Genome Assembly and Annotation - Information about interpretation of output metrics came from the QUAST manual: https://quast.sourceforge.net/docs/manual.html

SPAdes identified more contigs overall than ABySS. Some statistics had significant differences such as the N50 (272520 for ABySS and 193475 for SPAdes), NG50 (272520 for ABySS and 178662 for SPAdes), and auN (301881.7 for ABySS and 224465.2 for SPAdes). Something important to note is that ABySS did not detect misassemblies, while SPAdes has non-zero values for # misassemblies, # misassembled contigs, # local misassemblies, # scaffold gap loc. Mis. and # unaligned contigs. ABySS recognized larger areas of alignments with no misassemblies, relocations, translocations, indels, or inversions. This was not true for SPAdes which found more issues in the assembly.

The N50 value of 272520 on ABySS and 193475 for SPAdes means that half of the contigs were as long or longer than this many base pairs. A larger score indicates higher quality results. The L50 is the number of contigs that are above the N50 value. When we add a G into these, such as NG50 and LG50 we are now doing the calculations in regards to the entire reference genome, rather than just the assembly size. In addition to the N50 and L50, auN is yet another way to describe contiguity. The number of misassemblies in total includes all of the different types mentioned above like relocations, translocations, indels, or inversions. These misassemblies mean that there is some sort of gap in the sequence, such as the gene is separated on different chromosomes (translocations) or on opposite strands (inversions) for example.