

Table S1. Sapovirus genotypes determined in 112 infections among 82 Peruvian children less than 2 years old.

Genotype	Asymptomatic		Symptomatic		Undefined		Total	
	n	%	n	%	n	%	n	%
GI.1	5	14.3%	20	29.0%	3	37.5	28	25.0%
GI.2	1	2.9%	11	15.9%	1	12.5	13	11.6%
GI.6	1	2.9%	6	8.7%	0	0	7	6.3%
GI.7	3	8.6%	1	1.4%	0	0	4	3.6%
GII.1	3	8.6%	9	13.0%	1	12.5	13	11.6%
GII.2	6	17.1%	5	7.3%	0	0	11	9.8%
GII.3	1	2.9%	1	1.5%	0	0	2	1.8%
GII.4	4	11.4%	1	1.5%	0	0	5	4.5%
GII.5	6	17.1%	0	0.0%	0	0	6	5.4%
GII.6	1	2.9%	0	0.0%	1	12.5	2	1.8%
GII.7	0	0.0%	1	1.45%	0	0	1	0.9%
GII.8	2	5.7%	1	1.5%	0	0	3	2.7%
GIV.1	2	5.7%	6	8.7%	1	12.5	9	8.0%
GV.1	0	0.0%	7	10.1%	1	12.5	8	7.1%
Total	35	100.0%	69	100.0%	8	100.0%	112	100.0%

Note: Out of 175 sapovirus infection in 82 children, genogroups of sapovirus were defined in 113 infection of 69 children. Within 113, 14 genotypes were defined in 112 infections except one sample of asymptomatic infection of GII virus, whose genotype was not defined.