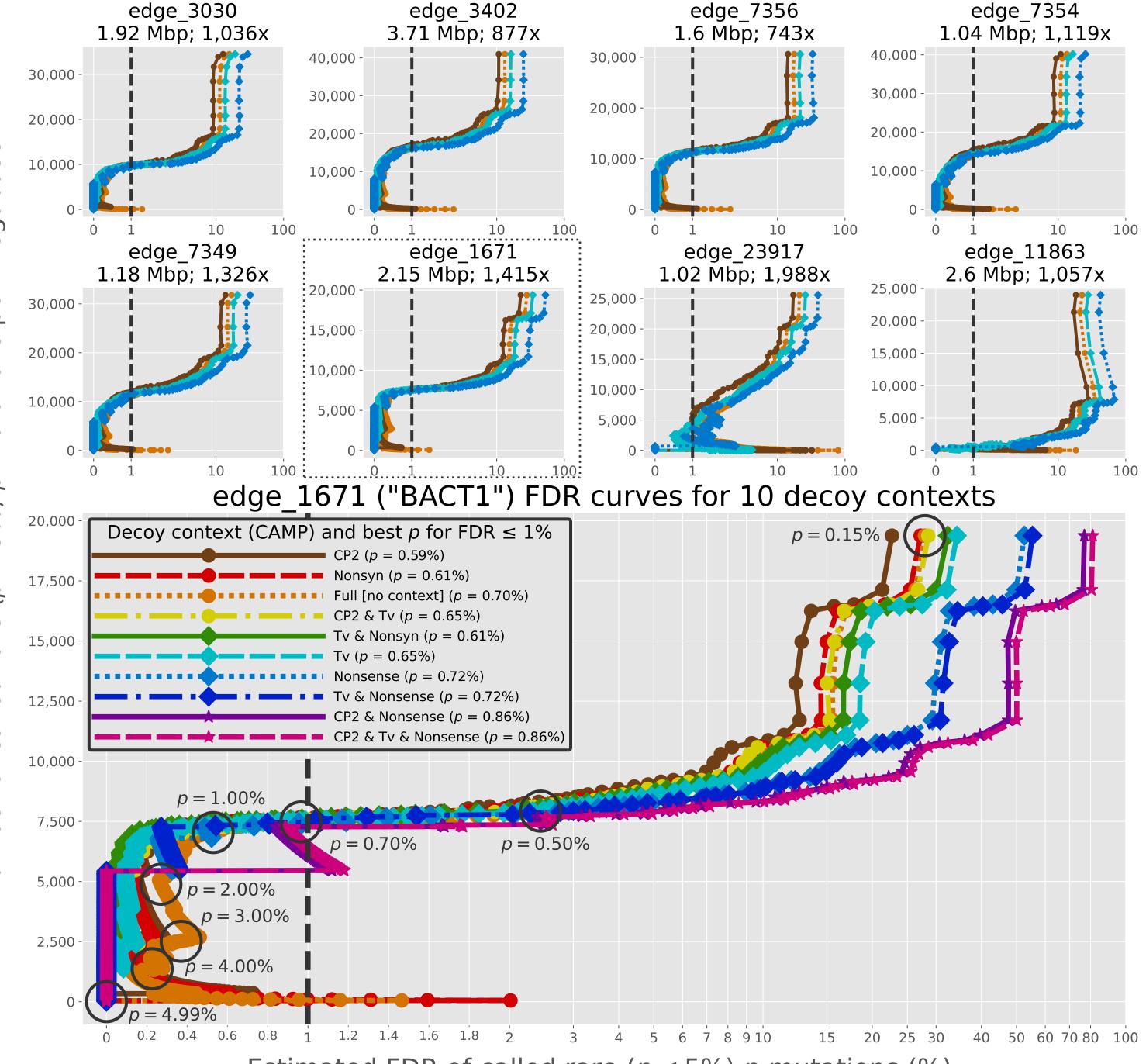
FDR curves for naïve p-mutation calling (p = 4.99% to p = 0.15%), using the 8 highest-diversity-index (p = 0.5%) target contigs ≥ 1 Mbp



Estimated FDR of called rare (p < 5%) p-mutations (%), using a log_{10} scale to highlight order-of-magnitude differences