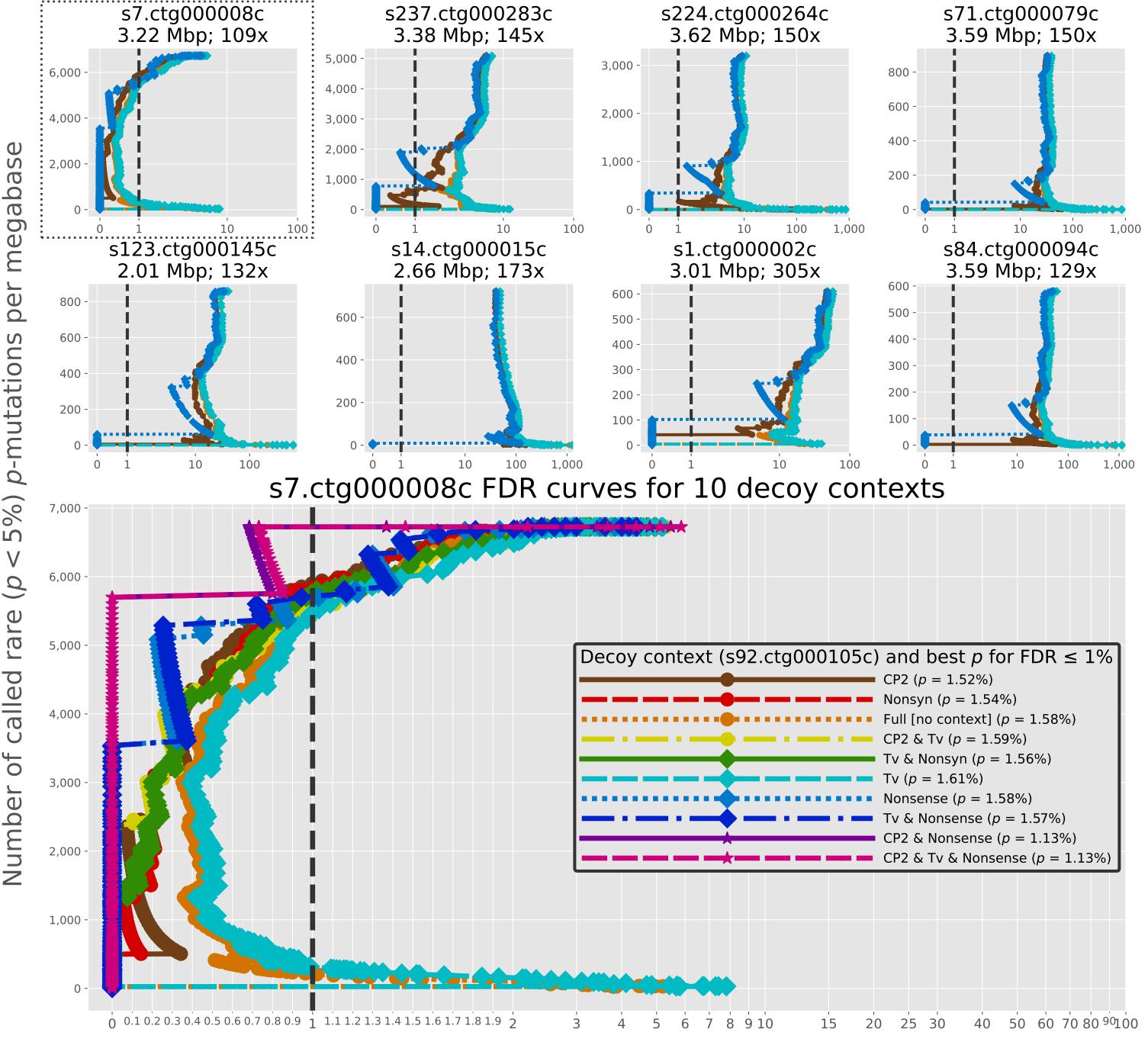
FDR curves for naïve p-mutation calling (p = 4.99% to p = 1.00%), using 8 target contigs ≥ 1 Mbp with average coverage $\geq 100x$



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