

Fig. 1: Unfiltered read depth vs. tag count for 1,152 samples

Red dots represent "BLANK" samples
Gray dots are samples with low sequencing depth (<10,000 reads)
Lines and associated numbers represent median values

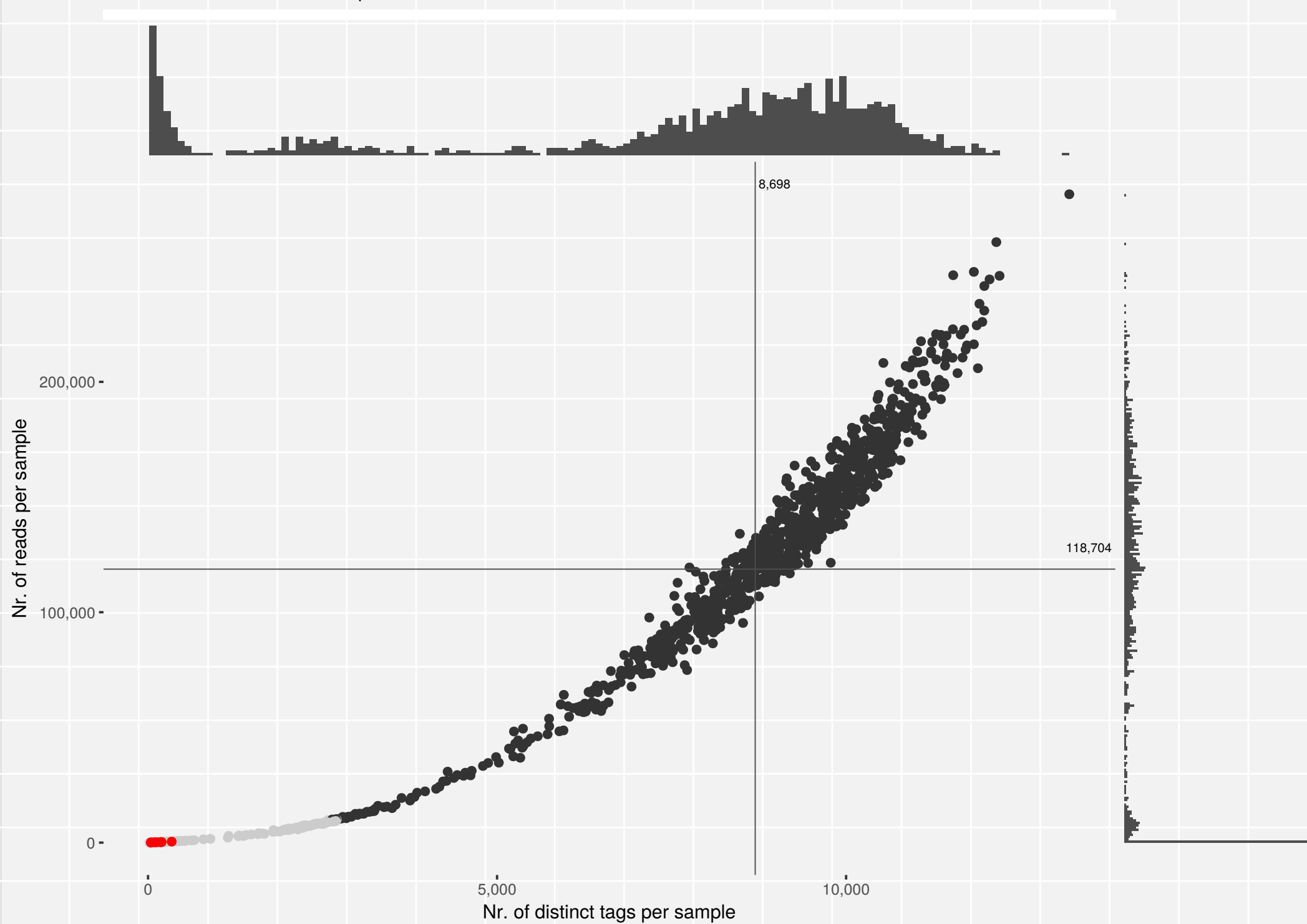


Fig. 2: Read counts per tag across 946 samples within sufficient sequencing depth

Read counts are normalized to 100K per sample

Colours indicate decomposition into three 'tag read depth' clusters

Cluster assignments with > 5% uncertainty are shown in gray.

Vertical bars represent mean read depth per tag within each cluster

View is truncated to max 200 reads per tag

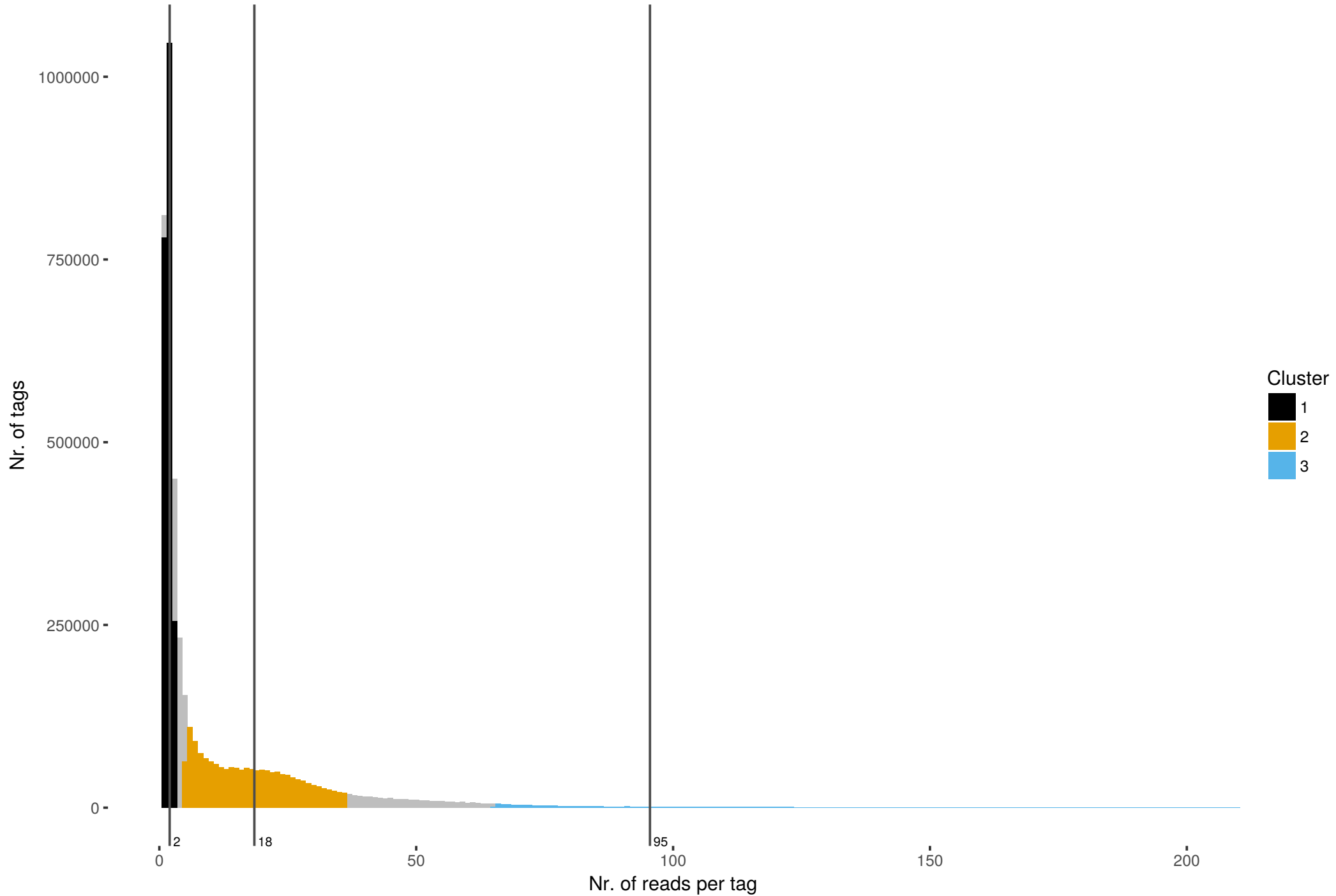


Fig. 3: Filtered read depth vs. tag count for 1,123 samples

Red dots represent "BLANK" samples

Gray dots represent samples with low sequencing depth (< 10,000 reads)

Lines and associated numbers represent median values

