

TABLE 2. Population structure of the uncultured fecal viral community as determined by mathematical modeling^a

Assumed avg genome size (kb)	Total no. of viral genotypes	% Abundance of most abundant virus ($a \times 100$)	Evenness parameter (b) ^b	Shannon index (H_{nats})
15	1,450 \pm 700	2.4 \pm 1.2	0.611 \pm 0.110	6.83
30	1,250 \pm 230	4.2 \pm 0.7	0.715 \pm 0.041	6.45
50	1,930 \pm 470	6.3 \pm 0.8	0.831 \pm 0.029	6.43

^a The total number of viral genotypes is equivalent to species richness. Evenness is a measure of how genotypes are distributed within the population. The Shannon index is a measure of diversity that incorporates both species richness and evenness.

^b Rank-abundance curve shape, $n_i = ai^{-b}$.