



Figure S1. Geographic origin distribution of sampled children who presented with diarrhea symptoms at KCH and were KHDSS residents. The diamonds indicate RVA positives and are colored by genetic cluster (see Figure 3 for details). The red empty circles indicate RVA negative cases.

Table S1: The global distribution of the identified G3 global genetic clusters

Global cluster name	Number of sequences	Includes Kilifi cluster	Years detected	Countries detected
Global/Clu_1	181	Clu_4/G3P[8]	2013, 2014, 2015, 2016, 2017, 2018	Australia, Taiwan, Japan, Indonesia, Thailand, USA, Dominican, Brazil, Italy, Germany, Hungary, Spain, Kenya
Global/Clu_2	116	Clu_3/G3P[8]	2013, 2014, 2015, 2016, 2018	India, Pakistan, China, Taiwan, Korea, Japan, Singapore, Australia, Italy, Spain, Russia, USA, Dominican, Ethiopia, Kenya
Global/Clu_3	47	Clu_5/G3P[8]	2013, 2014, 2016, 2017, 2018	Ethiopia, Kenya, Nigeria, Uganda, Indonesia
Global/Clu_4	3	-	2014	Peru
Global/Clu_5	1	-	2014	China
Global/Clu_6	10		2015, 2016, 2018	Kenya, Pakistan, Indonesia
Global/Clu_7	1	-	2016	Indonesia
Global/Clu_8	2	-	2013, 2016	Kenya, China
Global/Clu_9	1	-	2016	Kuwait
Global/Clu_10	2	-	2013, 2014	Belarus
Global/Clu_11	2		2013, 2015	Kenya
Global/Clu_12	1	-	2013	Nigeria
Global/Clu_13	1	-	2015	Thailand
Global/Clu_14	1	-	2016	Thailand
Global/Clu_15	1	-	2016	Thailand
Global/Clu_16	2	-	2014, 2016	Viet Nam, Korea
Global/Clu_17	1	-	2013	China
Global/Clu_18	2	-	2015, 2016	Indonesia