

TABLE S1. The *H. cinaedi* housekeeping genes used in this study.

Accession no. or locus tag	Gene name / Product	Gene length (bp)	PCR length (bp)	Polymorphism sites	No. of alleles	Representative organisms using the gene for MLST
Genes analyzed in 50 isolates from Japan and 6 reference strains^{#1}						
AY596254	23S rRNA / 23S rRNA	2718	762	4	5	-
HCCG_01345	<i>ppa</i> / inorganic pyrophosphatase	522	514	13	5	<i>Helicobacter pylori</i> , <i>Moraxella catarrhalis</i>
HCCG_00537	<i>aspA</i> / aspartate ammonia-lyase	1440	650	6	5	<i>Campylobacter jejuni</i> , <i>Campylobacter lari</i>
HCCG_00648	<i>aroE</i> / shikimate 5-dehydrogenase	792	688	21	6	<i>Staphylococcus aureus</i> , <i>Propionibacterium acnes</i>
HCCG_02167	<i>atpA</i> / ATP synthase subunit alpha	1515	646	5	5	<i>Helicobacter pylori</i> , <i>Campylobacter lari</i>
HCCG_01495	<i>tkt</i> / transketolase	1956	665	3	4	<i>Campylobacter jejuni</i> , <i>Campylobacter lari</i>
HCCG_01069	<i>cdtB</i> / cytolethal distending toxin B subunit	807	635	9	3	-
Genes analyzed in 8 isolates from 4 hospitals (2 for each hospital) and CCUG18818						
HCCG_01446	<i>glyA</i> / serine hydroxymethyltransferase	1251	639	6	4	<i>Campylobacter jejuni</i> , <i>Clostridium difficile</i>
HCCG_01783	<i>glnA</i> / glutamine synthetase	1479	677	5	2	<i>Campylobacter jejuni</i> , <i>Campylobacter lari</i>
HCCG_01698	<i>gltA</i> / type II citrate synthase	1284	649	6 ^{#2}	2	<i>Campylobacter jejuni</i> , <i>Campylobacter helveticus</i>
HCCG_01071	<i>efp</i> / elongation factor P	564	483	1	2	<i>Helicobacter pylori</i> , <i>Moraxella catarrhalis</i>
HCCG_00708	<i>hsp60</i> / Chaperonin GroEL	1644	569	1	2	<i>Yersinia ruckeri</i>
HCCG_01373	<i>sodA</i> / superoxide dismutase	639	639	4 ^{#2}	2	<i>Clostridium difficile</i>
HCCG_00654	<i>mutY</i> / A/G-specific adenine glycosylase	1044	655	1 ^{#2}	2	<i>Helicobacter pylori</i> , <i>Moraxella catarrhalis</i>
HCCG_02123	<i>yphC</i> / GTP-binding protein engA	1584	613	3 ^{#2}	2	<i>Helicobacter pylori</i>
HCCG_00133	<i>rpoB</i> / GTP-binding protein engA	8676	697	1	2	<i>Haemophilus parasuis</i> , <i>Corynebacterium diphtheriae</i>
HCCG_01182	<i>trpC</i> / bifunctional DNA-directed RNA polymerase subunit beta	1509	646	0	1	<i>Helicobacter pylori</i>
HCCG_00798	<i>glmM</i> / 2,3-bisphosphoglycerate-independent phosphoglycerate mutase	1470	644	0	1	<i>Campylobacter jejuni</i> , <i>Campylobacter lari</i>
HCCG_00755	<i>gyrB</i> / DNA gyrase subunit B	2319	692	0	1	<i>Escherichia coli</i> , <i>Acinetobacter baumannii</i>
HCCG_01929	<i>recA</i> / protein recA	1035	621	0	1	<i>Escherichia coli</i> , <i>Haemophilus influenzae</i>
HCCG_01104	<i>lepA</i> / GTP-binding protein lepA	1818	699	0	1	<i>Propionibacterium acnes</i> , <i>Burkholderia cepacia</i>

^{#1} The six reference strains include CCUG18818, CCUG18819, CCUG43521, MIT99-5915, MIT00-5434, and MIT01-5002

^{#2} The sequences in 8 isolates were identical and polymorphisms was detected between CCUG18818 and 8 isolates.