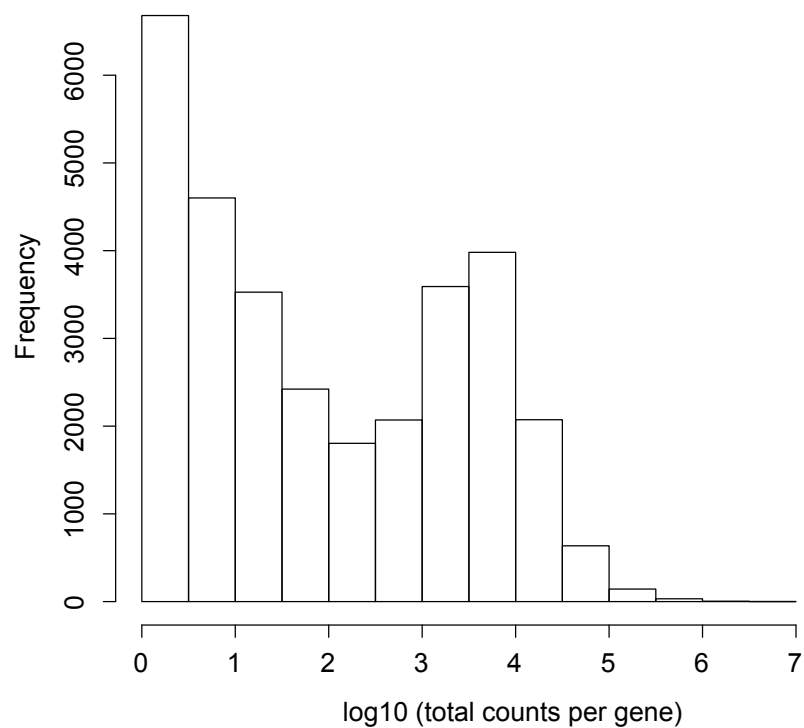




Additional file 11) A bimodal distribution in total counts per gene can be observed in the sequencing data. Read counts for each transcript in all samples was summed and the distribution was determined.