S1 Table: Method of Calculation of sequence-based diversity measures

TABLE 1 Description of sequence-based diversity measures

Diversity measure	Method of calculation
% diversity	Average pairwise genetic distance was calculated using the maximum composite likelihood model. MEGA 7.0.14 (www.megasoftware.net) was used to analyze gap-stripped sequence alignments. This value is reported as a percentage.
% complexity	[(no. of distinct variants)/(total no. of reads)] × 100
Shannon entropy (S)	$S = -\left(\dfrac{1}{\log N}\right)\sum_{i=1}^{n} p_i \log p_i$ where p_i is the proportion of reads consisting of each unique sequence pattern, N is the total no. of sequences, and n is the no. of distinct sequences