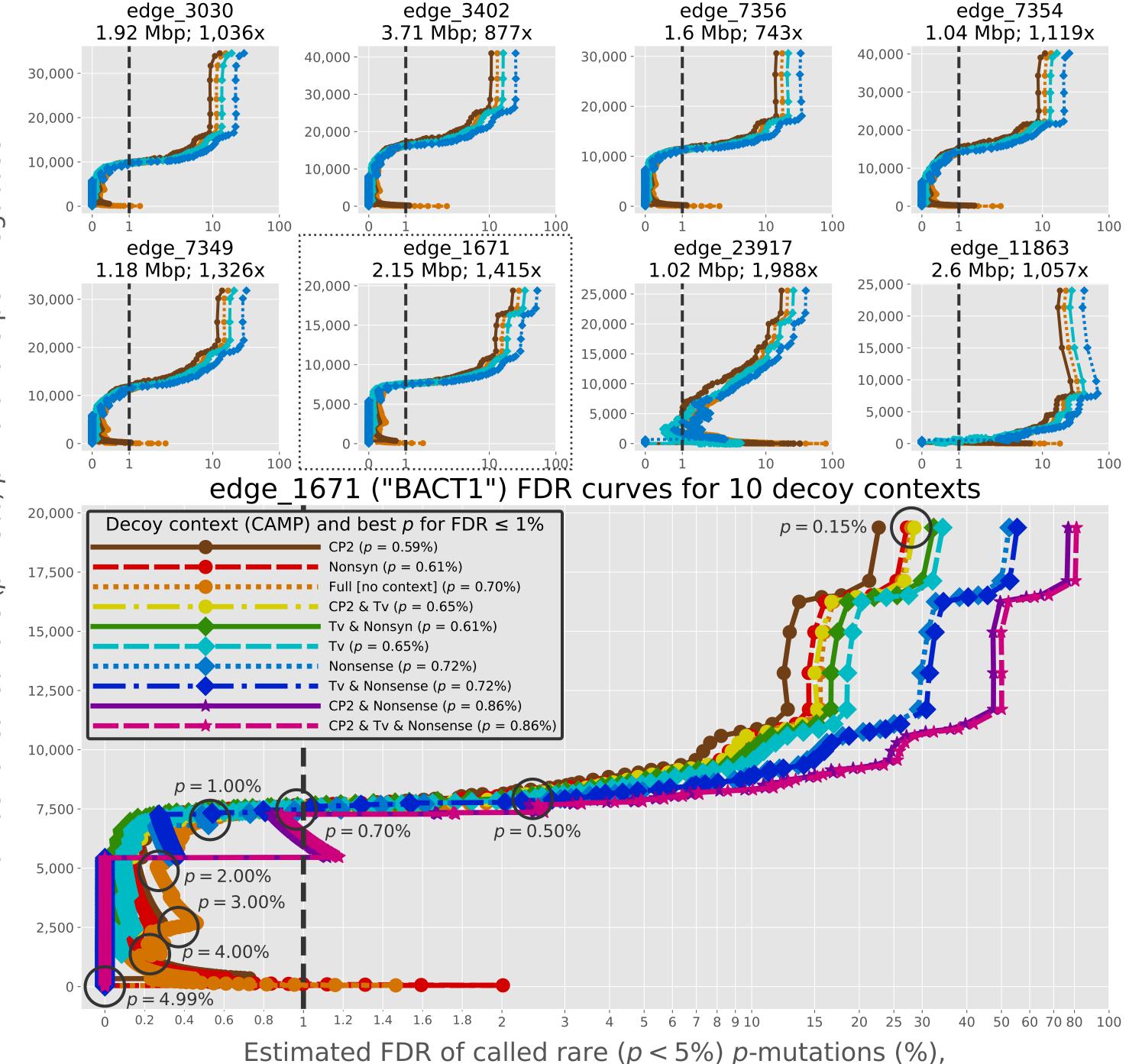
FDR curves for naïve p-mutation calling (p = 4.99% to p = 0.15%), using the 8 highest-diversity-index (p = 0.5%) target contigs ≥ 1 Mbp



using a log₁₀ scale to highlight order-of-magnitude differences