Convergent molecular evolution of toxins in the venom of advanced snakes (Colubroidea)

Xie, B.

Chapter 7. Supplementary Materials

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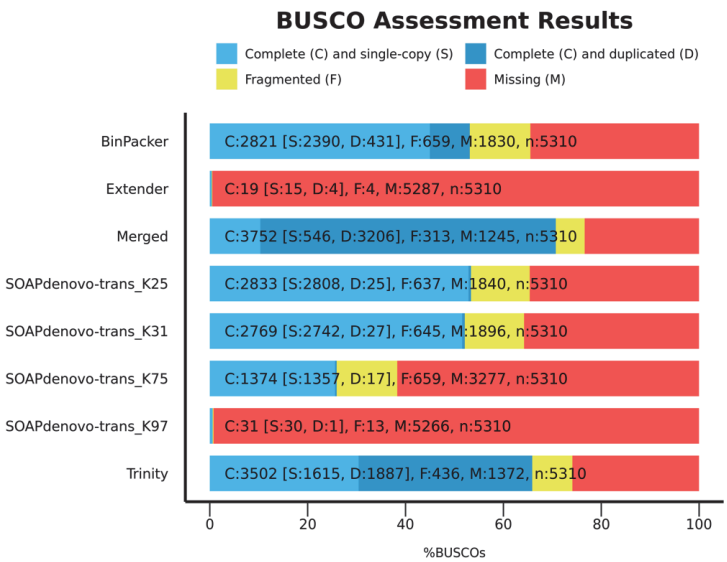
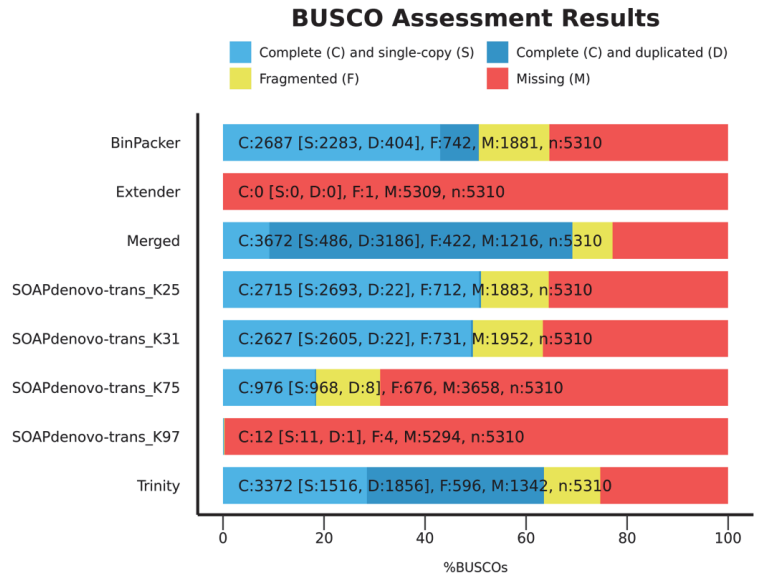
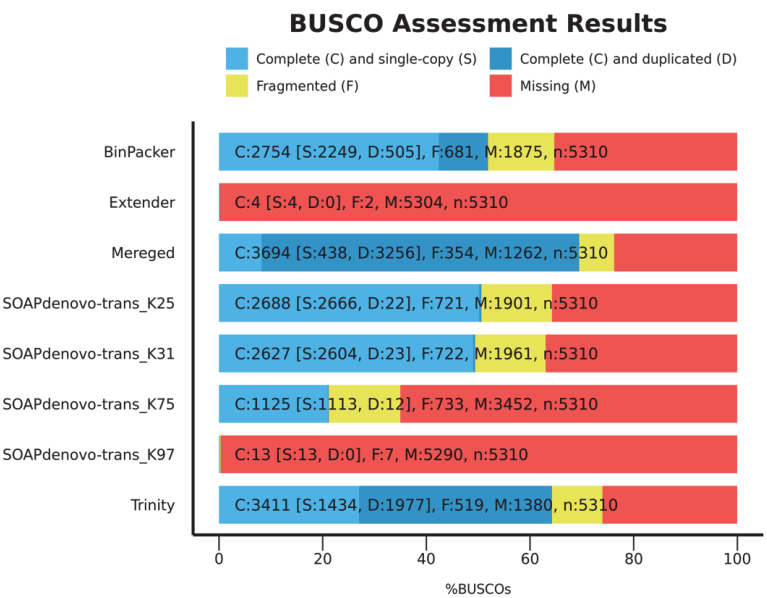
https://doi.org/10.1186/s12915-021-01208-9



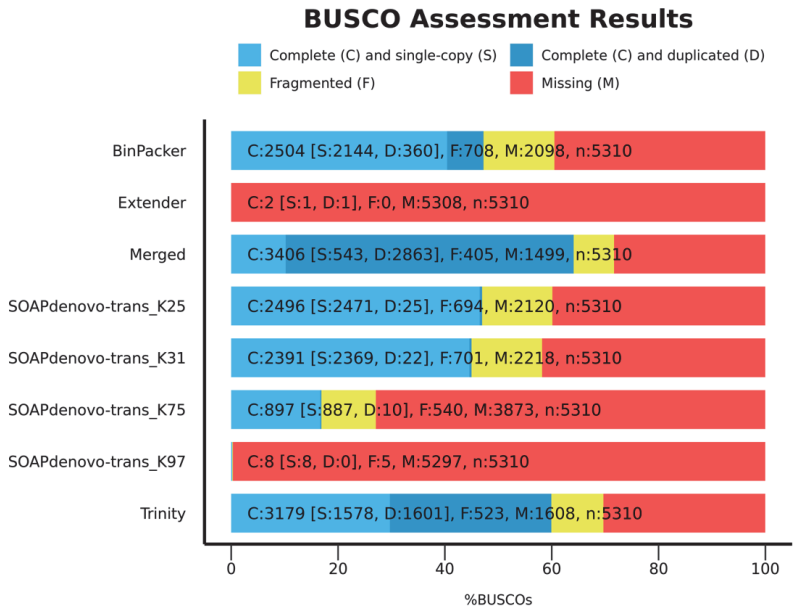
Supplementary Figure 1A: BUSCO completeness analyses of venom gland transcriptome assemblies for *Helicops leopardinus*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



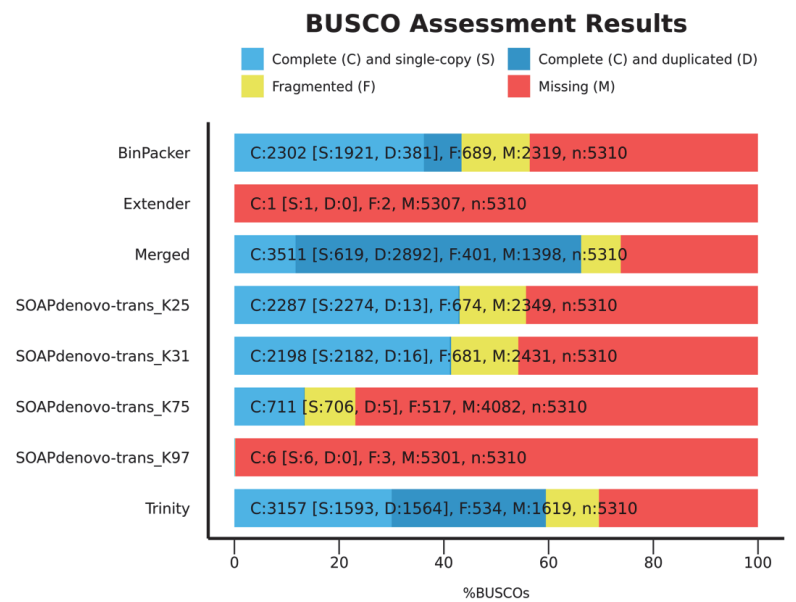
Supplementary Figure 1B: BUSCO completeness analyses of venom gland transcriptome assemblies for *Rhabdophis subminiatus*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



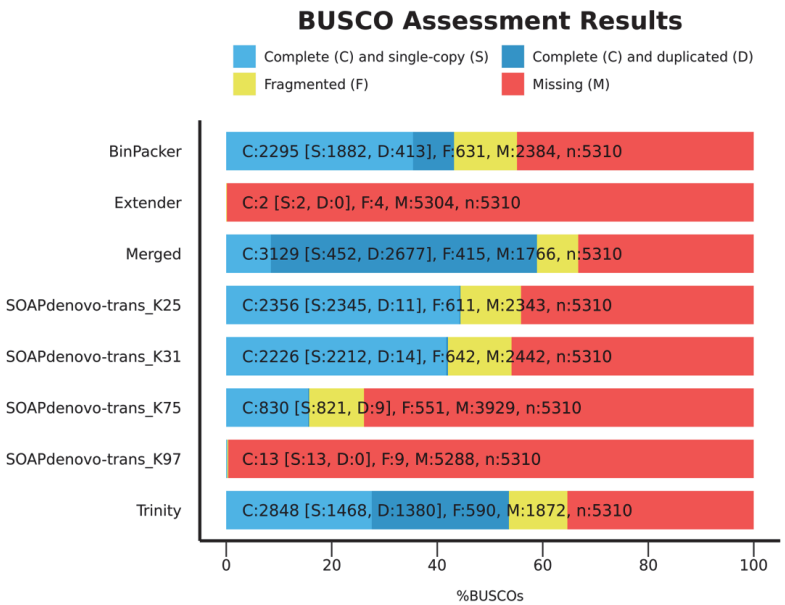
Supplementary Figure 1C: BUSCO completeness analyses of venom gland transcriptome assemblies for *Heterodon nasicus*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



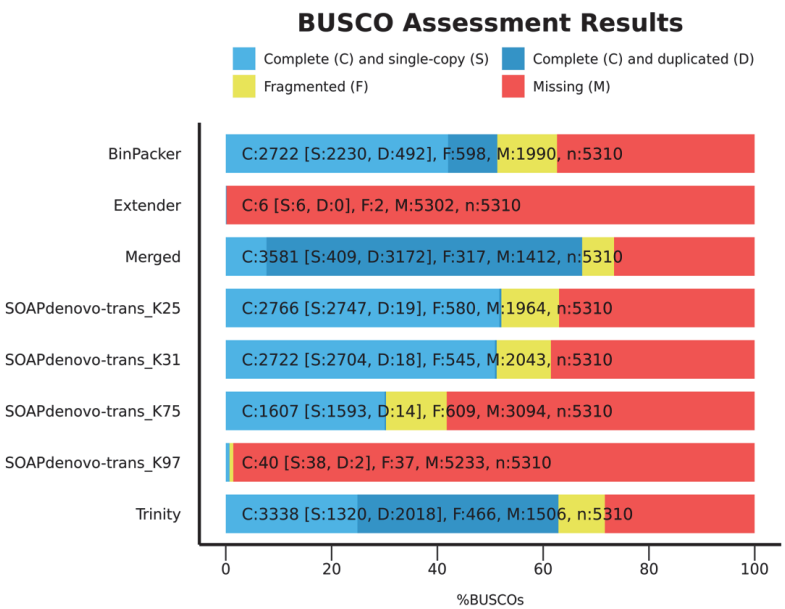
Supplementary Figure 1D: BUSCO completeness analyses of venom gland transcriptome assemblies for *Malpolon monspessulanus*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



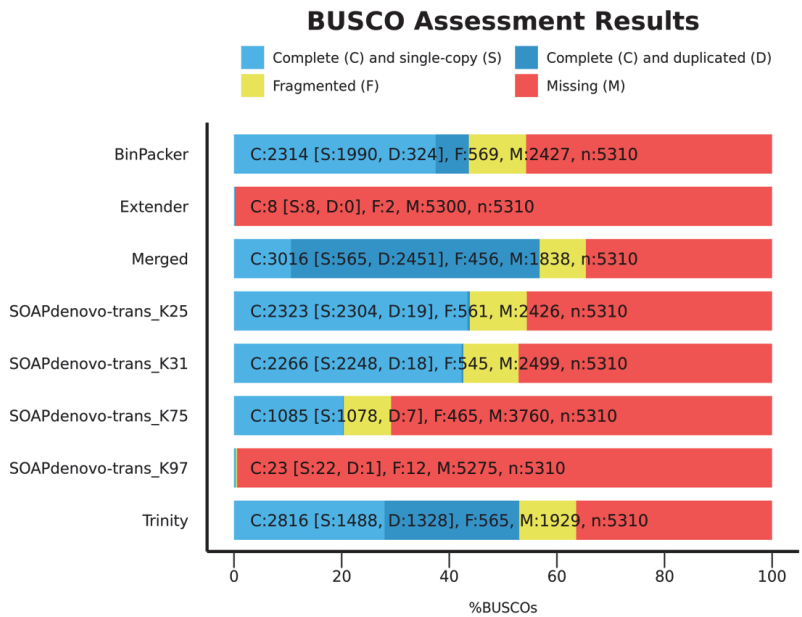
Supplementary Figure 1E: BUSCO completeness analyses of venom gland transcriptome assemblies for *Psammophis schokari*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



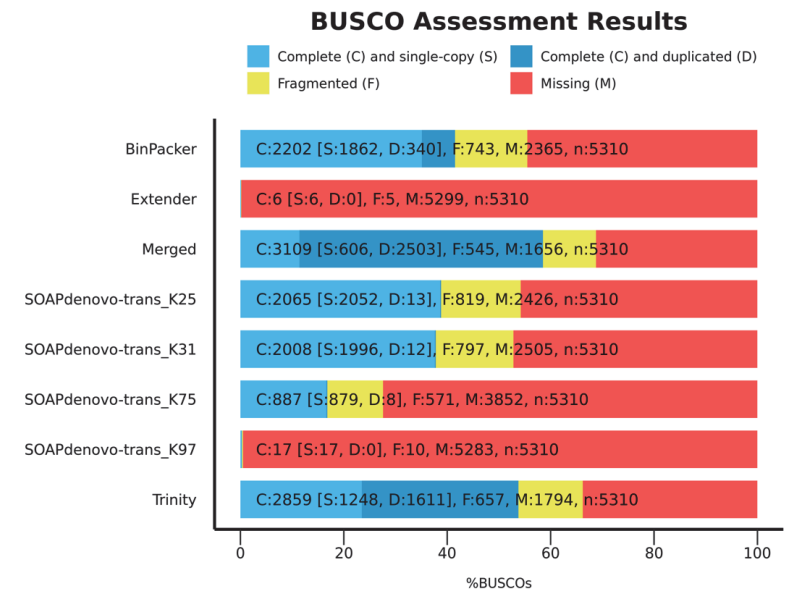
Supplementary Figure 1F: BUSCO completeness analyses of venom gland transcriptome assemblies for *Psammophis subtaeniatus*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



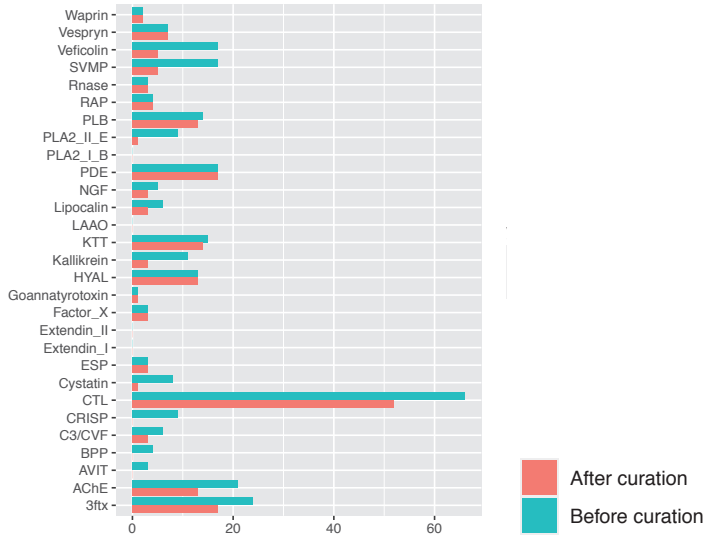
Supplementary Figure 1G: BUSCO completeness analyses of venom gland transcriptome assemblies for *Homalopsis buccata*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



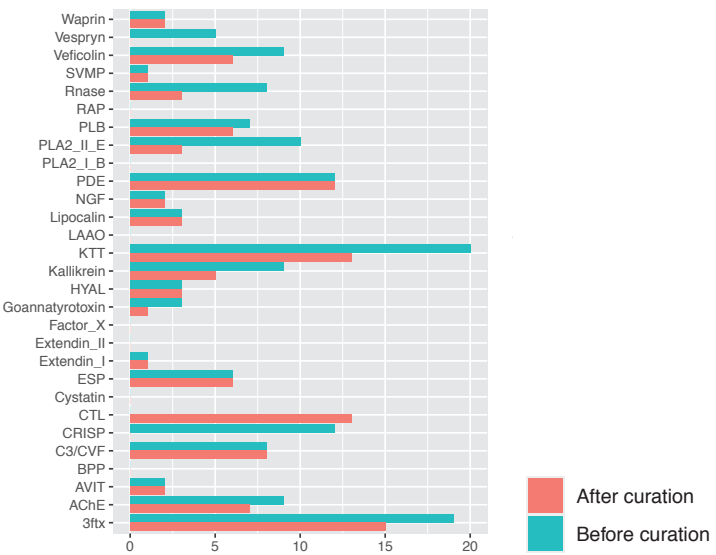
Supplementary Figure 1H: BUSCO completeness analyses of venom gland transcriptome assemblies for *Pseudocerastes urarachnoides*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



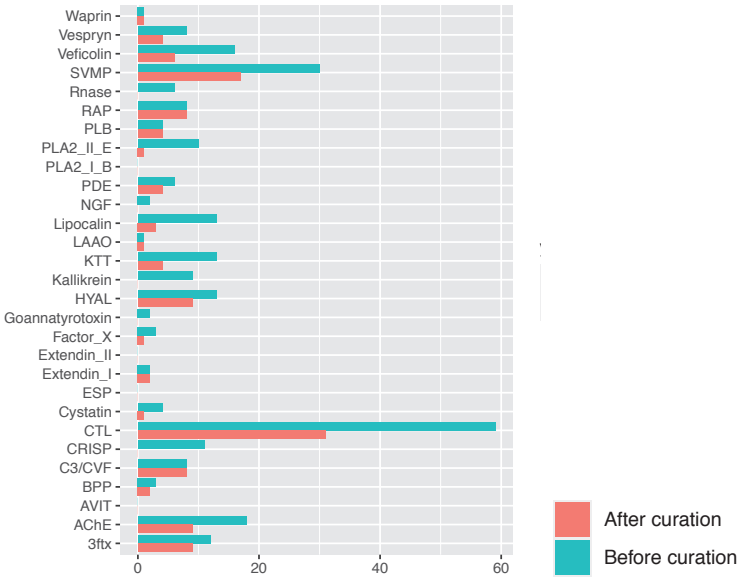
Supplementary Figure 1I: BUSCO completeness analyses of venom gland transcriptome assemblies for *Vipera transcaucasiana*. Snake contigs were matched against 5310 orthologous loci defined within Tetrapoda.



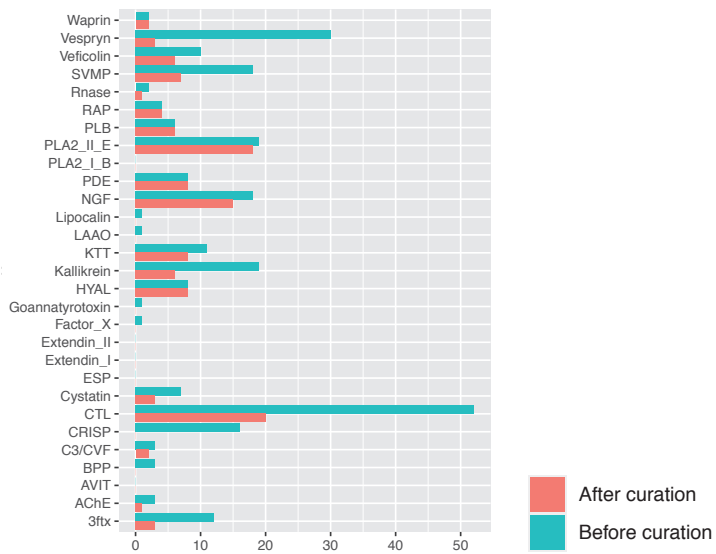
Supplementary Figure 2A: The statistics of toxins from *Helicops leopardinus* before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



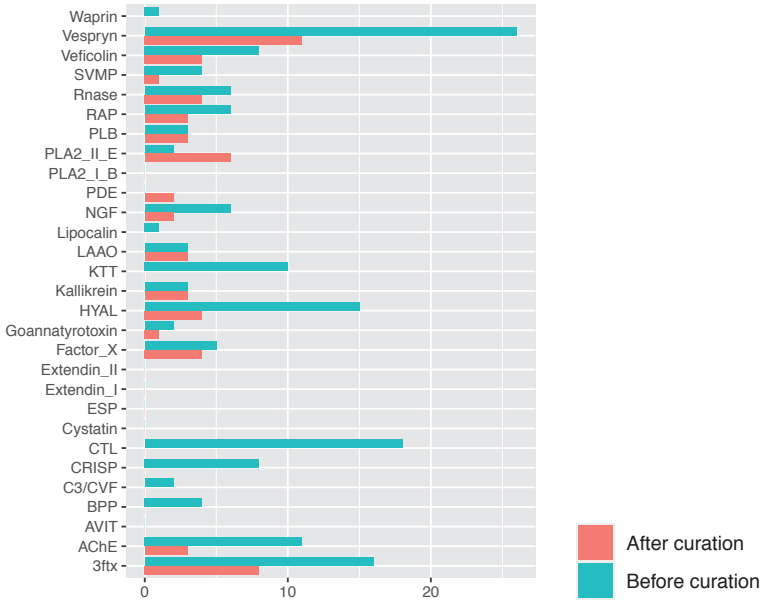
Supplementary Figure 2B: The statistics of toxins from *Rhabdophis subminiatus* before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



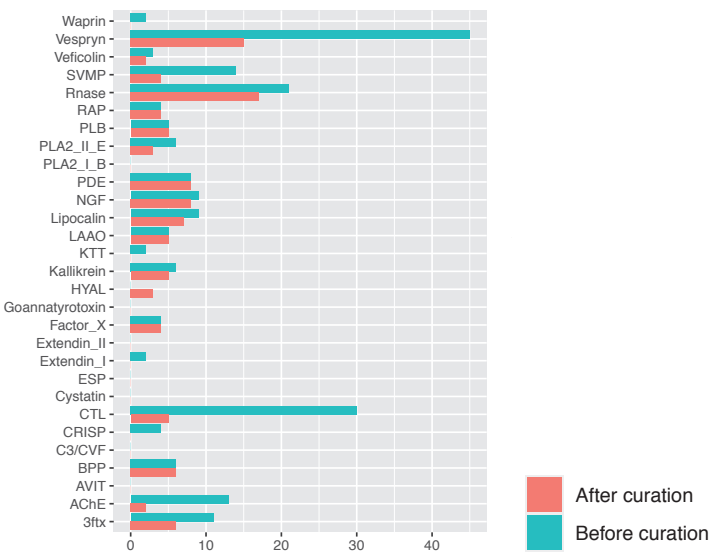
Supplementary Figure 2C: The statistics of toxins from *Heterodon nasicus* before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



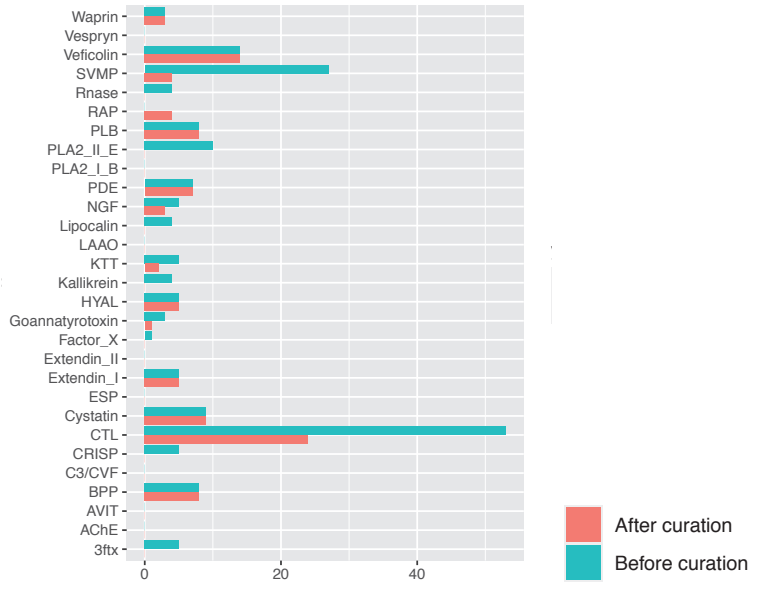
Supplementary Figure 2D: The statistics of toxins from *Malpolon monspessulanus* before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



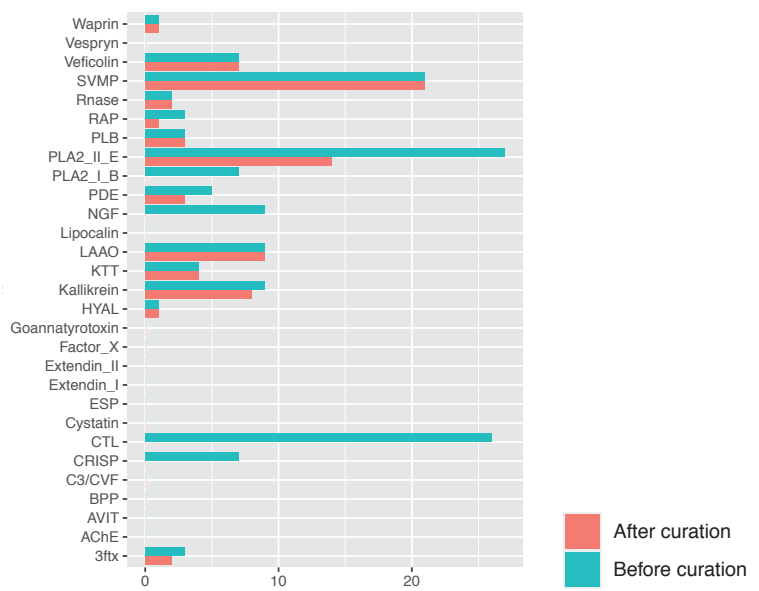
Supplementary Figure 2E: The statistics of toxins from *Psammophis schokari* before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



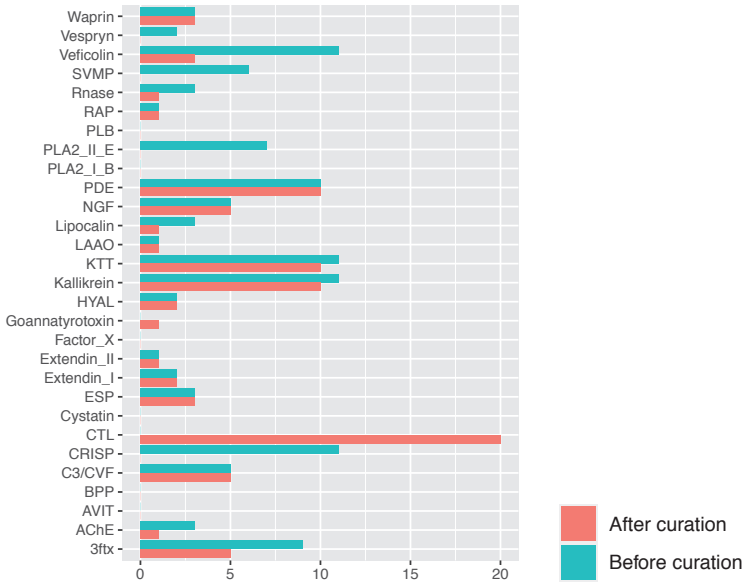
Supplementary Figure 2F: The statistics of toxins from *Psammophis subtaeniatus* before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



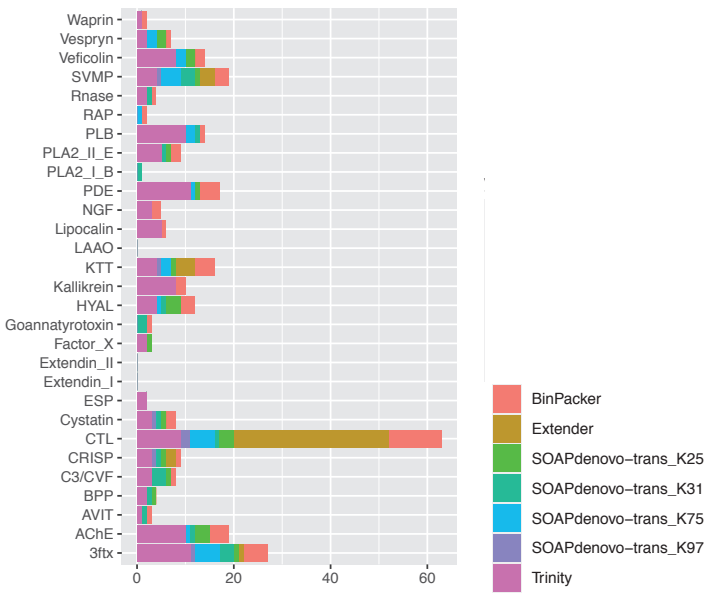
Supplementary Figure 2G: The statistics of toxins from *Homalopsos buccata* before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



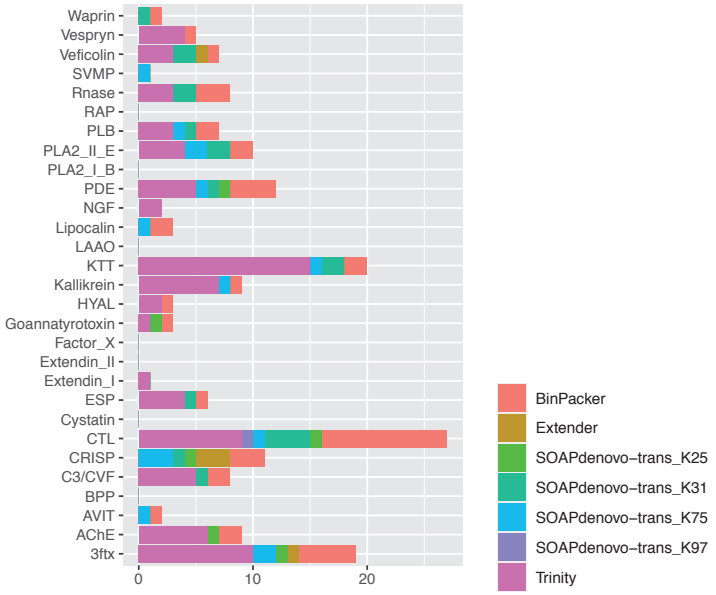
Supplementary Figure 2H: The statistics of toxins before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



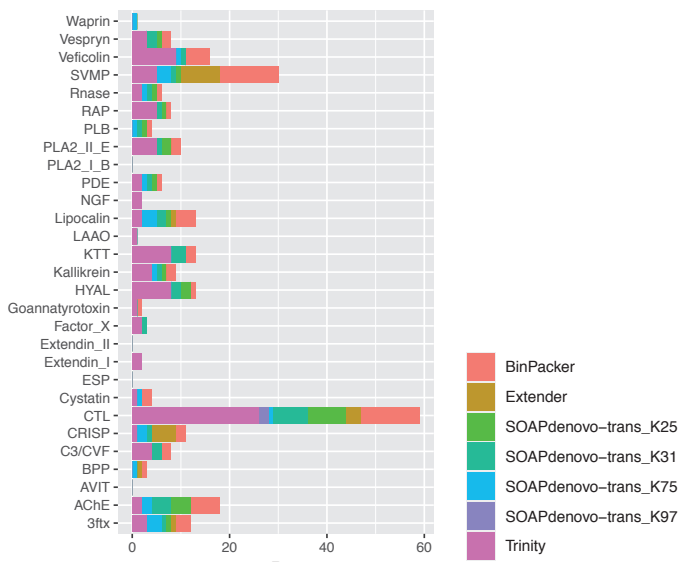
Supplementary Figure 2I: The statistics of toxins before and after curation. As can be seen, curation leads to a huge decline in the number of both toxin families diversities and toxin transcripts. Some toxin families are discarded as a whole. X axis is toxin family name and Y axis is the number of the corresponding toxin transcripts.



Supplementary Figure 3A: Toxin distribution of *Helicops leopardinus* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.

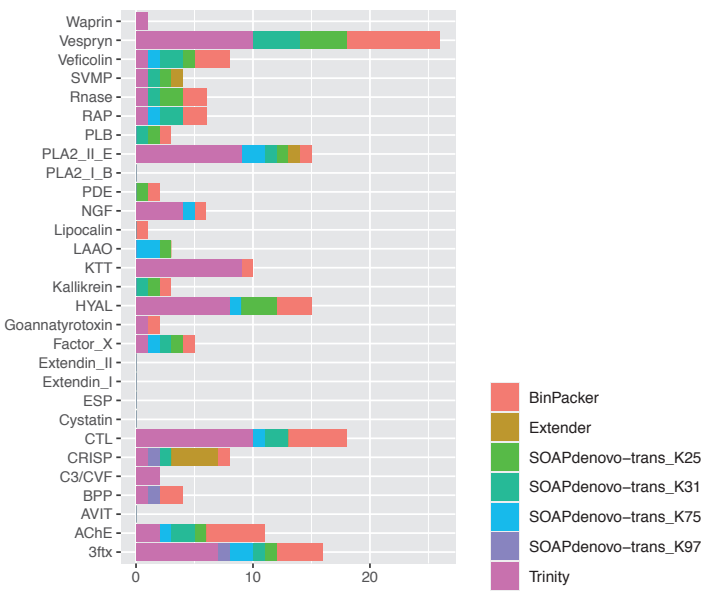


Supplementary Figure 3B: Toxin distribution of *Rhabdophis subminiatus* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.

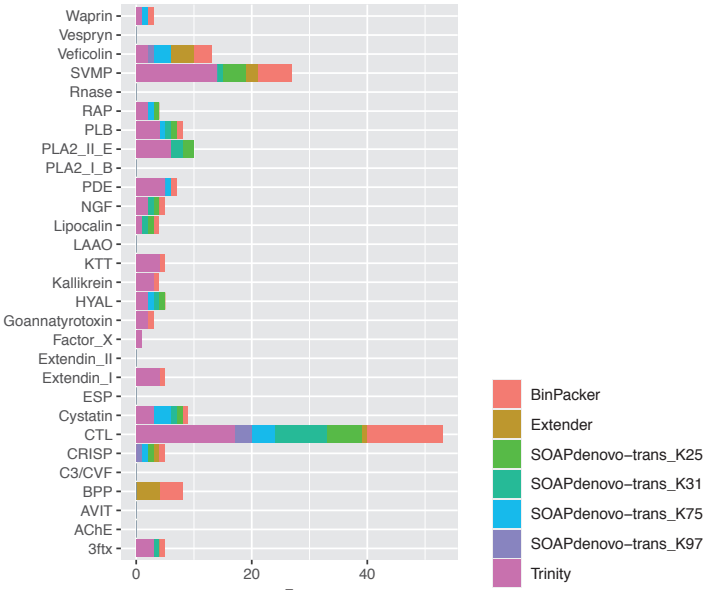


Supplementary Figure 3C: Toxin distribution of *Heterodon nasicus* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.

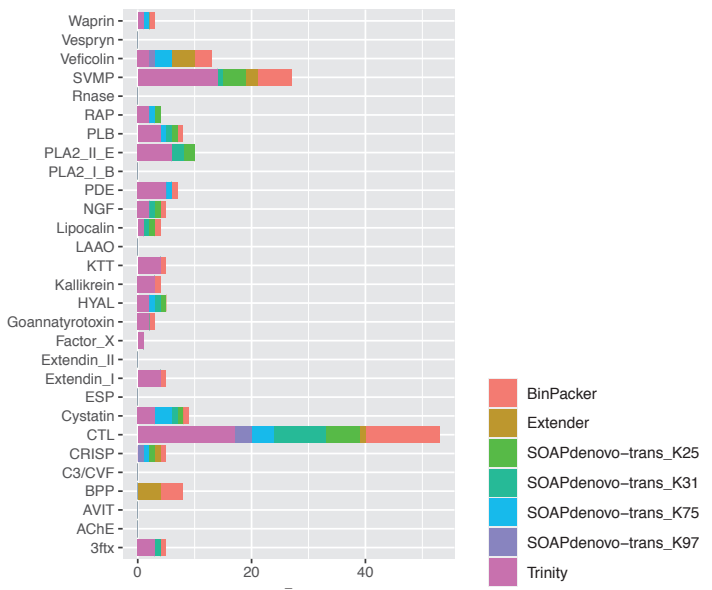
Supplementary Figure 3D: Toxin distribution of *Malpolon monspessulanus* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



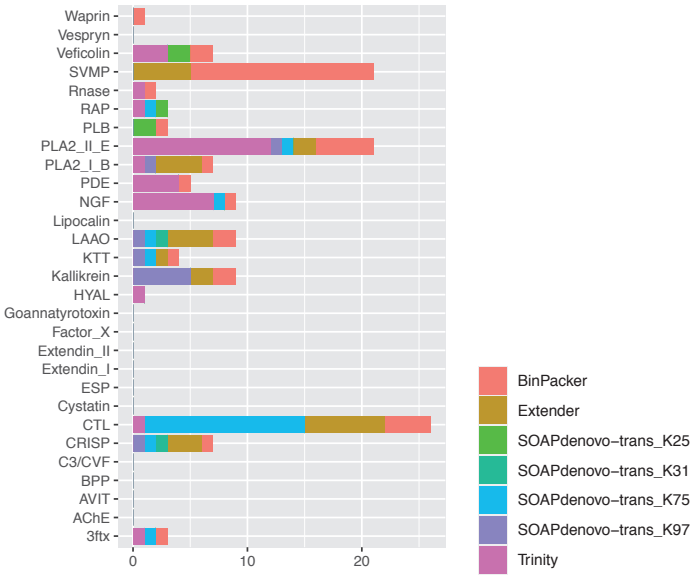
Supplementary Figure 3E: Toxin distribution of *Psammophis schokari* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



Supplementary Figure 3F: Toxin distribution of *Psammophis subtaeniatus* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.

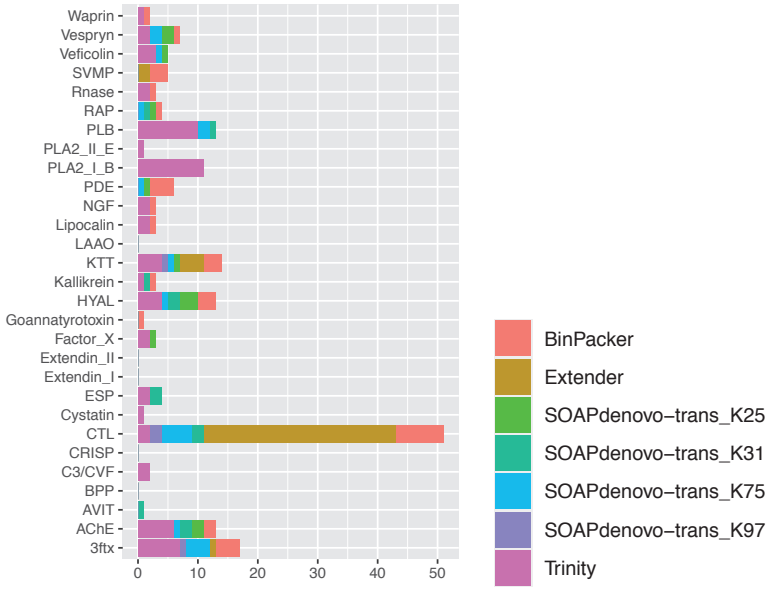


Supplementary Figure 3G: Toxin distribution of *Homalopsis buccata* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.

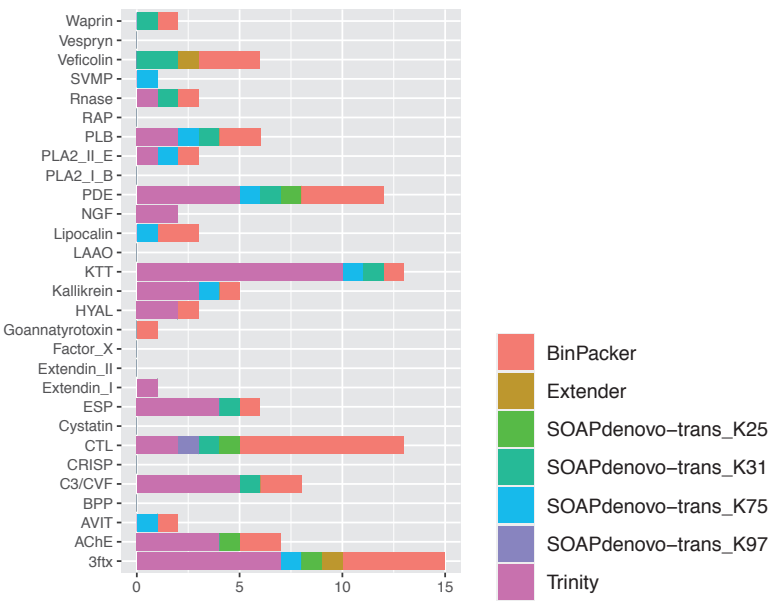


Supplementary Figure 3H: Toxin distribution of *Pseudocerastes urarachnoides* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.

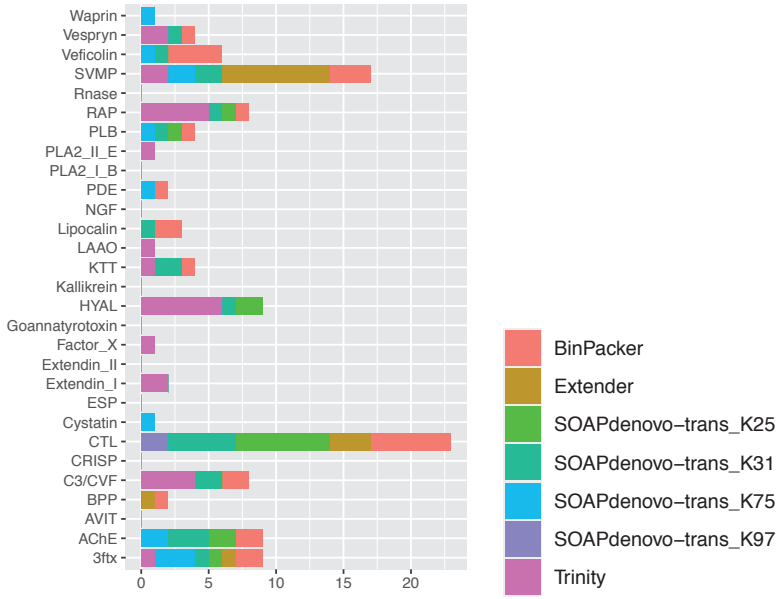
Supplementary Figure 3I: Toxin distribution of *Vipera transcaucasiana* before curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



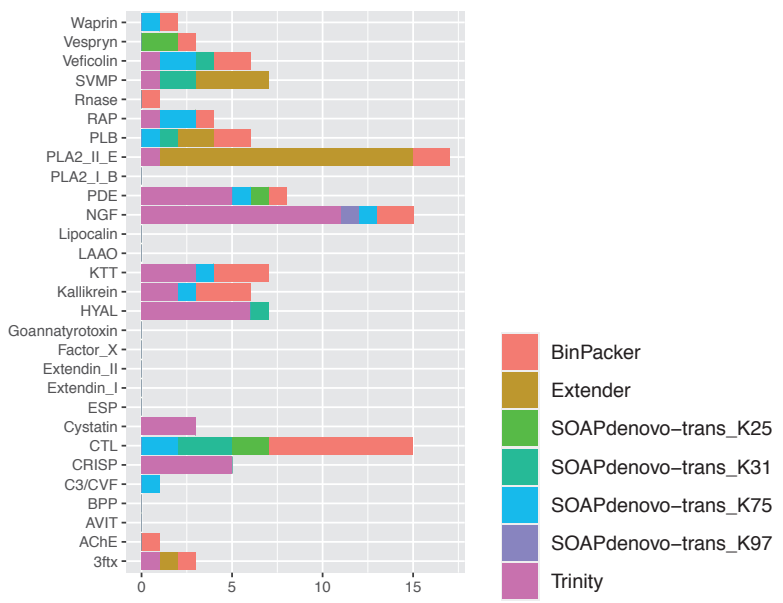
Supplementary Figure 4A: Toxin distribution of *Helicops leopardinus* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



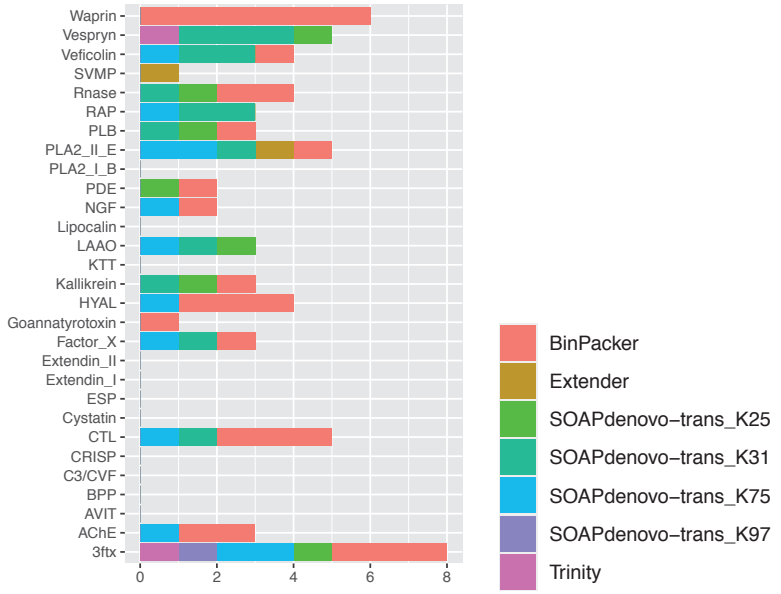
Supplementary Figure 4B: Toxin distribution of *Rhabdophis subminiatus* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



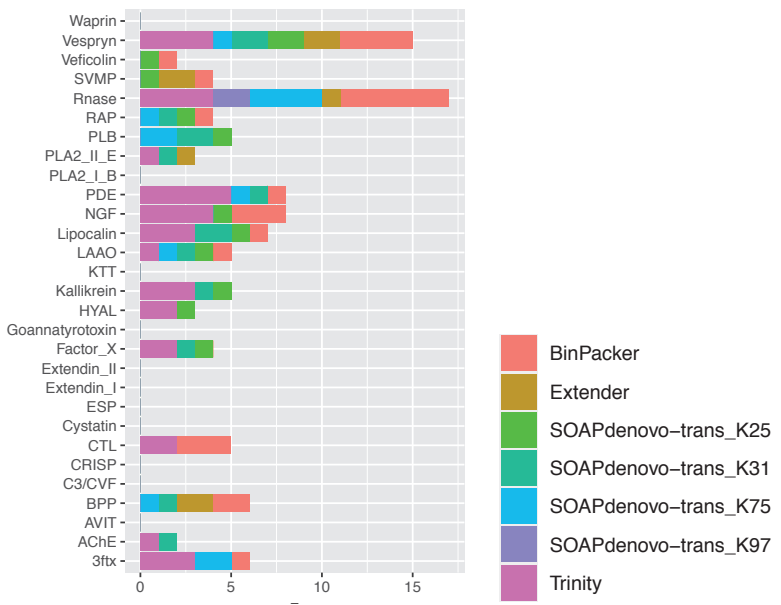
Supplementary Figure 4C: Toxin distribution of *Heterodon nasicus* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



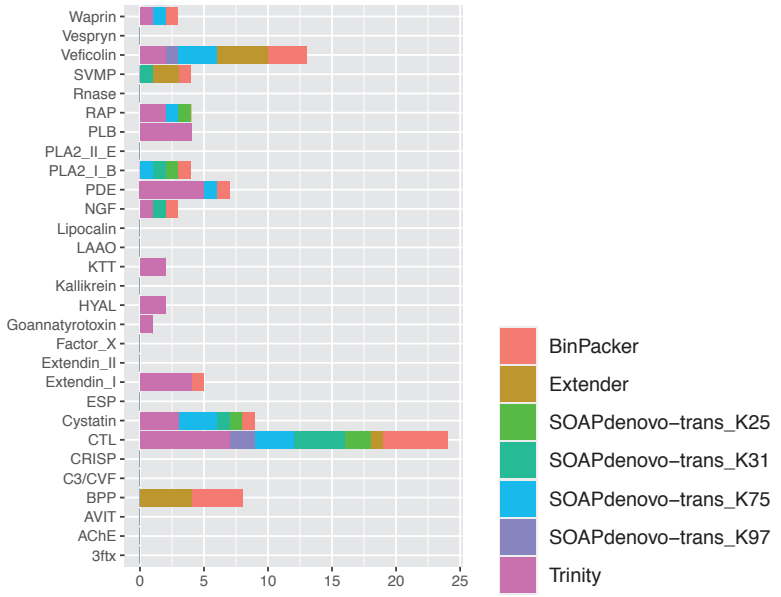
Supplementary Figure 4D: Toxin distribution of *Malpolon monspessulanus* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



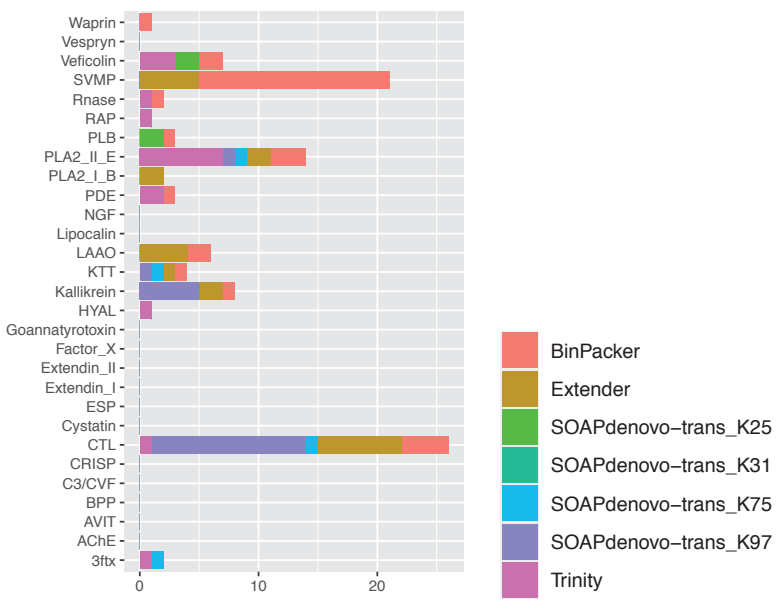
Supplementary Figure 4E: Toxin distribution of *Psammophis schokari* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



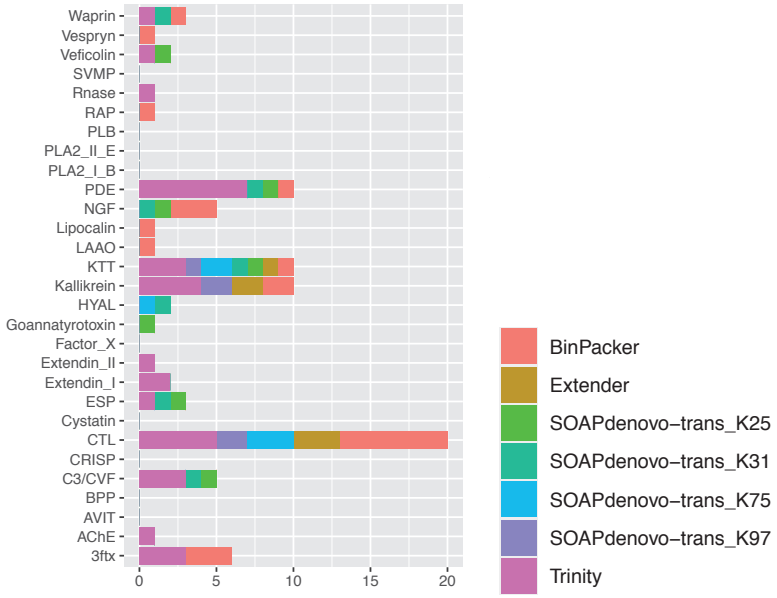
Supplementary Figure 4F: Toxin distribution of *Psammophis subtarniatus* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



Supplementary Figure 4G: Toxin distribution of *Homalopsis buccata* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



Supplementary Figure 4H: Toxin distribution of *Pseudocerastes urarachnoides* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.



Supplementary Figure 4I: Toxin distribution of *Vipera transcaucasiana* after curation. For each toxin family, the numbers of toxin transcripts recovered by different assembly methods are indicated by different colours.

Supplementary File 2: The settings for MrBayes

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log start replace;

set autoclose = no nowarn=no;

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prset applyto = (all) aamodelpr = mixed;

unlink revmat = (all) shape = (all) pinvar = (all) statefreq = (all) tratio = (all);

showmodel;

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sumt relburnin = yes burninfrac = 0.25 contype = halfcompat;

sump relburnin = yes burninfrac =0.25;

outgroup 1;

log stop;

end;

For the following **Supplementary Files**, they can be viewed via

https://figshare.com/articles/dataset/Supplementary_Files/15085353

Supplementary_File_1_inhouse_toxin_database.fasta

Supplementary_File_3_kunitz_alignment.fasta

Supplementary_File_4_kunitz_alignment.con.tre

Supplementary_File_5_lectin_alignment.fasta

Supplementary_File_6_lectin_tree.con.tre

Supplementary_File_7_SVMP_alignment.fasta

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Supplementary_File_9_SVMP_propeptide_alignment.fasta

Supplementary_File_10_SVMP_propeptide_tree.con.tre