

Table. S1. Strains sequenced in this study.

Strain	Isolation source	Accession #	Assembly method	Sequencing technology ^a	# of contig	Total read length	Genome size	Genome coverage	n50	GC content (%)
CAM57	Japanese human	MBFN00000000	Velvet 1.2.03	Hiseq 2500 (100bp x 2)	167	2,478,975,000	5,248,692	472.3	78,334	69.0
CAM177	Japanese human	MBFO00000000	Velvet 1.2.03	Hiseq 2500 (100bp x 2)	183	2,145,647,200	5,289,482	405.6	73,948	68.9
CAM78	Japanese human	MBFP00000000	Velvet 1.2.03	Hiseq 2500 (100bp x 2)	256	2,350,692,600	5,058,528	464.7	54,764	69.2
OCU462	Japanese bathroom	MBFQ00000000	Velvet 1.2.03	GAIIx (75bp x2)	483	3,917,873,625	5,811,762	674.1	25,525	68.0
OCU404	Japanese human	MKCW00000000	Velvet 1.2.03	Miseq (300bp X 2)	331	1,339,916,400	5,266,633	254.4	49,567	69.0
OCU466	Japanese human	LBGZ00000000	Velvet 1.2.03	Hiseq 2500 (100bp x 2)	168	1,335,438,200	5,635,307	237.0	235,001	68.6
OCU556	Japanese pig	MKCX00000000	Velvet 1.2.03	Hiseq 2500 (100bp x 2)	100	2,396,896,200	5,121,042	468.0	223,658	69.1
OCU491	Japanese pig	MKCY00000000	Velvet 1.2.03	GAIIx (75bp x2)	236	1,842,705,975	4,990,846	369.2	49,059	68.7
OCU464	Japanese human	CP009360, CP009405, CP009406	HGAP ver.2.0 Sprai ver 0.9.5.1.3	PacBio RSII	3 (one chr. +Two plasmids)	647,688,821	5,178,255 (chr.) 78,497 (p78k) 18,291 (p18K)	104.8	-	69.1 65.6 65.9
S2 ^b	Japanese human	CP018014	Canu 1.3, Falcon 0.6.4	PacBio RSII	1	379,054,874	5,186,756	73.0	-	69.1
P7 ^b	Japanese human	CP018020	Canu 1.3, Falcon 0.6.4	PacBio RSII	1	485,626,035	5,027,306	96.6	-	69.2
HP17	Japanese human	CP016818	Canu 1.3, Falcon 0.6.4	PacBio RSII	1	809,228,548	5,100,512	158.7	-	69.2

a. x 2 denotes paired-end sequencing.

b. P7 and S2 corresponds to 'OCU873s_P7_4s', and 'OCU901s_S2_2s' in Genbank/DDBJ/EMBL entry, respectively.