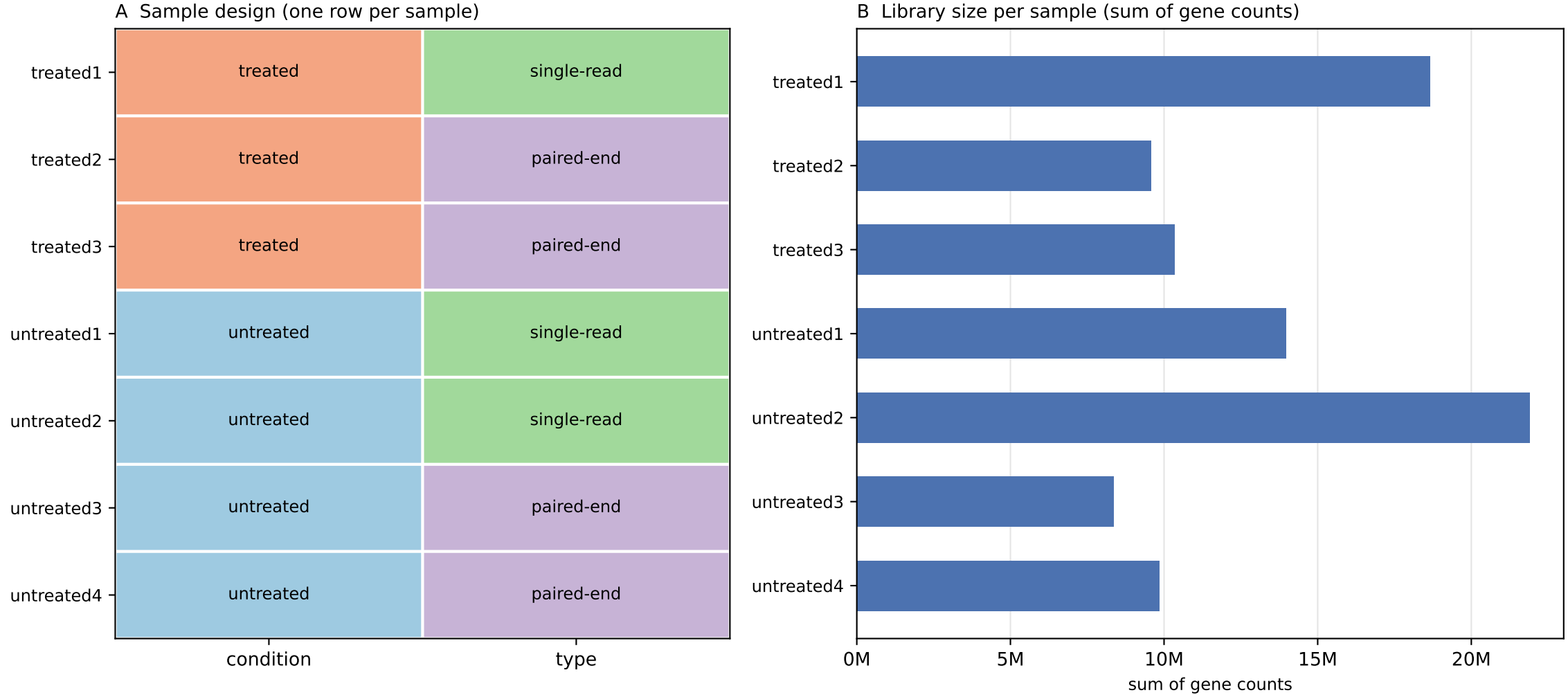


Reference levels: condition=untreated, type=single-read. Additive design, no interaction; no differential test run. Library size = column sums of gene counts.