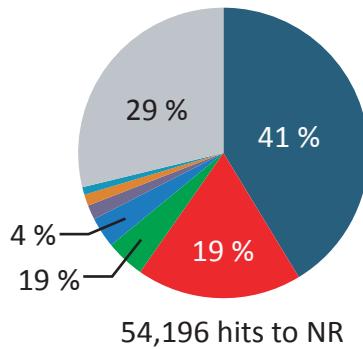


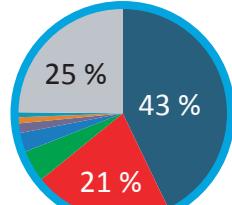
### Taxonomic distribution

#### A Pooled *E. spinax* transcriptome (119,749 unigenes)

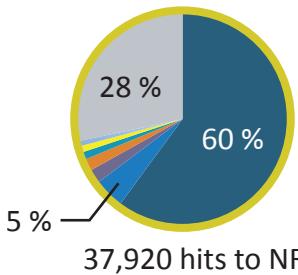


B

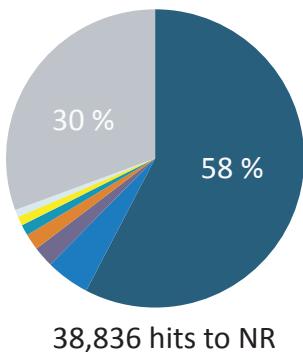
#### Ventral skin *E. spinax* transcriptome (93,569 unigenes)



#### Eye *E. spinax* transcriptome (94,365 unigenes)



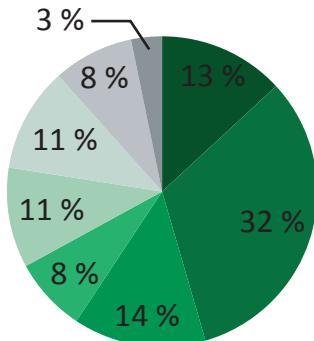
#### C Reference *E. spinax* transcriptome (104,390 unigenes)



- *Callorhinchus milii* □ *Anolis carolinensis*
- *Latimeria chalumnae* □ *Alligator mississippiensis*
- *Lepisosteus oculatus* □ *Others*
- *Chrysemys picta* ■ *Bradyrhizobium sp*
- *Xenopus tropicalis* ■ *Hordeum vulgare*
- *Chelonia mydas*

### E-value distribution

#### D Reference *E. spinax* transcriptome (104,390 unigenes)



- $x = 0$
- $0 < x \leq 1e^{-100}$
- $1e^{-100} < x \leq 1e^{-60}$
- $1e^{-60} < x \leq 1e^{-45}$
- $1e^{-45} < x \leq 1e^{-30}$
- $1e^{-30} < x \leq 1e^{-15}$
- $1e^{-15} < x \leq 1e^{-5}$
- $1e^{-5} < x$