1. The shortest K value resulted in a large number of contigs, with an extreme amount landing in the 0 and 100 buckets. As K increases the number of contigs goes down while the average contig length goes up.
2. A higher coverage cutoff appears to increase the size of the contigs while decreasing the number of them. In a De Bruijn graph, a correct assembly should have a high coverage value. Setting a low kmer coverage allows for more sequencing errors to make it into the final graph but doesn’t remove as much data. Setting a high coverage forces velvet to align some sequences that are slightly different than one another.
3. Increasing the minimum contig length makes the average contig length higher. The N50 is also be higher and the total genome length smaller.