

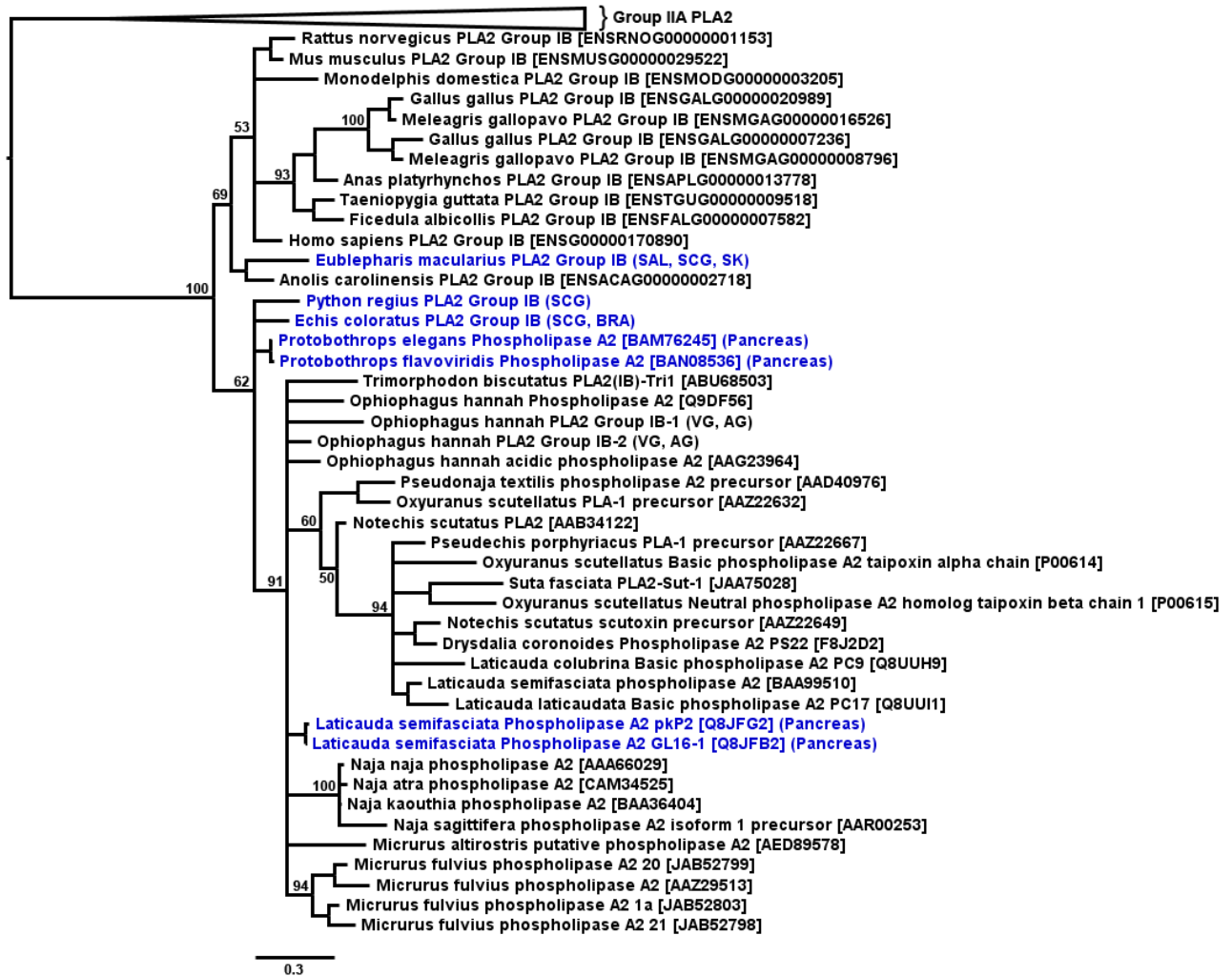
## Supplementary material

**Supplementary table S1.** Sequencing and assembly metrics for tissue assemblies, based on two individuals per tissue for leopard gecko (*Eublepharis macularius*), rough green snake (*Opheodrys aestivus*) and royal python (*Python regius*) skin, scent glands and salivary glands and corn snake scent gland and salivary gland. Only a single corn snake skin sample provided RNA of high enough quality for sequencing. *Echis coloratus* values are derived from four adult individuals for venom gland, two adult individuals for skin, scent gland, kidney and brain and one individual for liver and ovary. SAL, salivary gland; SCG, scent gland; VG, venom gland; KID, kidney; PE, paired-end.

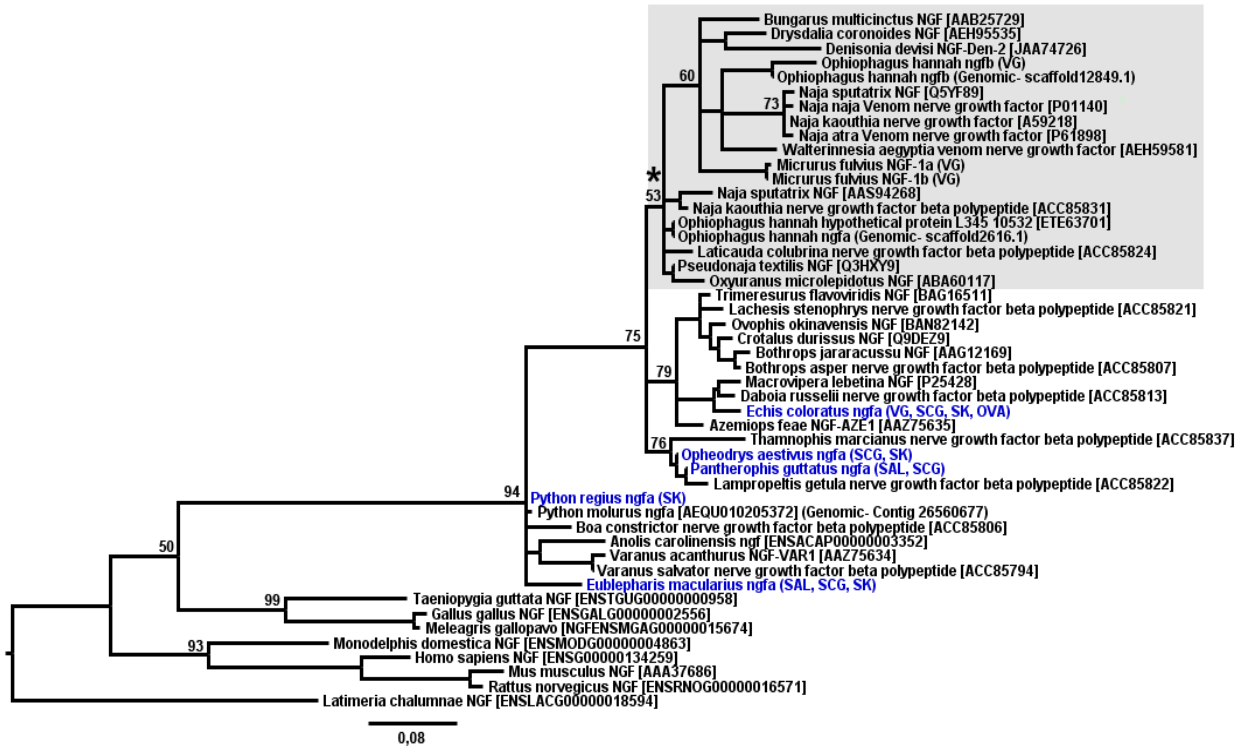
Species	Tissue	Total number of PE reads	Total number of bases	Number of contigs	Number of contigs >300bp	Contig N50 (bp)	Max contig (bp)
<i>Pgu</i>	SAL	25,655,661	5,131,132,200	64,595	43,565	1,916	17,102
	SCG	25,982,209	5,196,441,800	110,016	70,265	2,345	17,065
	Skin	7,862,371	1,572,474,200	51,199	35,969	1,329	19,348
<i>Oae</i>	SAL	24,959,242	4,991,848,400	65,393	42,558	1,780	17,524
	SCG	28,136,146	5,627,229,200	126,321	77,954	2,064	17,135
	Skin	16,398,925	3,279,785,000	92,597	57,242	1,918	33,155
<i>Pre</i>	SAL	28,035,045	5,607,009,000	73,492	48,727	2,265	33,655
	SCG	24,575,003	4,915,000,600	163,065	104,329	3,156	20,966
	Skin	15,643,272	3,128,654,400	67,200	47,819	1,864	25,879
<i>Ema</i>	SAL	29,882,110	5,976,422,000	111,345	73,027	2,439	24,285
	SCG	25,502,521	5,100,504,200	129,951	85,014	2,330	29,392
	Skin	14,675,568	2,935,113,600	92,506	61,456	2,057	27,091
<i>Eco</i>	VG	110,032,016	22,173,182,778	117,125	81,798	2,623	30,131
	SCG	27,206,987	5,441,397,400	138,852	87,389	2,444	36,612
	Skin	14,166,420	2,833,284,000	77,402	50,860	1,725	30,610
	Ovary	18,155,364	3,667,383,528	81,682	52,264	2,023	16,376
	KID	41,148,101	8,311,916,402	120,728	76,660	2,044	12,930
	Brain	31,934,884	6,450,846,568	195,958	134,236	3,552	20,155
	Liver	7,095,517	1,433,294,434	31,205	18,169	950	9,939

**Supplementary table S2.** Sequence and assembly metrics for king cobra (*Ophiophagus hannah*) venom gland, accessory gland and pooled tissue (heart, lung, spleen, brain, testes, gall bladder, pancreas, small intestine, kidney, liver, eye, tongue and stomach) data from Vonk et al. (2013).

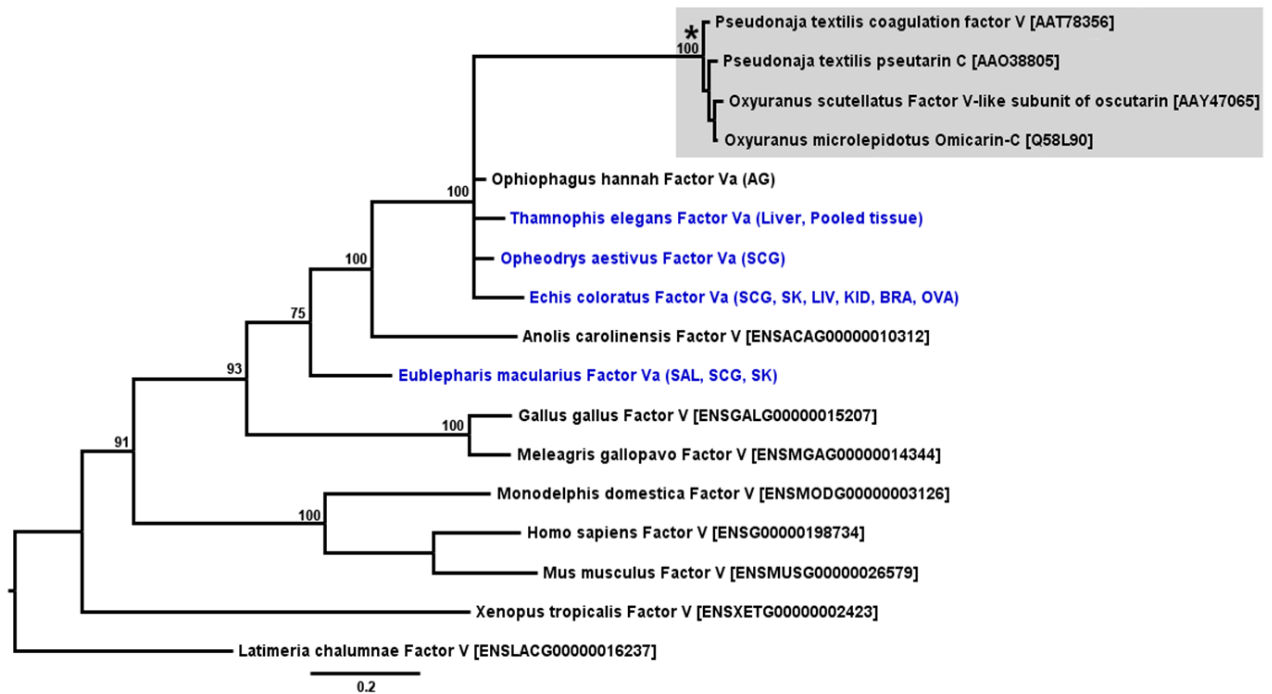
Tissue	Total number of reads	Total number of bases	Number of contigs	Number of contigs >300bp	Contig N50 (bp)	Max contig (bp)
Venom gland	15,166,590	834,162,450	6123	2,925	424	4,585
Accessory gland	11,209,677	616,532,235	9046	4,113	377	3,740
Pooled tissue	17,858,289	910,772,739	8877	4,135	413	5,733



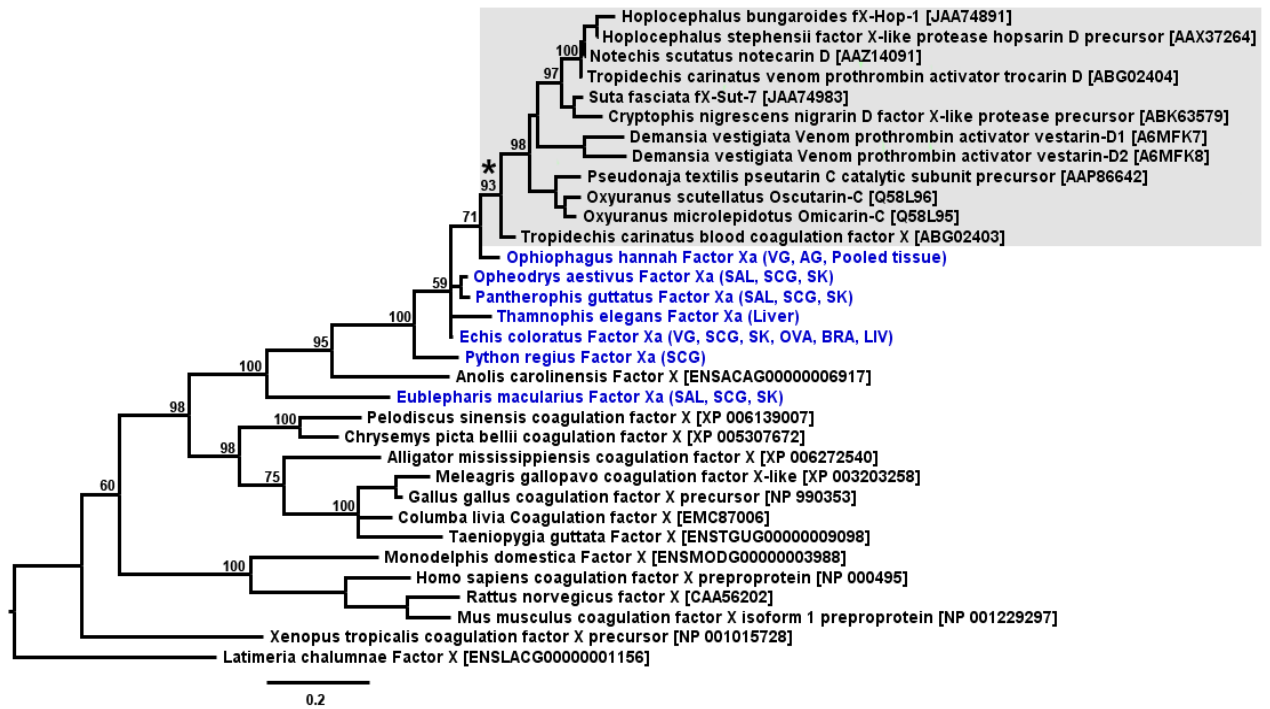
**Supplementary figure 1. Maximum likelihood tree of *Phospholipase A<sub>2</sub> group IB (PLA2 IB)* genes.** *Phospholipase A<sub>2</sub> group IB* genes are expressed in a diversity of tissues, including leopard gecko salivary glands. Following a gene duplication event somewhere in the advanced snake lineage one paralog has been restricted to the venom gland. Lineages for which body (non-venom gland) sequences are available are coloured blue and bootstrap values for 500 replicates are shown above branches.



**Supplementary figure 2. Maximum likelihood tree of nerve growth factor (ngf) genes.** *nerve growth factor* genes are expressed in a diversity of tissues, including venom and salivary glands. Following a gene duplication event (marked with \* and shaded) one paralog has been restricted to the venom gland. Lineages for which body (non-venom gland) sequences are available are coloured blue and bootstrap values for 500 replicates are shown above branches.



**Supplementary figure 3. Maximum likelihood tree of factor V genes.** *factor V* genes are expressed in a diversity of tissues, leopard gecko salivary glands. Following a gene duplication event (marked with \* and shaded) one paralog has been restricted to the venom gland. Lineages for which body (non-venom gland) sequences are available are coloured blue and bootstrap values for 500 replicates are shown above branches.



**Supplementary figure 4. Maximum likelihood tree of factor X genes.** *factor X* genes are expressed in a diversity of tissues, including venom and salivary glands. Following a gene duplication event (marked with \* and shaded) one paralog has been restricted to the venom gland. Lineages for which body (non-venom gland) sequences X-like are available are coloured blue and bootstrap values for 500 replicates are shown above branches.

## References for supplementary material

Vonk FJ, Casewell NR, Henkel CV, Heimberg AM, Jansen HJ, McCleary RJ, Kerckamp HM, Vos RA, Guerreiro I, Calvete JJ et al. 2013. The king cobra genome reveals dynamic gene evolution and adaptation in the snake venom system. *Proc Natl Acad Sci U S A*. 110:20651-20656.