Salmonellosis is one of the most frequent foodborne zoonoses representing a worldwide major public health concern. The main sources of infection for humans include meat products, eggs, vegetables, and water (1). Genomic diversity of Salmonella is increasingly studied, but at the same time, we have limited knowledge of Salmonella phage diversity. In this study, we isolated and characterized the bacteriophage 118970_sal3 infecting Salmonella enterica serovar Typhimurium. This bacteriophage belongs to the Myoviridae family and has a 39,464-bp double-stranded DNA (ds-DNA) genome containing 53 coding sequences (CDSs).

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