



## Immune genes are hotspots of shared positive selection across birds and mammals

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- What does this do overall for (tree-wide) positive selection detection rates?
- **Without** the error component, **40.4%** of all genes have signal for selection
- **With** the error component, **4.5%** of all genes have signal for selection
  - Nearly a 10x reduction in yield
  - This is actually more in line with what biologists are comfortable with.

Some of the ZOONOMIA data

N of taxa	Alignments analyzed	Fraction (%) where selection was detected P ≤ 0.05 (FDR q ≤ 0.10)		
		BUSTED	BUSTED-E	FDR discovery reduction X
8	7062	15.9 (5.8)	4.7 (0.1)	58.0
16	7165	24.9 (17.7)	7.4 (0.7)	25.3
32	7229	36.3 (33.4)	10.5 (2.3)	14.5
64	3950	57.8 (58.7)	17.7 (9.0)	6.5