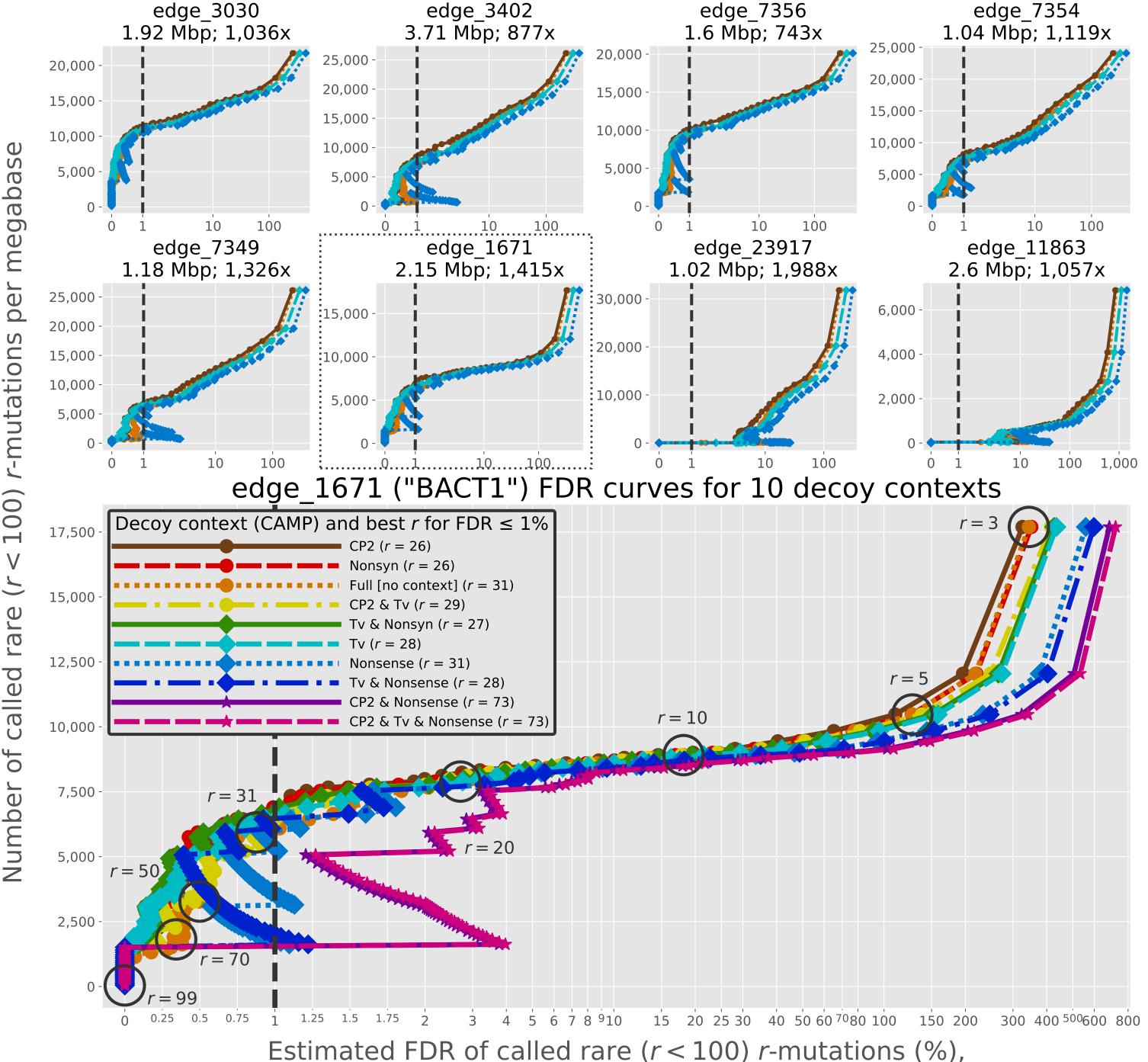
FDR curves for naïve r-mutation calling (r = 99 to r = 3), using the 8 highest-diversity-index (p = 0.5%) target contigs ≥ 1 Mbp



Estimated FDR of called rare (r < 100) r-mutations (%), using a log₁₀ scale to highlight order-of-magnitude differences