We used the ISI Web of Science database and Google Scholar to perform the literature review on six keyword sets: “population genetics”, “genetic domestication”, “genetic variant”, “whole genome resequencing”, “landscape genomics”, and “genome-wide association”. These keywords were chosen to get a broad representation of genomic studies broadly covering the fields of human health, agriculture/domestication, and biodiversity studies of wild populations. A “topic” search was used for the first five terms, whereas a “keyword-plus” search was used for the last term. After not finding many relevant papers for some keywords, we modified the terms and performed new searches in Google Scholar with the following modifications:

-“population genetics and DNA sequencing”, “population genomics and DNA sequencing”, and “population genetics, genomics, and DNA sequencing” instead of “population genetics”

-“Genome wide association and DNA sequencing” and “Genome wide association and DNA sequencing and restriction site ” instead of “genome wide association”.

-“genetic variant and DNA sequencing and Restriction site” instead of “genetic variant”

Search results were sorted by relevance and limited to the last five years (2018-’23, except for the “population genetics, genomics, and DNA sequencing” search). Within each keyword search, we identified and scored/measured the 25-30 publications (for a total of 173 papers) that included the analysis of raw sequence data (e.g., no review, synthesis, or theoretical papers) to determine if and what high-throughput sequence data quality control or filtering measures were conducted. Population samples were required (e.g., >8 individuals). We measured the following variables in each publication:

Field, Organism, Population type (wild, domesticated), Sequencing library type, Number of individuals in study, Read depth mean, Allele balance filter applied, Mapping quality filter value, Percent of reads mapped, Minimum read quality (Phred) to keep a read, PCR duplicates removed?, Contaminant species reads removed?, Adapters trimmed?, Software used, Number of loci before filters, Number of loci after filters, MAF filter 1, MAF filter 2, MAC filter, HWE filter applied (if yes, *p*-value), Heterozygosity or paralog filter applied?, Loci LD pruned or filtered?, *F*ST outliers removed?, Minimum individual missing data percent, Minimum locus missing data percent, Biallelic loci only?, Siblings removed?, Sex-linked loci removed?, Effect of filtering on which metric?, and Resultant effect of filtering.

See **Supplemental Table S1** to see all papers in the review and their values for the variables recorded.