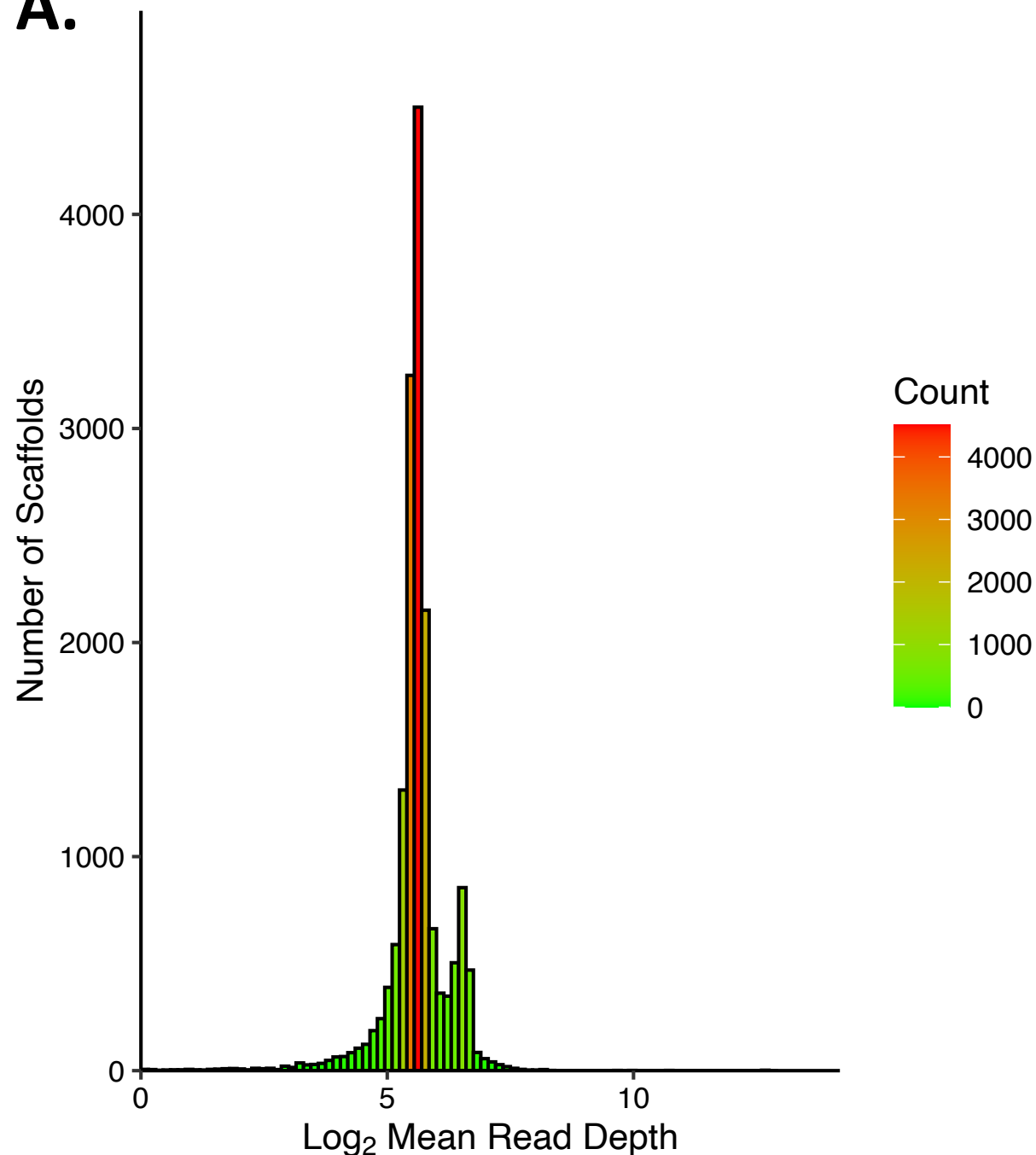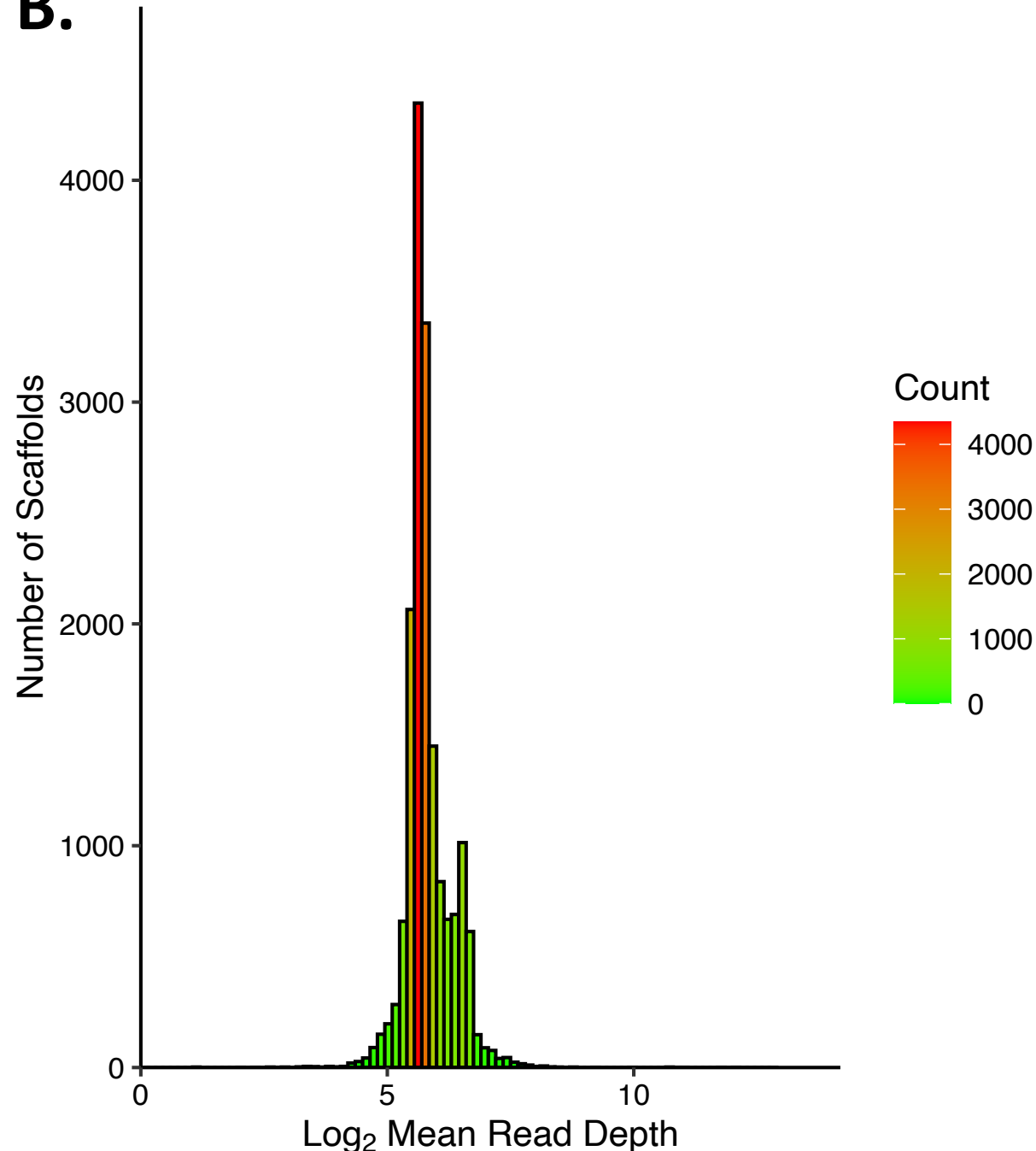**Figure S1. Scaffold mean read depth distributions in the final assembly.** Reads were aligned using BWAMEM (bwa v0.7.12) (Li 2013) with option –M and duplicates were removed using MarkDuplicates (picardTools v2.7.2; http://broadinstitute.github.io/picard/). Mean read depth for each scaffold was calculated by dividing the total read bases aligned to each scaffold by the length of each scaffold minus gaps. Read depth was then covered to a $\log_2$ scale. A.) Scaffolds mean read depth based on MAPQ scores of > 0. B.) Scaffolds mean read depth based on MAPQ scores of > 20.