**Supplementary material**

**Link to github repo**: <https://github.com/Rhia15/Dissertation.git>

**BUSCO scores for 53 initial genomes Table.1**

|  |  |  |
| --- | --- | --- |
| **common name** | **species name** | **busco\_genes amino acid collapsed isoformes** |
| Tree Shrew | *Tupaia chinensis* | 94.50% |
| Tasmanian | *Sarcophilus harrisii* | 97.90% |
| Elephant | *Elephas maximus* | 99.10% |
| Aardvark | *Orycteropus afer* | 96.80% |
| Sloth | *Choloepus didactylus* | 98.90% |
| Bat | *Desmodus rotundus* | 98.80% |
| Whale | *Balaenoptera musculus* | 98.90% |
| Molerat | *Nannospalax galili* | 96.70% |
| Human | *Homo sapiens* | 65.70% |
| Platypus | *Ornithorhynchus anatinus* | 97.70% |
| Rat / mouse | *Rattus norvegicus* | 64% |
| Ostritch | *Struthio* | 89.10% |
| guinea fowl | *Numida meleagris* | 96.40% |
| Golden eagle | *Aquila chrysaetos* | 95.30% |
| finch | *Taeniopygia guttata* | 93.70% |
| swift | *Apus apus* | 96.30% |
| cuckoo | *Cuculus canorus* | 98.00% |
| kittiwake | *Rissa tridactyla* | 97.60% |
| Tuatara | *Sphenodon punctatus* | 85.40% |
| Chinese softshell turtle | *Pelodiscus sinensis* | 87.50% |
| Goode's thornscrub tortoise | *Gopherus evgoodei* | 94.90% |
| Blue sea krait | *Laticauda laticaudata* | 75.20% |
| Leopard gecko | *Eublepharis macularis* | 99.50% |
| crocodile | *Crocodylus porosus* | 89% |
| leishan spiny toad | *Leptobrachium leishanense* | 93.30% |
| Tropic clawed frog | *Xenopus tropicalis* | 96.40% |
| BufoBufo | *Bufo bufo* | 97.20% |
| Bombina | *Bombina bombina* | 94.90% |
| GerSer | *Geotrypetes seraphini* | 97.80% |
| MicUni | *Microcaecilia unicolour* | 98.40% |
| RanTem | *Rana temporaria* | 96.70% |
| RhiBiv | *Rhinatrema bivittatum* | 98.30% |
| PleWal | *Pleurodeles waltl* | 93.80% |
| LitCat | *Lithobates catesbeianus* | 18.30% |
| XenLae | *Xenopus laevis* | 98.80% |
| NanPar | *Nanorana parkeri* | 94.60% |
| SpeBom | *Spea bombifrons* | 98.40% |
| aligator chinensis |  | 93.70% |
| najanja (indian cobra) |  | 70.50% |
| gorilla | *gorilla gorilla gorilla* | 99.00% |
| komodo |  | 97% |
| bearded |  | 98% |
| emu | *Dromaius novaehollandiae* | 95.30% |
| King cobra |  | 60.90% |
| Python |  | 91.00% |
| Brown snake |  | 96.30% |
| horse |  | 98.90% |
| Gray squirel |  | 99.40% |
| egretta |  |  |
| pigeon |  |  |
| Crested Ibis |  |  |
| White Rhino |  |  |
| Aligator Missipipiensis |  | 98.20% |
| Emperor penguin |  | 87.10% |
| King Cobra |  |  |
| Python |  | 91.00% |

**Table 2. Mammalian genomes – accession date- May 23rd 2023**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Superorder | Family | Species | Common name | Total length (GB) | Scaffold N50 (Mb) | Contig N50 (Kb) | Assembly level | Protein coding genes | Accession | Database | Reference |
| Metatheria | Dasyuridae | *Sarcophilus harrisii* | Tasmanian devil | 3.1 | 611.3 | 62.3 | Chromosome | 19,966 | GCF\_902635505.1 | NCBI RefSeq | [Stammnitz M *et al.,*](http://dx.crossref.org/10.1101/2022.05.27.493404) "The evolution of two transmissible cancers in Tasmanian devils", *bioRxiv*, 2022; |
| Afrotherian | Elephantidae (latest divergence) | *Elephas maximus indicus* | Elephant | 3.4 | 127.4 | 88 | Chromosome | 21,809 | GCF\_024166365.1 | NCBI | (Prado et al., 2023) |
| Xenarthra | Megalonychidae  (Late divergence) | *Choloepus didactylus* | Sloth | 3.2 | 146.2 | 21 | Chromosome | 23,549 | GCF\_015220235.1 | RefSeq | VGP BioProject PRJNA561937 |
| Laurasiatherian | Phyllostomidae | *Desmodus rotundus* | New world leaf-nosed bats | 2.1 | 160.1 | 6.8MB | Chromosome | 19,615 | GCF\_022682495.1 | NCBI | - |
| Laurasiatherian | Balaenopteridae | *Balaenoptera musculus* | Blue whale | 2.4 | 110.3 | 6.3Mb | Chromosome | 19,686 | GCF\_009873245.2 | NCBI | - |
| Laurasiatherian | Talpidae (early divergent) | *Nannospalax galili* | Upper Galilee mountains blind mole rat | 3.1 | 3.6 | 30.4 | Scaffold level | 20,986 | GCF\_000622305.1 | NCBI | [Fang X *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/24892994) "Genome-wide adaptive complexes to underground stresses in blind mole rats Spalax.", *Nat Commun*, 2014 Jun 3;5:3966 |
| Euarchontoglires | Tupaiidae (Early divergence) | *Tupaia chinensis* | Chinese Tree shrew | 2.8 | 3.7 | 25.9KB | Chromosome | 21,077 | GCF\_000334495.1 | RefSeq | [Fan Y *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/23385571) "Genome of the Chinese tree shrew.", *Nat Commun*, 2013;4:1426 |
| Monotremata | Ornithorhynchidae | *Ornithorhynchus anatinus* | Platypus | 1.9 | 83.3 | 15.1MB | Chromosome | 18,152 | GCF\_004115215.2 | NCBI RefSeq |  |
| Euarchontoglires | Homonidae | *Gorilla gorilla* | Gorilla | 3.6 | 151.6 | 151.6 | Chromosome | 23,010 | GCF\_029281585.1 | NCBI refseq |  |
| Laurasiatherian | Suidae | *Sus scrofa* | Pig | 2.5 | 88.2 | 88.2 | Chromosome | 20,790 | GCF\_000003025.6 | NCBI refseq | "An improved pig reference genome sequence to enable pig genetics and genomics research.", *Gigascience*, 2020 Jun 1;9(6) |
| Laurasiatherian | Rhinocerotidae | *Ceratotherium simum* | Rhino | 2.5 | 26.3 Mb | 93 kb | Scaffold | 33616 | GCF\_000283155.1 | NCBI RefSeq |  |

**Table 3. Aves genomes**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Order | Family | Species | Common name | Total length (Gb) | Scaffold N50 (Mb) | Contig N50 (Kb) | Assembly level | Protein coding genes | Accession | Database | Reference |
| Galliformes (Galonnserae)  Oldest | Numididae | *Numida meleagris* | Helmeted guinea fowl | 1 | 7.9 | 234.9 | Chromosome | 16,083 | GCF\_002078875.1 | NCBI RefSeq | - |
| Accipitriformes (Neognathae) older | Accipitridae | *Aquila chrysaetos chrysaetos* | Golden eagle | 1.2 | 46.9 | 21.9 | Chromosome | 16,702 | bAquChr1.2 | Ensembl |  |
| Passeriformes – recent divergence | Estrildidae | *Taeniopygia guttata* | Zebra finch | 1.1 | 71 | 9 Mb | Chromosome | 16,619 | bTaeGut1\_v1.p | Ensembl |  |
| Apodiformes (also an early divergent?) | apodidae | *Apus apus* | Common swift | 1.1 | 115.5 | 25.6 Mb | Chromosome | 14,765 | GCF\_020740795.1 | NCBI |  |
| Cuculiformes | Cuckoo | *Cuculus canorus* | Common cuckoo | 1.2 | 78.3 | 20.8MB | Chromosome | 16,774 | GCF\_017976375.1 | NCBI RefSeq | - |
| Charadriiformes | Laridae | *Rissa tridactyla* | Black-legged kittiwake | 1.4 | 88.2 | 15.7MB | Chromosome | 16,534 | GCF\_028500815.1 | NCBI RefSeq | - |
| paleognathae | Casuariidae | *Dromaius novaehollandiae* | Emu | 1.2 | 3.3 | 19,741 | Scaffold | 15,554 | GCF\_003342905.1 | NCBI Refseq | [Sackton TB *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/30948549) "Convergent regulatory evolution and loss of flight in paleognathous birds.", *Science*, 2019 Apr 5;364(6435):74-78  [Haddrath O *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/11370967) "Complete mitochondrial DNA genome sequences of extinct birds: ratite phylogenetics and the vicariance biogeography hypothesis.", *Proc Biol Sci*, 2001 May 7;268(1470):939-45 |
| Pelecaniformes | Threshkiornithidae | *Nipponia nippon* | Crested Ibis | 1.2 | 5.2 | 29.1kb | Scaffold | 15,032 | GCF\_000708225.1 | NCBI RefSeq |  |
|  |  |  | Pigeon | 1.1 | 14.2 | 26.6 | Scaffold | 15,575 | GCF\_000337935.1 | NCBI RefSeq |  |

**Table4. Reptilia genomes**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Order | Family | Species | Common name | Total length | Scaffold N50 (Mb) | Contig N50 (Kb) | Assembly level | Protein coding genes | Accession | Reference | Database |
| Rhynchocephalia | Sphenodontidae | *Sphenodon punctatus* | Tuatara | 4.3 | 3.1 | 27.1 | Scaffold | 17,648 | GCA\_003113815.1 | - | Ensembl |
| Testudines | Testudinidae (late divergence) | *Gopherus evgoodei* | Goodes thornscrub tortoise | 2.3 | 147.4 | 13Mb | Chromosome | 19,808 | GCA\_007399415.1 | VGP | Ensembl |
| Squamata | Gekkonidae (early divergence) | *Eublepharis macularis* | Leopard Gecko | 2.2 | 145.6 | 80.1 Mb | Chromosome | 20,469 | GCF\_028583425.1 | [Pinto BJ *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/36712019) "The revised reference genome of the leopard gecko ( *Eublepharis macularius* ) provides insight into the considerations of genome phasing and assembly.", *bioRxiv*, 2023 Feb 13; | NCBI RefSeq |
| Squamata | Varanidae | *Varanus komodoensis* | Komodo dragon | 1.5 | 23.8 | 20,696 | Scaffold | 17,968 | GCF\_004798865.1 |  |  |
| Squamata | Agamidae | *Pogona Viticeps* | Bearded dragon | 1.6 | 2.5Mb | 98,807 | Scaffold | 18,891 | GCF\_900067755.1 | [Georges A *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/26421146) "High-coverage sequencing and annotated assembly of the genome of the Australian dragon lizard Pogona vitticeps.", *Gigascience*, 2015;4:45 | NCBI RefSeq |
| Squamata | Elapidae | *Pseudonaja textilis* | Brown snake | 1.6 | 14.7Mb | 50.4kb | Scaffold | 19,358 | GCF\_900518735.1 |  | NCBI RefSeq |
| Crocodilia | Alligatoridae | *American Alligator* | Alligator mississipiensis | 2.1 | 7,093 | 18.6 MB | Scaffold | 18,942 | GCF\_000281125.3 | [St John JA](https://www.ncbi.nlm.nih.gov/pubmed/22293439)*[et al.,](https://www.ncbi.nlm.nih.gov/pubmed/22293439)* "Sequencing three crocodilian genomes to illuminate the evolution of archosaurs and amniotes.", *Genome Biol*, 2012 Jan 31;13(1):415 | NCBI RefSEq |

**Table5. Amphibia genomes**

|  |  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Order | Family | Species | Common name | Total length (Gb) | Scaffold N50 (Mb) | Contig N50 (Kb) | Assembly level | Protein coding | Genbank accession | Reference | Databse |
| Anura | Megophryidae | [*Leptobrachium leishanense*](https://www.ncbi.nlm.nih.gov/datasets/taxonomy/445787) | Leishan spiny toad | 3.5 | 394.7 | 1.9Mb | chromosome | 29,203 | GCA\_009667805.1 |  | Ensembl |
| Anura | Pipidae  May change it to ncbi | *Xenopus tropicalis* | Tropical clawed frog | 1.5 | 152 | 14.6 Mb | Chromosome | 22,107 | GCA\_000004195.4 | Published online: [Mitros T](http://dx.crossref.org/10.1016/j.ydbio.2019.03.015)*[et al.,](http://dx.crossref.org/10.1016/j.ydbio.2019.03.015)* "A chromosome-scale genome assembly and dense genetic map for Xenopus tropicalis", *Developmental Biology*, 2019;452(1):8-20 | Ensembl |
| Anura | Bufonidae | *Bufo bufo* | Common Toad | 5 | 635.7 | 4 Mb | chromosome | 21,517 | GCF\_905171765.1 | - | NCBI |
| Anura | Bombinatoridae | *Bombina bombina* | European fire-bellied toad | 10 | 1.2 | 3.8 Mb | Chromosome | 22,468 | GCF\_027579735.1 | [Rhie A *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/33911273) "Towards complete and error-free genome assemblies of all vertebrate species.", *Nature*, 2021 Apr;592(7856):737-746 | NCBI |
| Gymnophiona | Caeciliidae | *Geotrypetes seraphini* | Gaboon caecilian | 3.8 | 272.6 | 20.7 Mb | Chromosome | 19,223 | GCF\_902459505.1 | (Ovchinnikov et al., 2022) | NCBI |
| Gymnophiona | Siphonopidae | *Microcaecilia unicolour* | Tiny Cayenne caecilian | 4.7 | 376.1 | 3.7 Mb | Chromosome | 20,868 | GCF\_901765095.1 | (Ovchinnikov et al., 2022) | NCBI |
| Anura | Ranidae | *Rana temporaria* | Common frog | 4.1 | 481.8 | 6.3 Mb | Chromosome | 23,707 | GCF\_905171775.1 | (Streicher et al., 2021)  <https://www.pnas.org/doi/abs/10.1073/pnas.1501764112> | NCBI |
| Gymnophiona | Rhinatrematidae | *Rhinatrema bivittatum* | Two-lined caecilian | 5.3 | 486.9 | 3.2 Mb | Chromosome | 21,554 | GCF\_901001135.1 | - | NCBI |
| Anura | Pelobatidae | *Spea bombifrons* | Spadefoot toad | 987.7 Mb | 114.2 Mb | 21.2 Mb | Chromosome | 19,086 | GCF\_027358695.1 | [Rhie A *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/33911273) "Towards complete and error-free genome assemblies of all vertebrate species.", *Nature*, 2021 Apr;592(7856):737-746 | NCBI |
| Caudata | Salamandridae | *Pleurodeles waltl* | Iberian ribbed newt | 20.3 Gb | 1.2 Gb | 45.6 Mb | Chromosome | 13,359 | GCA\_026652325.1 |  | NCBI |
| Anura | Pipidae | *Xenopus laevis* | African clawed frog | 2.7 Gb | 155.3 | 22.5 Mb | Chromosome | 34,476 | GCF\_017654675.1 | [Roe BA *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/4019494) "The complete nucleotide sequence of the Xenopus laevis mitochondrial genome.", *J Biol Chem*, 1985 Aug 15;260(17):9759-74 | NCBI |
| Anura | Dicroglossidae | *Nanorana parkeri* | High Himalaya frog | 2.1 Gb | 1.1 | 32.8 kb | Scaffold | 18,958 | GCF\_000935625.1 | [Jiang L *et al.,*](https://www.ncbi.nlm.nih.gov/pubmed/25758045) "The complete mitochondrial genome sequence of the Xizang Plateau frog, Nanorana parkeri (Anura: Dicroglossidae).", *Mitochondrial DNA A DNA Mapp Seq Anal*, 2016 Sep;27(5):3184-5 | NCBI |

**A diagram with many colored circles

Description automatically generatedA diagram of colorful circles

Description automatically generatedA diagram of a number of dots

Description automatically generatedA diagram of a cell

Description automatically generatedA screen shot of a diagram

Description automatically generatedA screen shot of a diagram

Description automatically generatedA diagram of different colored circles

Description automatically generatedA screen shot of a diagram

Description automatically generatedA diagram of a diagram

Description automatically generated**

**a**

**Figure 1. Enrichments of the 10 significantly expanded orthogroups analysed in the main text (in order) (OG7, OG23, OG54, OG58, OG68, OG73, OG87, OG122, OG999, OG1255)**

**b**

**c**

**d**

**A diagram of circles and text

Description automatically generated**

A diagram of a diagram

Description automatically generatedA screen shot of a graph

Description automatically generatedA diagram of a cell

Description automatically generatedA diagram of a diagram

Description automatically generatedA diagram of different colored circles

Description automatically generatedA diagram of a number of dots

Description automatically generated

**Figure 2. Enrichments of the 6 significantly expanded orthogroups analysed in the main text (in order) (18, 100, 155, 148, 186, 430)**

**Table 6 – the raw data for domain architecture counts with eggNOG PFAM annotations mapped for each significantly expanded orthogroup at the amphibian stem lineage**

|  |  |  |
| --- | --- | --- |
|  | **Orthogroup 7** | |
| PFAM | amniote | amphibian |
| - | 5 | 0 |
| 7tm\_4 | 796 | 177 |
|  |  |  |
|  | **Orthogroup 17 (not mentioned in main text due to lack of studies)** | |
|  | amniote | amphibian |
| CBFD\_NFYB\_HMF,Histone | 8 | 0 |
| CENP-T\_C,Histone,Histone\_H2A\_C | 110 | 70 |
| Histone,Histone\_H2A\_C | 256 | 274 |
|  |  |  |
|  | **Orthogroup 54** | |
|  | amniote | amphibian |
| - | 0 | 3 |
| 7tm\_4 | 2 | 388 |
| Trypsin | 0 | 1 |
|  |  |  |
|  |  |  |
|  | **Orthogroup 58** | |
|  | amniote | amphibian |
| - | 7 | 10 |
| ADP\_PFK\_GK | 0 | 1 |
| CCDC73 | 0 | 1 |
| Chromo,MBD,Myb\_DNA-binding | 0 | 1 |
| DDE\_3,HTH\_Tnp\_Tc3\_2 | 0 | 1 |
| Ets | 0 | 2 |
| Gb3\_synth,Gly\_transf\_sug | 0 | 1 |
| Gelsolin,Sec23\_BS,Sec23\_helical,Sec23\_trunk,zf-Sec23\_Sec24 | 0 | 1 |
| PABP,RRM\_1 | 0 | 2 |
| PLA2\_inh,UPAR\_LY6 | 97 | 219 |
| RVT\_1 | 0 | 1 |
| Sulfotransfer\_1,WSC | 0 | 1 |
| Toxin\_TOLIP,UPAR\_LY6 | 0 | 1 |
| UPAR\_LY6 | 16 | 18 |
| zf-C2H2 | 1 | 0 |
|  |  |  |
|  | **Orthogroup 68** | |
|  | amniote | amphibian |
| BPL\_LplA\_LipB | 0 | 1 |
| C8,Cys\_knot,Mucin2\_WxxW,TIL,VWD | 31 | 54 |
| C8,Cys\_knot,TIL,VWD | 24 | 17 |
| C8,F5\_F8\_type\_C,Mucin2\_WxxW,TIL,VWD | 0 | 10 |
| C8,Mucin2\_WxxW,TIL,VWC,VWD | 53 | 75 |
| C8,Mucin2\_WxxW,TIL,VWD | 3 | 19 |
| C8,Mucin2\_WxxW,VWD | 3 | 2 |
| C8,TIL,VWA,VWA\_N2,VWC,VWD | 1 | 1 |
| C8,TIL,VWD | 33 | 14 |
| Cys\_knot,DAN | 0 | 1 |
| Cys\_knot,LCCL,VWC | 0 | 1 |
| FTO\_CTD,FTO\_NTD | 0 | 1 |
| Mucin2\_WxxW | 2 | 0 |
|  | **Orthogroup 73** | |
| PFAM | amniote | amphibian |
| - | 0 | 1 |
| 7tm\_4 | 0 | 1 |
| AAA | 1 | 0 |
| ADAM\_spacer1,I-set,Ig\_3,Kunitz\_BPTI,PLAC,TSP\_1,WAP | 0 | 2 |
| Alpha\_kinase,Sel1 | 0 | 4 |
| Antistasin,Kunitz\_BPTI,Lustrin\_cystein,Thyroglobulin\_1,WAP | 1 | 3 |
| Antistasin,Thyroglobulin\_1,WAP | 0 | 2 |
| Antistasin,VWC,WAP | 0 | 1 |
| Arm\_2 | 0 | 1 |
| ASC,CAP,Ldl\_recept\_a,Trypsin,WAP | 0 | 1 |
| ATP\_bind\_1 | 0 | 1 |
| BTB\_2,Ion\_trans | 1 | 0 |
| Cation\_ATPase\_N,E1-E2\_ATPase,Hydrolase,P5-ATPase | 1 | 1 |
| CCDC158 | 0 | 2 |
| Cementoin,WAP | 11 | 3 |
| CENP-K | 1 | 0 |
| DUF4504 | 0 | 4 |
| EGF | 0 | 1 |
| Elf-1\_N,Ets | 0 | 1 |
| Frizzled,Fz | 1 | 0 |
| Homeobox | 0 | 1 |
| KRAB,zf-C2H2,zf-H2C2\_2 | 1 | 0 |
| Kunitz\_BPTI | 5 | 8 |
| Kunitz\_BPTI,Lustrin\_cystein,MANEC,WAP | 0 | 2 |
| Kunitz\_BPTI,WAP | 6 | 14 |
| Methyltr\_RsmB-F,Methyltr\_RsmF\_N,P120R | 0 | 1 |
| Methyltransf\_4 | 0 | 3 |
| SYS1 | 1 | 0 |
| TRAM\_LAG1\_CLN8 | 0 | 2 |
| WAP | 109 | 126 |
| WAP,fn3 | 1 | 2 |
|  |  |  |
|  | **Orthogroup 122** | |
| PFAM | amniote | amphibian |
| - | 0 | 1 |
| Astacin | 15 | 15 |
| Astacin,CUB | 16 | 108 |
| Astacin,CUB,DERM | 1 | 4 |
| Astacin,CUB,DERM,ShK | 0 | 1 |
| Astacin,CUB,Kringle,ShK | 0 | 10 |
| Astacin,CUB,MAM | 9 | 9 |
| Astacin,CUB,MAM,Sushi | 0 | 1 |
| Astacin,CUB,ShK | 0 | 23 |
| Astacin,CUB,TSP\_1 | 0 | 3 |
| Astacin,EGF,MAM | 1 | 0 |
| Astacin,LRR\_8,Lectin\_C,ShK | 0 | 1 |
| Astacin,ShK | 0 | 11 |
| BTB,zf-C2H2 | 0 | 1 |
| CUB | 0 | 1 |
| CUB,DUF3481,F5\_F8\_type\_C,MAM | 0 | 1 |
| CUB,NTR | 0 | 1 |
|  |  |  |
|  |  |  |
|  | **Orthogroup 999** | |
| PFAM | amniote | amphibian |
| TAS2R | 149 | 159 |
|  |  |  |
| PFAM | **Orthogroup 87** | |
| adh\_short | 149 | 159 |
|  |  |  |
| PFAM | **Orthogroup 23** | |
| p450 | 302 | 349 |
|  |  |  |
|  | **Orthogroup 1255** | |
| PFAM | amniote | amphibian |
| C2-set\_2,I-set,Ig\_2,Ig\_3,V-set | 0 | 2 |
| C2-set\_2,ig | 0 | 11 |
| C2-set\_2,Ig\_2,Ig\_3,V-set | 0 | 7 |
| C2-set\_2,Ig\_2,Ig\_3,V-set,ig | 6 | 54 |
| C2-set\_2,V-set | 0 | 1 |
| CNH,Pkinase | 0 | 1 |
| Ig\_2,Ig\_3,V-set,ig | 0 | 1 |
| Ig\_3,V-set | 0 | 1 |
| Rhodanese | 0 | 1 |
| V-set | 0 | 1 |

**Please note: Phylopic silhouette references used for CAFÉ gene birth and death tree can be found in the GitHub repo, under phylopic.csv**