

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

- What is a key feature of genes that may be falsely flagged as positively selected?
- (Very) low proportions of (very) high omega values!