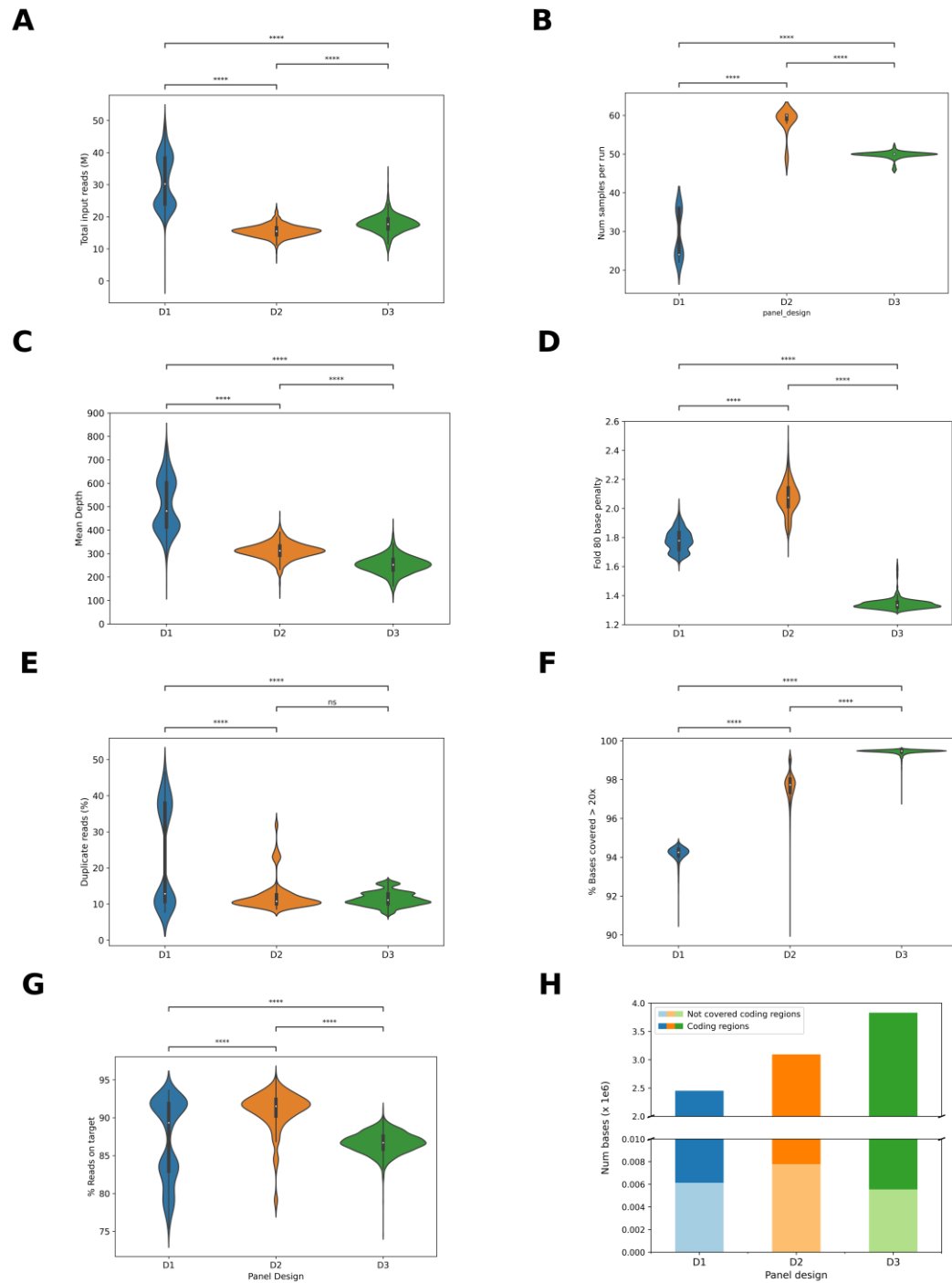




Additional File 4. Performance metrics for D1, D2 and D3. A-G. Violin plots presenting data comparisons between D1, D2 and D3 for **A**. Total input reads (in millions; M) **B**. Number of samples per sequencing run **C**. Mean Depth **D**. Fold 80 base penalty **E**. Duplicate reads **F**. % Bases covered > 20x **G**. % Reads on target. **** $p < 0.0001$ and ns = not significant, according to comparisons between two groups using the Wilcoxon test. A significance threshold of $p < 0.05$ was set to determine whether results are significantly different **H**. Bar plots presenting coding regions that were covered less than 50% in at least 95% of the samples for each pRARE version within the corresponding cohort.