1.  $\frac{1}{2}$  (a)  $\frac{1}{2}$  (b)  $\frac{1}{2}$  (c)  $\frac{1}{2}$  (d)  $\frac{1}{2}$  (e)  $\frac{1}{2}$  $\sim$   $\sqrt{C_1}$   $\sqrt{C_2}$   $\sqrt{C_3}$ 

 $\sim 1 - \sqrt{2} - \sqrt{2}$ 

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is the sected to the evolution of  $e$  into the evolution of a mode  $e$  and squame generate generate genomes genomes genomes genomes genomes and squamate generation of amounts and squamate generation of a model squamate ge and provide  $\mathcal{F}$  and provide much needed to existing information on  $\mathcal{F}$  in  $\mathcal{F}$  in  $\mathcal{F}$  and  $\mathcal{F}$  and  $\mathcal{F}$  in  $\math$  $t = \frac{1}{2}$  and  $t = \frac{1}{2}$  and  $t = \frac{1}{2}$  and  $t = \frac{1}{2}$  are multiple line  $\frac{1}{2}$  and  $\frac{1}{2}$  are multiple line  $\frac{1}{2}$  and  $\frac{1}{2}$  are multiple line including  $\frac{1}{2}$  and  $\frac{1}{2}$  are multiple line includi individuals of Heloderma, Pogona, and Varanus –  $\frac{1}{2}$  line  $\frac{1}{2}$  line  $\frac{1}{2}$  line  $\frac{1}{2}$  line  $\frac{1}{2}$ which also includes snakes and is proposed to have evolved to have evolved venoms on its and its and  $\mathcal{E}$ et al.  $2006$ ). These and other lizard genomes are expected to provide the providence of  $\mathcal{R}$  and  $\mathbf{e}$ evolutionary and comparative comparative context for understanding the origins of venoms in squamates, the origin number of the state venture evolved, and from  $\mathcal{E}_{\text{ref}}$ 

Squamate Genome Size

 $\mathbf{F}_{\mathbf{G}}e_n$  is  $\mathbf{F}_{\mathbf{G}}e_n = \frac{1}{2} \sum_{k=1}^{\infty} \frac{1}{k} \sum_{k=1}^{\infty} \frac{1}{k} \frac{1}{k} \sum_{k=1}^{\infty} \frac{1}{k}$  $t_{\rm t}$ the effort republic and  $\frac{1}{2}$  in  $\frac{1}{2}$  in  $\frac{1}{2}$  in  $\frac{1}{2}$  is one individual to  $\frac{1}{2}$  in  $\frac{1}{2}$  is one in  $\frac{1}{2}$  in  $\frac{1}{2}$  in  $\frac{1}{2}$  is one in  $\frac{1}{2}$  in  $\frac{1}{2}$  in  $\frac{1}{2}$  is o interest might be related to changes in genome size. In genome size  $\mathbb{R}$  , repetitive element content, organism  $\mathbb{R}$  and  $\mathbb{R}$  and longevity,  $\sigma$  rate  $\mathcal{P}_k$  rate and development rate all been proposed to correlate with genome  $\mathcal{P}_k$  $\mathcal{F}_{\text{c}}$  (Gregory 2001). There are a correlation between genome size and  $\mathcal{F}_{\text{c}}$  $\alpha_{\text{max}} = \frac{1}{2}$  in the  $\alpha_{\text{max}}$  value and inpact on cellular physiology, nuclear physiology, nuclear values, and and and and and and and and an impact on cellular values, and and an impact of  $\alpha_{\text{max}}$  $\mathcal{S}_\mathbf{c}$  ,  $\mathcal{S}_\mathbf{c}$  ,  $\mathcal{S}_\mathbf{c}$  (Gregory 2005). Some sizes have been estimated using the material materia Fig. 1 Box-plot comparisons of genome size estimates based on three different methods. For all panels, methods are abbreviatedFCM ow cytometry,SFC static ow cytometry,FD Feulgen density. a) Genome size estimates for all lizard and snake species that have been measured by all three mbt Gdsome size estimates for all snake and lizard species that have been measured by at least one of the three methods of the size estimates for lizard species that have been measured by at least one of the three methodsenome size estimates for snake species that have been

differences in accuracy and precision. Genome size estimates using each of the three techniques for all squamates with data currently available in the Animal Genome Database (Gretorare summarized in Fig.1, separated by technique. These estimates (Bighow multiple forms of bias across methods. Squamate genome size estimates from Feulgen density and static cytometry are bigger and have a much higher variance than other measurements. These two techniques are thus less precise and possibly less accurate the next ometry (Fig.1a). Thus, previous perspectives of high variance in genome size among squamate reptiles based on these estimates may be artifactual, due to the methodological inconsistency of the techniques used. There is a strong argument for careful interpretation of genome size estimates made by methods otherothan tometry methods.

The average squamate haploid genome size estimate based on tometry is 1.9 Gbpn  $\frac{1}{4}$ 90, range<sup> $4$ </sup> 1.3–3.0 Gbp; Fig.2b). This average is intermediate in size between birds (1.4 Gbp) and mammals (3.5 Gbp) and is also smaller than other non-avian reptiles (3.2 Gbp in Testudines and Crocodilia and 5.0 Gbp is phenodon(Janes et a 2010b). The average lizard genome size based on

ow cytometry is also 1.9 Gbp  $\frac{1}{4}$  58, range<sup> $\frac{1}{4}$ </sup> 1.3–2.8 Gbp; Fig.2c). The average snake genome size based onow cytometry is also 1.9 Gbn  $\ell_4$  32, range  $\ell_4$  1.5–3.0 Gbp; Fig. 2d). Previous work on the pattern of genome size evolution found that the Reptilia have experienced continuous gradual evolutionary change in genome size with no rapid shifts in genome size since the early reptile radiation (Organ et a 2008). Other research, however, has found that larger genomes evolve in size



Fig. 2 Comparison of generating comparison of  $\mathcal{C}$  and  $\mathcal{C}$  and Anolis carolinensis, Python molurus bivittatus, and Agkistrodon contortrix. Various repeat their overall contorted axis. Separation are shown on the horizontal axis. The vertical  $\text{axis}$  indicates the proportion of the total genome constituted by a repetitive element (Data based  $(2011$ and  $\alpha$  the repeat-masked complete  $\alpha$  the repeated complete  $\alpha$  the UCSC Genome  $\beta$ 

at  $\frac{1}{2}$   $\frac{1}{2}$ used the size of general three methods of  $\frac{1}{2}$  is unclear intervals in the intervals in  $\frac{1}{2}$  is unclear if  $\frac{1}{2}$  $m_{\text{eff}}$  in pactual theory is the impact of  $m_{\text{eff}}$  in the impact of  $m_{\text{eff}}$ 

### Squamate Genome Structure

#### The Mitochondrial Genome

 $G_{\text{eff}}$  typically invokes reference to the nuclear general general general general general general general general genomes  $G_{\text{eff}}$  $\alpha^*$  studied reptiles have been studied most thoroughly to date. This smaller organization is smaller organization or  $\alpha$  $\mathcal{X}, \mathcal{Y}, \mathcal{Y}, \mathcal{Y}$  and  $\mathcal{Y}$  protein-coding general to  $\mathcal{Y}$  and  $\mathcal{Y}$  is metabolism function,  $\mathcal{Y}$  is metabolism function,  $\mathcal{Y}$  is metabolism function,  $\mathcal{Y}$  is metabolism function,  $\mathcal{Y}$  i  $\frac{1}{\sqrt{2}}$ functions in mitochondrial general genome replication and transcription. Snake mitochondrial genomes mitochondrial genomes  $\sigma$ have been of particular interest because they evolved a number of characteristics that a number of characteristics that  $\frac{1}{2}$  $v_{\rm c}$ vertebrates. With the snakes  $\ell$  the snakes  $\ell$  the snakes  $\ell$  relatives), which are the most are the most ancestral extractions appear to have a duplicated  $\frac{1}{2}$  and  $\mathcal{F}_{\text{c}}$  regions are motion sequences are maintained at nearly identical  $\mathcal{F}_{\text{c}}$ se effects and mechanism mechanism mechanism mechanism mechanism of concerted evolution  $\mathcal{E}$ et al.  $200$  ). Molecular evidence suggests these control regions are both likely to act to act both  $\mathcal{S}$ as origins of  $\mathcal{S}$  and  $\mathcal{S}$  are probably also as probably also as probably also as probably  $\mathcal{S}$ et al. [2007;](#page-15-0) Castoe et al. It has been hypothesized that the that the that the that the these duplicate control regions are the that the tha  $m_1 + \frac{1}{2}$  function in the rapid metabolic upper snakes, which is associated with  $\frac{1}{2}$  is associated with feeding  $m_1 + \frac{1}{2}$ (Jiang et al. [2007;](#page-15-0) Castove et al. [2009b](#page-14-0)). In addition to large-scale genome structure, s  $s \mapsto s \mapsto s$  or  $\mathbb{R}$  and  $s$  include an extreme adaptive experience and included an extreme and included and included and included and included and included an extreme and included and included and included and include  $u_1 = \frac{1}{2} \int_0^2 \cos^2 \theta \sin^2 \theta$  and  $\int_0^2 \cos^2 \theta \sin^2 \theta$  replacements. The radical amino acid replacements. The radical replacements. The radical amino acid replacements. The radical amino acid replacement of  $\frac{1}{2}$  $T_{\text{ref}}$  findings in the snake of metabolism might function uniquely among vertebrates,  $\epsilon$ 



Nuclear Chromosomal Structure

 $C_{\rm K}$  chromosomal variation is far greater in the presence of  $\mathcal{S}_{\rm C}$  in manufacture to the presence of presence of  $\mathcal{S}_{\rm C}$  is the presence of  $\mathcal{S}_{\rm C}$  is the presence of  $\mathcal{S}_{\rm C}$  is the presence of  $\mathcal{F}_{\mathbf{S}}$  microchromosomes (Olmo [2005\)](#page-16-0).  $\mathcal{F}_{\mathbf{S}}$  is a structurally similar to  $\mathcal{F}_{\mathbf{S}}$  in  $\mathcal{F}_{\mathbf{S}}$  to  $\mathcal{F}_{\mathbf{S}}$  in  $\mathcal{F}_{\mathbf{S}}$  $\frac{1}{2}$   $\frac{1}{2}$  [1996\)](#page-16-0). They are three three to three tensions more general more general management of the  $(2000)$  $(2000)$ , and avian microchromosomes appear to have a higher recombination recombination recombination rate than  $\mathcal{E}_k$ ( $R_{\text{max}}$ ,  $\frac{1}{2}$ ). Compared with  $\frac{1}{2}$  and  $\frac{1}{2}$  in  $\frac{1}{2}$ ). Compared content in  $\frac{1}{2}$  in  $\frac{1}{2$  $\mathcal{F}_{\mathbf{z}}$ rochromosomes tends to be  $\mathcal{G}_{\mathbf{z}}$  rich and contains higher frequencies of  $\mathcal{G}_{\mathbf{z}}$ these  $\mathcal{F}_\infty$   $\mathcal{F}_\infty$  is a relatively deparate in repetitive elements (Hillier et al.  $200$  ).  $\sim$  1 d<sub>e</sub>ration 36.6 chromosomes ( $\frac{1}{2}$   $\approx$   $\frac{1}{2}$  de  $\frac{1}{2}$   $\sim$   $\frac{1}{2}$  de  $\frac{1}{2}$   $\sim$   $\frac{1}{2}$  de  $\frac{1}{2}$   $\sim$   $\frac{1}{2}$ into one  $\mathcal{E}_{\mathbf{X}}$  into  $\mathcal{E}_{\mathbf{X}}$  into  $\mathcal{E}_{\mathbf{X}}$  into  $\mathcal{E}_{\mathbf{X}}$  into  $\mathcal{E}_{\mathbf{X}}$  is the set of  $\mathcal{E}_{\mathbf{X}}$  i  $(1 \text{ or } 18.9, \frac{1}{2} \text{ or } 2.1-2)$  ( $\frac{1}{2}$   $\frac{1$  $\lambda$  . S. the most conserved karyotypes, with the most common diploid number being  $\lambda$  , we show snakes typically consistent pairs of macrochromosomes and  $p_{\rm w}$  pairs of microchromosomes and  $p_{\rm w}$  $(\hspace{1cm}1$  et  $2006$ ; Srikulnath et al. [2009](#page-16-0)). Lizards, in contrast, have large variations in contrast, have large v 2006

 $\sec \omega c + \cot \omega$  (Sry) and birds (Dmrt1), but not for  $\cot \omega$  is  $\cot \omega$  for  $\cot \omega$ to a  $\mathcal{R}_{\text{N}}$  in  $\mathcal{R}_{\text{N}}$  in  $\mathcal{R}_{\text{N}}$  in  $\mathcal{R}_{\text{N}}$  et  $\mathcal{R}_{\text{N}}$  et al.  $\mathcal{R}_{\text{N}}$  is the not therefore not the  $\mathcal{R}_{\text{N}}$  is the south state not the  $\mathcal{R}_{\text{N}}$  is the south state not the  $\$ sex-determining factor for snakes. Additionally, Dmrt1 from the chicken  $\mathcal{F}$  from the chicken  $\mathcal{F}$  changes. mapped to both  $\mathcal{E}_x$  and  $\mathcal{E}_y$  and  $\mathcal{E}_z$  in Gekko hokouensis, and analyses of the Anolis genomes of the Anolis genomes of the Anolis general section of the Anolis general section of the Anolis general section function in Dmrt1 is unlikely to be the sex-determination generation generatio  $C_{\alpha}$  is the search for a second in section locus in section locus in section locus in section locus in sex characteristics in section locus in section somes are not homological present  $\frac{1}{100}$  are consistent with sex consistent with sex chromosomes  $\frac{1}{100}$  consistent with sex chromosomes  $\frac{1}{100}$  consistent with sex chromosomes  $\frac{1}{100}$  consistent with sex evolving many times independent  $\mathcal{F}$  in reptiles (Ez $\mathcal{F}$  et al. [2009](#page-14-0)).

Genomic GC-Isochore Structure

 $G=\mathcal{A}$  is the large tracts of generatively relatively relatively relatively homogeneous base of  $\mathcal{B}$ composition that varies over  $\mathcal{E}_\text{c}$  over  $\mathcal{E}_\text{c}$  is  $\mathcal{E}_\text{c}$  is  $\mathcal{E}_\text{c}$  is correlated varies positively correlated varies  $\mathcal{E}_\text{c}$  is correlated varies of  $\mathcal{E}_\text{c}$  is correlated varies of with  $\mathcal{Y}$  in portant generation recombination recombination records recorded  $\mathcal{Y}$ , density,  $\mathbf{e}_i$ modifications, introduced  $\mathcal{E}$  introduced the importance as function times, in portance as functional general general general geno- $\mathcal{F}$  idic elements et al. [2010b\)](#page-15-0). The Anolis carolinensis general to lack  $\mathcal{G}$  and  $\mathcal{G}$  $\mathcal{L}_{\text{in}}$ isochores, which was an unexpected result and  $\mathcal{L}_{\text{in}}$  and  $\mathcal{P}_{\text{max}} = \mathcal{P}_{\text{max}}$  genomes  $\mathcal{P}_{\text{max}}$  structure structure than  $\mathcal{G} = \mathcal{P}_{\text{max}}$  structure than Anolis  $(\textcolor{red}{\mathcal{C}}_c,\textcolor{red}{\mathcal{C}}_c,\textcolor{red}{\mathcal{C}}_c)$ . These findings may suggest that some results is  $\mathfrak{C}$  isochore since since since since since  $\mathfrak{C}$  $\cdot$   $\mathfrak{g}_{\mathbf{C}}$  is  $\mathfrak{g}_{\mathbf{C}}$  anolis  $\mathfrak{g}_{\mathbf{C}}$  is an analyzed in an analyzed  $\mathfrak{g}_{\mathbf{C}}$  is anolis.

Ultraconserved Regions

 $U_{\mathcal{S}}$ , or some  $U_{\mathcal{S}}$  (ULSE), or small stretches of the general stretches of the general stretches  $\mathcal{S}_{\mathcal{S}}$ distantly related vertebrates, have been popular for inferring the phylogenetic relationships  $\mathcal{F}_{\text{c}}$ among vertex organisms ( $\beta \sim \beta$  discovered et al. 2012); Crawford et al. 2012  $\beta$  al. 2012 a dramatically increased substitution rate in  $\mathcal{A}$  $s = \frac{1}{10}$ snakes. Squamates, therefore, appear to show a shift in conserved regions that  $\frac{1}{10}$ here otherwise remained relatively static in other research  $\mathcal{E}$  research  $\mathcal{E}$  $\mathcal{E}_{\text{c}}$  and  $\mathcal{E}_{\text{c}}$  for  $\mathcal{E}_{\text{c}}$  (LCNSs), and  $\mathcal{E}_{\text{c}}$  of  $\mathcal{E}_{\text{c}}$  of  $\mathcal{E}_{\text{c}}$  and  $\mathcal{E}_{\text{c}}$  and  $\mathcal{E}_{\text{c}}$  and  $\mathcal{E}_{\text{c}}$  and  $\mathcal{E}_{\text{c}}$  and  $\mathcal{E}_{\text{c}}$  and  $\mathcal{E}_{\text{c}}$  an  $f(x) = \frac{1}{2} \int_{0}^{\pi} \frac{1}{2} \$ differing roles and constraints in generation in the reptile reptile line  $\mathbf{c}$  ( $\mathbf{c}$  al. 2009, 2010a). Future studies on studies on studies may provide a ditional into the evolution of the evolution  $\mathcal{Y}^{\text{t}}$  $\frac{1}{2}$  conserved genomic elements and the functional consequences of changes in such conserved  $\frac{1}{2}$  $e^x$  regions in squamates.

Transposable Element Diversity

Although  $\frac{1}{\sqrt{2}}$  and  $\frac{1}{\sqrt{2}}$  is structure and diversity is structure and diversity is structure and diversity is strongly slanted and diversity is structured and diversity is structured and diversity is strongly towards manners manners manners manners manners on reptilian genome structure and content is new structur  $j_{\rm c}$   $\sim$  so emerge ( $\cos$   $\frac{1}{2}$ ,  $\frac{1}{2}$   $\approx$  2.00120  $\sin(19.5)$   $\frac{1}{2}$   $\frac{1}{$ 1.  $($ 



# Microsatellite Seeding by Transposable Elements



## Genomics of Squamate Venom Toxins

Genetic and Genomic Structure of Squamate Venom Toxins

 $T$  ability to the ability to lever through technologies for  $\mathcal{F}_t$ , the genomic, transcriptomic, and  $\mathcal{F}_t$ protection and  $\frac{1}{2}$  and  $\frac{1}{2}$  and  $\frac{1}{2}$  improve our understanding of the squamate and the squamate and the squamate lineage and the squamate lineage and the squamate lineage and the squamate lineage and the s  $e^{\frac{1}{2}(\omega_1-\omega_2-\omega_3-\omega_4)}$  so squamate of toxing a developing a deeper knowledge of toxin general structure, and the tox gences and  $\mathcal{E}_{\text{g}}$  in  $\mathcal{E}_{\text{g}}$  and in which they have evolved in  $\mathcal{E}_{\text{g}}$  and  $u_1, u_2, \ldots, u_n, u_n \in \mathcal{Y}$  originary originary origins and regulation of the  $\mathcal{Y}$  $k \leq n$  about squame ventom general version general general general genomic it is based on the context because it is  $\delta$  cDNAs of ventor gland transcripts, the transcripts in the transcripts in  $\delta$  about the transcripts exonscripts in  $\delta$  about the transcripts in  $\delta$  about the transcripts in  $\delta$  about the transcripts in  $\delta$  about and UTRS. Because there is no multiple opportunities for  $\frac{1}{2}$  $\beta$  ivity and  $\beta$  is  $\beta$  in  $\beta$  in  $\beta$  in  $\beta$  in  $\beta$  is equal modificiency, positive effective effective

identi ed such effects, it is reasonable that there may be epigenetic regulatory effects that additionally modulate expression of venoms. Among vertebrates, snakes in particular possess a tremendous number of unique or extreme phenotypes. A greater understanding of the molecular and genomic basis of these phenotypes holds exciting potential to increase broad understanding of the function and functional exibility of the vertebrate genome and to illuminate the mechanisms by which such unique phenotypes can be evolutionary created from the raw material of the common vertebrate genome plan.

As more squamate genome and gene expression data become available, the toxinological community might consider a careful reevaluation of the precise language used for putative toxins

### <span id="page-14-0"></span>References

 $\lambda$  ,  $\lambda$ analysis with birds and  $\frac{1}{2}$  birds and  $\frac{1}{2}$  and  $\frac{2011}{7}$   $\frac{3}{2}$ .  $B_{\mathcal{A}}$   $\mathcal{A}$ ,  $\frac{1}{2}$  as a  $\frac{1}{2}$  de novo methods of genome assemblation  $\frac{1}{2}$  in the  $\frac{1}{2}$  in three vertebrates  $\frac{1}{2}$  $\therefore$   $\mathcal{S}$   $\therefore$   $\mathcal{S}$   $\therefore$   $\mathcal{S}$   $\therefore$   $\mathcal{S}$   $\therefore$  201 210.  $C_0$  and  $C_1$  and  $C_2$  and  $C_3$  and  $C_4$  marriage of  $C_1$  marriage of  $C_2$  marriage of  $C_3$  and  $C_4$  and  $C_5$  the convenience to address the convenience to address the convenience to address the convenience of performance and  $\mathcal{S}_c$  and  $\mathcal{S}_c$  and  $\mathcal{S}_c$  and  $\mathcal{S}_c$  and  $\mathcal{S}_c$ .  $\mathcal{S}_c$ . 2010; $\mathbf{6}$ , 128 – 1.  $\mathbf{C}$   $\mathbf{C}$  ,  $\math$ original evolution of metalloproteinases in the venom of snakes. The venom of snakes. The venom of  $\sim$  5.4. 2012;60.11  $C_{\alpha}$ ,  $C_{\alpha$  $\mathcal{E}_{\text{MC}}$  in  $\mathcal{E}_{\text{LC}}$  is in such that  $\mathcal{E}_{\text{LC}}$  is the snakes. PLOS  $\mathcal{E}_{\text{MC}}$  2008;  $\overline{C}$ ,  $P=\frac{1}{2}$  Police  $\frac{1}{2}$  and  $\frac{1}{2}$  equive episode of convergent molecular evolution. Processes the convergent molecular evolution. Processes the convergent molecular evolution. Processes the convergent molecular ev  $\frac{1}{2}$ ,  $\frac{1}{2}$ ,  $\frac{106}{3}$ ,  $\frac{1}{2}$ ,  $\frac{1}{2}$  $C_{\text{c}}$ ,  $\overline{G}$ ,  $C_{\text{c}}$ ,  $C$  $\frac{1}{2}$ ne mutation gradients and control region usage in squamate in squamate  $\frac{1}{2}$ gence  $\frac{1}{2}$  denominate Genet Genet Genet  $\frac{1}{2}$  12-2.  $C_{\mathcal{A}}$  a,  $C_{\mathcal{A}}$ , de  $\mathcal{A}$ ,  $C_{\mathcal{A}}$  are  $\mathcal{A}$ , et al. Sequencing the  $\mathcal{A}$  sequencing python (Python molurus bivittatus) as a model for studying extreme and snakes. Genome adaptations in snakes. Genome Biol.  $2011$   $12$   $1-$  8  $\mathcal{L}_1 \mathbf{C}$  ,  $\mathbf{K}_1 \leq \mathcal{L}_2$  ,  $\mathcal{L}_2 \leq \mathcal{L}_3$  ,  $\mathcal{L}_3 \leq \mathcal{L}_4$  ,  $\mathcal{L}_5 \leq \mathcal{L}_5$  ,  $\mathcal{L}_6 \leq \mathcal{L}_7$  ,  $\mathcal{L}_8$  ,  $\mathcal{L}_9$  ,  $\mathcal{L}_1 \leq \mathcal{L}_2$  ,  $\mathcal{L}_3$  ,  $\mathcal{L}_5$  ,  $\mathcal{L}_7$  ,  $\mathcal{L}_8$  ,  $w_e = \frac{1}{2} \int_{\mathbb{R}^3} \int_{\mathbb{R}^3} e^{-\int_{\mathbb{R}^3} e^{-\int$  $\mathbf{J}_{\mathbf{e}}$ ,  $\mathbf{J}_{\mathbf{e}}$ ,  $\mathbf{J}_{\mathbf{e}}$ ,  $\mathbf{J}_{\mathbf{e}}$ ,  $\mathbf{J}_{\mathbf{e}}$ ,  $\mathbf{J}_{\mathbf{e}}$ ,  $\mathbf{J}_{\mathbf{e}}$  $C_{\mathcal{A}} \bullet \mathcal{A}$ ,  $C_{\mathcal{A}}$  $P^3$  multi-organisation organisation transcriptome resource for the Burmese python molurus bivittatus).  $\qquad e^{-\int_{\Re}^{\bullet} e^{-2\theta} 1 \cdot \mathbf{R}^{-1}}$ .  $C_R$ ,  $G \underset{\mathbf{c}}{\downarrow} G$ ,  $\underset{\mathbf{c}}{\downarrow} G$ ,  $\underset$ 

<span id="page-15-0"></span> $G_{\alpha}$ ,  $S_{\alpha}$ ,  $S_{\alpha$  $\frac{1}{2}$  transfer of transposition transpose phyla. Nature. No 2010;464:1347–50.  $G = \frac{1}{100}$ ,  $\frac{1}{100}$  $\mathbf{S}$  spin transpose in squame reptiles. Molecules reptiles. Molecules  $\mathbf{C}$ 

<span id="page-16-0"></span> $\mathcal{S} \times \mathcal{S} \times \mathcal{S} \times \mathcal{S}$  and  $\mathcal{S} \times \mathcal{S}$  and  $\mathcal{S} \times \mathcal{S}$ 

Index Terms:

Gere e  $\mathcal{G}$  be assembly 13  $\mathcal{F}_{\text{te}}$  size estimation  $\mathcal{F}_{\text{te}}$  extending  $\mathcal{F}_{\text{te}}$  $G_{\text{tot}}$  General General General B  $H_1$   $H_2$   $H_3$  $\frac{1}{\sqrt{2}}$  Mitochondrial general general general general general general general genome  $\frac{1}{\sqrt{2}}$  $\mathcal{S}$   $\mathcal{S}$   $\mathcal{S}$   $\mathcal{S}$   $\mathcal{S}$   $\mathcal{S}$  $\sim$   $\frac{1}{2}$ ,  $\frac{1}{2}$  12–13  $T_{\text{revo}}$  element 8–10, 1  $U_1$ <sup>E</sup>  $U_2$  of  $U_3$   $C_3$   $C_4$   $C_5$  $\vec{v}$   $\vec{v}$   $\vec{v}$   $\vec{v}$   $\vec{v}$   $\vec{v}$   $\vec{v}$   $\vec{v}$  $ve$   $ve$   $ve$   $ve$   $ve$