

Table S1. Description of human and animal sample information with corresponding Illumina and ONT approaches: MinION (M), MinION with ViroCap (MV) and NextSeq with ViroCap (NV).

Sample ID	Approach	Total reads (trimmed)	Average sequence length (bp)	Average quality score
H1	M	400,045	601	9.32
	MV	405,861	619	10.71
	NV	26,283,927	2x76	35.72
H2	M	248,570	762	9.15
	MV	509,945	763	10.70
	NV	15,751,626	2x76	35.76
H3	M	289,919	770	9.18
	MV	576,312	748	11.15
	NV	21,680,167	2x76	35.74
H4	M	374,101	570	9.69
	MV	673,011	693	10.95
	NV	20,042,629	2x75	35.79
A1	M	475,457	1.028	9.65
	MV	387,513	860	10.87
	NV	36,399,004	2x76	35.73
A2	M	200,087	642	9.60
	MV	1,136,036	818	10.99
	NV	21,117,574	2x76	35.20
A3	M	128,940	873	9.59
	MV	381,625	794	11.04
	NV	8,970,518	2x76	35.58
A4	M	567,188	809	9.24
	MV	430,525	818	11.25
	NV	60,152,651	2x76	35.69