System/Organism	Natural / Lab	Population size (N)	Selection coeff. (s)	Beneficial mut. rate (U)	Regime	Estimated mutation bias	Comment
70 avian taxa; Hb-O2 affinity adaptations to elevation Storz et al. [16]	natural	small to moderate	moderate to large	small because few genes	OF	6 fold for mutations	Excess of CpG adaptive mutations compared to number predicted by null model where CpG status irrelevant to adaptation
De novo gene birth in overlapping reading frame in 80 capsid viral species Willis & Masel [40]	natural	large	unknown	tiny	OF because tiny U	$> 465 : 92 = 5$	Mutation bias greater if longer ORFs are more likely to be adaptive
Meta-analysis of adaptive mutations Stoltzfus & McCandlish [15]	natural & lab	mixed	mixed	mixed	Mixed, OF + MM	$3 - 7$ fold for mutations, $2 - 4$ fold for unique mutations	Excess transitions
M. tuberculosis; antibiotic resistance Payne et el. [9]	natural clinical isolates	large	large 100 fold increase in MIC	small $10^{-9} - 10^{-7}$	OF or MM	$1.6 - 41.6$ fold for mutations	Excess transitions for 9 out of 11 different antibiotics
P. aeruginosa; antibiotic resistance MacLean et al. [14]	lab	$10^4 - 10^9$	$0.12 - 0.96$	$8.3 \times 10^{-10} - 2.5 \times 10^{-8}$	OF or MM	Allele-specific mutation rate varies by 30 fold	In 11 adaptive mutations, chances of evolving correlated with respective mutation rates [10], and uncorrelated with selection coefficients
ssDNA bacteriophages ID8, ID11, NC13, WA13; phage growth Sackman et al. [12]	lab	$10^5 - 10^9$	$0.11 - 0.64$	$1.1 \times 10^{-3} - 5.3 \times 10^{-3}$ (total mut. rate)	OF or MM	24 fold for mutations, 11 fold for unique mutations	Excess transitions
ssDNA bacteriophage ID11; phage growth Rokyta et al. [11]	lab	$10^4 - 10^8$	$0.11 - 0.39$	$1.1 \times 10^{-3} - 5.3 \times 10^{-3}$ (total mut. rate)	OF or MM	$8 - 9$ fold among relative mutation rates	OF model used to estimate relative mutation rates. Ranking of s differs from [12].
HIV-1; evolved in cultures of human T-cells Bertels et al. [39]	lab	$1 \times 10^3 - 6 \times 10^6$	large	high	MM	5 fold for mutations, 6 fold for unique mutations	Excess transitions
E. coli; evolved with DHFR inhibited using antibiotic Schober et al. [37]	lab	$6 \times 10^6 - 7.2 \times 10^8$	large	high	MM	unavailable	Mutations rewiring broken metabolic network to less efficient configuration favored over those restoring original efficient configuration
E. coli; adaptation following inactivation of DHFR Rodrigues et al. [38]	lab	$1.6 \times 10^7 - 4.8 \times 10^7$	large	small	MM	unavailable	Mutations rewiring broken metabolic network to less efficient configuration favored over those restoring original efficient configuration
E. coli; antibiotic resistance Couce et al. [13]	lab	$7.2 \times 10^7 - 3.6 \times 10^9$	large $0.00158 - 1$	high $3 \times 10^{-4} - 1 \times 10^{-2}$	MM or DM	$100 - 300$ fold ($\Delta mutH$), $500 - 10{,}000$ fold ($\Delta mutT$)	Different mutational profiles of $\Delta mutT$ (elevates transversions, excl. usual transition adaptations) v. $\Delta mutH$ (elevates transitions)