Sample ID	Reads to align (R1+R2+R0)	Aligned reads (%) [1]	Aligned reads, filtered (%) [1,2]	Aligned in pair (%) [3]	Properly paired (%) [3,4]	Singleton (%) [3]
GHA-Obuasi-2014	100,593,664	61,708,566 (61%)	56,122,278 (56%)	55,690,966 (99%)	48,551,862 (87%)	260,831 (0.5%)
BEN-Kpome-2015	99,049,555	77,760,764 (79%)	70,065,274 (71%)	69,590,103 (99%)	65,309,148 (93%)	250,733 (0.4%)
CMR-Mebellom-2014	98,674,983	60,566,286 (61%)	55184243 (56%)	54,726,342 (99%)	47,294,648 (86%)	280,747 (0.5%)
COD-Kinshasa-2015	107,938,818	63,691,312 (59%)	56,850,352 (53%)	55,619,705 (98%)	49,126,540 (86%)	803,615 (1.4%)
COD-Mikalayi-2015	108,730,737	88,874,076 (82%)	80,470,521 (74%)	79,871,664 (99%)	71,656,064 (89%)	320,287 (0.4%)
UGA-Tororo-2014	96,991,083	78,309,572 (81%)	71,449,749 (74%)	70,908,959 (99%)	61,732,826 (86%)	324,735 (0.5%)
MWI-Chikwawa-2014	90,976,162	30,929,682 (34%)	28,399,605 (31%)	28,158,651 (99%)	24,343,506 (86%)	155,992 (0.5%)
MWI-Chikwawa-2002	100,344,549	82,126,137 (82%)	74,115,352 (74%)	73,528,738 (99%)	67,567,770 (91%)	328,021 (0.4%)
MOZ-Manhica-2016	168,020,763	75,930,322 (45%)	63,776,575 (38%)	62,922,778 (99%)	54,270,794 (85%)	293,960 (0.5%)
MOZ-Morrumbene-2002	103,013,413	74,942,373 (73%)	67,568,570 (66%)	66,783,585 (99%)	62,829,476 (93%)	572,374 (0.8%)

[1] % of reads to align.

[2] Aligned reads filtered to remove duplicates and reads with mapping quality <10.

[3] % of filtered aligned reads.

[4] Properly paired: both the read and its mate are mapped to opposing strands of the reference sequence, with 3' ends innermost and 5' ends within the allowed distance from each other (0-500 bp).