The majority of enteric outbreaks in Montana are most likely caused by norovirus, but only 61% were confirmed by laboratory testing. Even fewer, 60% of those with specimens submitted, have multiple specimens needed to perform genomic sequencing. Genomic sequencing identifies circulating or emerging strains and can help us predict the severity of a norovirus season. Since 2012, the most predominant strain has been GII.4 Sydney, which is consistent with U.S. trends.