-10	Neurotoxicity
19	PTE.KTSPI.ID13	KTSPI	0	13014.64	0	24.49	2.10203E-09	Unknown
20	PTE.VFV.ID02	vFVa	0.01	19.41	120.29	15.24	1.02582E-07	Coagulopathy
21	PTE.KTSPI.ID06	KTSPI	2233.64	262.38	123604.24	12.98	1.77478E-07	Coagulopathy
22	PTE.VFX.ID06	vFXa	0	5019.31	1.15	15.77	2.24634E-07	Coagulopathy
23	PTE.KTSPI.ID02	KTSPI	202	27.7	9912.88	12.74	3.50726E-07	Unknown
24	PTE.VFX.ID01	vFXa	74.99	0	54.45	12.42	1.86708E-06	Coagulopathy
25	PTE.PLA2.ID07	PLA2	166.15	22869.13	0.56	10.89	1.51211E-05	Coagulopathy
26	PTE.VFV.ID01	vFVa	156.85	0.1	2072.04	14.06	4.32801E-05	Coagulopathy
27	PTE.KTSPI.ID17	KTSPI	0	27.42	3731.9	12.89	8.05014E-05	Unknown
28	PTE.KTSPI.ID03	KTSPI	0	4361.37	0.21	12.25	0.000359305	Unknown
29	PTE.KTSPI.ID08	KTSPI	377.44	16617.46	2.12	9.13	0.000479738	Coagulopathy
30	PTE.PLA2.ID10	PLA2	0	14081.05	0.25	8.64	0.070450417	Neurotoxicity
31	PTE.PLA2.ID03	PLA2	0	0.63	5.84	6.72	0.12004098	Coagulopathy
32	PTE.PLA2.ID04	PLA2	0	1.34	4.65	6.30	0.131285302	Coagulopathy

33	PTE.PLA2.ID09	PLA2	0	5.53	13.11	4.44	NA	Coagulopathy
34	PTE.VFX.ID05	vFXa	16.57	1.01	0.03	0.10	NA	Coagulopathy

Table S3. Overview of differential venom gene expression analysis between hatchling and adults venom glands of strap-snouted brown snake (*Pseudonaja aspidorhyncha*) identified by DESeq2 algorithm. Only the venom gene families that include procoagulant toxins are shown. Abbreviations: KTSPi, Kunitz-type serine protease inhibitor; PLA₂, phospholipase A₂; vFXa, venom factor Xa; vFVa, venom factor Va; TPM, transcripts per million.

	Toxin-ID	Venom gene	Hatchlings TPM	Adult 1 TPM	Adult 2 TPM	log2FoldChange in adults	Adjusted p-value	Toxin activity
1	PAS.PLA2.ID5	PLA2	77.1	32667.58	35018.28	12.20	7,15086E-57	Coagulopathy
2	PAS.PLA2.ID4	PLA2	6.16	5736.19	5258.40	13.30	3,95109E-49	Coagulopathy
3	PAS.VFX.ID2	vFXa	2.05	539.51	355.78	11.61	7,22212E-30	Coagulopathy
4	PAS.VFV.ID1	vFVa	0.35	1185.2	253.97	13.76	1,25975E-22	Coagulopathy
5	PAS.KTSPi.ID6	KTSPi	7347.22	0	0.00	-12.89	1,03311E-13	Unknown
6	PAS.VFV.ID2	vFVa	0.01	26.14	5.51	15.90	4,51732E-10	Coagulopathy
7	PAS.VFX.ID3	vFXa	3.25	22.51	1063.08	10.41	4,9471E-08	Coagulopathy
8	PAS.KTSPi.ID3	KTSPi	0	10124.28	0.00	29.79	2,26961E-08	Coagulopathy
9	PAS.VFV.ID4	vFVa	0.01	0	35.52	27.90	8,32894E-08	Coagulopathy
10	PAS.VFX.ID1	vFXa	0.45	971.28	0.11	13.68	6,5524E-06	Coagulopathy
11	PAS.PLA2.ID1	PLA2	1.65	4010.58	0.21	14.35	5,84465E-06	Coagulopathy
12	PAS.PLA2.ID3	PLA2	16.17	1.3	10519.67	10.91	6,84579E-05	Coagulopathy
13	PAS.KTSPi.ID1	KTSPi	130.8	15574.02	217.03	8.69	0,000118794	Unknown
14	PAS.KTSPi.ID4	KTSPi	80.26	44580.93	2.61	12.02	0,000123778	Coagulopathy
15	PAS.KTSPi.ID9	KTSPi	6.04	13915.87	2.41	14.59	0,000238469	Unknown
16	PAS.PLA2.ID2	PLA2	33.19	0.24	0.45	-3.41	0,002145386	Coagulopathy
17	PAS.KTSPi.ID5	KTSPi	2439.83	4.49	0.00	-6.24	0,007912785	Unknown
18	PAS.KTSPi.ID2	KTSPi	1463.17	5735.28	131.54	5.08	0,030616594	Unknown
19	PAS.VFV.ID3	vFVa	26	0.51	504.58	6.06	0,055552905	Coagulopathy
20	PAS.KTSPi.ID7	KTSPi	1320.14	5835.96	317.22	4.92	0,146349415	Unknown
21	PAS.KTSPi.ID8	KTSPi	4307.6	1095.37	242.17	1.02	0,642680766	Unknown
22	PAS.KTSPi.ID11	KTSPi	20.84	0	3.26	1.11	0,643960331	Unknown
23	PAS.KTSPi.ID10	KTSPi	36.62	1554.32	1886.93	-1.02	#N/A	Unknown

Table S4. Overview of differential venom gene expression analysis between hatchling and adults venom glands of ringed brown snake (*Pseudonaja modesta*) identified by DESeq2 algorithm. Only the venom gene families that include procoagulant toxins are shown. Abbreviations: KTSPi, Kunitz-type serine protease inhibitor; PLA₂, phospholipase A₂; TPM, transcripts per million.

	Toxin-ID	Venom gene	Hatchlings TPM	Adult 1 TPM	Adult 2 TPM	log2FoldChange in adults	Adjusted p-value	Toxin activity
1	PMO.PLA2.ID01	PLA2	1156.69	4785.43	9655.76	10.18	4,78783E-92	Coagulopathy
2	PMO.KTSPi.ID03	KTSPi	113.98	5883.73	21596.84	14.49	1,26743E-64	Unknown
3	PMO.KTSPi.ID02	KTSPi	42428.23	0	0	-11.46	2,15257E-19	Unknown
4	PMO.KTSPi.ID06	KTSPi	0	78.82	260.08	12.80	2,06403E-12	Unknown
5	PMO.KTSPi.ID04	KTSPi	24762.36	3294.17	16221.63	6.20	7,50352E-12	Unknown
6	PMO.PLA2.ID02	PLA2	204.77	4775.93	9.46	10.83	6,84318E-09	Coagulopathy
7	PMO.KTSPi.ID05	KTSPi	0	10.47	83.75	10.73	6,27557E-08	Unknown
8	PMO.KTSPi.ID01	KTSPi	151.86	7639.96	2.14	11.51	0,000100521	Unknown
9	PMO.KTSPi.ID07	KTSPi	822.91	3.57	4.18	-0.31	0,75824653	Coagulopathy
10	PMO.KTSPi.ID08	KTSPi	476.42	0	0.93	-2.47	#N/A	Unknown

Table S5. Overview of venom and tissue samples included in this study.

Abbreviations: QLD, Queensland; SA, South Australia; SVL, snout–vent length.

Species	Snake ID	Locality	Developmental life stage	Size (SVL; cm)	Included in following venom analysis:			
					Proteomics	Transcriptomics	Clotting assay	Prothrombin assay
<i>P. aspidorhyncha</i>	PAS1	Cunnamulla, QLD	Hatchling	NA	Yes	Yes	Yes	Yes
<i>P. aspidorhyncha</i>	PAS2	Cunnamulla, QLD	Hatchling	NA	Yes	Yes	Yes	Yes
<i>P. modesta</i>	PMOD1	Mixed heritage	Hatchling	NA	Yes	Yes	Yes	No
<i>P. modesta</i>	PMOD2	Mixed heritage	Hatchling	NA	Yes	Yes	Yes	No
<i>P. textilis</i>	CB1A	Myola, QLD	Hatchling	NA	Yes	Yes	Yes	Yes
<i>P. textilis</i>	CB2B	Myola, QLD	Hatchling	NA	Yes	Yes	Yes	Yes
<i>P. aspidorhyncha</i>	01	Cunnamulla, QLD	4 months	NA	Yes	No	Yes	Yes
<i>P. aspidorhyncha</i>	02	Cunnamulla, QLD	4 months	NA	Yes	No	Yes	Yes
<i>P. aspidorhyncha</i>	03	Cunnamulla, QLD	4 months	NA	Yes	No	Yes	Yes
<i>P. textilis</i>	01	Myola, QLD	4 months	NA	Yes	No	Yes	Yes
<i>P. textilis</i>	02	Myola, QLD	4 months	NA	Yes	No	Yes	Yes
<i>P. textilis</i>	03	Myola, QLD	4 months	NA	Yes	No	Yes	Yes
<i>P. textilis</i>	04	Myola, QLD	4 months	NA	Yes	No	Yes	Yes
<i>P. textilis</i>	05	Myola, QLD	4 months	NA	Yes	No	Yes	Yes
<i>P. textilis</i>	06	Myola, QLD	4 months	NA	Yes	No	Yes	No
<i>P. textilis</i>	07	Myola, QLD	4 months	NA	Yes	No	Yes	No
<i>P. aspidorhyncha</i>	01	Cunnamulla, QLD	6 months	41.0	Yes	No	Yes	Yes
<i>P. aspidorhyncha</i>	02	Cunnamulla, QLD	6 months	34.2	Yes	No	Yes	Yes
<i>P. aspidorhyncha</i>	03	Cunnamulla, QLD	6 months	37.1	Yes	No	Yes	Yes
<i>P. textilis</i>	01	Myola, QLD	6 months	35.5	Yes	No	Yes	Yes
<i>P. textilis</i>	02	Myola, QLD	6 months	37.0	Yes	No	Yes	Yes
<i>P. textilis</i>	03	Myola, QLD	6 months	35.6	Yes	No	Yes	Yes
<i>P. textilis</i>	04	Myola, QLD	6 months	38.4	Yes	No	Yes	Yes
<i>P. textilis</i>	05	Myola, QLD	6 months	39.6	Yes	No	Yes	Yes

<i>P. aspidorhyncha</i>	01	Cunnamulla, QLD	12 months	62.0	Yes	No	Yes	Yes
<i>P. aspidorhyncha</i>	02	Cunnamulla, QLD	12 months	57.5	Yes	No	Yes	Yes
<i>P. aspidorhyncha</i>	03	Cunnamulla, QLD	12 months	55.5	Yes	No	Yes	Yes
<i>P. textilis</i>	01	Myola, QLD	12 months	75.5	Yes	No	Yes	Yes
<i>P. textilis</i>	02	Myola, QLD	12 months	67.0	Yes	No	Yes	Yes
<i>P. textilis</i>	03	Myola, QLD	12 months	71.0	Yes	No	Yes	Yes
<i>P. textilis</i>	04	Myola, QLD	12 months	69.5	Yes	No	Yes	Yes
<i>P. textilis</i>	05	Myola, QLD	12 months	73.0	Yes	No	Yes	Yes
<i>P. aspidorhyncha</i>	PAS25	Middleback Ranges, SA	Adult	NA	Yes	Yes	Yes	Yes
<i>P. aspidorhyncha</i>	PAS26	Middleback Ranges, SA	Adult	NA	Yes	Yes	Yes	Yes
<i>P. modesta</i>	PMOD8	Mixed heritage	Adult	NA	Yes	Yes	Yes	No
<i>P. modesta</i>	PMOD16	Mixed heritage	Adult	NA	Yes	Yes	Yes	No
<i>P. textilis</i>	CB440	Adelaide region, SA	Adult	NA	Yes	Yes	Yes	Yes
<i>P. textilis</i>	CB489	Adelaide region, SA	Adult	NA	Yes	Yes	Yes	Yes

Table S6. Overview of snout–vent length data for ancestral state estimation analysis. The snout–vent length data for *Pseudonaja mengdeni* (previously mentioned as *P. "nuchalis"* "Orange with black head"), *Pseudonaja nuchalis* (previously mentioned as *P. "nuchalis"* "Darwin morph") and *Pseudonaja aspidorhyncha* (previously mentioned as *P. "nuchalis"* "Southern morph" South Australia) was based on their previously described subspecies within the former *P. nuchalis* clade. Asterisk (*) indicates standard deviation instead of standard error. Abbreviations: NSW, New South Wales; NT, Northern Territory, QLD, Queensland; SA, South Australia; SE, standard error; SVL, snout–vent length.

	Adult males			Adult females		
Species	Mean SVL (cm)	SE (cm)	Sample size (N)	Mean SVL (cm)	SE (cm)	Sample size (N)
<i>Oxyuranus scutellatus</i>	156.4	3.6	55	140.0	4.4	23
<i>Oxyuranus microlepidotus</i>	132.0	6.8	13	143.8	6.3	6
<i>Oxyuranus temporalis</i>	137.0	0	1	129.3	9.0	3
<i>Pseudonaja guttata</i>	67.9	1.8	65	70.7	1.8	52
<i>Pseudonaja modesta</i>	35.9	0.5	127	41.2	0.6	38
<i>Pseudonaja ingrami</i>	120.3	4.7	9	122.6	4.4	6
<i>Pseudonaja mengdeni</i>	90.6	2.0	54	85.7	2.7	27
<i>Pseudonaja nuchalis</i>	94.5	2.9	22	81.1	2.7	19
<i>Pseudonaja textilis</i> NSW	110.1	2.4	90	102.7	1.9	45

<i>Pseudonaja textilis</i> QLD and NT	120.3	2.3	76	101.8	2.8	54
<i>Pseudonaja textilis</i> SA	96.1	2.4	44	89.0	3.9	38
<i>Pseudonaja</i> <i>inframacula</i>	92.9	3.0	34	82.6	3.1	22
<i>Pseudonaja</i> <i>aspidorhyncha</i>	99.9	2.6	46	93.9	3.8	19
<i>Pseudonaja affinis</i>	108.5	2.7	49	108.8	2.6	35
<i>Vermicella annulata</i> NSW	42.1	1.0	38	54.4	1.5	38
<i>Vermicella annulata</i> QLD	36.8	0.9	46	54.4	1.2	42
<i>Vermicella intermedia</i>	35.45	5.79*	13	41.5	7.6*	15
<i>Vermicella multifasciata</i>	33.33	7.6*	3	25.0	0*	1
<i>Vermicella snelli</i>	39.5	0*	1	42.5	4.2*	5
<i>Vermicella vermiformis</i>	43.25	3.18*	2	48.3	1.7*	3
<i>Neelaps bimaculatus</i>	29.3	0.8	25	33.6	0.9	22
<i>Neelaps calonotos</i>	20.5	0.2	30	22.4	0.3	32