

Table S1. Basic genome statistics for the *Giardia* samples sequenced in this study from Creston, BC. H=human, W=water, B=beaver. *Sample VANC/90/UBC/45 has bacterial contamination and the largest contig corresponds to *Clostridium* spp. The largest contig corresponding for *Giardia* sp. is 260,011 bp.

Sample ID	Source	Genome size	GC (%)	# contigs (> 1 kb)	Largest contigs	N50	Reads aligned	Fold Coverage	Rate of alignment (Bowtie2)		
									WB (A1)	DHA (A2)	GS_B (B)
VANC/90/UBC/ 41	H	11,625,828	47.99	641	260,011	51,753	2,564,933	88.33	0.99%	0.93%	91.24%
VANC/90/UBC/ 42	H	11,138,540	49.24	713	168,072	52,859	3,153,295	138.16	92.93%	96.67%	1.02%
VANC/90/UBC/ 43	H	10,773,986	48.89	507	191,820	57,584	2,459,041	101.63	99.22%	92.91%	0.54%
VANC/90/UBC/ 45*	H	13,523,024	48.21	579	1,388,027	66,812	5,871,828	80.56	0.48%	0.46%	41.84%
VANC/90/UBC/ 46	H	11,473,860	47.95	603	261,363	53,309	1,752,804	43.52	1.15%	1.10%	87.44%
VANC/90/UBC/49	W	11,975,651	47.94	924	139,974	44,592	3,509,694	86.21	1.05%	0.99%	86.83%
VANC/90/UBC/50	W	11,458,722	47.99	588	260,290	54,278	2,254,481	57.78	1.22%	1.15%	85.83%
VANC/90/UBC/52	B	10,950,575	48.98	577	148,917	59,116	3,316,403	95.77	99.08%	91.72%	0.72%
VANC/90/UBC/ 71	H	10,802,051	48.91	526	246,364	57,191	1,646,856	56.24	97.58%	92.50%	0.57%
VANC/90/UBC/ 40	W	11,472,656	47.92	691	262,713	60,043	3,026,736	119.72	0.71%	0.68%	93.27%
VANC/90/UBC/ 44	H	11,487,245	47.97	686	258,661	57,567	3,224,387	125.50	0.78%	0.74%	92.60%
VANC/90/UBC/ 60	H	11,352,332	47.78	693	261,166	56,348	839,242	33.00	0.62%	0.59%	91.68%